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ABSTRACT BOOK

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Oral Abstracts

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: Genomic data linking transmission between the different reservoirs
Abstract No: 14785

Fluidity of Antimicrobial Resistance between Humans, Food Animals and Water and Soil Environments in South Africa: A Genomic Illustration

Sabiha Essack*[1] ; Luther King Abia-Akebe[1] ; Daniel Amoako[1] ; Tracy Beetar-King[1] ; Dorcas Fatoba[1] ; Joshua Mbanga[1]
[1]Antimicrobial Research Unit/ University of KwaZulu-Natal/ South Africa

Introduction and Objectives or Purpose

Antimicrobial resistance (AMR) is considered the quintessential One Health issue as it exists and can be transferred within and between humans, animals and the environment. We delineated the molecular epidemiology of bacterial AMR in humans, food animals and associated water and soil environments using whole genome sequencing and bioinformatics analysis.

Methods

The World Health Organization's (WHO) Global Antimicrobial Surveillance System (GLASS) protocol and the WHO Advisory Group on the Integrated Surveillance of AMR (AGISAR) farm-to-fork protocol was used for the human and food animal investigations in public sector hospitals and intensive chicken and pig production farms respectively. For environmental AMR surveillance, we collected water samples bimonthly from the influent and effluent of waste water treatment plants (WWTPs) receiving water from hospitals and farms. We also investigated soil fertilized by chicken litter before (Day 0, 1, 2, 3, 5, 7, 9) and after (Day 0, 1, 3, 7, 14 and weekly thereafter) litter application. Isolates were subjected to microbial culture and sensitivity testing, and, whole genome sequencing and bioinformatics analysis to delineate the resistome, virulome, mobilome, clonality and phylogeny.

Results or Focus

Using Escherichia coli, Enterococci and Staphylococcus aureus as indicator bacteria, we found evidence of the fluidity of drug-resistant bacterial strains, antibiotic resistance genes and mobile genetic elements at the human:food animal:environment interfaces.

Conclusion or Scope

While such genomic studies have shown the prevalence of similar bacterial strains, similar resistance genes and similar mobile genetic elements in human, food animal and environmental compartments of the One Health triad, we are yet to establish the transmission dynamics and the risks associated with the prevalence of AMR at the interfaces.

Acknowledgement

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Keywords: antimicrobial resistance; One Health; whole genome sequencing; resistome, mobilome

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: Genomic data linking transmission between the different reservoirs
Abstract No: 14920

A COLLABORATIVE EFFORT ON GENOMIC SURVEILLANCE OF AMR IN JAKARTA: A ONE HEALTH STUDY FROM CONCEPTUALISATION TO IMPLEMENTATION

Nelly Puspandari[2] ; Dwi Febriyana[2] ; Tati Febrianti[2] ; Wirabrata[2] ; Imron Suandy[1] ; Desrina Sitompul[8] ; Asih Hartanti[2] ; Adam Robert[3] ; Thomas Weaver[8] ; Ageng [3]
[2]Centre for Health Resilience and Health Resource Policy/ Health Policy Agency, Indonesia Ministry of Health / Indonesia, [1]Directorate of Veterinary Public Health, Directorate General of Livestock and Animal Health/ Indonesia Ministry of Agriculture / Indonesia, [8]Fleming Fund Country Grant to Indonesia/ DAI/ Indonesia [2]Fleming Fund Country Grant to Indonesia/ Health Security Partners / Indonesia [3]Antimicrobial Chemotherapy and Resistance/ Liverpool School of Tropical Medicine / United Kingdom [3]National Research and Innovation Agency / Eijkman Research Centre/ Indonesia

Introduction and Objectives or Purpose

Bacterial genomics increases our understanding of genes and mobile genetic elements within bacterial populations, providing an early warning system for emerging resistances. This study capitalised on a unique set of strains to strengthen genomic surveillance capabilities and inform One Health AMR decision-making.

Methods

Through the Global Surveillance Extended Spectrum Beta Lactamase Escherichia coli Tricycle programme, the Government of Indonesia (GoI) collected samples from humans, animals, and the environment, resulting in over 1000 ESBL-producing E. coli strains. We selected over 300 isolates for whole genome sequencing, providing the first city-wide, One Health, genomic overview of ESBL-producing E. coli in Indonesia. Indonesia's Ministry of Health (MoH) led the co-design process, employing a One Health approach. A robust stratified random strain selection method maximised representativeness and diversity of strains and resulting genomes. Bioinformatic analyses prioritised subtyping, phylogenetics, gene content and location; phenotypic and epidemiological data will overlay genomic analyses.

Results or Focus

This study was founded on two years of cross-sectoral relationship building, planning, and training led by the GoI and the FFCGI; characterised by a strong culture of openness, respect, and trust under GoI leadership, despite operational challenges posed by the pandemic. This study aligns with Tricycle programme and other One Health initiatives, adding value to previous work. It strengthened Indonesian capabilities in genomic surveillance, study design and implementation, generating a collection of robust genomes which will inform policy and become a foundation for future genomic surveillance. It also highlighted the prohibitive cost of sequencing in Indonesia, that hinders AMR containment strategies.

Conclusion or Scope

The study exemplifies One Health in action. It will increase understanding of the relatedness, dynamics, ecology, selection factors and transmission pathways of a critical AMR indicator bacteria species within and between host populations and environmental sources, setting the foundations for integrating sequencing into routine cross-sectoral AMR surveillance in Indonesia.

Keywords: Genomic; Surveillance; AMR; environment; Indonesia

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: Genomic data linking transmission between the different reservoirs
Abstract No: 15017

The Saint John's Island Resistome project: a tractable microcosm of antibiotic resistance transmission across One Health domains in Singapore

Yann Felix Boucher*[1 2 3] ; Jia Yee Ho[1 2] ; Evelyn Goh[1 2] ; Dalong Hu[1 2] ; Haripriya Sadhasivan[1 2] ; Deborah Kang[2]
[1]Saw Swee Hock School of Public Health/ National University of Singapore/ Singapore, [2]Singapore Centre for Environmental Life Sciences Engineering/ National University of Singapore/ Singapore, [3]Yong Loo Lin School of Medicine, Department of Microbiology and Immunology, Infectious Diseases Translational Research Program/ National University of Singapore/ Singapore

Introduction and Objectives or Purpose

Monitoring of Antimicrobial Resistance (AMR) genes in the environment or clinical samples is readily feasible using PCR-based molecular approaches. However, tracing their transmission pathways or even simply identifying the organisms carrying them remains a challenge. Their low abundance in the environment has also limited the usefulness of metagenomics to provide further information about their dispersal and associations, while achieving pure cultures of isolated colonies of AMR bacteria is time consuming and usually targets particular antibiotics and carrier species.

Methods

To overcome these limitations, a combination of high throughput PCR-based screening and culture-enriched metagenomics was used to look for AMR genes in Singapore's St-John's Island coastal microcosm. All three One Health domains were targeted, with weekly sampling over an entire year of recreational seawater users, marine animals, seagrasses, algae, sediments and seawater. Bacterial biomass associated with each sample type was collected and culture enrichments were performed on all samples using liquid and solid selective media targeting ESKAPE bacteria. Samples were screened for the presence of 30 AMR genes using mPCR-RLB and DNA from positive samples (biomass and culture enrichments) was sequenced using a combination of Illumina and Nanopore technologies.

Results or Focus

Sequencing from the culture enrichments containing tens to hundreds of genotypes yielded near-complete genomes of several AMR-containing ESKAPE bacteria. This made the use of core genome Multi-locus sequence typing possible, which yielded clear links between different One Health domains. Furthermore, avid seawater users displayed significantly more AMR bacteria in their gut microbiome than people not going in seawater for recreation.

Conclusion or Scope

Results suggest that this approach, if the sampling scope is wide and diverse enough, can help determine carrier organisms of AMR genes and their transmission pathways. This method can also help evaluate the risk posed by AMR bacteria to recreational water users.

Keywords: AMR; One Health; bacteria; water; metagenomics

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: Plasmid-mediated resistance
Abstract No: 15211

Rise of carbapenem resistant Klebsiella pneumoniae in young infants in Bangladesh: an 18-year genomic epidemiological study (2004-2021)

Yogesh Hooda*[1] ; Afroza Tanni[2] ; CHRF Genomics Team [2] ; Monir Hossain[3] ; Mahboob Haq[3] ; Arif Mohammad Tanmoy[2] ; Samir K Saha[4] ; Senjuti Saha[2]
[1]Biochemistry and Molecular Biology/ Child Health Research Foundation/ Bangladesh (□□□□□□□□), [2]Genomics/ Child Health Research Foundation/ Bangladesh (□□□□□□□□), [3]Neonatology/ Bangladesh Shishu Hospital and Institute/ Bangladesh (□□□□□□□□), [4]Clinical Microbiology/ Child Health Research Foundation/ Bangladesh (□□□□□□□□)

Introduction and Objectives or Purpose

Klebsiella pneumoniae is a major cause of neonatal sepsis globally. With increasing antimicrobial resistance in Klebisella sp., the mortality associated with these neonatal infections is steadily rising. While many studies have looked at the burden of neonatal Klebsiella infections in high-income countries, limited data is available from low-and-middle-income countries, especially in South Asia. These gaps limit the institution of evidence-based policies and stymie the design of pharmaceutical interventions to address this emerging crisis.

Methods

We collected blood cultures positive for Klebsiella sp. at four study site hospitals in Bangladesh from 2004 to 2021. Clinical features including hospital stay, symptoms, outcome etc. were also recorded. Whole genome sequencing was performed on a representative set of isolates from children <60 days. Comparative genomic analysis was performed to identify the underlying antimicrobial resistance genes, O-antigen and K-capsule types.

Results or Focus

In total 1,769 Klebsiella isolates were collected over the 18-year study period. 82% of infections occurred in children under 2 months and these children were 2.4 (95%CI: 1.8-3.2) times more likely to die. The number and mortality of infections has been steadily increasing from 30% before 2015 to 52% in 2021. 579 isolates (42%) were sequenced and these belonged to 130 distinct sequence types (STs) including several unique STs. The 10 most common STs represented 54% of sequences and each year had a unique mix of STs causing infections. Concomitant to increasing mortality, rise in carbapenem resistance was also observed since 2015. Carbapenem resistance increases the odds ratio of dying by 3.1 (95%CI: 2.2-4.6). High rates of diversity were also in seen in O-antigen (top 10 O-types: 92% of genomes) and K-capsule (top 10 K-types: 59% of genomes).

Conclusion or Scope

The numbers and mortality of Klebisella infections among young infants is increasing in Bangladesh since 2015. This increase in mortality correlates with rising rates of carbapenem resistance.

Keywords: Klebsiella pneumoniae, neonates, antimicrobial resistance, vaccine antigens, carbapenem

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 14861

BENEFITS OF POLITICAL ECONOMY ANALYSES ON ANTIMICROBIAL RESISTANCE: CROSS-EXAMINATION OF PEA IMPACTS IN BANGLADESH, PAKISTAN, AND INDONESIA

Nicole DeCastro[*8] ; Dr. Rumana Huque[1] ; Sanya Tahmina[1] ; Mark Rasmuson[1 8] ; Solomon Benigno[8] ; Richard Burrough[8] ; Dr. Fayaz Ahmad[2] ; Umar Banoori [2]
[8]Global Health/ DAI/ United States [1]Fleming Fund Country Grant to Bangladesh/ DAI/ Bangladesh (□□□□□□□□) [8]Fleming Fund Country Grant to Indonesia/ DAI/ Indonesia [2]Fleming Fund Country Grant to Pakistan/ DAI/ Pakistan (پاکستان)

Introduction and Objectives or Purpose

Pakistan, Bangladesh, and Indonesia are three countries at high risk for the emergence of AMR. Each country presents unique AMR and health security challenges that benefit from the results of Political Economy Analyses(PEA). This form of analysis promotes a programmatic One Health approach to reducing the burden of AMR, antimicrobial use, and antimicrobial consumption.

Methods

PEAs in each country were conducted from 2020-2021 by identifying gaps, surveying stakeholders, identifying policies realted to the AMR National Action Plan and using PEA data to create a plausible pathways of change. Slightly different approaches were taken in each setting, but all three countries followed three steps:

1. Identify the problem
2. Map the structural factors, institutions (formal and informal), and stakeholders' interests
3. Identify political economy drivers and obstacles, and inform solutions that promote change

Results or Focus

This approach helps shape countries' implementation strategies by illuminating the underlying interests, incentives, historical legacies, and social trends, to inform how these factors affect or impede change. Despite differences between Indonesia, Pakistan, and Bangladesh - the PEAs identify key stakeholders to make strategic decisions and ensure the sustainability of investments at the national and international level.

Conclusion or Scope

PEA findings identified cross-cutting enablers and barriers, shortcomings, entry points, and opportunities for changing the incentives of stakeholders in favour of AMR containment efforts. The PEA frameworks make it easier for each country to think and work politically by identifying sustainable opportunities to improve programmes and policies across sectors, at all levels of government. Application of findings:

- Bangladesh: Revising the national strategic framework to cost the National Action Plan.
- Indonesia: Adopted by the Government of Indonesia and are actively used as evidence for AMR policymakers
- Pakistan: Key PEA messages packaged into a "Policy Brief" that is actively used by government for advocacy and data collection mechanisms and dashboards of key AMR indicators

Keywords: Antimicrobial resistance; political economy analyses; Coordination; governance; Advocacy

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 14988

Understanding networks in rural Cambodian farming communities and how they influence antibiotic use

Jane Lim*[1] ; Sokchea Huy[2] ; Chhay Ty[2] ; Khieu Borin[2] ; Li Yang Hsu[1] ; Clarence C Tam[1]
[1]Saw Swee Hock School of Public Health/ National University of Singapore/ Singapore, [2]Research/ Centre for Livestock and Agriculture Development (CelAgrid) / Cambodia (□□□□□□□)

Introduction and Objectives or Purpose

Although smallholder backyard farming systems play a major economic role in many Cambodian households, biosecurity and preventive animal health services in these settings are limited, often leading to an over-reliance on antibiotics. However, data are lacking on the factors influencing antibiotic use in these communities.

Methods

Between January and July 2019, we conducted a mixed methods, social network study in two rural Cambodian farming communities. This included a household census (n = 248), network surveys (n = 145) and in-depth interviews (n = 28) to investigate how social and contextual influences can influence both human and animal antibiotic use behaviours.

Results or Focus

In both villages, participants most commonly accessed antibiotics or learned animal antibiotic use practices through village-level informal sources such as pharmacies, health centres or animal health workers. While most participants reported not using antibiotics for animal growth promotion or illness prevention, misconceptions surrounding both antibiotic effectiveness and resistance were common. Social networks capturing informal, work-related and health-related social ties showed that familial connections and geographic proximity were of primary importance for information sharing. Using exponential random graph models, we demonstrated that familial ties, and closer geographic and geodesic distance, were associated with similarity in overall antibiotic knowledge and attitudes.

Conclusion or Scope

Our findings indicate that in backyard farming communities, the informal private sector plays a major role in provision of antibiotics and antibiotic-related information, but that such information is often maintained within close social groups. This demonstrates the importance of engaging village-level informal sources in the provision of antibiotic-related information for both human and animal health, as well as in potential interventions to encourage appropriate antibiotic behaviours in lower-resourced settings.

Acknowledgement

We thank the CelAgrid and USIRP administrative team and data collectors for their assistance in data collection

Keywords: Antimicrobial Resistance (AMR); social networks; antibiotic use; One Health

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 15067

TRENDS OF HUMAN AND VETERINARY ANTIMICROBIAL CONSUMPTION IN FIJI FROM A “ONE HEALTH” PERSPECTIVE

Royford Magiri*[1] ; Chaminda Dissanayake[2] ; Eric Rafai[3] ; Ashodra Gautam[3] ; Keith Hayes[4] ; Walter Okello[4] ; George Mutwiri[5] ; Paul A. Iji[1]
[1]Veterinary Science/ Fiji National University/ Fiji, [2]Biosecurity/ Biosecurity Authority of Fiji (BAF)/ Fiji, [3]FPBS/ Ministry of Health and Medical Services, Fiji/ Fiji, [4]Research / Commonwealth Scientific and Industrial Research Organization/ Australia, [5]School of Public Health/ University of Saskatchewan/ Canada

Introduction and Objectives or Purpose

Globally, the demand for animal protein is increasing leading to increased antimicrobial use in food producing animals. Antimicrobials are used in modern of animal production, which put more pressure on evolution of antibiotics resistance bacteria. Despite the negative effects on animal and human health, there are no assessment of antibiotics consumption by the human and livestock sector in Fiji and other Pacific Island countries. The study objective was to evaluate patterns and class of antimicrobial used human and livestock sector from 2015 to 2019 in Fiji.

Methods

The data was collected from the official antimicrobial import records held by Biosecurity Authority of Fiji (BAF) for animal use and Ministry of Health and Medical Services, Fiji for human consumption data.

Results or Focus

In 2017, 131.55kg of antibiotics were imported and used; 129.93kg in food animals while 1.62kg was used in companion animals. In the following year (i.e., 2018), 134.58kg of antibiotics were imported and used; 134.08kg in food animals while 0.50kg in companion animals. Lastly, in 2019, 156.90kg of antibiotics were imported and used; 153.56kg in food animals while 3.34kg in companion animals. This study has revealed that the tetracyclines, sulfonamides, beta-lactams and macrolides are the most commonly used drugs in food-producing animals in Fiji. Our study shows a considerable overlap between antibiotic classes sold for use in both human and veterinary medicine. Of the overlapping antibiotic classes, beta lactam/penicillin, tetracycline, sulfonamide, and macrolide antibiotic classes were found to be used in both human and animal health sectors. Overall, human drug stores had a broader range of antibiotics available for sale when compared to veterinary drugs.

Conclusion or Scope

The data is crucial for risk analysis and planning, and can be used to evaluate resistance surveillance data, success of initiatives to promote prudent antimicrobial usage, and strategies to reduce antimicrobial resistance.

Acknowledgement
The study was supported by CSIRO.

Keywords: Antimicrobial use, one health, Humans, Animals

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 15305

Antimicrobial use patterns and resistance among peri Urban poultry farmers in Wakiso and rural farmers in Soroti, Uganda

Irene Mbatidde*[1] ; Dickdon Ndoboli[1] ; Bernd-Alois Tenhagen [2] ; Arshnee Moodley[3] ; Dreck Ayebare[1] ; Savino Biryomumaisho[4] ; Eddie Wampande[4] ; Kristina Rosel[3] ; Dishon Muloi[3] ; John Elmerdahl Olsen[5]
[1]Animal and Human Health/ International Livestock Research Insititute/ Uganda, [2]Federal Institute for Risk assessment, Germany/ Freie University Berlin/ Germany (Deutschland), [3]Animal and Human Health/ International Livestock Research Institute/ Kenya, [4]Veterinary medicine/ Makerere University, Uganda/ Uganda, [5]Microbiology/ University of Copenhagen, Denmark/ Denmark (Danmark)

Introduction and Objectives or Purpose

A cross sectional study was carried out to 1) describe the antimicrobial use patterns among peri urban and rural poultry farmers 2) establish resistant profiles of Salmonella and E. coli among the poultry farms 3) Establish factors associated with antimicrobial use at the poultry farms

Methods

402 farms randomly selected between October 2021 – March 2022. A structured questionnaire was used to capture AMU data. Regression analysis was performed using Stata/SE 17.0.

For microbiology, two samples were collected from one chicken coop per farm: a boot sock and a composite. Traditional methods were used to isolate and identify Salmonella spp.

Quantification of AMR E.coli was done by serial dilution and plating on MacConkey agar with and without antibiotic (namely cefotaxime and colistin). AST and genotypic characterization of Isolates is ongoing in the laboratory

Results or Focus

Tetracycline was the most used antibiotic class (44.5% of farms). The purpose was treatment 75.8%, 38.2% prophylaxis and 7.3% growth promotion.Frequent use of multivitamins containing antibiotics like colistin and frequent use of human antibiotics in Soroti. Poor biosecurity,vaccination chalenges and low diagnostic services were observed.

Logistic regression showed a significant relationship between; Easy access to vet services and AMU (Z=6.65 P=0.00). Having disease prevention training and AMU (Z=2.77, p= 0.01). Practicing proper biosecurity and AMU (Z=10.4, p=0.000)

Resistant E.coli was at 45.5 % of farms for colistin and 51.7% for cefotaxime in Wakiso. While in Soroti, 62% for colistin and 62.5% for cefotaxime. CFU counts ranges were colistinR E.coli = 1 x 102 – 4.6 x 105 cfu/g and Cefotaxime E.coli 1 x 102 – 1.1 x 106 cfu/g

Conclusion or Scope

There was frequent and imprudent AMU, More than 40% of farms have colistin^R and cefotaxime^R but do not report the direct use of these antibiotics. Training, biosecurity, and access to veterinary services can promote rational AMU

Acknowledgement

Funded by BMZ

Keywords: Antimicrobial use, resistance, poultry farms

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Environmental AMR monitoring
Abstract No: 14696

Genotypic profile of XDR Escherichia coli isolated from broilers in Ilorin, North Central Nigeria

Ahmad I Al-Mustapha[*1 2 3] ; Shafi Abdullahi Alada[1] ; Ibrahim A Raufu[1] ; Katarina Eskola[1] ; Michael SM Brouwer[2] ; Victoria Adetunji[2] ; Annamari Heikinheimo[1]

[1]Department of Food Hygiene and Environmental Health/ University of Helsinki/ Finland (Suomi), [2]Department of Veterinary Public Health and Preventive Medicine/ University of Ibadan/ Nigeria [3]Department of Veterinary Services/ Kwara State Ministry of Agriculture and Rural Development/ Nigeria [1]Department of Veterinary Microbiology/ University of Ilorin/ Nigeria [2]Department of bacterial genomics/ Wageningen University and Research/ Netherlands

Introduction and Objectives or Purpose

The occurrence of multidrug resistant (MDR) bacteria in poultry poses public health threat man. Hence, this study assessed the occurrence of MDR Escherichia coli in broilers in Kwara State, Nigeria.

Methods

Presumptive E. coli were isolated via the EURL guideline of 2017 by using nonselective media and confirmed via MALDI-ToF. Five extensively drug-resistant (XDR) isolates were selected for WGS to detect AMR genes, phylotype, sequence type, serotype, as well as diversity of mobile genetic elements.

Results or Focus

Of the 181 caecal samples, 73 presumptive E. coli isolates were obtained. The prevalence of MDR E. coli in broilers was 82% (n=67/73). Altogether, 50.6% (n=37/73) of the isolates were XDR. WGS showed that the isolates were of diverse sequence types and phylogroups (ST165/B1, ST115/A, ST901/B1, ST4087/F, and ST8324/A). The isolates were of diverse serotypes: O80:H19; Unknown:H7; O109:H4; O117:42; and O127:H42 and were clonally diverse. The XDR E. coli isolates encoded resistance to fluoroquinolones (qnrS1, qnrB19, gyrA(P.S83L)), fosfomycin (fosA3), sulfamethoxazole (sul1, sul2, sul3), ampicillin and cephalosporins bla$_{\text{TEM-1B,}}$ bla$_{\text{EC}}$, bla$_{\text{CTX-M-14,}}$ bla$_{\text{CTX-M-55}}$), trimethoprim (dfrA1, dfrA17, dfrA36), aminoglycosides (ant(2')-Ia, aac(3)-IId, aadA1), chloramphenicol (catA1 and floR), tetracycline [tet(A), tet(B), tet(M)], and macrolides [mef(B) and mph(A)]. There was a positive correlation between phenotypic resistance patterns and the antibiotic resistance genes that were detected in the sequenced isolates. The XDR isolates also harbored two DRGs (qacE and sitABCD) which conferred resistance to hydrogen peroxide and quaternary ammonium compounds. The pan-genome of the XDR isolates harbored several mobile genetic elements (IncFIB(AP001918), IncFII, IncFII(pRSB107), IncFIC(FII), p0111, IncHI2A, IncFII(pCoo), Col156, Col440I, ColRNAI, ColpVC, and Col(pHAD28) and virulence-associated genes (sitA, astA, cea, cvac, iss, hylF, iucC, tsh, uphT, terC, papC) which were conserved in all sequenced XDR isolates.

Conclusion or Scope

Our findings suggest that poultry are potential carriers of clonally diverse, pathogenic, MDR/XDR E. coli which may have detrimental zoonotic potentials on human health.

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Environmental AMR monitoring
Abstract No: 14733

Surveillance of antibiotic-resistant genes (ARGs) associated with tuberculosis treatment from wastewater treatment plants (WWTPs) in Sub-Saharan Africa

Hlengiwe Mtetwa[*1 2] ; Isaac Dennis Amoah[2] ; Sheena Kumari[2] ; Faizal Bux[2] ; Poovendhree Reddy[1]
[1]Department of Community Health Studies/ Durban University of Technology/ South Africa, [2]Institute of Water and Wastewater Technology (IWWT)/ Durban University of Technology/ South Africa

Introduction and Objectives or Purpose

Despite global control efforts, tuberculosis (TB) continues to pose a serious health threat, placing enormous strain on the healthcare systems of many poor nations, particularly in Sub-Saharan Africa. Surveillance using clinical diagnostics and hospitalization data is inadequate due to limited access to healthcare. This study, therefore, applies the Wastewater-based Epidemiology approach to the surveillance of tuberculosis resistance in six sub-Saharan African countries and the contribution of treated wastewater to the dissemination of TB-related ARGs into the environment.

Methods

This study evaluated influent and effluent wastewater samples for TB surveillance in six sub-Saharan African countries (Ghana, Nigeria, Kenya, Uganda, Cameroon, and South Africa) using droplet-digital PCR.

Results or Focus

There was a significant difference between antibiotic-resistant gene (ARG) concentrations in wastewater samples from the selected countries (p-value<0.05); South African samples exhibited the highest concentrations of 4.3(±2,77), 4.8(±2.96), 4.4(±3,10) and 4.7(±3,39) log copies/ml for genes conferring resistance to first-line TB drugs (katG, rpoB, embB and pncA respectively) in untreated wastewater. This may be attributed to the higher prevalence of TB/MDR-TB in SA compared to other African countries. Other ARGs associated with resistance to second-line TB drugs such as delamanid and bedaquiline were detected in high concentrations (4.8(±3,67 and 3.2(±2,31 log copies/ml for ddn and atpE respectively) in countries such as Cameroon where these drugs are not yet part of the MDR-TB treatment regimens, which may be attributed to migration. ARG associated with resistance to aminoglycosides (rrs gene) such as streptomycin was abundant in all the countries due to the common use of this antibiotic for infections other than TB.

Conclusion or Scope

Therefore, these findings warrant the need for an additional surveillance and monitoring system to collect data at a community level. Linking WBE and the One Health approach in monitoring and management of the occurrence and spread of drug-resistant TB in the population could contribute to early mitigation.

Keywords: Wastewater-based epidemiology; droplet digital PCR; Multi-drug-resistant TB; Sub-Saharan Africa

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Environmental AMR monitoring
Abstract No: 14910

MIGRATORY BIRDS IN BANGLADESH HARBOUR MULTIDRUG RESISTANT NON-TYPHOIDAL SALMONELLA OF PUBLIC HEALTH SIGNIFICANCE

Roderick Card*[1] ; Thomas Chisnall[1] ; Ruhena Begum[1] ; Md Samun Sarker[1] ; Muhammad Hossain[1] ; Md Shahjalal Sagor[1] ; Mohammad Mahmud[1] ; Mohammed Samad[1]
[1]Department of Bacteriology/ Animal and Plant Health Agency/ United Kingdom [1]Antimicrobial Resistance Action Center/ Bangladesh Livestock Research Institute/ Bangladesh (□□□□□□□□□)

Introduction and Objectives or Purpose

Non-typhoidal Salmonella provide an exemplar for the One Health approach as it encompasses public health, veterinary control, food safety, and environmental considerations. The contribution of environmental aspects is currently the most poorly defined. This study's purpose was to determine the carriage of non-typhoidal Salmonella in migratory birds in Bangladesh, and assess the potential for risk to public and animal health.

Methods

Cloacal swabs (n=451) were collected in years 2018-2020 from Tanguar and Hakaluki Haors, important wetland ecosystems in North-eastern Bangladesh. Salmonella were isolated according to ISO6579-1:2017 and the serovar determined. Resistance towards 14 antimicrobials was assessed by broth microdilution and interpreted using EUCAST ECOFF values. AMR genotype and Sequence Type (ST) were established by whole-genome sequencing.

Results or Focus

The prevalence of Salmonella was 13.5% (61 positive swabs) and six serovars identified: Salmonella Perth (ST2245), Kentucky (ST198), Albany (ST292), Infantis (ST32), Weltevreden (ST365), and Brancaster (ST2133). Salmonella Perth and Weltevreden isolates were fully susceptible and harboured no acquired AMR genes. All other isolates were multidrug resistant, commonly possessing resistance to the first line antimicrobials ampicillin, chloramphenicol, sulfamethoxazole, and trimethoprim; and the second line antimicrobial ciprofloxacin. There was excellent correspondence between resistance phenotype and AMR genes, many associated with Salmonella Genomic Islands. High-level ciprofloxacin resistance correlated with mutations in the chromosomal gyrB and/or parC genes.

Conclusion or Scope

We have demonstrated that migratory birds are a reservoir of multidrug resistant non-typhoidal Salmonella serovars which have high prevalence in livestock and in human cases. Migratory birds can act as a reservoir and a route for dissemination to people and livestock. Bangladesh lies on two migratory flyways indicating that birds have the potential to disseminate Salmonella over long distances and between countries. The risk to public and animal health can be mitigated by measures including continued surveillance and implementation of good farm biosecurity practices.

Acknowledgement

Fleming Fund

Keywords: Salmonella; migratory birds; multidrug resistance; AMR

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Environmental AMR monitoring
Abstract No: 15065

One Health Applications of Antimicrobial Resistance Detection using CZ ID – An Open Source Cloud-based Pipeline and Analysis Tool for Metagenomic Pathogen Detection

Katrina Kalantar*[1] ; Chaz Langelier[2] ; CZ ID Team [1] ; Elizabeth Fahsbender
[1]Science/ Chan Zuckergerg Initiative/ United States, [2]Infectious Diseases/ Chan Zuckerberg Biohub/ United States

Introduction and Objectives or Purpose

Metagenomic next-generation sequencing (mNGS) has enabled the rapid, unbiased detection and identification of microbes and their antimicrobial resistance (AMR) genes without pathogen-specific reagents, culturing, or a priori knowledge of the microbial landscape. mNGS data analysis requires a series of computationally intensive processing steps to accurately determine the microbial and AMR gene composition of a sample. Most mNGS data analysis tools require bioinformatics expertise and access to powerful local server-class hardware resources, which presents an obstacle for many research laboratories, especially in resource-limited environments.

Methods

To overcome these barriers, we have developed an extension of the CZ ID portal, specifically aimed at analysis of AMR from complex samples. CZ ID is an open source cloud-based metagenomics pipeline that serves as a service for global pathogen detection and monitoring (https://czid.org/). It consists of an informatics pipeline as well as an interactive web application, which serves to reduce the barrier to entry for mNGS data analysis. The CZ ID pipeline accepts raw mNGS data, characterizes the associated taxonomic relative abundance and antimicrobial resistance profiles, and visualizes the results to facilitate data interpretation and hypothesis generation.

Results or Focus

Here we present four exemplary applications of the CZ ID platform for evaluation of AMR independently or integrated with microbial detection, in a variety of One Health contexts. These include assessment of AMR in hospitalized COVID-19 patients with secondary bacterial infections, wastewater surveillance for AMR pathogens, AMR gene acquisition during international travel, AMR surveillance of commercial pig farm slurry, and identification of AMR pathogens in patients with sepsis and pneumonia.

Conclusion or Scope

Our results demonstrate how these tools can enable bench scientists, clinicians, and bioinformaticians to gain insight from mNGS datasets for both known and novel pathogens.

Acknowledgement

Keywords: metagenomics; antimicrobial resistance; bioinformatics; software;

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14685

Using antimicrobial use surveillance to measure the effects of a pragmatic antimicrobial stewardship trial in 135 veterinary practices

Laura Hardefeldt*[1 2] ; Brian Hur[1 3] ; Kirsten Bailey[1 2] ; Ri Scarborough[1 2] ; Suzanna Richards[1 2] ; Helen Bilman-Jacobe[1 2] ; James Gilkerson[1 2] ; Glenn Browning[1 2]
[1]Asia-Pacific Centre for Animal Health/ University of Melbourne/ Australia, [2]National Centre for Antimicrobial Stewardship/ Peter Doherty Institute/ Australia, [3]School of Computing and Information Systems/ University of Melbourne/ Australia

Introduction and Objectives or Purpose

Comprehensive antimicrobial stewardship programs (ASPs) have been widely implemented in medical practice to improve the appropriateness of antimicrobial prescribing. The aim of this project was to assess the effectiveness of three ASPs on veterinary antimicrobial use, and on the prescribing of highly important antimicrobials, in a large number of veterinary practices.

Methods

In October 2018, general practices were assigned to one of three levels of ASP; education only (CON), intermediate (AMS1) and comprehensive (AMS2) programs. De-identified prescribing data (1 October 2016 – 31 October 2020) was sourced from VetCompass Australia (version 0.5). A Poisson regression model was fitted to identify the effect of the interventions on the the incidence rates of antimicrobial therapy. High prescribing practices were defined as the top 25% of prescribers in the pre-trial period.

Results or Focus

Veterinary clinics (n=135) were enrolled in the study; 43 practices allocated to CON, 46 AMS1 and 46 to AMS2. In the two years preceding the trial, the overall incidence rate (IR) of antimicrobial prescribing to dogs and cats was 3.7 per 100 consultations, which declined by 36% (2.4/100) in the implementation period, and by 50% (1.9/100) during the post-implementation period. Compared to CON, in AMS2 there was a 4% and 6% reduction in the overall IR of antimicrobial prescribing, and a 24% and 24% reduction in IR of high importance antimicrobial prescribing, attributable to the intervention in the implementation and post-implementation periods, respectively. A greater mean difference in the IR of antimicrobial prescribing was seen in high-prescribing clinics.

Conclusion or Scope
We have shown the value of antimicrobial use surveillance in veterinary practice. These interventions had a positive impact in a large group of general veterinary practices resulting in both a decline in overall antimicrobial use and a shift away from high importance rated antimicrobials, with the greatest impact seen in high-prescribing practices.

Acknowledgement
Australia Research Council Linkage Project Sceme. Greencross Vets.

Keywords: antimicrobial stewardship; dogs; cats; antimicrobial use; surveillance

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14689

BARRIERS TO COMPREHENSIVE VETERINARY CARE IN POULTRY FARMS IN BANGLADESH AND THEIR IMPACT ON RISING ANTIMICROBIAL RESISTANCE: A QUALITATIVE STUDY

Abdullah Sattar*[1] ; Nusrat Irin[1] ; Afsana Sultana[2] ; Meherjan Islam[1] ; Esrat Jahan Esha[1] ; Rashed Mahmud[1] ; Tony Barnett[3] ; Ivo Syndicus[3] ; Eve Houghton[3] ; Md. Ahasanul Hoque[1]
[1]Department of Medicine and Surgery, Faculty of Veterinary Medicine / Chattogram Veterinary and Animal Sciences University/ Bangladesh (□□□□□□□□), [2]Animal Health Research Division/ Bangladesh Livestock Research Institute (BLRI)/ Bangladesh (□□□□□□□□), [3]Veterinary Epidemiology, Economics and Public Health Group, Pathobiology and Population Sciences Department/ Royal Veterinary College/ United Kingdom

Introduction and Objectives or Purpose

With the recent expansion of Bangladesh's poultry sector and increasing number of farms, providing quality veterinary services to farms has become challenging. This qualitative study explores what and how veterinary services are accessed by poultry farmers, assesses farmers' knowledge of antimicrobials, and how these two factors may contribute to antimicrobial resistance (AMR).

Methods

Researchers conducted semi-structured interviews with exotic broiler and Sonali poultry farmers (n=35), feed dealers (n=29), and veterinarians (n=45) in ten districts of Bangladesh. Interviews explored disease management practices on farms, access to veterinary services, and farmers' antimicrobial usage and understanding.

Results or Focus

For most independent or dealer-dependent poultry farms, treatment is initially determined based on the farmer's or dealer's own experience, only seeking veterinary counsel if these interventions fail. Some farmers are hesitant to seek veterinarians' suggestions due to their fear of superfluous and costly prescriptions. There are limitations on the veterinarians' side too. Many are expected to cover farms across huge regions, making it difficult for them to respond promptly, particularly to farmers in remote locations. Sometimes, veterinarians have to depend on feed dealers to gain access to farms, limiting the farms they can serve and leaving farmers to rely on non-expert advice. These gaps between farmers have exacerbated the overuse or misuse of medications, including antimicrobials. Insufficient knowledge of antibiotics by farmers, as evidenced by the study, results in liberal and/or unintentional use of antibiotics, without regard for the potential consequences. In comparison, disease and medication use are minimal in company-regulated contract farms because of veterinarians' routine inspections and prompt services.

Conclusion or Scope

Insufficient farm-level veterinary care has contributed to the irrational antimicrobial usage in poultry, which has in turn aggravated AMR issue. More accessible veterinary services, AMR awareness, and legislation prohibiting antibiotic abuse with effective monitoring systems can help address this rising threat.

Acknowledgement

UKRI GCRF One Health Poultry Hub

Keywords: Veterinary service; poultry farm; Knowledge; AMR

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 15105

STRENGTHENING ONE HEALTH GOVERNANCE OF AMR/AMU SURVEILLANCE – THE FLEMING FUND EXPERIENCE

Joanna McKenzie[*1] ; Stanley Fenwick[2] ; Raghu Sriram[3] ; Winfred Amia[4] ; Emannuel Azore[5] ; Perdita Hilary Lopes[6] ; Antionette Brigitte Ngandjio[7] ; Manisha Bista[8] ; Darunee Tuntasuvan[9] ; Toby Leslie[10]
[1]School of Veterinary Science/ Massey University/ New Zealand, [2]One Health Lead/ Mott MacDonald/ Thailand (□□□), [3]Lead Clinical Microbiologist/ Mott MacDonald/ India, [4]Regional One Health Specialist/ Mott MacDonald/ Uganda, [5]Regional Microbiologist/ Mott MacDonald/ Uganda, [6]Regional One Health Specialist/ Mott MacDonald/ Ghana (Gaana), [7]Regional Microbioligst/ Mott MacDonald/ Ghana (Gaana), [8]Regional One Health Specialist/ Mott MacDonald/ India, [9]Regional One Health Specialist/ Mott MacDonald/ Thailand (□□□), [10]Global Technical Lead/ Mott MacDonald/ United Kingdom

Introduction and Objectives or Purpose
One Health (OH) underpins the United Kingdom (UK) Department of Health and Social Care's (DHSC) Fleming Fund (FF) program to strengthen antimicrobial resistance (AMR) and antimicrobial use (AMU) surveillance within 24 countries in Africa and Asia (2018-2023). The program strengthens governance and implementation of OH AMR/AMU surveillance. After several years of FF program implementation, we evaluated the multisectoral structure and functionality of the two major AMR surveillance governance organisations, the national AMR Coordinating Committee (AMRCC) and the multisectoral technical working group (TWG) , to understand how they supported a OH approach, program outputs and lessons learned for future programs.

Methods

A questionnaire was completed for each country by Mott MacDonald's Regional One Health Technical Teams, covering leadership, membership, activities and outputs of the AMRCCs and TWGs, plus challenges, success factors and lessons learned. A combination of descriptive quantitative analysis and qualitative thematic analysis identified progress and major themes for the areas of interest.

Results or Focus

The AMRCC and TWGs contributed to multisectoral governance of AMR/AMU surveillance to varying extents through multisectoral leadership and membership, supporting a multisectoral national action plan, raising AMR awareness amongst communities and government decision-makers, policy advocacy, stakeholder engagement, facilitating surveillance in multiple sectors to produce policy-relevant information and strengthening information sharing and understanding between the sectors. Further detailed results will be presented on challenges, successes and lessons learned for implementation of future OH programs.

Conclusion or Scope
Areas identified for further strengthening governance of OH AMR/AMU surveillance programs include, but are not limited to: enhanced secretariat support, regular meetings and clear action plans, efficient data sharing systems, greater engagement of the environment and agriculture sectors, strengthened OH interpretation of surveillance data from different sectors, policy formulation and advocacy, and enhanced design and implementation of prioritised AMR/AMU surveillance programs.

Acknowledgement

Possawat Jorakate (Thailand) and Manish Pathak (India), Regional Microbiologists, Mott MacDonald.

Keywords: One Health; AMR surveillance; multi-sectoral; governance; Fleming Fund

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 15151

Legislation on restrictions on antimicrobials intended for animal consumption in Viet Nam: Where do we go from here?

Juan Carrique-Mas[1] ; Le Thi Hue[*2] ; Nguyen Thu Thuy[2] ; Pawin Padungtod[1]
[1]Emergency Center for Transboundary Animal Diseases/ Food and Agriculture Organization of the UN/ Vietnam (Việt Nam), [2]Veterinary Drugs Administration/ Department of Animal Health, MARD/ Vietnam (Việt Nam)

Introduction and Objectives or Purpose

Objectives

(a) To present recent legislative initiatives in Viet Nam on antimicrobial use (AMU) stewardship, specifically restrictions on AMU in animal production; (b) to describe activities in support of these regulations; and (c) to discuss a way forward for Viet Nam in the context of the broader Southeast Asian region.

Methods

Since 2013 Viet Nam with the support of international organizations has taken bold steps to improve antimicrobial stewardship (AMS) in the human and animal sectors. Since 2018 new regulations involve restrictions on AMU in animal production based on purpose, stage of herd/flock development, farm size and antimicrobials class (based on WHO criteria). In addition, regulations on veterinary prescription requirements have also been issued. In parallel, initiatives that support the dissemination and compliance with these regulations are being developed, alongside new IT systems that enhance antimicrobial product management and AMU surveillance in the field. Guidelines for the safe and effective use of antimicrobials on animals are also being developed.

Results or Focus

We will present the up-to-date list of restrictions on AMU in animal production in Viet Nam, alongside current activities that underpin AMS efforts, management of antimicrobial products (import, manufacturing, and distribution) quality control, and the monitoring of AMU at farm/retail. Given the increasing role of transnational companies, we advocate for a common set of guiding principles and aims on AMU restrictions. These will be outlined alongside theoretical basis for conducting risk assessments to monitor impact.

Conclusion or Scope

For regulations to be meaningful, they should lead to measurable reductions in AMR and treatment outcomes. The new regulations in Viet Nam provides a unique opportunity to evaluate the impact of policy interventions across the country. As a rule, any new legislation should be preferably assessed to achieve an optimal balance cost-benefit outcome, keeping in mind that antimicrobials should be available to be used when strictly necessary.

Topic: Antimicrobial Resistance (AMR): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15287

Roadmap from COVID-19 surveillance to a sustainable One Health & AMR surveillance ecosystem

Michael Oberholzer*[1]
[1]Global Product Management/ Illumina/ United States

Introduction and Objectives or Purpose

The COVID-19 pandemic has ushered in a new era of infectious disease surveillance. Globally, public health professionals utilized genomics to understand SARS-CoV-2 spread and evolution, uncovering vital clues that inform public health decision-making and the development of new diagnostics, therapeutics, and vaccines. Through the development of the COVIDSeq™ Test, COVIDSeq Assay, and Illumina's SARS-CoV-2 NGS Data Toolkit, Illumina is proud to have supported the expansion of resources for public health surveillance during the COVID-19 pandemic. The pandemic highlighted the need for a sustained, unified, and pathogen-agnostic genomic surveillance efforts through a One Health approach to strengthen global health security and prevent the catastrophic cost of future pandemic. In this talk, Michael will share the vision of Illumina's infectious disease and microbiology product portfolio development to address critical public health and infectious disease surveillance needs.

Keywords: one health; genomic surveillance; AMR; public health; pandemic preparedness

Topic: Impact on and Innovations in Clinical Practice (IICP): Management of Non-Communicable Diseases (NCD) - pivoting during a pandemic and beyond: Chronic NCD management in outbreaks: Leveraging mobile technology to improve patient care
Abstract No: 14832

Rapid development of a mobile health application to facilitate remote care for COVID-19 patients with non-communicable diseases during a pandemic

Jamaica Pei Ying Tan[1] ; Joanne Sze Win Lee[*1] ; Xiaofeng Lei[2] ; Yong Liu[2] ; Siow Mong, Rick Goh[2] ; Teck Choon Tan[3] ; Chen Ee Lee[3] ; Franklin Chee Ping Tan[3] ; Lian Leng Low[1]
[1]Population Health and Integrated Care Office/ Singapore General Hospital (SGH)/ Singapore, [2]Institute of High Performance Computing (IHPC)/ Agency for Science, Technology and Research (A*STAR)/ Singapore, [3]Office for Service Transformation/ Singapore Health Services (SingHealth)/ Singapore

Introduction and Objectives or Purpose

An increasing amount of evidence suggests higher risks of infection and poorer prognoses for COVID-19 patients with Non-Communicable Diseases (NCDs). Mobile health (mHealth) solutions facilitate remote monitoring and continuity of care for COVID-19 patients with NCDs, while minimizing physical interactions. This study describes the rapid development of an mHealth application, DrCovid+, that is cost-effective and a timely enabler amidst the pandemic.

Methods

The application prototype was developed following the Rapid Application Development (RAD) approach. Decision makers, physicians, nurses, healthcare administrators, and research engineers were engaged. The process began with requirements gathering to define the project scope, followed by an iterative user-design process involving prototyping, testing, and improvement prior to final development and implementation. Co-designing principles were applied to ensure collaborative efforts and practical requirements were met.

Results or Focus

DrCovid+ was developed on Telegram and hosted on a cloud server. It features a secure patient enrolment process with multi-lingual communication capabilities and the option of automatic and/or personalized push messaging to collect patients' vital signs, including blood pressure, heart rate, and body temperature. This information is stored in a backend dashboard for remote monitoring, facilitating continuity of care for COVID-19 patients with NCDs. DrCovid+ was deployed in the Singapore General Hospital COVID Virtual Ward, an effective and accessible home-based recovery programme for complex COVID-positive patients. From 1st November 2021 to 31st May 2022, 630 patients have been enrolled, leading to 4071 bed-days and 102 man-days saved and more than 1,000 video consultations have been performed.

Conclusion or Scope

The rapid development of DrCovid+ underlines the importance of timely and continual response for COVID-19 patients with NCDs. It served to meet the exponential increase in patient load and demand for healthcare resources through remote clinical management. It further highlights the importance of leveraging innovative solutions and rethinking care models for chronic NCDs to future-proof rising population health challenges.

Acknowledgement

SGH,SingHealth,A*STAR

Keywords: mHealth; rapid development; remote care; COVID-19; Non-Communicable Diseases

Topic: Impact on and Innovations in Clinical Practice (IICP): Management of Non-Communicable Diseases (NCD) - pivoting during a pandemic and beyond: Chronic NCD management in outbreaks: Leveraging mobile technology to improve patient care
Abstract No: 14845

STROKE CARE DURING COVID NEEDS MORE THAN A STROKE TELECLINIC!

Fung Peng Woon[1] ; Peck Kee Lim[2] ; Yi Ping Quek[2] ; Il Fan Tan[2] ; Deidre De Silva*[3]
[1]Neurology/ Singapore General Hospital/ Singapore, [2]Neurology (Nursing)/ National Neuroscience Institute/ Singapore, [3]Neurology/ National Neuroscience Institute (Singapore General Hospital campus)/ Singapore

Introduction and Objectives or Purpose

The COVID-19 pandemic affected some aspects of stroke care. Whilst hyperacute stroke treatment and acute hospitalisation care remained intact, we identified other gaps in care. These include limited access to outpatient rehabilitation and care centres; no face to face support services by voluntary welfare organisations; and fear/concern to seek help as a vulnerable group. We aimed to provide an alternate avenue to provide post-stroke support and information for stroke survivors and caregivers.

Methods

We developed a mobile application with collaboration from a multidisciplinary group. The healthcare group's Office of Innovation assisted to link up with the Integrated Health Information Systems team and an industry partner to provide technical expertise in application development and security. The healthcare team comprising of doctors, nurses and allied health contributed to the stroke education contents and rehabilitation training videos. Stroke survivors/caregivers from a stroke support organisation provided feedback and participated in user acceptance testing. The launch and publicity of the application were supported by colleagues from marketing/communication.

Results or Focus

The Stroke Buddy housed under SingHealth's Health Buddy mobile application was launched on 26 March 2021. It currently features 23 articles/videos stroke care tips, 24 videos on training exercises for patients and tutorials for caregivers, and stroke community resources. Patients can access recovery tools such as the Post-Stroke Checklist, personalise their own exercise and wellness programme, track their blood pressures and set medication reminders. There were 7,467 active users and 5,724 screen views for Stroke Buddy from March 2021 to June 2022.

Conclusion or Scope

Stroke Buddy is a one-stop portal for stroke speciality care that leverages on the existing Health Buddy's features in providing a wide range of e-services that empowers stroke survivors and their caregivers to self-manage their condition in their post-stroke and rehabilitation journey.

Keywords: stroke, post-stroke support, mobile application, stroke rehabilitation

Topic: Impact on and Innovations in Clinical Practice (IICP): Management of Non-Communicable Diseases (NCD) - pivoting during a pandemic and beyond: Rethinking NCD care models: Lessons from COVID-19
Abstract No: 14975

The One Health Clinic: Leveraging the Human-Animal Bond for care access in the unhoused population

Erin Tabor*[1] ; Alice Tin[2] ; Kathryn Kuehl[3] ; Julianne Meisner[1] ; Vickie Ramirez[1] ; Anina Terry[4] ; Peter Rabinowitz[1]
[1]Department of Environmental and Occupational Health Sciences/ Center for One Health Research/University of Washington/ United States, [2]Family Medicine/ Swedish Health Center/ United States, [3]College of Veterinary Medicine/ Washington State University/ United States, [4]Youth Clinic at New Horizons/ Neighborcare Health/ United States

Introduction and Objectives or Purpose

In 2018, the University of Washington's Center for One Health Research and Washington State University's College of Veterinary Medicine collaborated to create the One Health Clinic in Seattle, Washington for people experiencing homelessness with pets. The Clinic was the first of its kind to leverage the human-animal bond to reduce barriers to healthcare while offering integrated human and veterinary care, with human and veterinary teams working in tandem to create a single management plan for the human-animal unit. This presentation introduces the One Health Clinic (OHC) concept and reports on the relationship among OHC clients, Emotional Support Animal (ESA) status of animals, human mental health diagnoses, and the relationship between ESA and housing status.

Methods

We performed a chart review of human medical and veterinary medical records for visits to the OHC in 2019 to abstract clinical information about diagnoses, treatments, type of animal, housing status, environmental factors, and whether the animal was a documented emotional support animal.

Results or Focus

Among 95 charts reviewed, the three most common reasons for seeking human healthcare were mental health (34.7%), contraception (22.1%), and substance use (15.8%). 30.5% of the animals seen in 2019 were considered ESAs, and 72% of the ESAs were dogs. With each additional psychiatric diagnosis, the odds of having an animal considered to be an ESA decreased by 83.3% (PR: 0.167, CI: 0.0192, 0.764). There was a non-significant trend of individuals who were not housed having a lower-odds of having an ESA.

Conclusion or Scope

These initial findings support the clinical importance of the human-animal bond, as seen in the relationship between human mental health, companion animal status and housing status in the unhoused population. It also suggests that One Health Clinic service models provide a unique opportunity for providing care to this population through an integrated approach to the human-animal unit.

Keywords: human-animal bond; emotional support animal; integrated healthcare; homelessness with pets

Topic: Impact on and Innovations in Clinical Practice (IICP): Management of Non-Communicable Diseases (NCD) - pivoting during a pandemic and beyond: Rethinking NCD care models: Lessons from COVID-19
Abstract No: 15267

MULTISECTORAL AND COMMUNITY ENGAGEMENT IN PRIMARY HEALTH CARE INITIATIVE TO COMBATING COVID-19 PANDEMIC: LESSON-LEARNT FROM MOBILE HEALTH STATIONS IN VIETNAM

Giang Nguyen Hoang*[1] ; Thang Nguyen Thi[1] ; Linh Nguyen Thi Phuong[1] ; Vinh Nguyen The[1] ; Giang Tran Nguyen Thien[1] ; Linh Dao Phuong[1] ; Dung Nguyen Thi[1] ; Minh Bui Ngoc[1] ; Oanh Tran Thi Mai[1]
[1]Department of Public Health/ Health Strategy and Policy Institute/ Vietnam (Việt Nam)

Introduction and Objectives or Purpose

The COVID-19 pandemic caused serious impacts on people’s health and unprecedented pressure on the healthcare system in Vietnam. Mobile Health Station (MHS) was initiated to be a gatekeeper of the health system, ensuring access to community-based COVID-19 care and primary health care (PHC). This study assessed performance and identified challenges in implementing MSH during the COVID-19 outbreak in Vietnam.

Methods

A cross-sectional study using a mix-method design was conducted in two provinces. The quantitative study includes secondary data collection on supporting conditions and service provision of MSH; a self-administered survey with MSH’s staff to access knowledge and practice. The qualitative study employed focused group discussions with stakeholders (local authorities, health managers, health providers, and affected communities) to understand implementation challenges and lesson-learned.

Results or Focus

MSHs were activated in 90.9% of communes, covering 72% of COVID-19 patients in catchment areas. Of which, 80.5% were provided COVID-19 home care, such as diagnosis, health monitoring, and consultation, via phone call/smartphone-based messaging apps. The MSHs collaborated with existing PHC facilities and Community COVID Care Groups, providing COVID-19 testing and vaccination, counseling, regular care for chronic conditions, referral, and welfare support for disadvantaged groups. The MSH received strong political and resource commitment from the local authorities and stakeholders and continuous technical support from health managers. However, the study highlights barriers hampering MSHs from fulfilling their designated roles, including stressful and risky working conditions due to understaffing issues and excessive workload; limited capacity; insufficient financial support; poor medical supplies; inadequate medical and protective devices.

Conclusion or Scope

Despite tremendous challenges, stakeholders’ engagement contributed to the early success of the MSH in guaranteeing timely access to COVID-19 care and essential PHC services during the pandemic. The development of financial, organizational, and operational mechanisms is crucial to sustaining the model in response to the current pandemic or future health security threats in Vietnam.

Keywords: COVID-19, Vietnam, Mobile Health Station, Primary Health Care

Topic: Impact on and Innovations in Clinical Practice (IICP): Multidrug Resistant Organisms (MDRO) - roles, responsibilities and interests of the non-ID physicians: The interdependence of animal and human health - MDRO in pet animals and livestock
Abstract No: 14662

U.S. Food and Drug Administration (FDA) and U.S. Department of Agriculture (USDA) Integrated Antimicrobial Resistance Data Dashboards from Companion Animals

Olgica Ceric*[1] ; Amy Merril[1] ; Beth Harris[2] ; Jennifer Rodriguez[2] ; Christine Foxx[3] ; Christina Loiacono[2] ; Sarah Peloquin[1] ; Jake Guag[1] ; Claudine Kabera[1] ; Gregory Tyson[1]
[1]Center for Veterinary Medicine/ U.S. Food and Drug Administration/ United States, [2]National Animal Health Laboratory Network/ USDA-APHIS-VS-DB/ United States, [3]Oak Ridge Institute for Science and Education Research Participation Program/ Oak Ridge Institute for Science and Education Research Participation Program/ United States

Introduction and Objectives or Purpose

The FDA's Veterinary Laboratory Investigation and Response Network (Vet-LIRN) and the USDA's National Animal Health Laboratory Network (NAHLN) monitor antimicrobial resistance (AMR) in animal pathogens routinely isolated by veterinary clinics and diagnostic laboratories across the U.S. A cross-agency collaborating group was formed to develop a centralized data collection and reporting process across participating laboratories from both networks. The group consists of members from FDA's Vet-LIRN and National Antimicrobial Resistance Monitoring System (NARMS), and USDA's NAHLN.

Methods

More than 40 laboratories from both networks provided antimicrobial sensitivity test (AST) data on Escherichia coli, Salmonella spp., and Staphylococcus intermedius group species in dogs, using a commercially available testing platform. Laboratories sequenced a subset of isolates and submitted the whole genome sequencing data to public sequencing repositories. Both networks followed Clinical and Laboratory Standards Institute (CLSI) AST testing methods

Results or Focus

The first integrated report for 2018 data was released in December 2020 as a part of NARMS's Integrated Report Summary for 2018. The report included dashboards with minimum inhibitory concentration (MIC) data for approximately 2,300 isolates. This was the first time that integrated AMR monitoring data from dogs, collected from FDA and USDA's networks, became available in the U.S. The second joint report for 2019 data was released in March 2022, which includes MIC data for approximately 4,000 isolates. Dashboards for the second report also included resistance mechanisms from genomics data, along with the percent resistance and MIC distributions for each of the antibiotics included in the panels.

Conclusion or Scope

By developing a centralized data collection and reporting process across laboratories from FDA and USDA networks, data can be monitored for trends in AMR phenotypes and genotypes to identify new or emerging resistance profiles, to help monitor the continued efficacy of antibiotics over time, and to provide information to all stakeholders regarding these trends.

Keywords: AMR Monitoring; Companion animals; Integrated AMR data

Topic: Impact on and Innovations in Clinical Practice (IICP): Multidrug Resistant Organisms (MDRO) - roles, responsibilities and interests of the non-ID physicians: Use of bioinformatics for the control and containment of infectious diseases
Abstract No: 14943

Scale-up of Infection Prevention and Control Capacity for Public Health Emergency Response through Virtual Learning

Samuel Alabi[*1] ; Olaoluwa Akinloluwa[1] ; Titilope Ajayi[1] ; Chinwe Ochu[2]
[1]Integrated Response to Public Health Emergencies in Nigeria Plus Project/ Pro-Health International/ Nigeria, [2]Knowledge Management/ Nigeria Centre for Disease Control/ Nigeria

Introduction and Objectives or Purpose

Following the index COVID-19 case in February 2021, a spike in incidence rate and hospitalization triggered the institution of emergency public health measures in Nigeria. There was an urgent need to address healthcare worker (HCW) knowledge and practice gaps in the clinical management of Severe Acute Respiratory Infections (SARI), and the institution of infection prevention practices for border health security personnel: human and animal.

Methods

Severe Acute Respiratory Infection training and Nigeria Centre for Disease Control’s Infection Prevention and Control training programme. The team proceeded to developing the Instructional Design Document, laying out the instructional roadmap of the curriculum using the One Health Approach. This was a necessary step as the target audience included human and animal healthcare workers. The implementation plan allowed for a single window of multisectoral and multidisciplinary review and field testing. Feedback from the process directed rewriting scripts to better suit the training audience and optimize audiovisuals. The development process was completed in 6 weeks and the platform made available to end users in May 2020.

Results or Focus

Public health measures to control the spread of COVID-19 such as ‘lockdowns’ presented a unique challenge to providing capacity building to thousands of healthcare workers and border health security personnel during a period of uncertainty and acute public health information gaps. We collaboratively developed and deployed a remote learning solution to reach HCW and border health security personnel across Nigeria.

Conclusion or Scope

The approach is suitable for rapidly scaling-up healthcare worker capacity building outside of the traditional classroom setting during a large-scale public health emergency.

Acknowledgement

This intervention was possible thanks to funding from the US Centers for Disease Control and Prevention

Keywords: Capacity Building, Virtual Learning, large scale public health emergency, response

Topic: Impact on and Innovations in Clinical Practice (IICP): Multidrug Resistant Organisms (MDRO) - roles, responsibilities and interests of the non-ID physicians: Using Clinical Decision Support System (CDSS) to guide antibiotic prescriptions
Abstract No: 15314

MACHINE LEARNING TO GUIDE ANTIBIOTIC USE IN SUSPECTED BACTERIAL PNEUMONIA: PROOF OF CONCEPT

Sarah Tang*[1] ; Andrea Kwa[1] ; Jasmine Chung[2] ; Yvonne Zhou[1] ; Daniel Chang[3] ; Piotr Chlebicki[2] ; Winnie Lee[1]
[1]Pharmacy/ Singapore General Hospital/ Singapore, [2]Infectious Diseases/ Singapore General Hospital/ Singapore, [3]Allied Health / Singapore General Hospital/ Singapore

Introduction and Objectives or Purpose

Accurate diagnosis of acute bacterial pneumonia (ABP) is often elusive. The lack of diagnostic gold standard, exacerbated by overlapping syndrome with non-infective/non-bacterial respiratory conditions, have contributed to antibiotic over-prescribing. This in turn drives drug resistance, healthcare costs and patient morbidity. We explored feasibility of developing a classification model to identify instances when antibiotics should be initiated or withheld in cases when ABP is suspected.

Methods

All inpatients in Singapore General Hospital during Y2015-2020 and had ICD-10 codes for ABP or mimicking conditions (e.g., fluid overload) were included. Population was divided into 80% and 20% for training and testing respectively. Only cases with ICD-10 codes for ABP and manually assessed to be true by the hospital antimicrobial stewardship unit were labelled as ground truth “Yes” (i.e., antibiotics should be initiated). Cases with ICD-10 codes for other conditions were labelled as ground truth “No” (i.e., antibiotics could be withheld). Patient information (e.g., clinical notes, radiology reports, vital signs) were extracted from our hospital’s electronic data repository. Machine learning techniques (logistic regression, support vector machines, random forest and XGBoost) were applied and assessed for their relative performance.

Results or Focus

There were a total of 18,589 episodes. In view of a significantly imbalance dataset (ground truth “No” 84.5%), random under-sampling was performed. Final population sizes for training and testing were 4,617 and 1,156 respectively. XGBoost proved the best performance: AUC was 82.6%, F1 score 83.1%, accuracy 82.6%, precision 80.7%, negative predictive value 84.7%, and recall 85.6%. Chest scan report, procalcitonin, presence of cough, oxygen saturation and auscultation findings documented at start of episode were the 5 most important features in determining presence of ABP requiring antibiotics.

Conclusion or Scope

We developed a machine learning model to support decision-making on antibiotic initiation for suspected ABP. Further work is needed to optimize this model and evaluate its impact on clinical practice.

Keywords: machine learning; antimicrobial stewardship; clinical decision support tool; bacterial pneumonia

Topic: One Health Science (OHS): Discovery and Surveillance: Digital-aided events based syndromic and genomics surveillance
Abstract No: 15375

AUSTRAKKA – A NATIONAL PATHOGEN GENOMICS SURVEILLANCE PLATFORM BRIDGING THE GAP IN DATA SHARING, INTEGRATION AND ANALYSIS

Benjamin Howden*[1] ; Tuyet Hoang[1] ; Torsten Seemann[1] ; Mathilda Wilmot[1] ; Patiyan Andersson[1] ; Connie Lam[2] ; Vitali Sintchenko[2] ; Amy Jennison[3] ; Clare Sloggett[1] ; Son Nguyen[3]
[1]Microbiology and Immunology/ Microbiological Diagnostic Unit Public Health Laboratory, University of Melbourne/ Australia, [2]NSW Health Pathology/ Institute of Clinical Pathology & Medical Research/ Australia, [3]Forensic and Scientific Services/ Queensland Health/ Australia

Introduction and Objectives or Purpose

AusTrakka, a central and secure system for data sharing and analysis of genomics data governed by the Communicable Diseases Genomics Network, was rapidly deployed in 2020 in response to the need for national SARS-CoV-2 genomic surveillance and outbreak investigations. Since then, AusTrakka has seen significant increases in engagement and interest in utilising the system for other public health priority pathogens from human and non-human sources.

Methods

To date, AusTrakka has hosted over 120,000 genomes, including SARS-CoV-2, Salmonella and Listeria. Analyses and reports, including phylogenetic trees, sample metadata tables, and report summaries for SARS-CoV-2 variants of concern, have been made available to users in real-times. The development of AusTrakka has been highly consultative, built by public health laboratories for public health laboratories. A key outcome of AusTrakka has been the provision of analysis capacity to jurisdictions with limited resources, enabling laboratories to view their genomic data in a highly secure manner within the national context to identify matches or clusters requiring further public health investigation.

Results or Focus

The global strengthening of pathogen genomics capacity for public health has revealed the demand for technical solutions that provides jurisdictions and sectors with capacity to integrate and analyse genomic data to inform public health action and decision-making more readily. Barriers to data sharing and coordination has been overcome where there are agreed frameworks that recognise data custodianship, governance, and usage of data. Experience in deploying AusTrakka in Australia has shown that technical solution supported by an agreed governance system can enable a networked operational model between laboratories, health providers and government bodies.

Conclusion or Scope

There is opportunity adapt the principles of the AusTrakka system, to bridge the gap for cross-sectoral data integration for enhanced genomic surveillance.

Acknowledgement

Communicable Diseaes Genomics Network

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Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15259

Working on NTDs to prevent epidemics through the strengthening of health systems

Deborah Nadal*[1] ; Bernadette Abela-Ridder[1]
[1]Control of Neglected Tropical Diseases/ World Health Organization/ Switzerland (Schweiz)

Introduction and Objectives or Purpose

Health emergencies, from localized disease outbreaks to pandemics, can push health systems to a breaking point. This is more likely to happen, and to cause severe damage, where health systems are already fragile. Therefore, it is imperative to build and maintain robust health systems, especially in under-resourced areas. It is acknowledged that the benefits of adopting a One Health approach include the strengthening of human, animal, and environmental public health systems – at their interface. We argue that endemic diseases, and Neglected Tropical Diseases (NTDs) in particular, represent a strategic area of One Health intervention towards this goal.

Methods

Through some of the examples that we have collected from NTD stakeholders during the creation of the document “One Health: Approach for action against NTDs 2021–2030” (WHO, 2022), and the results of a survey on the impact of the pandemic on global rabies control efforts, we will present some of the ways through which One Health-centered NTDs management can produce benefits far beyond these health issues. Instances include the building of core capacities such as responsive surveillance systems, delivering integrated health programs, and engaging with local communities and local healthcare personnel in a long-term fashion. Based on a rapid landscape review of available literature, we will also reflect on what incentives could be adopted to sustainably scale up One Health projects into long-term programs embedded into health systems.

Conclusion or Scope

Pandemic preparedness is considered an essential “global public good”. The elimination of NTDs, for the massive burden that they silently impose on over one billion people, is equally important. Designing and operationalizing One Health plans for NTDs builds health systems that meet the needs of all communities (while relieving the poor from healthcare-related financial burden), are more likely to effectively cope with new health threads, and can go through public health crises unbroken.

Keywords: control of Neglected Tropical Diseases; health system strengthening; One Health incentives; preparedness

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15331

Towards wastewater surveillance of arbovirus outbreaks

Francisca Chandra*[1] ; Federica Armas[1] ; Wei Lin Lee[1] ; Desmond Chua[2] ; Hongjie Chen[1] ; Germaine Kwok[2] ; Xiaoqiong Gu[1] ; Stefan Wuertz[2 3] ; Eric Alm[1 4] ; Janelle Thompson[2 5]
[1]Antimicrobial Resistance IRG/ Singapore MIT Alliance for Research and Technology/ Singapore, [2]Singapore Center for Environmental Life Sciences Engineering/ Singapore Center for Environmental Life Sciences Engineering/ Singapore, [3]School of Civil and Environmental Engineering/ Nanyang Technological University/ Singapore, [4]Biological Engineering/ Massachusetts Institute of Technology/ United States, [5]Asian School of the Environment/ Nanyang Technological University/ Singapore

Introduction and Objectives or Purpose

Clinical surveillance of arboviruses underreport the true prevalence as the majority of cases are asymptomatic or mild and self-managed. Reports of urinary shedding of several arboviruses suggest the possibility of wastewater surveillance(WWS).

Methods

To investigate the plausibility of wastewater surveillance of arboviruses, we first compiled urinal shedding rates of arboviruses and calculated their theoretical wastewater titers. We built a simple model of arboviral WWS sensitivity(i.e.how many infections in a given background of healthy population) given volume processed. We empirically tested the decay rates of arboviral RNA signals in wastewater at environmentally relevant temperatures to inform sampling strategy. Finally, we have also benchmarked viral concentration methods to determine the best protocol for arboviral WWS.

Results or Focus

While arboviruses are shed 2-3 logs lower than fecally-shed viruses(e.g.poliovirus, norovirus,and SARS-CoV-2), it is comparable with urine-shed viruses(e.g.polyomavirus) that have been surveyed in wastewater. We determined that arboviral RNA signals persist in wastewater matrices in the span of 2-4 days, but can persist for much longer if refrigerated at 6’C. To process the wastewater samples, we recommend using the centrifugal ultrafiltration method as it has the highest recovery efficiency, with the main caveat of small processing volume. Our proposed wastewater sampling and processing protocol can potentially survey an arboviral outbreak of at least 10 cases in a neighbourhood of 400 people.

Conclusion or Scope

Our work has shown that arboviral WWS is possible with an optimised protocol and a neighbourhood-sized catchment. While it is more challenging than WWS of fecally-shed viruses, due to their need for refrigeration and higher processing volume, arboviral WWS can potentially reduce surveillance cost and alleviate socio-economic burdens of arboviral outbreaks.

Acknowledgement

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Keywords: Wastewater surveillance; arbovirus; disease outbreak management

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 14732

WASTEWATER-BASED EPIDEMIOLOGY SURVEILLANCE AS AN EARLY WARNING SYSTEM FOR SARS-COV-2 INDONESIA

Vicka Oktaria*[1 2] ; Indah Kartika Murni[1 3] ; Amanda Handley[4 5] ; David T McCarthy[6] ; Celeste M Donato[4 7] ; Titik Nuryastuti[8] ; Endah Supriyati[9] ; Ida Safitri Laksono[1 3] ; Jarir At Thobari[1] ; Julie E Bines[4 10 7]

[1]Center for Child Health – Pediatric Research Office/ Faculty of Medicine, Public Health and Nursing, Universitas Gadjah Mada/ Indonesia, [2]Department of Biostatistics, Epidemiology and Population Health/ Faculty of Medicine, Public Health and Nursing, Universitas Gadjah Mada/ Indonesia, [3] Child Health Department/ Faculty of Medicine, Public Health and Nursing, Universitas Gadjah Mada/ Indonesia, [4]Enteric Diseases Group/ Murdoch Children's Research Institute/ Australia, [5]Medicines Development for Global Health/ Medicines Development for Global Health/ Australia, [6]Environmental and Public Health Microbiology Lab (EPHM Lab), Department of Civil Engineering/ Monash University/ Australia, [7]Department of Paediatrics/ The University of Melbourne/ Australia, [8]Department of Microbiology/ Faculty of Medicine, Public Health and Nursing, Universitas Gadjah Mada/ Indonesia, [9]Center for Tropical Medicine/ Faculty of Medicine, Public Health, and Nursing, Universitas Gadjah Mada/ Indonesia, [10]Department of Gastroenterology and Clinical Nutrition/ Royal Children's Hospital Melbourne/ Australia

Introduction and Objectives or Purpose

The potential of wastewater-based epidemiology (WBE) surveillance as an early warning system (EWS) for community COVID-19 transmission in low-and middle-income (LMIC) settings needs further investigation. We aim to investigate the potential of WBE as an EWS tool to predict changing trends of community COVID-19 case transmissions.

Methods

We conducted a routine WBE surveillance in three districts in Yogyakarta, Indonesia, from 27 July 2021 to 7 April 2022), which covered two periods of COVID-19 pandemic wave (Delta and Omicron wave surge). Samples were collected on a weekly or fortnightly basis with grab and passive sampling methods with real-time PCR performed for identification of SARS-CoV-2 in the environmental samples. The correlation between environmental data and local epidemiology of sub-district COVID-19 confirmed cases and the changing trends were analyzed using time-series analysis in STATA.

Results or Focus

A total of 1,233 samples (Phase 1, 24 weeks, 27 July 2021 to 7 January 2022) and 214 samples (Phase 2, 12 weeks, 18 January to 7 April 2022) were collected. Data collected from manholes were highly correlated with cases in the community (N gene $r = 0.8699$, $P<0.001$; ORF1ab gene $r = 0.9090$, $p<0.001$) and more likely to mimic the trend of incidence of COVID-19 in the community than data from septic tanks and others. There was an approximately 1-week lag time between wastewater and community case detection.

Conclusion or Scope

A WBE surveillance for SARS-CoV-2 in Indonesia showed its potential as an EWS in predicting changing trends of community SARS-CoV-2 transmission. However, to ensure its routine implementation as well as sustainability, a multisectoral collaboration between government, stakeholders, academicians, and the community is required.

Acknowledgement

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Keywords: wastewater surveillance; environmental sampling; SARS-CoV-2; COVID-19; Indonesia

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 14831

BEHAVIORAL-BIOLOGICAL SURVEILLANCE OF EMERGING INFECTIOUS DISEASES AMONG A DYNAMIC COHORT IN THAILAND

Su Yadana[*1] ; Thaniwan Cheun-Arom[1] ; Hongying Li[1] ; Emily Hagan[1] ; Emma Mendelsohn[1] ; Leilani Francisco[5] ; Thiravat Hemachudha[2] ; Peter Daszak[1] ; Kevin Olival[1] ; Supaporn Wacharapluesadee[3] ; Alice Latinne; Stephanie Martinez; Opass Putcharoen; Janthira Homvijitkul; Onarnong Sathaporntheera; Nit Pattanapreeda; Pongtorn Chartpituck; Supalak Yamsakul; Krairoek Sutham; Supharoek Komolsiri; Sonjai Pornphatthananikhom; Sininat Petcharat; Weenassarin Ampoot
[1]Program/ EcoHealth Alliance/ United States, [1]Department of Biology, Faculty of Science/ Ramkhamhaeng University/ Thailand (□□□), [5]Research/ Henry M. Jackson Foundation for the Advancement of Military Medicine/ United States [2]Thai Red Cross Emerging Infectious Diseases Clinical Center/ King Chulalongkorn Memorial Hospital/ Thailand (□□□) [3]Thai Red Cross Emerging Infectious Diseases-Health Science Centre, Faculty of Medicine, World Health Organization Collaborating Centre for Research and Training On Viral Zoonoses/ Chulalongkorn Hospital, Chulalongkorn University/ Thailand (□□□)

Introduction and Objectives or Purpose

Research to understand the high-risk behaviors associated with disease transmission at the human-animal interface is limited, and few consider regional and local contexts. This study employed an integrated behavioral–biological surveillance approach for the early detection of novel and known zoonotic viruses in potentially high-risk populations to identify risk factors for spillover and to determine potential foci for risk-mitigation measures.

Methods

Participants were enrolled at two community-based sites (n = 472) and two hospital sites (n = 206) in Thailand. A behavioral questionnaire was administered to understand participants' demographics, health history, and animal-contact behaviors and attitudes. Biological specimens were tested for coronaviruses, filoviruses, flaviviruses, influenza viruses, and paramyxoviruses using pan (consensus) RNA Virus assays.

Results or Focus

Overall 61/678 (9%) of participants tested positive for the viral families screened which included influenza viruses (75%), paramyxoviruses (15%), human coronaviruses (3%), flaviviruses (3%), and enteroviruses (3%). The most salient predictors of reporting unusual symptoms (i.e., any illness or sickness that is not known or recognized in the community or diagnosed by medical providers) in the past year were having other household members who had unusual symptoms and being scratched or bitten by animals in the same year. Many participants reported raising and handling poultry (10.3% and 24.2%) and swine (2%, 14.6%), and several participants also reported eating raw or undercooked meat of these animals (2.2%, 5.5%, 10.3% respectively). Twenty four participants (3.5%) reported handling bats or having bats in the house roof. Gender, age, and livelihood activities were shown to be significantly associated with participants' interactions with animals. Participants' knowledge of risks influenced their health-seeking behavior.

Conclusion or Scope

This study highlights important differences among demographic and occupational risk factors as they relate to animal contact and zoonotic disease risk, which can be used by policymakers and local public health programs to build more effective surveillance strategies and behavior-focused interventions.

Keywords: surveillance; emerging infectious diseases; zoonotic disease risk; spillover; high-risk behaviors

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 14993

HIGHLY DIVERGENT SARS-COV-2 FROM NORTH AMERICAN DEER WITH PROBABLE DEER-TO-HUMAN TRANSMISSION

Samira Mubareka[*1 2] ; Bradley Pickering[3 4 5] ; Oliver Lung[3 6] ; Finlay Maguire[7 8] ; Peter Kruczkiewicz[3] ; Jonathon Kotwa[2] ; Tore Buchanan[9] ; Jennifer Guthrie[10 11] ; Claire Jardine[12 13] ; Jeff Bowman[9 14]

[1]Laboratory Medicine and Pathobiology/ University of Toronto/ Canada, [2]Biological Sciences/ Sunnybrook Research Institute / Canada, [3]National Centre for Foreign Animal Disease/ Canadian Food Inspection Agency, Winnipeg, Manitoba, Canada/ Canada, [4]Department of Veterinary Microbiology and Preventative Medicine/ College of Veterinary Medicine, Iowa State University/ United States, [5]Department of Medical Microbiology and Infectious Diseases/ University of Manitoba/ Canada, [6]Department of Biological Sciences/ University of Manitoba/ Canada, [7]Computer Science/ Dalhousie University/ Canada, [8]Department of Community Health & Epidemiology, Faculty of Medicine/ Dalhousie University/ Canada, [9]Wildlife Research and Monitoring Section/ Ontario Ministry of Natural Resources and Forestry/ Canada, [10]Laboratory/ Public Health Ontario/ Canada, [11]Department of Microbiology & Immunology/ Western University/ Canada, [12]Ontario-Nunavut/ Canadian Wildlife Health Cooperative/ Canada, [13]Department of Pathobiology/ University of Guelph/ Canada, [14]Environmental and Life Sciences Graduate Program/ Trent University/ Canada

Introduction and Objectives or Purpose

Novel wildlife reservoirs of SARS-CoV-2 may enable spillover to other species, and/or spillback into humans. In North America, there is recurrent spillover of SARS-CoV-2 from humans to white-tailed deer (WTD; Odocoileus virginianus). We sought to determine the regional genomic epidemiology of SARS-CoV-2 in Canadian WTD through a multidisciplinary biosurveillance program, the Wildlife Emerging Pathogens Initiative (Wild EPI), and characterize SARS-CoV-2 in this population.

Methods

During autumn 2021, 213 nasal swabs and 292 retropharyngeal lymph nodes (RPLN) were analyzed from 298 hunter-harvested adult WTD from southwestern (N=247, 83.0%) and eastern (N=51, 17.0%) regions of the province of Ontario, Canada. PCR and culture in VeroE6 cells expressing human ACE2 and TMPRSS2 were used for SARS-CoV-2 detection and isolation respectively. Consensus genomes were generated through a combination of amplicon and capture probe-based methods and characterized using maximum-likelihood and parsimony-based phylogenetics and mutational signature analyses.

Results or Focus

Five nasal swabs and 16 RPLN were confirmed positive for SARS-CoV-2 by PCR from 17 (5.7%) individual WTD; all positive animals were from southwestern Ontario. Five high quality SARS-CoV-2 sequences were generated and clustered together as a new and highly divergent lineage of SARS-CoV-2, harbouring 76 consensus mutations and designated as B.1.641 within the B.1 PANGO lineage. Six non-synonymous mutations in S corresponded to a 6-nucleotide deletion and 5 substitutions. A genome-wide elevated proportion of C>U changes relative to other global, B.1 lineage, and animal-derived viral sequences was observed. The well-supported deer-derived B.1.641 monophyletic group also clustered with a B.1.641 virus from an epidemiologically-linked human case with correlating geotemporal data and exposure history. Infectious virus was isolated from four positive deer nasal swabs.

Conclusion or Scope

Our findings suggest extensive parallel evolution of SARS-CoV-2 in North American wildlife, with unsustained deer-to-human transmission.

Acknowledgement

Wild EPI also includes H. McClinchey, M. Gagnier, A. Masse and L. Nituch, in collaboration with M. Cote and A. McGeer Keywords: SARS-CoV-2; wildlife; genomic epidemiology; transmission; reservoir

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15014

Extensive movement and recombination of SARS-related coronaviruses across China and Southeast Asia

Spyros Lytras*[1] ; Jonathan Pekar[2] ; Joel Wertheim[3] ; Joseph Hughes[1] ; Simon Dellicour[4] ; Philippe Lemey[5] ; David Robertson[1]
[1]MRC - University of Glasgow Centre for Virus Research/ University of Glasgow/ United Kingdom, [2]Department of Biomedical Informatics/ University of California San Diego/ United States, [3]Department of Medicine/ University of California San Diego/ United States, [4]Spatial Epidemiology Lab (SpELL)/ Université Libre de Bruxelles/ Belgium, [5]Department of Microbiology/ KU Leuven/ Belgium

Introduction and Objectives or Purpose

The emergence of SARS-CoV in 2002 and SARS-CoV-2 in 2019 has led to increased sampling of related coronaviruses circulating in animals, primarily horseshoe bats. Understanding the distribution, diversity and relatedness of the Sarbecoviruses – the taxonomic group encompassing SARS-related coronaviruses - can help us prevent future spillovers but also predict the evolutionary trajectory of the SARS-CoV-2 pandemic.

Methods

Coronaviruses readily exchange parts of their genomes in a process called recombination, contributing to their functional and antigenic properties. We used the genomes of all known Sarbecoviruses to explore the extent of recombination taking place between these viruses. Accounting for these patterns, we disentangled the unique evolutionary histories of all non-recombinant genomic segments. These inferences were combined with sampling times and locations of the viruses to model the temporal and geographic movements of their proximal ancestors.

Results or Focus

We find multiple recombination events across the evolution of the SARS-related coronaviruses, suggesting frequent co-infections of their bat reservoir hosts. Recombination breakpoints cluster at specific genome regions, indicative of the viruses preferentially swapping genes, such as Spike, to change their functional and/or antigenic properties. The strikingly different evolutionary histories that each genomic segment represents highlight how crucial it is to account for recombination instead of inferring trees from whole-genome sequences or just the RdRp. Integrating geographic information in the recombination-aware tree reconstructions reveals extensive ancestral movement across China and Southeast Asia in the past couple of centuries, with few viruses dispersing many kilometers away in just a few years.

Conclusion or Scope

Understanding the recombination patterns of Sarbecoviruses provides insights about their diversity and phylogeography, and help us predict how this process will impact the future evolution of SARS-CoV-2 in humans. At the same time, reconstructing the detailed movements of all known SARS-related coronaviruses can aid in both predicting future spillovers and uncovering the origins of the current pandemic.

Keywords: SARS-CoV-2; origins; phylogeography; surveillance; coronaviruses; recombination; virus evolution

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15029

ASIAN HOUSE SHREWS (SUNCUS MURINUS) IN SINGAPORE HARBOUR A NOVEL ORTHONAIROVIRUS

Dolyce Low[*1] ; Lena Ch’ng[1] ; Martin Linster[1] ; Mackenzie Kwak[1] ; Rong Zhang[1] ; Sophie Borthwick[1] ; Erica Neves; Yvonne Su[1] ;
Gavin Smith[1 4 3 5] ; Ian Mendenhall[1 3]
[1]Emerging Infectious Diseases/ Duke-NUS Medical School/ Singapore [1]Department of Biological Sciences/ National University of Singapore/ Singapore [4]Centre for Outbreak Preparedness/ Duke-NUS Medical School/ Singapore [3]SingHealth Duke-NUS Global Health Institute/ Duke-NUS Medical School/ Singapore [5]Duke Global Health Institute/ Duke University/ United States

Introduction and Objectives or Purpose

The genus Orthonairoviruses is segmented RNA viruses, classified taxonomically under the family Nairoviridae, orderBunyavirales. They are predominantly tick-borne and can infect a wide range of mammals and birds. Orthonairoviruseshave been documented to cause human illness, with Crimean-Congo hemorrhagic fever virus (CCHFV) being the most pathogenic with high case fatality. In this study, we describe a novel Orthonairovirus, Cencurut virus (CENV) discovered in the Asian house shrew (Suncus murinus) from Singapore.

Results or Focus

CENV was detected in the lung, spleen and kidney tissues of 27/37 shrews, with the highest viral loads detected in the kidneys. A nymphal tick (Amblyomma helvolum) was collected from the snout of an infected shrew and harboured similarly high CENV loads, likely due to the consumption of an infected blood meal. Full genome sequencing of CENV revealed approximately 5% nucleotide diversity across three genome segments (small, medium and large genes), suggesting high genetic diversity across the shrew population in Singapore. Phylogenetic analysis of individual gene segments showed relatedness to Thiafora and Erve viruses (Thiafora orthonairovirus genogroup), which were previously discovered in shrews from Senegal and France, respectively. Studies have demonstrated zoonotic potential of Orthonairoviruses, from the detection of CCHFV antibodies in humans across several countries, as well as implicated Erve virus in causing severe headaches in humans. However, there are few Orthonairovirus reports within Southeast Asia, which is likely due to a lack of surveillance.

Conclusion or Scope

This study highlights the importance of Orthonairovirus surveillance in Southeast Asia, especially in synanthropic species such as Asian house shrew that are widely distributed across the region.

Keywords: metagenomics; phylogeny; Cencurut virus; Thiafora

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15084

BAT CORONAVIRUSES SURVEILLANCE IN 3 LIMESTONE KARSTS IN LAOS

Chittaphone Vanhnollat*[1] ; Khamsing Vongphayloth[1] ; Bounsavane Douangboubpha[2] ; Somphavanh Somlor[1] ; Daosavanh Sanamxay[2] ; Watthana Theppangna[3] ; Paul Brey[1] ; James Strong[4]
[1]-/ Institut Pasteur du Laos/ Lao People's Democ. Rep., [2]Faculty of environmental science/ National university of Laos/ Lao People's Democ. Rep., [3]Department of Livestock and Fisheries/ National Animal Health Laboratory/ Lao People's Democ. Rep., [4]Public Health Agency of Canada/ National Microbiology Laboratory Branch/ Canada

Introduction and Objectives or Purpose

Although there are many unresolved questions about the origin of SARS-CoV-2 virus, several studies pose a high possibility of zoonotic spillover from bats. From our initial study, we have shown that coronaviruses (CoVs) are abundantly present in various bat species in Laos. In this study, we continue to evaluate the diversity of bat CoVs in Laos.

Methods

Four live-capture missions were conducted in 3 different locations of limestone karsts in Laos including Vientiane (twice: VT-1 and VT-2), Luangnamtha (LNT), and Khammoune (KM) province over the period of 5 months (February - June 2022). Anal swab samples of various bat species were collected to screen for CoVs using RT-PCR assay and the positive samples were subjected to Sanger sequencing. The identity of sequences obtained was confirmed by NCBI BLASTn search.

Results or Focus

Among 1,205 bats captured and sampled, the pan-coronavirus screening revealed an overall positivity percentage of 12.78% (154 of 1,205 anal swabs). By locations, KM yielded the highest positivity rate 21.34% (102 of 478), followed by 9.92% (26 of 262) in LNT, 6.56% (24 of 366) in VT-2, and 2.02% (2 of 99) in VT-1 respectively. Analysis of the partial RdRP gene of coronavirus indicated that the coronavirus-detected samples were mainly clustered in the unclassified coronavirus group. Our analysis also revealed a high genetic diversity, by which various sub-viral groups were identified in both Alphacoronavirus and Betacoronavirus genera. The sub-genera that fell within the described Alphacoronavirus included Decacovirus, Rhinacovirus, and some unclassified alphacoronaviruses. Of the Betacoronavirus we also found the following sub-genera: Nobecovirus, Sarbecovirus, and unclassified betacoronavirus.

Conclusion or Scope

This study reiterated our previous findings that CoVs have high genetic diversity and are widely circulating in bats within upper Mekong region. For the mitigation of future risks, it is highly necessary to continue long-term longitudinal studies of virus density and circulation in Laos and region.

Keywords: bat coronavirus; genetic diversity; SARS-CoV-2; Laos

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15221

Descriptive Epidemiology and Response to Human Monkeypox Re-emergence in Nigeria Using One Health Approach, 2017 – 2021

Bola Lawal*[1] ; Lateefat Amao[2] ; Lois Olajide[1] ; Oladapo Ogunbode[3] ; Odianosen Ehiakhamen[2] ; Oyeladun Okunromade[1] ; Elsie Ilori[1] ; Ifedayo Adetifa[1]
[1]Surveillance and Epidemiology/ Nigeria Center for Disease Control/ Nigeria, [2]Health Emergency, Preparedness and Response / Nigeria Center for Disease Control/ Nigeria, [3]Prevention, Programmes and Knowledge management/ Nigeria Center for Disease Control/ Nigeria

Introduction and Objectives or Purpose

Human monkeypox is a zoonotic infectious disease caused by an orthopoxvirus transmitted to humans by contact with infected animals and humans. Following the re-emergence of monkey in Nigeria in 2017, the country has continued to record sporadic cases. We described the epidemiology of human monkeypox in Nigeria from 2017 to 2022 and the country's response.

Methods

Using the WHO case definition for monkeypox, a retrospective data review of monkeypox cases reported in Nigeria from 2017 to July 2022 was conducted. Descriptive analysis was conducted to describe the epidemiology of monkeypox cases reported with respect to person, place and time. We reviewed the country's control measures including guidelines and manuals developed and reports of outbreak investigation and response conducted. Analysis was done using Microsoft Office Excel and QGIS.

Results or Focus

Of the 925 suspected cases reported in the country from 2017 to July 2022, 383 (41.4%) were laboratory confirmed cases across 30 states with the southern part of the country accounting for majority (80.9%) of the confirmed cases. Twelve deaths (CFR:3.1%) were recorded among confirmed cases. No seasonal pattern was observed in the distribution of the cases over time. The year 2022 accounted for the highest morbidity with 157 (41.0%) confirmed cases and mortality (4 deaths). There was a male preponderance [253 (66.1%)] and cases 31–40years old [134 (33.1%)] constituted the highest age-group. A multi-sectoral multi-disciplinary measure using a one health approach was used to respond to the re-emergence of monkeypox in the country.

Conclusion or Scope

With the re-emergence of monkey in Nigeria, the country has continued to record sporadic cases with an unprecedented high number of cases this year. Nigeria's response to this re-emergence using a one health approach provides a valuable reference for public health policy makers in responding to other zoonotic diseases.

Acknowledgement

We acknowledge the national monkeypox Technical Working Group.

Keywords: Monkeypox, Re-Emergence, One-Health, Surveillance

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15315

Cumulative evidence supports wastewater-based COVID-19 pandemic surveillance in a middle-income African country

Chinwe Iwu-Jaja*[1] ; Nkosenhle Ndlovu[1] ; Laurette Mhlanga [2] ; Cari Van Schalkwyk[2] ; Juliet Pulliam[2] ; Said Rachida[1] ; Mukhlid Yousif[1] ; Setshaba Taukobong[1] ; Mokgaetji Macheke[1] ; Kerrigan McCarthy[1]
[1]Centre for Vaccines and Immunology/ National Institute for Communicable Diseases/ South Africa, [2]The South African Centre for Epidemiological Modelling and Analysis (SACEMA)/ Stellenbosch University/ South Africa

Introduction and Objectives or Purpose

Wastewater-based epidemiology (WBE) has been a valuable tool to complement clinical epidemiology for decades. We present results of WBE for SARS-CoV-2 in wastewater from South African wastewater treatment plants (WWTPs) and describe the relationship between SARS-CoV-2 levels and laboratory-confirmed case burden by district.

Methods

The South African Collaborative Covid-19 Surveillance System (SACCESS) network tested influent wastewater from 87 WWTPs in nine provinces between June 2021 and May 2022 (2nd to 4th pandemic 'waves'). Weekly samples (one-litre wastewater) were collected, underwent concentration, and RNA extraction. Positive samples for SARS-CoV-2 were quantified and log-transformed. The relationship between SARS-CoV-2 concentrations and clinical cases were investigated using correlation and a linear regression model. We also investigated the possibility of predicting a wave of infection by testing the sensitivity of 'rules' using the change in positivity rate of SARS-CoV-2 clinical tests as a gold standard, and generating receiver-operating curves.

Results or Focus

In most plants studied, SARS-CoV-2 levels showed a significant strong positive linear correlation with clinical cases. Our regression model demonstrated a significant association between viral load and caseload after adjusting for testing laboratory, size, sampling frequency, and location ($p<0.001$, CI=0.00008-0.00011). Successive increases were detected before and during pandemic waves, and decreased afterwards indicating the potential to predict oncoming 'waves'. However, none of the 'tests' had sensitivity above 60%. Of all rules, a 50% increase in log copies in the week of interest compared to the rolling mean of the previous 5 or 6 weeks predicted the 'gold standard' one week ahead.

Conclusion or Scope

Our study showed that SARS-CoV-2 RNA monitoring in wastewater is a good indicator of community disease burden and ongoing transmission of COVID-19. Predictive signals of oncoming 'waves' may become apparent if testing methodology is more sensitive and testing frequency increased. There is also need to investigate alternative approaches for meaningful signals from wastewater, of oncoming waves.

Keywords: Wastewater based epidemiology epidemiology, SARS-CoV-2, COVID-19 pandemic, environmental surveillance, South Africa

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15341

ENVIRONMENTAL SAMPLING AND VIRAL METAGENOMICS: A TOOL TO EXPAND AND ENHANCE GENOMIC SURVEILLANCE AT HIGH RISK HUMAN-ANIMAL INTERFACES?

Ynze Siegers[*1] ; Vireak Heang[1] ; Sokhoun Yann[1] ; Gavin Smith[2 3 4] ; Cadhla Firth[5] ; Erik Karlsson[1]
[1]Virology/ Institut Pasteur du Cambodge/ Cambodia (□□□□□□□), [2]Programme in Emerging Infectious Diseases/ Duke-NUS Medical School/ Singapore, [3]SingHealth Duke-NUS Global Health Institute/ SingHealth Duke-NUS Academic Medical Centre/ Singapore, [4]Duke Global Health Institute/ Duke University/ United States, [5]EcoHealth Alliance/ EcoHealth Alliance/ United States

Introduction and Objectives or Purpose

The ability to quickly assess zoonotic disease at high-risk interfaces is paramount for effective early warning systems and preventative actions. Current surveillance systems rely primarily on sampling individual animals – a costly and time-consuming practice, and prevents widespread coverage. Incorporation of environmental sampling (ES) such as water sources, air, and surfaces into sampling casts a wider net at high-risk interfaces, potentially improving expanded sampling on a longitudinal basis.

Methods

Individual animal and ES samples were collected at key live bird markets (LBMs) and bat caves/roosts in Cambodia. PCR based screening was performed for several viral pathogens including Orthomyxoviruses, Coronaviruses, and Paramyxoviruses. In parallel, targeted, enriched viral metagenomic sequencing (TEMVS) was performed using Twist Bioscience Comprehensive Viral Research Panel on Illumina MiSeq platform and analyzed using several commercial software packages.

Results or Focus

In LBMs, ES reflected avian influenza viral (AIV) diversity found in individual animal samples. In bat cave/roost ES, Paramyxovirus, Coronavirus and Astrovirus were detected in feces. Only paramyxoviruses were detected in air and urine. TEMVS significantly improved sensitivity and genome coverage of AIV whole genome sequencing compared to in-house protocols. In addition, metagenomic methods simultaneously identified numerous animal, plant, and occasionally human pathogens that are understudied in Cambodia.

Conclusion or Scope

ES coupled with TEMVS is a powerful tool to improve/expand surveillance capacity. However, current (commercial) metagenomic analysis software requires more exhaustive reference databases to detect emerging pathogens at human-animal interfaces. Overall, coupling TEMVS with ES can: improve pathogen surveillance; reduce cost; improve biosafety and animal welfare, and reduce occupational exposure risks; and, act as a first-line of detection for high-risk human-animal interfaces.

Keywords: surveillance; zoonosis; metagenomics; EID; environmental

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15367

Sampling solutions and risk-based prioritisation for wastewater surveillance of SARS-CoV-2

Judith Chui Ching Wong[1] ; Martin Tay[*1] ; Lei Lei [1] ; Janet Ong[1] ; Li Hui Goh[2] ; Dzulkhairul Maliki[1] ; Kelvin Bryan Tan[3] ; Lee Ching Ng[1]
[1]Environmental Health Institute/ National Environment Agency/ Singapore, [1]-/ NM3 Tech Pte Ltd/ Singapore, [2]Singapore's National Water Agency/ PUB/ Singapore [3]Policy Research and Evaluation Division/ Ministry of Health/ Singapore

Introduction and Objectives or Purpose

Wastewater based epidemiology (WBE) is an effective COVID-19 surveillance tool which complements clinical surveillance. However, challenges exist in the wastewater sampling process, such as sampling deep manholes beyond sampling depths of commercially available solutions, and the selection of suitable sampling points for surveillance.

Methods

Here, we describe the development and fabrication of deep manhole autosamplers which allow samples to be drawn from depths greater than 25m, as well as the use of geospatial and data analytic tools to identify suitable sampling sites. Sites with higher likelihood of transmission were identified and prioritised. We performed autocorrelation analyses on SARS-CoV-2 viral load in wastewater and the reported cases at each of sampling points to evaluate the effectiveness of WBE as an early warning system.

Results or Focus

Pump technology from the oil and gas industry was adapted for sampling deep manholes, with two prototypes consecutively tested in the field. The final design passed durability and quality checks of more than 500 sampling cycles and the deep manhole autosamplers have since been deployed across 30 sites islandwide.

Analyses of COVID-19 cases surrounding 203 wastewater sampling points covering different site types (i.e. community hubs, integrated transport hubs and shopping malls) show that community hubs have a higher rate of COVID-19 incidence, facilitating a risk-based prioritisation surveillance sites. A positive correlation between population density and COVID-19 incidence was also observed. Corroboration of SARS-CoV-2 virus load in wastewater and COVID-19 cases show that wastewater signals were a lead or contemporaneous indicator for majority (54.4%-59.4%) of the sites, with a greater number of sites showing wastewater signals as the lead indicator during the Omicron wave.

Conclusion or Scope

The work here accentuates the importance of engineering ingenuity and data-driven prioritisation for effective implementation of a WBE programme as a public health surveillance tool.

Acknowledgement

NEA's Microbiology and Molecular Epidemiology Division

PUB, Singapore's National Water Agency

Keywords: Wastewater surveillance, COVID-19, SARS-CoV-2, Wastewater-based epidemiology, Sampling technology

Topic: One Health Science (OHS): Discovery and Surveillance: Vector borne diseases
Abstract No: 14932

Mosquitoes as flying syringes: using blood meal for fast and effective virus surveillance in humans and wildlife

Carla J S P Vieira[*1 2] ; Narayan Gyawali[1] ; Michael B Onn[3] ; Martin A Shivas[3] ; Damien Shearman[4] ; Jonathan Darbro[4] ; Andrew Van den Hurk[5] ; Francesca D Frentiu[2] ; Gregor J Devine[1]

[1]Mosquito Control Laboratory/ QIMR Berghofer Medical Research Institute/ Australia, [2]School of Biomedical Sciences and Centre for Immunology and Infection Control/ Queensland University of Technology/ Australia, [3]Entomology Laboratory, Public Space Operations/ Brisbane City Council/ Australia, [4]Metro North Public Health Unit/ Queensland Health/ Australia, [5]Public and Environmental Health, Forensic and Scientific Services/ Queensland Health/ Australia

Introduction and Objectives or Purpose

Emerging zoonotic arboviruses often have complex transmission cycles involving multiple domestic and/or wild vertebrates, and mosquito vectors. Monitoring of the emergence, dynamics and prevalence of these viruses requires sampling from a wide variety of hosts and environments. Vertebrate immune responses to viral infections produce antigen-specific antibodies that may be detected by immunological assays, providing a critical tool for vector-borne disease surveillance. However, seroprevalence studies for zoonoses are challenging both logistically and in terms of the ethics and safety required for sampling from humans, and wild and domestic animals. We aimed to explore the use of mosquito blood meals as a method of determining vertebrate host seroprevalence in relation to Ross River virus (RRV) ecology.

Methods

We combined mosquito surveys with molecular and serological assays to investigate RRV transmission pathways across five urban sites in Brisbane, Australia, from March 2021 to May 2022. We assessed mosquito blood meals for the presence of antibodies to RRV using a micro-plaque reduction neutralisation test (mPRNT). In addition, host origins of mosquito blood meals were identified through amplification and sequencing of the Cytochrome b gene.

Results or Focus

Blood meals were recovered from 14 mosquito species totalling 480 individuals captured. Blood-fed mosquitoes comprised mainly Culex annulirostris (68.7%) and Cx. orbostiensis (9.4%). Host origins of 307 mosquito blood meals were identified, with humans (52%) and cow (6.8%) the dominant blood meal sources. This contrasts with previous Australian studies in which humans represented a relatively small proportion of blood meals. RRV seroprevalence was 52% in the 253 blood meal samples of human origin and 71% in 21 samples from cows.

Conclusion or Scope

Our results show that blood-fed mosquitoes captured in the wild contain enough host blood to detect antibodies to specific arboviruses. In tandem with barcoding techniques that identify the host blood-source, this technique can help suggest potential transmission pathways.

Acknowledgement

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Keywords: Ross River virus; zoonosis; vectors; host blood meal; neutralisation assay

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Diagnostic and discovery platforms
Abstract No: 15039

A RECOMBINANT CHIMERIC CEDAR VIRUS BASED PLATFORM AS A RAPID SURROGATE NEUTRALIZATION ASSAY FOR PATHOGENIC HENIPAVIRUSES

Moushimi Amaya[*1] ; Randy Yin[1] ; Lianying Yan[1] ; Viktoriya Borisevich[2 3] ; Antony Dimitrov[1] ; Robert Cross[2 3] ; Kimberly Bishop-Lilly[4] ; Thomas Geisbert[2 3] ; Christopher Broder[5]
[1]Department of Microbiology and Immunology/ Uniformed Services University / Henry M. Jackson Foundation for the Advancement of Military Medicine Inc./ United States, [2]Department of Microbiology and Immunology/ University of Texas Medical Branch/ United States, [3]Galveston National Laboratory/ Galveston National Laboratory, University of Texas Medical Branch/ United States, [4]Genomics and Bioinformatics Department/ Naval Medical Research Center/ United States, [5]Department of Microbiology and Immunology/ Uniformed Services University/ United States

Introduction and Objectives or Purpose

The pathogenic henipaviruses, Nipah virus (NiV) and Hendra virus (HeV), infect humans and animals with high rates of morbidity and mortality. The lack of vaccines and therapeutics approved for human use along with their highly pathogenic nature requires the handling of NiV and HeV at Biosafety level 4 (BSL-4) containment. Consequently, this can hamper certain tasks needed in henipavirus vaccine or antibody-based countermeasure development such as the analysis of neutralizing antibody responses. The principal henipavirus targets of neutralizing antibodies and vaccine immunogens are the attachment (G) glycoprotein and the fusion (F) glycoprotein that facilitate virus attachment and membrane fusion resulting in virus entry and infection.

Methods

Here, using an established reverse genetics platform for recombinant Cedar (rCedV), the F and G glycoprotein genes of the non-pathogenic rCedV henipavirus were replaced with those of NiV-Bangladesh (NiV-B) or HeV to generate replication competent non-reporter chimeric viruses (rCedV-NiV-B and rCedV-HeV) and reporter versions containing a green fluorescent protein (GFP) or a luciferase protein.

Results or Focus

The rCedV chimeras induced a robust Type I interferon response when compared to rCedV and use only ephrin-B2 and -B3 as entry receptors. Neutralization potencies of well-characterized cross-reactive NiV/HeV F/G specific monoclonal antibodies against rCedV-NiV-B-GFP and rCedV-HeV-GFP highly correlated with those measured using authentic NiV-B and HeV when tested by plaque reduction neutralization test (PRNT). A rapid high-throughput fluorescence reduction neutralization test (FRNT) was also established and was highly correlative with the PRNT. We also evaluated the applicability of the FRNT for analyzing G glycoprotein immunized animal sera.

Conclusion or Scope

Together, the results demonstrate the utility of the rCedV chimera platform as an authentic henipavirus-based surrogate neutralization assay for pathogenic henipaviruses that is rapid, cost-effective, and can be used outside BSL-4 containment.

Keywords: Cedar virus; Henipavirus; chimera; neutralization assay

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Diagnostic and discovery platforms
Abstract No: 15373

MULTIPLEX ASSAYS: AN ATTRACTIVE OPTION FOR SIMULTANEOUS SURVEILLANCE OF INFLUENZA, RESPIRATORY SYNCYTIAL VIRUS, AND SEVERE ACUTE RESPIRATORY SYNDROME CORONAVIRUS-2.

Narjis BOUKLI[1] ; Kimlay Chea[1] ; Leangyi Heng[1] ; Seangmai Keo[1] ; Kimhoung Sour[1] ; Sophea In[1] ; Panha Chhim[1] ; Bunthea Chhor[1] ; Lomor Kruy[1] ; Erik Karlsson[*1]
[1]Virology Unit/ Institut Pasteur du Cambodge/ Cambodia (□□□□□□□)

Introduction and Objectives or Purpose

Viral respiratory infections (VRI) ranked as the fourth leading cause of death globally in 2019. The COVID-19 pandemic has increased their share of responsibility in morbidity/mortality. Therefore, it is critical to utilize current surveillance systems such as the Global Influenza Surveillance and Response System (GISRS) to integrate SARS-CoV-2. Recently, several companies have marketed multiplex assays (MPA), which detect simultaneously SARS-CoV-2, Flu, and RSV in a single test. Virus detection, cost and testing burden are critical criteria to compare MPA to make a better choice.

Methods

We evaluated the PowerChek^{TM} SARS-CoV-2, Influenza A & B, RSV Multiplex Real time PCR Kit II (Kogene Biotech), Xpert Xpress SARS-CoV-2/Flu/RSV test (Cepheid) and TaqPath^{TM} COVID-19, FluA/B, RSV Combo Kit (ThermoFisher), in comparison with to individual standard WHO/US-CDC and FAO assays (Standards) currently used. Performance criteria were: (1) the sensitivity (limit of detection; LoD) assessed utilizing in-house isolates of SARS-CoV-2 (Wuhan, Alpha, Omicron variants), human seasonal influenza (A/H1N1, A/H3N2 and A/H5N1, B/Victoria and B/Yamagata) and avian influenza (A/H5N1, A/H5N8, A/H7N4, and A/H9N2); and (2) detection of SARS-CoV-2, influenza and RSV in residual clinical specimens collected under public health surveillance and response. Subsequently, we compared implementation parameters, and evaluated the costs.

Results or Focus

Utility for multiple subtypes, LoD, and detection of virus in clinical samples are comparable between the three MPA compared to Standards. Costs, testing burden, and implementation parameters differ and could influence choice depending on capacity and sustainability parameters.

Conclusion or Scope

VRI surveillance could benefit from the use of MPA. They represent a cost-effective solution to detect the return of influenza activity, alongside monitoring COVID-19 trends, and outbreaks of RSV. They can also serve to detect spillover of avian viruses, especially in resource-limited settings. Minimizing the delay to diagnostic and sparing human resources in laboratories is critical to meet the challenging objectives of pandemic response.

Keywords: SARS-CoV-2; Influenza viruses; Respiratory syncytial virus; COVID-19; multiplex real-time PCR; surveillance systems

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Focus on pandemic prone pathogens
Abstract No: 15208

Advancing One Health for Global Health Security: What does the evidence say?

Jakob Zinsstag*[1] [2]
[1]Epidemiology and Public Health/ Swiss Tropical and Public Health Institute/ Switzerland (Schweiz), [2]Faculty of Science/ University of Basel/ Switzerland (Schweiz)

Introduction and Objectives or Purpose

In this work, we review the contributions of human-animal-environmental (ONE-HEALTH [OH]) approaches to improving global health security (GHS) across a range of health hazards and summarise contemporary evidence of incremental benefits of an OH approach. We assessed how OH approaches were reported to FAO, WOAH and WHO, within the respective monitoring and evaluation frameworks of the International Health Regulations (IHR, 2005) and the Performance of Veterinary Services (PVS). We reviewed OH theoretical foundations, methods and case studies. Examples from joint health services and infrastructure, surveillance-response, antimicrobial resistance (AMR) surveillance, food safety and food security, environmental hazards, water and sanitation, and zoonoses control clearly show incremental benefits of OH approaches.

Results or Focus

OH approaches appear to be most effective and sustainable in the prevention, preparedness and early detection/investigation of evolving risks/hazards and the evidence base for their application is strongest in the control of endemic and neglected tropical diseases. For benefits to be maximised and extended, improved One Health Operationalisation (OHO) is needed with strengthening of multisectoral coordination mechanisms at global, regional and national levels.

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Author collective:

Jakob Zinsstag[1,2], Andrea Kaiser-Grolimund[1,2], Kathrin Heitz-Tokpa[7], Rajesh Sreedharan[3], Juan Lubroth[4], François Caya[5], Matthew Stone[5a], Hannah Brown[6], Bassirou Bonfoh[7], Emily Dobell[8], Dilys Morgan[8], Nusrat Homaira[9], Richard Kock[10], Jan Hattendorf[1,2], Lisa Crump[1,2], Stephanie Mauti[1,2], Victor del Rio Vilas[12], Sohel Saikat[3], Alimuddin Zumla[11], David Heymann[,12,13], Osman Dar[12] Stephane de la Rocque[3]

Institutional Affiliations:

[1]Swiss Tropical and Public Health Institute

[2]University of Basel, Switzerland

[3]World Health Organization

[4]Lubroth One Health Consultancies, Italy

[5]World Organisation for Animal Health

[5a]Spade Solutions, New Zealand

[6]Durham University, United Kingdom

[7]Centre Suisse de Recherches Scientifiques en Côte d'Ivoire

[8]Public Health England

[9]University of New South Wales, Australia

[10]Royal Veterinary College, United Kingdom

[11] University College London, United Kingdom.

[12]Chatham House, United Kingdom

[13]London School of Hygiene & Tropical Medicine,

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Focus on pandemic prone pathogens
Abstract No: 15223

Global epidemiology of animal influenza infections

Michael Ward[*1] ; ZhiJie Zhang[2] ; Jiaqi Huang[2] ; Shuang Xiao[2]
[1]Sydney School of Veterinary Science/ The University of Sydney/ Australia, [2]School of Public Health, Department of Epidemiology and Biostatistics/ Fudan University/ China (□□)

Introduction and Objectives or Purpose

Influenza virus, with a global distribution, diverse animal host range and multiple virus subtypes, has caused several pandemics. To better prepare for the emergence of new subtypes and the possible threat of the next pandemic, the global status of animal influenza needs to be defined and documented. Here we create a global and comprehensive database of animal influenza events and present key epidemiological features.

Methods

We created a global database of animal influenza events by an exhaustive search of the scientific and primary literature on animal influenza-related events, using systematic review methodology. The temporal, spatial and host distribution of animal influenza and the diversity of influenza subtypes in different regions were analyzed.

Results or Focus

A total of 70,473 records and 4,712 events of animal influenza throughout the world were identified from the databases searched. Events involving subtypes H5N2, H7N7, and H7N9 were relatively constant, with a slow upward trend during the past decade. Asia was the region with the most clusters of events. Poultry was the main host reported in Asia and Africa, and wild birds in Europe and North America. We found that wild birds carried a very rich array of virus subtypes, a warning for the possible generation of reassortment viruses with pandemic potential.

Conclusion or Scope

Our database provides a comprehensive overview of the current status of animal influenza events throughout the world. Influenza surveillance should be strengthened in some countries and regions to prevent the emergence of new subtypes. Importantly, improvement of the global influenza surveillance system and sharing of surveillance data is very much needed to predict the next pandemic.

Acknowledgement
Funding provided by a Univerdity of Sydney - Fudan University partnership award is acknowledged.

Keywords: Animal influenza; Spatio-temporal distribution; Virus subtypes; Influenza surveillance; Systematic review.

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Focus on pandemic prone pathogens
Abstract No: 15380

The One Health integrated surveillance system reveals the growth of Rift Valley fever outbreaks in Sudan

Ayman Ahmed*[1] ; Jakob Zinsstag[2]
[1]Clinical Pathology & Immunology / Institute of Endemic Diseases, University of Khartoum/ Sudan, [2]Epidemiology and Public Health/ Swiss Tropical and Public Health Institute (Swiss TPH)/ Switzerland (Schweiz)

Introduction and Objectives or Purpose

Rift Valley fever (RVF) is an arboviral disease caused by RVF virus (RVFV; genus Phlebovirus, family Phenuiviridae) and several species of mosquitoes are involved in the transmission of RVF. This study, aims to investigate the magnitude and spread of RVF outbreak in Sudan in 2020. RVF is endemic in Sudan; however, outbreaks of RVF are commonly occur in the central and southern region of the country.

Methods

Following the unusual emergence of RVF cases in Northern State, both alert and active surveillance were initiated throughout the country. Using the well-established clinical case-definition, we collected blood samples from suspected cases and sent them to the National Public Health Laboratory for molecular analysis. Following a One Health strategy, in addition to coordinating with the animal surveillance, we tested mosquito pools for RVF using qPCR.

Results or Focus

This study reports the first outbreak of RVF in Northern State. About 2225 cases and 56 fatalities from RVF were confirmed among humans, the majority of them (99%) were reported from the Northern State, however, infections were also confirmed in East Darfur, Kassala, Khartoum, River Nile, and West Kordofan. Additionally, around 2,000 deaths and/or abortions were reported among domestic animals, including cattle, goats, and sheep. Furthermore, three pools of Culex mosquitoes were tested positive for the presence of RVF.

Conclusion or Scope

This is the first study to implement an integrated One Health surveillance and response system to investigate in Sudan. Outbreaks of RVF were more confined in the central and southern regions of the country; however, here we report an alarming shift in the geographical distribution of RVF outbreaks in the country. We identified that the major risk factors for this change in disease epidemiology were socioeconomic, political instability, and climate change factors. Further entomological investigations are warranted to confirm the main vector of RVF in Sudan.

Keywords: Rift Valley fever; Outbreaks; Pandemic; Integrated One Health Strategy; Global Health Security; Food Security

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15051

MONKEYPOX - A DESCRIPTIVE ANALYSIS OF OUTBREAKS IN NIGERIA 2017-2022

Chinenye Emelife*[1] ; Zirra Abraham[2] ; Ahmed Nasir[1] ; Robinson Nnaji[1] ; Jenom Danjuma[3] ; Bola Lawal[1] ; Odianosen Ehiakhamen[1] ; Oyeladun Okunromade[1] ; Elsie Ilori[1] ; Ifedayo Adetifa[1]
[1]Surveillance and Epidemiology/ Nigeria Centre for Disease Control/ Nigeria, [2]Emergency Centre for Transboundary Animal Diseases (ECTAD)/ Food and Agricultural Organization (FAO)/ Nigeria, [3]Prevent Epidemic/ Resolve to Save Lives / Nigeria

Introduction and Objectives or Purpose

Monkeypox is a zoonotic disease caused by Orthopoxvirus genus of the Poxviridae family, characterized by smallpox-like symptoms. It is endemic in West and Central Africa. In Nigeria prior to 2017, the last reported case of Monkeypox was in 1978. This study aims to describe the trend and distribution of Monkeypox cases in Nigeria from 2017 – 2022.

Methods

Descriptive analysis of secondary data from national situational reports for Monkeypox were carried out using Epi Info and QGIS to determine trends and spatial distribution of Monkeypox cases across Nigeria.

Results or Focus

A total of 383 cases were reported in Nigeria, of which 88 (23.0%) in 2017, 49 (12.8%) in 2018, 47 (12.3%) in 2019, 8 (2.1%) in 2020, 34 (8.9%) in 2021 and 157 (40.0%) in 2022. Prior to 2022, outbreaks have been reported in 20 (54.1%) states out of the 36 states and the Federal Capital Territory across 4 geopolitical zones (South-east, South-south, South-west and North-central). However, in 2022 cases were reported in 10 additional states from North-east, South-west, North-central, and North-west geopolitical zones. About 65% of the total cases were reported among individuals between the ages of 21 – 40 years. The male to female ratio is 1:9. In 2017, cases peaked in October while in 2022 there has been a continued rise in the number of cases since May. The case fatality rate from 2017 to 2022 is 3.1%.

Conclusion or Scope

Nigeria has continuously experienced sustained monkeypox outbreaks since 2017. The increased number of cases observed in May and around September of 2017 and 2022 respectively is likely due to heightened surveillance and increased interaction at the human-animal interface due to farming activities. South-south zone of the country accounts for the highest-burden of Monkeypox. Enhanced surveillance at the human-animal-environment-wildlife interface and further research is required to improve early detection and effective response.

Keywords: Monkeypox, Outbreak, Nigeria.

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15171

Adoption of an implementation science approach to achieve zero COVID-19 transmissions in staff at a large community care facility in Singapore during the COVID-19 pandemic

WEIEN CHOW*[1] ; Elaine Lum[2] ; Arif Tyebally[3] ; Sze Ling Chan[4] ; Lai Chee Lee[5] ; Moi Lin Ling[5] ; Hiang Khoon Tan[5] ; Nigel CK Tan [6]
[1]Changi General Hospital/ Singapore Health Services/ Singapore, [2]Health Services & Systems Research/ Duke-NUS Medical School/ Singapore, [3]KK Women's and Children's Hospital/ Singapore Health Services/ Singapore, [4]Health Services Research Centre/ Singapore Health Services/ Singapore, [5]Singapore General Hospital/ Singapore Health Services/ Singapore, [6]National Neuroscience Institute / Singapore Health Services/ Singapore

Introduction and Objectives or Purpose

During the height of the COVID-19 pandemic in Singapore in 2019, a 3200-bed medical facility was setup at the Singapore Expo convention centre to isolate and treat patients with mild COVID-19 infection. The unprecedented scale of the pandemic response led to many uncertainties and frequent changes to the pandemic response system and processes. The objective of this study is to use the implementation science approach to elicit critical factors which enabled zero COVID-19 transmissions to healthcare staff at the community care facility.

Methods

Retrospective analysis was conducted using the integrated Promoting Action on Research Implementation in Health Services (i-PARIHS) framework. The infection prevention control innovation at the community care facility comprised five key elements: physical environment, work practices, tools and technology, staff training, and audits. Contextual assessment was conducted for baseline and 100th day of operations. Actions taken to improve scores between these timepoints were mapped against the Expert Recommendations for Implementing Change (ERIC) tool to surface key implementation strategies.

Results or Focus

Positive shifts were observed in all constructs of the i-PARIHS framework, between baseline and 100th day. The largest shifts were in work practices, tools and technology, and staff training. Key implementation strategies used included: rapid Plan-Do-Study-Act (PDSA) cycles, identifying champions, team building, creating a culture of collaborative learning, multi-disciplinary teamwork, transparency in communications and decision-making, and skilful facilitation.

Conclusion or Scope

The adoption of the implementation science approach was found to be relevant and useful to comprehensively capture the interventions, strategies and lessons learnt to achieve zero COVID-19 transmissions in staff during a pandemic. The implementation science approach may be used to inform preparedness planning of future pandemics and improve overall outbreak response.

Acknowledgement

We would like to acknowledge the close collaboration and partnership between Singapore Health Services and our external partners and resilience of our healthcare staff and patients in overcoming the COVID-19 pandemic.

Keywords: COVID-19; implementation science; infection prevention control; pandemics

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15365

ENHANCING EPIDEMIC PREPAREDNESS THROUGH COMMUNITY BASED SURVEILLANCE IN KENYA.

Naomi Ngaruiya*[1] ; Vivian Jepkorir[1]
[1]Health (Human and Animal health)/ Kenya Red Cross Society/ Kenya

Introduction and Objectives or Purpose

Communities play key role in diseases outbreak prevention, detection and response. Red Cross epidemic and pandemic preparedness program funded by IFRC and USAID empowers communites to take early action to control diseases. The program leverages on One Health approach to establish community-based surveillance (CBS) as a preparedness model yielding early detection and action to halt outbreaks of Zoonotic diseases to human at the onset . This paper reports on the mid-stage CBS implementation experience and results since September 2019 to September 2021 in four counties in Kenya and the recommendations for supporting the CBS.

Methods

890 Community Health Volunteers (CHVs) and Community Disease Reporters (CDRs) from Health and Veterinary departments were trained on simple Community case definitions to detect potential epidemic alerts and report immediately by mobile applications. The receiving supervisor cross-checks the alert and triggers real-time response actions which are conducted collaboratively through one health platform.

Results or Focus

To improve health literacy on zoonotic diseases and other epidemic prone diseases, CHVs and CDR reached 70,000 households, 769 schools and 200 groups with preventive health messages. To date 702 priority disease alerts have been sent via SMS by CHVs and CDRs out of which 500 were animal alerts and 202 human alerts. The average accuracy of volunteers to identify alerts matching community case definitions is 51% . Alerts were detected and authorities notified within 24 hours at an average of 94%. Challenges experienced are securing free SMS channels for alerts, timely response activities and integration of CBS to the national Disease surveillance systems in Ministry of Health and Veterinary.

Conclusion or Scope

Community engagement in prevention, detection and response actions and one health collaboartions are important for effective control of large scale dieases outbreak. Communities are central change agents in preventing epidemics and pandemics.

IFRC and USAID technical support.

Keywords: One Health Approach, Community Based Surveillance , Community Health Volunteers

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Sharing of pathogens, resources and data
Abstract No: 15037

FROM THEORETICAL TO TECHNICAL: LESSONS LEARNED FROM ASSESSMENT OF ZOONOTIC SARS-COV-2 COORDINATED SURVEILLANCE IN THE UNITED STATES

Ria Ghai[*1] ; Gunel Ismayilova[2] ; Amanda Liew[1] ; Jane Rooney[3] ; Laura Miles[3] ; Oriana Beemer[3] ; Junxia Song[2] ; Sean Shadomy[1] ; Casey Barton Behravesh[1]
[1]One Health Office/ U.S. Centers for Disease Control and Prevention (CDC)/ United States, [2]Animal Health Programme/ Food and Agriculture Organization of the United Nations/ Italy (Italia), [3]Animal and Plant Health Inspection Services (APHIS) / U.S. Department of Agriculture (USDA)/ United States

Introduction and Objectives or Purpose

Siloing surveillance activities and infrastructure within specific sectors can limit our ability to respond to zoonotic and emerging disease threats. Coordinated surveillance using a One Health approach has been proposed to harmonize activities across sectors by optimizing data collection and sharing. The Surveillance and Information Sharing Operational Tool (SIS OT) is a coordinated surveillance tool that we used to retrospectively assess the capacity of the coordinated surveillance system for zoonotic SARS-CoV-2 events in the United States.

Methods

In March 2020, the U.S. Centers for Disease Control and Prevention (CDC) and the U.S. Department of Agriculture (USDA) began developing coordinated surveillance for SARS-CoV-2. As part of infrastructure development, in early 2021, CDC launched an online One Health surveillance system that allows state and local One Health partners to input case data in real-time, accessible by the jurisdiction and federal agencies. We assessed overall national surveillance for zoonotic SARS-CoV-2 using the SIS OT's framework of 32 capacity-building activities, which assigns a level for each activity (Level 1 – Baseline; Level 2 – Intermediate, Level 3 – Advanced, or Complete).

Results or Focus

Since the beginning of the pandemic, >450 One Health SARS-CoV-2 case investigations and >2000 consultations have been reported. SIS OT assessment identified lower capacity scores (Level 1 and 2) on 12 activities (37.5%) and higher capacity scores (Level 3 or Complete) on 20 activities (62.5%). Lower capacity scores corresponded with lack of formalized assessments and evaluation plans necessitated by the urgency with which the infrastructure was built. Higher scores corresponded to multisectoral data harmonization, sharing, and security.

Conclusion or Scope

Important successes identified through assessment of the US's surveillance infrastructure for zoonotic SARS-CoV-2 include the strength of One Health coordination occurring across all jurisdictional levels, and the development of plans and systems that can be rapidly applied to other emerging zoonotic diseases in the future.

Keywords: coordinated surveillance; operational tools; SARS-CoV-2; One Health assessment

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Sharing of pathogens, resources and data
Abstract No: 15128

Landscape analysis of wildlife stakeholders and information sharing to operationalize One Health

Gisella Stephanie De Oliveira Dias da Silva *1 ; Gisela Vasconcelos Gioia 1 ; Racine N'Diaye 2 ; Willington Bessong Ojong 3 ; Pawin Padungtod4 ; Frank Mubiru3 ; VanThu Nhu4 ; Alpha Camara2 ; Emma Gardner1 ; Sophie Von Dobschuetz1
1ECTAD/ Food and Agriculture Organization of the United Nations / Italy (Italia), 2ECTAD/ Food and Agriculture Organization of the United Nations / , 3ECTAD/ Food and Agriculture Organization of the United Nations / Uganda, 4ECTAD/ Food and Agriculture Organization of the United Nations/ Vietnam (Việt Nam)

Introduction and Objectives or Purpose

To provide a baseline assessment of existing gaps in surveillance and information sharing at the wildlife-livestock-human interface, and to create dialogue and plans to strengthen the collaboration between natural resources, animal and public health sectors, the Food and Agriculture Organization of the United Nations (FAO) piloted a survey in Guinea, Uganda, and Vietnam to map existing surveillance and monitoring activities in wildlife, identify implementing institutions and clarify current data sharing mechanisms with government entities and One Health (OH) Platforms.

Methods

A questionnaire covering methodology, objectives, geographical level, and time period of activities conducted by institutions engaged in surveillance and monitoring of wild mammals and birds was hosted on an online platform and shared with respondents identified by FAO country teams.

Results or Focus

Thirty-one representatives from 28 institutions replied. Fourteen institutions collected data on farming and trade of wild mammals and birds, ten institutions collected data on distribution and movement, 13 institutions collected data on health and infectious diseases, six institutions were involved in outbreak investigations, and 11 institutions provided training or developed guidelines related to wildlife. In total, the survey registered 131 activities. Data from 54 activities were shared with the government by 17 institutions, while five respondents reported limitations in information sharing, the lack of convenient sharing mechanisms being the main constraint.

Conclusion or Scope

Since several wildlife surveillance and monitoring activities are ongoing in a country, much data is readily available, providing ample opportunity to collaborate and leverage existing capacities of national and sub-national monitoring and disease surveillance in wildlife. The survey identified an eminent need to facilitate information-sharing mechanisms.

The national OH Platform can play an important role in leveraging available resources and capacities for surveillance of wildlife, request data to enable evidence-based decision making, and invite relevant institutions to contribute to the development of joint risk assessments, surveillance planning and disease control.

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Clinical, epidemiology and molecular drivers of disease susceptibility
Abstract No: 14917

Assessing acute febrile diseases of unknown cause in Africa through the ANDEMIA network

Adriano Mendes*[1] ; Kgothatso Meno[1] ; Caitlin MacIntyre[1] ; Clarence Yah[1] ; Marietjie Venter
[1]Department of Molecular Virology/ University of Pretoria/ South Africa

Introduction and Objectives or Purpose

The African network for improved diagnostics, epidemiology and management of common infectious agents (ANDEMIA) is multi-country network targeting three syndromes commonly caused by infectious diseases within four African countries.

Methods

In order to investigate the aetiology and epidemiology of febrile and neurological disease in South Africa, we enrolled cases of fever or history of fever with neurological symptoms from sentinel hospitals in the Pretoria and Mpumalanga provinces. Health control cases were also enrolled. Whole blood and cerebrospinal fluid (CSF) samples from cases and controls were screened with a multiplex-PCR based protocol targeting 30 common, zoonotic and arboviral pathogens called the fever chip.

Results or Focus

Active surveillance has been on-going since 2018 and to date 1193 febrile and/or neurological disease patients have been enrolled and 464 healthy controls. The case definition ensured that only patients with acute febrile disease were enrolled and symptoms ranged from exclusively fever to fever with accompanying neurological symptoms such as seizures, meningitis and encephalitis. Approximately 16% of febrile patients in site 1 (Pretoria) were positive versus 6% amongst controls. Approximately 22% of cases were positive in site 2 (Mpumalanga) hospitals with only 3.5% in the controls. Epstein-Barr virus (EBV) accounted for 75% and 90% of the cases from each site. Over and above molecular testing, IgM serology was employed in two pilot studies in order to determine if a greater number of positive cases could be identified. Both Sindbis virus IgM and West Nile virus IgM antibodies were detected in PCR negative fever cases.

Conclusion or Scope

The ANDEMIA study has thus far shown that many children presenting with febrile and neurological signs are EBV positive. Over and above EBV and despite multiplex PCR testing, many febrile and neurological cases remain unresolved and may require broader serological testing in order to address the cause of disease.

Keywords: ANDEMIA; fever; neurological; surveillance;

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Clinical, epidemiology and molecular drivers of disease susceptibility
Abstract No: 14955

THE INCIDENCE OF SINDBIS VIRUS IN HORSES WITH FEBRILE AND NEUROLOGICAL SIGNS AND MOLECULAR CHARACTERISATION OF STRAINS IN SOUTH AFRICA.

Kgothatso Meno*[1] ; Milehna Guarido[2] ; Isabel Fourie[2] ; Adriano Mendes[1] ; Marietjie Venter[1]
[1]Medical Virology/ University of Pretoria/ South Africa, [2]Medical Virology/ University of Pretoria/ South Africa

Introduction and Objectives or Purpose

Sindbis virus (SINV), is an alphavirus with worldwide distribution but limited genetic data on strains circulating in Africa. The incidence of SINV in horses with febrile and neurological signs during an outbreak in 2017, was investigated by IgM serology. SINV strains present in South Africa were investigated by sequencing PCR positive animal and mosquitoes detected between 2008-2020.

Methods

RNA extraction was performed on clinical samples from animals, and 15 positive mosquito pools in the Northern parts of South Africa. A nested RT-PCR of the nsP4 and E2 glycoprotein was used to amplify positive samples for Sanger sequencing. Virus isolation followed by next generation sequencing using the Illumina® iSeqTM, were performed for the positive samples. A total of 155 horse specimens collected during the arbovirus season of 2017 were screened using an IgM immunofluorescence assay and confirmed with a neutralization assay.

Results or Focus

A total of 29/2748 animals tested positive for SINV using the nsP4 in the clinical samples, of which 45.0% died. A total of 34 nsP4 sequences obtained from animals and mosquitoes grouped with other African isolates and historical South African strains. A total of six E2 protein sequences were obtained. Four 2014 mosquito pools clustered with a Kenya 2013 strain, whilst 2018 (mosquito) and 2020 (horse) sequences clustered with the Saudi Arabia 1980 strains in genotype IC. Complete SINV genomes were obtained for the same 2014 mosquito pools which clustered in genotype IA. SINV IgM was detected in 54/155 horse cases and 29/54 neutralized SINV. 30-40% IgM positive cases experienced ataxia, paresis, and there was statistical significance associated with recumbency.

Conclusion or Scope

This study confirmed that SINV strains identified in animals with neurological signs were similar to those present in local mosquitoes. Close genetic clustering with strains from Kenya and the Middle East suggest wide distribution of SINV likely by bird reservoirs.

Keywords: Sindbis virus; Febrile; Neurological; RT-PCR; Serology

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Clinical, epidemiology and molecular drivers of disease susceptibility
Abstract No: 14984

Predictors of Mortality among Middle East Respiratory Syndrome Coronavirus (MERS-CoV) patients globally (2017-2022): a retrospective cohort study

Paul Yonga*[1] ; Robert Rono[2]
[1]Infectious Diseases/ CA Medlynks Clinic and Laboratory/Fountain Health Care Hospital/ Kenya, [2]Epidemiology/ Baringo County Government/ Kenya

Introduction and Objectives or Purpose

The Middle East Respiratory Syndrome Coronavirus (MERS-CoV) is a significant clinical and public health concern due to its high case fatality rate. Current literature on the predictors has been from single centre studies, with minimal knowledge on the predictors of mortality amongst patients with MERS-CoV globally, hence the purpose of this study.

Methods

This was a retrospective cohort study amongst MERS-CoV cases reported to the World Health Organization via the Disease Outbreak Network and PROMED over a five-year period (2017-2022). Univariate and multivariate analyses were utilized to determine the predictors of mortality amongst the patients with MERS-CoV.

Results or Focus

618 patients were included in the final analysis with a male-to-female ratio of 3.3:1 (n=473). 11.7% (n=72) of the patients were health care workers and 94.3% (n=583) of the participants were cases reported in Saudi Arabia. 27.4% (n=169) of the participants were reported to have died. On multivariate analysis, the presence of comorbidities (aHR=2.19; 95% CI: 1.26-3.80), age equal to or above 60 years (aHR=1.77; 95% CI: 1.27-2.47), and age equal to or above 65 years (aHR=2.28; 95% CI: 1.65-3.14) were significant predictors of mortality.

Conclusion or Scope

The elderly (age above 60 years) and people with comorbidities are at significantly higher risk of mortality due to MERS-CoV. Hence, guidance, surveillance, and collaboration amongst human health and animal health practitioners globally are needed as one health in countries gains prominence.

Acknowledgement

We thank WHO and PROMED for availing these disaggregated data through the Disease Outbreak Network and email alerts.

Keywords: Mortality; MERS-CoV; Cohort

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Clinical, epidemiology and molecular drivers of disease susceptibility
Abstract No: 15021

Implications of Advanced Genomic Technologies to Combat the Prevalence of Zoonotic Infections in Developing Countries

Maryam Javed*[1]
[1]Institute of Biochemistry and Biotechnology/ University of veterinary and animal sciences/ Pakistan (پاکستان)

Introduction and Objectives or Purpose

Developing countries like Pakistan are facing rising concerns over prevalence of zoonotic infection at animal-human interface. As Pakistan is an agrarian country, so animal interaction is inevitable. Bovine tuberculosis (bTB) is a neglected endemic zoonosis, causing lot of mortalities every year. In a report from WHO, Pakistan is ranked fifth amongst the high burden countries in the world. Previous methods of controlling bTB, like vaccination, antibiotics, have raised the concern of animal product consumers regarding microbial resistance. Enhancing the genetic resistance is promising new alternate to combat bTB. Many of countries have opted this new approach and have reported useful data in cattle but very limited efforts have been put into the river buffaloes. River buffaloes of Indo-Pak region are world famous for their superior genetic potentials and inter-breed variations that provides substantial basis for identification of significant selection signatures.

Methods

Present research was planned to explore SLC11A1 gene in river buffalo which is known as natural resistance-associated macrophage protein 1. For its genetic characterization, blood was collected from tuberculin negative (n=267) and tuberculin positive (n=194) animals. DNA was extracted and Sanger's method of DNA sequencing was used. Significance of each variation was tested by Hardy Weinberg equilibrium ($P<0.05$). Association was performed by one way ANOVA.

Results or Focus

Sequence comparison of two groups provided a total of three variations. Results illustrated only one variation found significantly associated with better immunity against bTB. For purpose of some additional and supportive information phylogenetic analysis was also being performed by neighbor joining method with bootstrap value-1,000. Tree indicated that river buffaloes are in closest proximity to Bos taurus and its genetic distance from other species may also be seen in Figures provided.

Conclusion or Scope

Genetic markers identified in this study can be useful in future breeding selection programs against bTB resistance.

Acknowledgement

NA

Keywords: bTB; SLC11A1; Buffalo; Polymorphism; Association; Phylogenetic tree

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Clinical, epidemiology and molecular drivers of disease susceptibility
Abstract No: 15041

Pilot survey of cystic echinococcosis in Masaai livestock-keeping communities of Northern Tanzania

Francesca Tamarozzi[1] ; Tito Kibona[2] ; William A De Glanville[3] ; Tauta Mappi[2] ; Elly Adonikamu[4] ; Anande Salewi[4] ; Kennedy Misso[4] ; Adriano Casulli[5] ; Blandina T Mmbaga[2] ; Sarah Cleaveland[*3]
[1]Dept Infectious-Tropical Diseases and Parasitology/ IRCCS Sacro Cuore Don Calabria Hospital/ Italy (Italia), [2]./ Kilimanjaro Clinical Research Institute/ Tanzania, United Republic of, [3]Institute of Biodiversity, Animal Health & Comparative Medicine/ University of Glasgow/ United Kingdom, [4]./ Kilimanjaro Christian Medical Centre/ Tanzania, United Republic of, [5]Dipartimento Malattie infettive/ Istituto Superiore di Sanità/ Italy (Italia)

Introduction and Objectives or Purpose

Maasai communities of northern Tanzania are suffering from a very high prevalence of cerebral coenurosis (Taenia multiceps/Coenurus cerebralis), causing high mortality in small ruminants. Given the close similarity between the life cycle of T. multiceps and Echinococcus granulosus sensu lato (causing cystic echinococcosis [CE] in humans), this raises concerns about an increased risk of human CE. We aimed to estimate the prevalence of human abdominal CE and livestock infection in Maasai communities of northern Tanzania.

Methods

Human CE was diagnosed by abdominal ultrasound in 5 communities of Longido and Ngorongoro districts and through inspection of ruminants in local abattoirs. DNA was extracted from 1 cyst/animal, prioritizing hepatic cysts. Molecular identification was performed using PCR, followed by RFLP, Multiplex-PCR, and sequencing of COX1 PCR product of non-E. granulosus s.l. samples.

Results or Focus

Ultrasound was performed on 823 voluteers. Six hepatic CE cases (3 with active cysts), were diagnosed in Ngorongoro (1.3% prevalence). Of the 697 ruminants inspected, 34.4% had parasitic cysts. Molecular identification, achieved for 140/219 cysts, identified Taenia hydatigena in 48.6% and E. granulosus s.l. in 51.4%: E. granulosus sensu stricto (G1-G3) in 87.5% cases; E. ortleppi (G5) in 9.7%, E. canadensis (G6-10) in 1 cyst. E. granulosus s.l. was identified in livestock from both Longido and Ngorongoro (35.3% and 91.2% of genotyped cysts, respectively). The 3 human active cysts removed surgically were G1-G3.

Conclusion or Scope

Multiple species/genotypes of E. granulosus s.l. are circulating in Maasai communities of northern Tanzania. More precise estimation of prevalence of human CE in this area and understanding of specific risk factors for CE among communities is needed. Interventions targeting transmission routes common to both E. granulosus s.l. and T. multicepswould have dual benefits for preventing both human and livestock disease.

Acknowledgement
Prof Venance Maro (KCMC, Tanzania), Dr Azzurra Santoro and Federica Santolamazza (ISS, Italy), Mr Fadhili, Mr Amani (KCRC, Tanzania)

Keywords: Echinococcus granulosus sensu lato; cystic echinococcosis; Maasai communities of northern Tanzania; prevalence; genotypes; ultrasound

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Clinical, epidemiology and molecular drivers of disease susceptibility
Abstract No: 15169

Situation analysis of Kyasanur Forest Disease in Kannangi of Tirthahalli taluk, Shivamogga District, Karnataka, India, January

Mohamed Jainul Azarudeen*[1] ; Vaisakh TP[1] ; Sushma Choudhury; Tanzin Dikid[1] ; Meera Dhuria[1] ; SK Jain[1] ; Sujeet kumar Singh[1] ; Kiran SK
[1]Epidemiology/ National Centre for Disease Control/ India

Introduction and Objectives or Purpose

Kyasanur Forest Disease(KFD) is a tick-borne viral haemorrhagic fever, endemic in central districts of Karnataka state of India. Tirthahalli Taluk, Shivamogga district recorded highest KFD incidence for 2014-19. In January 2020, Kannangi area of Tirthahalli reported clustering of laboratory confirmed(by RT-PCR) KFD cases. We conducted a situational analysis; assessed knowledge, practices and preparedness for prevention of KFD in Kannangi.

Methods

We defined KFD case as “acute onset fever with headache /myalgia /extreme weakness /nausea / vomiting /diarrhea /pain abdomen /neurological/hemorrhagic manifestations in a person residing within 2 kms of monkey death or lab confirmed KFD in Kannangi from 1 December 2019 to 28 January 2020. We did house-to-house case search; We studied knowledge, practices and vaccination status by interviewing one person per household(case from case household and eldest family member from non-case household). We assessed health facility preparedness for KFD prevention and control using semi-structured questionnaires and record reviews.

Results or Focus

We surveyed 196 households, found 10 cases, four monkey deaths. Median age of cases was 63.5 years(range:16-72), seven were males, three were confirmed by RT-PCR. Attack rate was 15/1000(10/674) population, Six(60%) believe KFD spreads through tick bite and had awareness about prevention measures. Five(50%) visited forest in last two months four spent >3 hours collecting dry leaf in forest, eight(80%) reported presence of ticks on their livestock. All households had domestic pets and livestock near their premises, 53%(258/674) received two doses and 73%(489/674) one dose of KFD vaccine. Median distance of affected villages to health facility was 5 kms. We found deficiency of human resource, cold chain and records

Conclusion or Scope

Rise in KFD in Kannangi likely due to lack of awareness, non-vaccination, proximity to livestock infested with ticks and deficiency in health services. We recommend to create awareness on disease transmission, vaccination and treat livestock for infestation.

Keywords: Tick bites, monkey fever, KFD, KFD Vaccine

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Clinical, epidemiology and molecular drivers of disease susceptibility
Abstract No: 15290

Participatory survey of risk factors and pathways for Rift Valley fever in pastoral and agropastoral communities of Uganda.

Dan Tumusiime*[1 2 3] ; Ard Nijhof[1] ; Martin Groschup[4] ; Julius Lutwama[5] ; Kristina Roesel[6] ; Bernard Bett[6]
[1]Dahlem Research School/ Freie Universität Berlin/ Germany (Deutschland), [2]Animal and Human Health Program/ International Livestock Research Institute/ Uganda, [3]Animal Health/ Ministry of Agriculture, Animal Industry and Fisheries/ Uganda, [4]Institute of Novel and Emerging Infectious Diseases/ Friedrich-Loeffler-Institut / Germany (Deutschland), [5]Arbovirology/ Uganda Virus Research Institute/ Uganda, [6]Animal and Human Health/ International Livestock Research Institute/ Kenya

Introduction and Objectives or Purpose

Rift Valley fever (RVF) is a mosquito-borne viral zoonosis caused by Rift Valley fever virus (RVFv) of the order Bunyavirales, family Phenuiviridae and genus Phlebovirus.

In Uganda, RVF control measures have not adequately included local community knowledge on predisposing risk factors and disease identification.

Purpose: To assess community knowledge on RVF identification and risk factors and the possibility of integrating it into an early warning system and strategies for veterinary and public health service delivery in Uganda.

Methods

Participatory Epidemiology survey was conducted using semi-structured interviews, matrix scoring for clinical manifestation of RVF and other livestock diseases; Proportional piling to assess for risk factors influencing RVF occurrence; disease calendar; Qualitative ranking to assess RVFv risk pathways; Cattle serosurvey.

Results or Focus

-RVF was ranked the eleventh most important cattle disease with a relative burden of 2.8% among other cattle diseases. Pastoralists' agreement on the relative burdens of these diseases was moderately strong ($W = 0.4108$) and statistically significant ($p<0.001$).

-Perceived risk factors: infected mosquitoes (21.7%), excessive rainfall (13.4%), flood prone areas (12.9%), bushlands (11.9%) and livestock movement (9.5%). Others- Proximity to water bodies (9.3%), handling abortus material (6.9%), high livestock density (5.6%), rice and banana fields (5.5%) and proximity to wildlife (3.2%).

-Participants exhibited good knowledge of recognizing clinical signs of cattle diseases including to a limited extent, RVF, in their herds

-Perceived risk pathways for the entry of RVFv in the four districts were via infected mosquitoes, infected domestic ruminants, infected aborted foetuses and fluids and infected wild animals -Cattle seroprevalence: 22.1%-62.4%.

Conclusion or Scope

PE approach is key in surveillance of livestock diseases in remote pastoral communities. Findings are central for designing an effective national RVF surveillance system.

Acknowledgement

BMZ, CGIAR, DTRA, Cattle farmers in the study districts and staff of Butebo, Napak, Lyantonde and Isingiro district local governments.

Keywords: Participatory survey; Rift Valley fever; Pastoralist knowledge; Risk factor; Risk pathway

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Clinical, epidemiology and molecular drivers of disease susceptibility
Abstract No: 15319

National sero-prevalence and spatial distribution of Brucella spp. in Kenya

James Akoko*[1] ; Athman Mwatondo[1 2] ; Lillian Wambua[1] ; Richard Nyamota[1] ; Mathew Muturi[1 2] ; John Gachohi[3] ; Samson Konongoi[4] ; Bernard Bett[1]
[1]Animal and Human Health/ International Livestock Research Institute/ Kenya, [2]Epidemiology/ Zoonotic Disease Unit/ Kenya, [3]Global Health Programme, Nairobi, Kenya/ Washington State University/ Kenya, [4]Epidemiology/ Kenya Medical Research Intitute/ Kenya

Introduction and Objectives or Purpose

Brucellosis, caused by several species of Brucella, is a global zoonotic disease of high economic and public health importance. The disease is endemic in Kenya but the national burden on livestock is poorly understood. We conducted a study to establish the national prevalence and develop a risk map for Brucella spp. in Kenya.

Methods

We randomly generated 265 geolocations across the country, based on agroecological zones and livestock populations. The closest herd to selected geolocation was identified for consenting. Up to 25 cattle were sampled per herd, followed by the administration of a structured questionnaire. 6593 cattle samples were tested for Brucella immunoglobulin G (IgG) antibodies using an Enzyme-linked immunosorbent assay (ELISA). The potential risk factors were assessed using a random-effects binary logistic regression model with a herd as the random effect.

Results or Focus

The national prevalence of brucellosis was 6.8 % (95% CI 6.2-7.4), with varied spatial distribution between the different ecological zones (P-value = <0.0001) and herd sizes (P-value = <0.0001). The odds of seropositivity were significantly higher in female (OR=1.3, 95% CI 1.0-1.8) and adult (OR=2.4, 95% CI 1.7-3.5) animals compared to males and calves. Similarly, adult female animals with a history of abortion (OR= 2.2, 95% CI 1.3-3.6), and those with multiple syndromes of brucellosis (OR = 2.8, 95% CI 1.2-6.6) had higher seropositivity compared to those without. At the herd level, the risk of transmission was increased by having animals with a history of abortion (OR of 2.4; 95% CI: 1.2-4.6), the birth of weak calves (OR of 4.3; 95% CI: 1.6-11.8) and swollen testis (OR=4.4; 95% CI 1.1-17.8).

Conclusion or Scope

Brucella seroprevalence was higher in arid and semi-arid ecological zones, where pastoralism is practiced. This study provides baseline epidemiological data for the development of targeted control programs for brucellosis in Kenya.

Acknowledgement
NA

Keywords: Brucellosis, zoonotic disease, epidemiology, Brucella, Kenya

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Clinical, epidemiology and molecular drivers of disease susceptibility
Abstract No: 15413

Molecular dynamics changes of rotavirus genotypes and its recombination with animal strains among pediatric patients in Indonesia during 2015-2020

Laura Navika Yamani[*1 2 3] ; Rury Mega Wahyuni[3] ; Takako Utsumi[3 4] ; Zayyin Dinana[2 3] ; Anisa Lailatul Fitria[3] ; Aussie Tahta Maharani[3] ; Juniatuti Juniastuti[2 3 5] ; Soetjipto Soetjipto[3] ; Maria Inge Lusida[2 3 5] ; Ikuo Shoji[4]
[1]Faculty of Public Health, Department of Epidemiology/ Universitas Airlangga/ Indonesia, [2]Research Center on Global Emerging and Re-emerging Infectious Diseases, Institute of Tropical Disease/ Universitas Airlangga/ Indonesia, [3]Indonesia-Japan Collaborative Research Center for Emerging and Re-emerging Infectious Diseases, Institute of Tropical Disease/ Universitas Airlangga/ Indonesia, [4]Center for Infectious Diseases, Kobe University Graduate School of Medicine, Kobe, Japan/ Kobe University/ Japan (□□), [5]Faculty of Medicine, Department of Microbiology/ Universitas Airlangga/ Indonesia

Introduction and Objectives or Purpose

Group A rotavirus (RVA) is the most important cause of severe gastroenteritis in children worldwide, and effective RVA vaccines have been introduced in many countries. Here, we performed a molecular epidemiological analysis of RVA infection in pediatric patients in Indonesia, 2015-2020.

Methods

The total of 700 stool samples were collected and none of the patients in this cohort had been immunized with an RVA vaccine. Then, G-P combinations of RVA genotypes in all samples were analyzed using multiplex reverse transcription-PCR (RT-PCR).

Results or Focus

The common G-P combination of RVA genotypes detected in Indonesia were all equine-like G3P[8] and G3P[6] in 2015-2017, human G1P[8], G1P[6], G3P[8], and G3P[6] in 2018, equine-like G3P[8] and G3P[6]; human G1P[8], G1P[6], G3P[8], G3P[6], and G9P[8] in 2019, and equine-like G3P[6]; human G1P[8], G1P[6], G3P[8], G3P[6], G9P[8], and G2[8] in 2020. Equine-like G3 rotavirus originated in Australia and is a recombinant inter-genotype between human and equine RVA strains. In addition, several sequences of RVA isolated from pediatric patients were found in a gene segment of bovine rotavirus strains, such as the NSP4 gene. Rotavirus is a zoonotic disease with many gene segment, that are VP1-VP4, VP6, VP7 and NSP1-NSP5 genes, Therefore, it is likely to generate genetic recombination within and between genotypes and even between human and animal strains. Interestingly, the equine-like strains were exclusively detected again eventhough they were completely replaced by a typical human genotype (G1 and G3).

Conclusion or Scope

The dynamic changes in RVA genotypes from equine-like G3 to typical human G1/G3 in Indonesia can occur even in the country with low RVA vaccine coverage rate. The mechanism of the dynamic changes in RVA genotypes needs to be explored.

Acknowledgement

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Keywords: rotavirus, equine-like G3 strain, bovine-like strain, typical human genotype, genotypes change, Indonesia

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 14791

Human behavior strategies to mitigate zoonotic spillover risk

Hongying Li[*1] ; Libao Zhang[2] ; Guangjian Zhu[1] ; Shiyue Li[3] ; Emma Mendelsohn[1] ; Wei Zhang[4] ; Aleksei Chmura; Mark Fielder[5] ; Zhengli Shi[4] ; Peter Daszak[1]
[1]Research/ EcoHealth Alilance/ United States, [2]Research/ Institute of Zoology, Guangdong Academy of Sciences/ China (□□), [3]School of Health Sciences/ Wuhan University/ China (□□), [4]Research/ Wuhan Institute of Virology, Chinese Academy of Sciences/ China (□□), [5]School of Life Sciences/ Kingston University/ United Kingdom

Introduction and Objectives or Purpose

Human behavior in contacting animals has been implicated as a primary driver for the emergence of several high-impact zoonotic diseases. This seven-year research in Southern China aimed to showcase the application of different human behavior studies in developing evidence- and context-based behavioral change strategies for zoonotic spillover risk mitigation.

Methods

From 2015 to 2022, 5,192 residents from Southern China were enrolled in studies employing mixed methods of ethnographic interviews, serological-behavioral surveillance, and behavior change theories-based surveys to characterize at-risk human-animal contacts, identify the behavioral determinants and develop context-based behavioral change strategies for zoonotic risk mitigation.

Results or Focus

Eighty-eight ethnographic interviews and 55 field observations were conducted to elucidate the frequent human-animal interactions and low levels of environmental biosecurity in local communities. Residents (n=1,596) from the same areas were then enrolled in serological-behavioral surveillance, with nine participants (0.6%) serologically tested positive for bat coronaviruses, and 265 (17%) participants reported SARI and/or ILI symptoms in the past year associated with animal contacts. Further studies focusing on the wildlife trade revealed a low level of knowledge and perceived risk among 947 adults regarding zoonotic spillover and identified the factors in attitudes, social norms, and perceptions that strongly determine the behaviors in wildlife consumption among 2,561 adults. Health-focused behavior change recommendations for zoonotic risk mitigation were developed based on the evidence and are being assessed for acceptability and accessibility among the target populations.

Conclusion or Scope

These studies showcase the integration of different behavioral research methods to build evidence of zoonotic spillover events associated with at-risk behaviors and translate evidence into risk mitigation practices tailored to different populations, demonstrating the value of human behavior research in understanding and addressing the driving factors of zoonotic spillover.

Acknowledgement

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Keywords: Behavior; human-animal contact; zoonotic spillover; wildlife trade; China

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 14876

SMALL MAMMALS AS RESERVOIRS OF EMERGING PATHOGENS CAUSING LETHAL ENCEPHALITIS IN ANIMALS AND HUMANS

Viola Haring*[1] ; Kore Schlottau[2] ; Valerie Allendorf[3] ; Sina Nippert[1] ; Angele Breithaupt[4] ; Florian Pfaff[2] ; Donata Hoffmann[2] ; Martin Beer[2] ; Dennis Rubbenstroth[2] ; Rainer G. Ulrich[1]
[1]Institute of Novel and Emerging Infectious Diseases/ Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health/ Germany (Deutschland), [2]Institute of Diagnostic Virology/ Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health/ Germany (Deutschland), [3]Institute of International Animal Health/One Health / Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health/ Germany (Deutschland), [4]Department of Experimental Animal Facilities and Biorisk Management/ Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health/ Germany (Deutschland)

Introduction and Objectives or Purpose

The aetiologic agent of meningoencephalitides often remains elusive. Neurotropic viruses (such as herpes viruses or West Nile virus), but also Borna disease virus 1 (BoDV-1), variegated squirrel borna virus 1 (VSBV-1), or the novel rustrela virus (RusV), a relative of human rubella virus, can induce lethal non-suppurative myeloencephalitis in humans and/or other mammals. Previous studies indicate the latter viruses to be transmitted from small mammals. BoDV-1 was detected in bicoloured white-toothed shrews (Crocidura leucodon), VSBV-1 in captive squirrels (mainly Callosciurus prevostii and Sciurus variegatoides) and RusV in yellow-necked field mice (Apodemus flavicollis), but little was known about their distribution within small mammal populations.

Methods

Here, we report the screening of brain tissue by BoDV-1, VSBV-1 and RusV specific RT-qPCRs of almost 10,000 rodents and insectivores from Europe. In selected positive animals, virus distribution in tissues was evaluated by immunohistochemistry and/or in-situ hybridisation.

Results or Focus

BoDV-1 was detected not only in Crocidura leucodon, but also in several lesser white-toothed shrews (Crocidura suaveolens) and in a single greater white-toothed shrew (Crocidura russula); all shrews originated from known BoDV-1 endemic areas. Further analysis showed a broad viral tissue distribution with highest loads in neural tissue. We did not detect VSBV-1 RNA in endemic species, like red squirrels (Sciurus vulgaris). These findings support the assumption of the import of a VSBV-1-carrying squirrel from its country of origin. Interestingly, in Germany we detected RusV RNA only in Apodemus flavicollis.

Conclusion or Scope

Identification and characterization of a reservoir host is important to establish protective measures and prevent the circulation of pathogens. Further studies will focus on the identification of the so far unknown reservoir of VSBV-1.

Acknowledgement
Daniel Nobach, Frauke Ecke, Markus Bauswein

Keywords: reservoir, rodents, insectivores, meningoencephalitis, Bornaviridae

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 14927

A POWERFUL TOOL IN NEED OF AN INSTRUMENT: APPLICATION OF WEARABLE TECHNOLOGIES FOR MEASUREMENT OF HUMAN-ANIMAL CONTACT NETWORKS

Julianne Meisner*[1] ; Edmund Seto[2] ; J. Russell Stothard[3] ; Janelisa Musaya[4]
[1]Department of Global Health/ University of Washington/ United States, [2]Department of Environmental and Occupational Health Sciences/ University of Washington/ United States, [3]Department of Tropical Disease Biology/ Liverpool School of Tropical Medicine and Hygiene/ United Kingdom, [4]College of Medicine/ University of Malawi/ Malawi

Introduction and Objectives or Purpose

Zoonotic diseases spillover into human populations along complex networks involving animal and human hosts, and network modeling is a potentially powerful tool for refining zoonotic disease surveillance and intervention deployment. We report here on literature searchers and pilot studies to characterize suitable approaches to human-animal contact network analysis.

Methods

We searched infectious disease epidemiology, sociology, wildlife biology, and veterinary medical literature for methods to measure and model networks. Concurrently we deployed 8 low-cost GPS collars to all animals within a small, schistosome-infected, and mobile herd on the Lake Malawi shoreline over 12 weeks, and customized devices using long-range radio (LoRa) technologies to capture within- and between herd contact among livestock in northern Kenya.

Results or Focus

Self-report and Bluetooth technologies are used to measure human contact for infectious disease modeling. Movement records are used for livestock, and a variety of approaches---including camera traps, focal follows, and GPS devices, often combined with modeling---are used for wildlife. We found one study measuring human-animal contact, which used surveys validated by daily diaries. Contact data from animal geotaggers and human self-report can be converted to aggregate relational data and combined using methods for estimating statistics of generative network models. In Malawi, GPS-tagged animal movements demonstrated daily water contact at several discrete water contact points, and a highly-repetitive cycle of temporal and spatial activities. Later in 2022, we will deploy 50 custom-built LoRa collars among livestock in northern Kenya and combine these data with surveys and daily diaries.

Conclusion or Scope

Both direct and indirect human-animal contact are highly heterogenous, yet the topography of human-animal contact networks has not been well-characterized, and most zoonotic disease models assume random mixing or rely on poorly-justified parameters. Wearable animal geotaggers combined with approaches from other disciplines to capture sensitive contacts and estimate network parameters represent a promising way forward.

Keywords: epidemiology; contact networks; zoonoses; Malawi; Kenya; livestock

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 15024

FOREST FRAGMENTATION DRIVES ZOONOTIC MALARIA PRESENCE IN NON-HUMAN PRIMATE HOSTS

Emilia Johnson*[1 2 3] ; Reuben Sunil Kumar Sharma[4] ; Pablo Ruiz Cuenca[2 5 6] ; Milena Milena Salgado-Lynn[7 8 9] ; Chris Drakeley[10] ; Jason Matthiopoulos[1] ; Luca Nelli[1] ; Kimberly Fornace[1 2 3]
[1]School of Biodiversity, One Health & Veterinary Medicine/ University of Glasgow/ United Kingdom, [2]Department of Disease Control / London School of Hygiene & Tropical Medicine/ United Kingdom, [3]Centre on Climate Change and Planetary Health/ London School of Hygiene & Tropical Medicine/ United Kingdom, [4]Faculty of Veterinary Medicine/ Universiti Putra Malaysia/ Malaysia, [5]Lancaster Medical School/ Lancaster University/ United Kingdom, [6]Neglected Tropical Diseases/ Liverpool School of Tropical Medicine/ United Kingdom, [7]School of Biosciences/ Cardiff University/ United Kingdom, [8]Wildlife Health, Genetic and Forensic Laboratory/ Sabah Wildlife Department/ Malaysia, [9]Danau Girang Field Centre/ Sabah Wildlife Department/ Malaysia, [10]Department of Infection Biology/ London School of Hygiene & Tropical Medicine/ United Kingdom

Introduction and Objectives or Purpose

Land conversion is understood to increase the risk of emergent zoonotic diseases. In simians and humans, infection risk has been linked to fragmented habitats. However, the role of fragmentation on disease dynamics in wildlife hosts is rarely quantified at macroecological scales due to the lack of systematic surveys. In Southeast Asia, non-human primates (NHPs) host Plasmodium knowlesi, a prominent zoonotic malaria. We examine reported primate P. knowlesi to investigate how landscape impacts parasite prevalence.

Methods

A georeferenced dataset of PCR-confirmed P. knowlesi in NHPs across Southeast Asia was assembled from published and unpublished literature. Using systematic tools developed for epidemiological studies, we conducted a regional meta-analysis of P. knowlesi prevalence in simian hosts. Environmental covariates were assembled from remote sensing data and generalised linear mixed models were fitted to prevalence at multiple spatial scales.

Results or Focus

123 observations on a total of 4931 NHPs were identified, primarily Long-tailed macaques (Macaca fascicularis) (88.6%, n=4368/4931). Overall prevalence was 9.6% (CI95% 6.3–13.4), with considerable regional heterogeneity (I^2=96.6%; CI95% 95.7–97.3) and high estimates in Malaysian Borneo (52.4%, CI95% 22.8–81.3). We demonstrate a strong relationship between forest fragmentation (20km, $p<0.0001$) and P. knowlesi in NHPs, suggesting that zoonotic malaria prevalence is maximised at intermediate levels of habitat complexity.

Conclusion or Scope

Findings provide evidence that P. knowlesi in primate hosts is partially driven by landscape change across Southeast Asia and support a previously hypothesised trade-off between epidemiological and ecological mechanisms in determining P. knowlesi infection in wildlife reservoirs. With higher prevalence in NHPs showing geographical overlap with human infection foci, parasite prevalence in NHPs may be a key spatial driver of human spillover risk. Given the clear intersection between human epidemiology and wildlife ecology it is essential that infection dynamics within wildlife reservoirs are considered in public health interventions.

Keywords: disease ecology; forest fragmentation; land use change; malaria; zoonoses

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 15083

Larval Ecology of Anopheles mosquitoes with Reference to Plasmodium knowlesi malaria in Kudat District, Sabah, Malaysia

Wilfredo Aure*[1] [2] ; Nelia Salazar[2] ; Sylvia Daim[1] ; Tock Hing Chua[1]
[1]Faculty of Medicine and Health Sciences/ Universiti Malaysia Sabah / Malaysia, [2]Medical Entomology Department/ Research Institute for Tropical Medicine/ Philippines

Introduction and Objectives or Purpose

A longitudinal survey of larval habitats was conducted to better understand how landuse types have affected mosquitoes with reference to Plasmodium knowlesi malaria from May 2015 to April 2016 in District of Kudat, Sabah, Malaysian Borneo.

Methods

Larval collections were done in target sampling blocks by dipping and reared to adult for species identification.

Results or Focus

Five anopheline and three culicine were collected. Species recovered were Anopheles balabacensis, An. barbirostris, An. lesteri, An. borneensis, An. umbrosus, Aedes albopictus, Culex gelidus and Toxorhynchites sp. An. balabacensis were found in the six land use types. Ninety-five out of 368 breeding habitats were positive for Anopheles larvae. The physico-chemical factors associated with Anopheles larvae were: turbidity, shadiness, water vegetation, surface area, temperature, pH, TDS and EC. Species diversity was high in coconut, clearing sites and rubber plantation but low in forest and settlement. The relative importance of land use types and larval habitats was analysed by Kruskal-Wallis H test by ranks. In decreasing order Anopheles larvae were found highest in rubber tree, coconut, clearing site, oil palm and least in forest and settlement area. Important larval habitats of An. balabacensis were intermittent stream, artificial container and puddle. Eighteen breeding sites of An. balabacensis were within (500 m) flight range of the species and houses at risk for malaria..

Conclusion or Scope

Results of the study could provide understanding on the biology and ecology of mosquito vector's larvae as well as contribute to the development of novel strategies on vector control

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Keywords: Plasmodium.knowlesi, larval survey, Anopheles balabacensis, malaria in Sabah

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 15104

A PROSPECTIVE COHORT STUDY OF INFLUENZA A RISK AMONG SWINE WORKERS AND COMPARISON HOUSEHOLDS IN SOUTH-CENTRAL CAMBODIA

Monivan CHHOUR*[1] ; Monidarin CHOU[1] ; Sokmony YIB[1] ; Chanleakhena PHOEUNG[1] ; Vonthanak SAPHONN[1] ; Hannah HOLT[2] ; Michael ZELLER[3] ; Yvonne SU[3] ; Gavin SMITH[3] ; James RUDGE[2]
[1]Rodolphe Mérieux Laboratory/ University of Health Sciences Cambodia/ Cambodia (□□□□□□□), [2]Department of Global Health and Development/ London School of Hygiene and Tropical Medicine/ United Kingdom, [3]Emerging Infectious Diseases Programme/ Duke-NUS Medical School/ Singapore

Introduction and Objectives or Purpose

Cross-species transmission of influenza A viruses, including between pigs and humans, can lead to reassortment and emergence of novel viruses with pandemic potential. However, evidence on spillover rates, and how these vary across demographic and occupational groups, is limited. Here we describe a prospective cohort study which aims to elucidate zoonotic influenza risk at the swine-human interface in south-central Cambodia.

Methods

Eight districts in four provinces were selected using probability proportional to pig population size sampling, and households with and without occupational exposure to live pigs were recruited. Questionnaires were administered to obtain demographic and behavioural data, and sera collected for Influenza A antibody screening. Follow-up surveys and serological assay development are ongoing.

Results or Focus

Despite delays due to the COVID-19 pandemic, 942 individuals in 615 households were recruited to date. Households are categorized into: i) smallholders (n=190); ii) traders/butchers (n=95); iii) commercial farm workers (n=98); and, iv) non-occupational households (i.e. without pig ownership or occupational exposure; n=233). Frequency and types of swine exposure varied significantly across groups. Blood samples were collected from 783 (83.1%) of individuals. Preliminary ELISA screening reveals the majority are positive for influenza A IgG antibodies, with 36.5% “strongly positive” when grouped using expectation-maximization algorithm. Sera will be tested for evidence of seroconversion to viruses circulating in Cambodian pigs using microbead-based assays.

Conclusion or Scope

This study is part of the larger PigFluCam+ project. Combined with data from slaughterhouse surveillance and pig network surveys, the study will help identify high-risk groups and practices zoonotic influenza in relation to swine production and trade.

Acknowledgement

The project is sponsored by the United States Department of the Defense, Defense Threat Reduction Agency. The content of the information does not necessarily reflect the position or the policy of the federal government, and no official endorsement should be inferred.

Keywords: Influenza; swine workers; cohort study; zoonotic risk; Cambodia

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 15109

CHARACTERIZING INFLUENZA EPIDEMIOLOGY AND DYNAMICS AT THE SWINE-HUMAN INTERFACE IN CAMBODA: THE PIGFLUCAM+ PROJECT

James Rudge[*1] ; Hannah Holt[1] ; Arata Hidano[1] ; Sothyra Tum[2] ; Monidarin Chou[3] ; Ty Chhay[4] ; William Leung[1] ; PigFluCam+ Consortium[1 2 3 4 5] ; Yvonne Su[5] ; Gavin Smith[5]
[1]Department of Global Health and Development/ London School of Hygiene and Tropical Medicine/ United Kingdom, [2]National Animal Health and Production Research Institute/ General Directorate of Animal Health and Production/ Cambodia (□□□□□□□), [3]Rodolphe Mérieux Laboratory/ University of Health Sciences/ Cambodia (□□□□□□□), [4]LDC/ Livestock Development for Community Livelihood/ Cambodia (□□□□□□□), [5]Emerging Infectious Diseases Programme/ Duke-NUS Medical School/ Singapore

Introduction and Objectives or Purpose

Coordinated research and surveillance at the human-livestock interface is needed to better respond to emerging infectious disease threats. The PigFluCam+ project is a multi-partner research collaboration to characterize zoonotic and pandemic risk in relation to pig rearing systems in south-central Cambodia, with a focus on influenza.

Methods

Data are collected through 3 main study components: (A) pig sector surveys to characterize production practices and trading networks; (B) virological and serological surveillance among slaughterhouse pigs; and (C) a human cohort study among households with and without occupational exposure to live pigs. Swabs are screened for influenza A M-gene and positive samples sequenced. Sera are tested using ELISA and multiplex bead-based immunoassays. Data are being used to inform mathematical models of enzootic and zoonotic transmission dynamics.

Results or Focus

Of 3,836 pig nasal swabs tested to date, 67 (1.7%) were positive for influenza A M-gene; batches from commercial farms were more likely to test positive compared with those from smallholders. The majority of HA sequences were closely related to pandemic human H1N1 virus, while H1N1 classical swine and H3N2 human seasonal lineages were also detected. A total of 945 individuals from 651 households with contrasting pig exposure types and frequencies have been enrolled into the human cohort, with follow-up and serological analysis ongoing.

Conclusion or Scope

The study design and findings can inform risk-based strategies for early detection and mitigation of emerging disease threats in the Lower-Mekong region, where livestock systems are changing rapidly. Key findings, challenges and lessons learned will be discussed.

Acknowledgement

The project depicted is sponsored by the U.S. Department of Defense, Defense Threat Reduction Agency. The content of the information does not necessarily reflect the position or the policy of the federal government, and no official endorsement should be inferred.

Keywords: influenza A virus; pig production; zoonotic risk; transmission dynamics; Cambodia

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 15129

AVIAN INFLUENZA IS OFTEN MASKED BY RESPIRATORY CO-INFECTIONS IN SMALL-SCALE POULTRY FARMS IN BANGLADESH – A POTENTIAL DRIVER FOR ZOONOTIC SPILLOVER

MD RAFIQUL ISLAM[*1] ; Mohammad Mijanur Rahman[1] ; Mohammed Nooruzzaman[1] ; Congriev Kumar Kobiraj[1] ; Tanjin Tamanna Mumu[1] ; Ismail Hossain[1] ; ABM Jalal Uddin[1] ; Emdadul Haque Chowdhury[1]
[1]Department of Pathology/ Bangladesh Agricultural University/ Bangladesh (□□□□□□□□)

Introduction and Objectives or Purpose

Highly pathogenic avian influenza (HPAI) is still considered as a pandemic threat. Stumping out and/or vaccination are practiced in different countries to control HPAI in poultry over the last two decades. However, H5 HPAI viruses still prevail across the globe. The present study was undertaken to better understand the circulation of H5 HPAI virus in poultry in Bangladesh in the context of respiratory co-infections.

Methods

We investigated respiratory disease events in 167 small-scale commercial poultry farms in Mymensingh, Tangail, Kishoreganj and Sirajganj districts of Bangladesh during 2019-2021. Pooled samples of oropharyngeal swabs from live birds or respiratory tissues from dead birds were tested for molecular detection of avian respiratory pathogens including avian influenza virus (AIV), Newcastle disease virus, infectious bronchitis virus, infectious laryngotracheitis virus, Mycoplasma gallisepticum, and Avibacterium paragallinarum. Representative 11 isolates of H5 AIV were subjected to whole genome sequencing.

Results or Focus

One or more respiratory pathogens were detected in 113 farms out of 167 investigated farms. AIV was detected in 66 farms often concurrently with other pathogens. H5, H9, H5 + H9, and non-H5-non-H9 AIVs were detected in 31, 13, 14, and 8 farms, respectively. Birds of most of the H5 AIV positive farms did not present typical clinical signs or high mortality. On longitudinal observation of 20 such farms showed only 1.05 to 5.50% mortality but a marked drop in egg production. On full genome sequencing all the 11 H5 isolates belonged to clade 2.3.2.1a H5N1 virus.

Conclusion or Scope

Despite the absence of typical devastating HPAI outbreaks in small-scale commercial poultry production, H5N1 viruses are widely circulating in Bangladesh in an enzootic pattern, which are often masked by other respiratory infections. Although the reasons of this changed dynamics of H5 AIV in small-scale poultry production have not been established, this remains as a potential driver for zoonotic spillover.

Keywords: Avian influenza, infection dynamics, co-infection, Bangladesh

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 15293

“Sink” Surveillance – longitudinal environmental monitoring for avian influenza viruses in ruban live bird markets in Bangladesh, 2016-2020

Eric Brum[1] ; Md. Zakiul Hasan[*1] ; Mohammad Taifur Rahman[1] ; Md. Mohibul Hassan Afrad[1] ; Abdus Samad; Zulfeker Ali; Inkeyas Uddin; Himel Barua; Paritosh Kumar Biswas
[1]Emergency Centre for Transboundary Animal Disease (ECTAD) / FAO/ Bangladesh (□□□□□□□□)

Introduction and Objectives or Purpose

Influenza A virus has potential threat for poultry and public health. In 2016, Government of Bangladesh initiated Sink Surveillance programme in Dhaka and one year later in Chattogram live bird markets (LBMs) to investigate the prevalence of influenza A viruses in a cost-effective manner. This study aims to evaluate the trend of circulating Influenza A viruses in the poultry market chain in Bangladesh for five years.

Methods

A total of 7960 environmental samples were collected monthly from 106 Dhaka (n=4946) and 70 Chattogram (n=3014) LBMs during the period. The samples were tested for the presence of membrane protein (M) genes of influenza A viruses using real-time PCR. The M gene positive samples were further examined to investigate the association with hemagglutinin genes (H5, H7 and H9).

Results or Focus

The average monthly prevalence of influenza A virus, including of H5 and H9 subtypes, peaked in 2016 (Inf A 65%, H5 39%, H9 31%) and then gradually declined until 2018 in Chattogram (Inf A 23%, H5 2%, H9 8%) in 2019 in Dhaka (Inf A 32%, H5 11%, H9 12%). Prevalence began increasing in 2019 in Chattogram (Inf A 35%, H5 7%, H9 17%) and in 2020 in Dhaka (Inf A 51%, H5 18%, H9 26%). All H5 subtype viruses detected to date have been highly pathogenic avian influenza (HPAI) H5N1. No H7 subtype virus was detected during the study period.

Conclusion or Scope

Influenza A viruses, including HPAI H5N1, have been consistently detected year-around from environmental samples collected at urban LBMs since 2016, suggesting persistent, endemic circulation. Monthly prevalence observed in Dhaka has been higher compared to Chattogram LBMs, consistent with the source-sink hypothesis for pathogen accumulation in urban markets. Following a steady decline in prevalence between 2018 and early 2019, prevalence of influenza A viruses began increasing in 2020, suggesting resurgence following COVID-19 lockdowns in 2020.

Acknowledgement

Keywords: Sink Surveillance; Avian Influenza, Live Bird Market; Disease Monitoring

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 15309

Mixed species farming in Vietnam: potential risk of cross-species transmission and zoonotic disease emergence

Cuong Nguyen*[1] ; Chuyen Nguyen Khac[2] ; Thanh Nguyen Van [2] ; Guy Thwaite E.[1] ; Peter Daszak[3] ; Duy Pham Thanh[1] ; Cadhla Firth[3]
[1]Molecular Epidemiology / Oxford University Clinical Research Unit (OUCRU)/ Vietnam (Việt Nam), [2]Epidemiology / Sub-Department of Animal Health, Dak Lak Province, Vietnam/ Vietnam (Việt Nam), [3]NA/ EcoHealth Alliance / United States

Introduction and Objectives or Purpose

Viet Nam sits within a critical Southeast Asian emerging infectious disease hotspot with diverse wildlife and a rapidly increasing human population. In this region, wildlife farming is a growing but inadequately regulated industry that exhibits many features thought to contribute to increased risks of cross-species transmission and zoonotic disease emergence. We tested the hypothesis that viral diversity and cross-species transmission increases with species diversity on mixed-species farms, and this pattern will be amplified by the co-occurrence of wildlife species.

Methods

Using a metatranscriptomics-based approach, we analyzed the fecal viromes from a unique set of farmed animals in the Central Highlands of Viet Nam, where a variety of wildlife (e.g., bamboo rats, civets, wild boar, porcupines) and domestic species (e.g., chickens, ducks, pigs, goats) are farmed both together and separately. Farms were selected to encompass a range of species complexity, from single-species farms, to those where more than 8 species were present. We assessed the presence and prevalence of a subset of viruses identified from these data using PCR to identify the presence and frequency of cross-species transmission of viruses between animal species, as well as estimate their zoonotic potential and potential consequences for animal health.

Results or Focus

We identified high fecal viral diversity in eight animal species across all farming conditions, with samples from domestic pigs and wild boar containing the broadest diversity of viruses. Preliminary data also suggests that viral sharing may be frequent on mixed-species farms, with several viruses identified in two-to-five different animal species located on the same farm.

Conclusion or Scope

Mixed-species farms create new interfaces between wildlife, domestic animals, and people that may provide opportunities for cross-species transmission of viruses to occur. The risk of cross-species transmission and disease emergence may be further driven by the present of species like domisticated pigs/wild boar, and co-located with wild species.

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Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Molecular epidemiology and evolution
Abstract No: 15040

DIVERSITY AND SPILLOVER RISK OF SWINE ACUTE DIARRHEA SYNDROME-RELATED CORONAVIRUSES IN CHINA AND SOUTHEAST ASIA

Cadhla Firth[*1] ; Alice Latinne[1] ; Li-Biao Zhang[2] ; Kevin Olival[1] ; Cecilia Sánchez[1] ; Ben Hu[3] ; Bei Li[3] ; Hongying Li[1] ; Zheng-li Shi[3] ; Peter Daszak[1]
[1]NA/ EcoHealth Alliance/ United States, [2]Institute of Zoology/ Guangdong Academy of Sciences/ China (□□), [3]Chinese Academy of Sciences/ Wuhan Institute of Virology/ China (□□)

Introduction and Objectives or Purpose

Bats are the likely reservoir hosts of several significant emerging coronaviruses affecting human and livestock health. In this study, we assessed the diversity, evolution, and geographic distribution of two alphacoronaviruses with significant potential for emergence: swine acute diarrhea syndrome (SADS-CoV), which has caused significant mortality in pigs and is capable of infecting primary human airway epithelial cells in vitro; and its close relative, HKU2-CoV, previously identified in horseshoe bats (Rhinolophus spp.).

Results or Focus

Our phylogenetic analyses revealed substantial diversity of HKU2-like viruses circulating in bats in China. We observed strong phylogenetic clustering by location, which is suggestive of infrequent long-distance transmission of these viruses between locations in southern China. Using ancestral state reconstruction analysis, we found that Rhinolophus sinicus/thomasi and R. affinis are likely to have played significant roles in the evolution of these viruses in southern China and that R. affinis is the most likely reservoir host of the virus that spilled over into pigs as SADS-CoV.

We developed species distribution models for the four primary bat hosts of HKU2-like viruses (R. affinis, R. pusillus, R. sinicus/thomasi, and R. stheno), and combined these with pig and human population data to identify areas of potential spillover risk in Southeast Asia. Specific areas with both high pig counts and high predicted bat occurrence probability were identified primarily in southern China, and throughout Vietnam and Laos. Hotspots of risk where high human population density overlaps with bat host distribution were present in southern China, central Thailand, peninsular Malaysia, and Sumatra

Conclusion or Scope

Increased surveillance of pigs and people in these regions may facilitate the timely detection of bat alphacoronavirus spillover events and mitigate the risk of future outbreaks in both people and pigs.

Methods

We use a combination of phylogenetic analyses and species distribution modelling to understand the emergence, spread, and future risk of HKU2-CoV-like viruses.

Acknowledgement

Additional authors: Guangjian Zhu, Shirley Chen, Noam Ross, Kai Zhao, Wei Zhang, Aleksei Chmura

Keywords: Bats, coronaviruses, pigs, spillover risk, Southeast Asia

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Predictive risk models
Abstract No: 14680

Identification and quantification of risk factors driving vector-borne zoonotic infections in northern Italy

Roberto Rosa*[1] [2] ; Giovanni Marini[2] ; Annapaola Rizzoli[2]
[1]Centre Agriculture Food Environment/ University of Trento/ Italy (Italia), [2]Research and Innovation Centre/ Fondazione Edmund Mach/ Italy (Italia)

Introduction and Objectives or Purpose

Changes in climate, land use and biodiversity are considered among the most important factors affecting zoonotic diseases emergence. Transmission of vector-borne infections are particularly sensitive to these changes due to the complexity of their cycle, where the transmission of a pathogen depends on the interaction between vectors and their reservoir hosts. In this study we focus on the effect of climatic and ecological drivers shaping vector-borne infection dynamics. Specifically, we present recent advances regarding two emerging vector-borne viruses in Europe, focusing on northern-Italy: tick-borne encephalitis virus (TBEv) and West Nile virus (WNv).

Methods

Both statistical and mechanistic models, informed by eco-epidemiological data, were carried out to: (i) assess the effect of major predictors on the timing and abundance of vectors and their transmitted pathogens; (ii) simulate vector population dynamics and pathogen infection rates in both vectors and animal reservoir hosts; (iii) estimate human transmission risk

Results or Focus

For the TBEv case study, a specific combination of climatic conditions and the densities of rodents and deer hosts are the main determinants in shaping feeding tick dynamics and TBEv circulation. For WNv, we found that anomalous warm spring temperatures amplify virus transmission at the beginning of the season, increasing virus prevalence in mosquito and avian populations during the summer, which caused a higher estimated risk for human transmission.

Conclusion or Scope

Changes in vector:host ratio are critical in determining the intensity of pathogen transmission and consequently infection risk for humans. Quantifying vector-borne disease risk, in different biomes, under the global change scenarios is particularly challenging, requiring long-term studies based on a multidisciplinary approach in a One-Health framework. In this complex context, quantitative models can provide early-warning systems for assessing transmission risk and allowing targeted public health actions by strengthening advanced surveillance and prevention programs.

Acknowledgement

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Keywords: human-animal-environment interactions; predictive models; vectors-borne pathogens

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Predictive risk models
Abstract No: 14840

MAPPING THE RISK OF TAENIA SOLIUM IN LAO PDR

Andrew Larkins*[1] ; Mieghan Bruce[1] ; Sarah Keatley[1] ; Boualy Keokhamphavanh[2] ; Bounnaloth Insisiengmay[2] ; Amanda Ash[1]
[1]Centre for Biosecurity and One Health/ Murdoch University/ Australia, [2]Department of Communicable Diseases/ Ministry of Health/ Lao People's Democ. Rep.

Introduction and Objectives or Purpose

Taenia solium is considered the most significant global food-borne pathogen. It is the leading cause of preventable epilepsy in low and middle-income countries and challenging to definitively diagnose. Acting on the WHO call for increased control of T. solium in hyperendemic areas, the objective of this study is to identify high-risk areas in Laos without the demanding resource requirements of national disease occurrence surveys that are often hampered by the nature of current diagnostic tools.

Methods

National census data were examined using multicriteria decision analysis to map the risk of T. solium at district and village-levels. Village risk scores were calculated using linear combination of risk factors that were weighted using an analytic hierarchy process. District risk scores were calculated as the mean village score for a given district. Risk scores were categorised using the Fisher-Jenks algorithm. One-at-a-time sensitivity analysis was completed and summarised as the variance of results across all scenarios. Results will be compared against available biological data.

Results or Focus

24% of villages and 14% of districts were classified as high risk, with high-risk locations present across the country. When examined with sensitivity analysis, two main areas of high risk and low variability are revealed. The first in northern Laos is consistent with current knowledge and past projects. The second in the south-east has yet to be investigated. Validation of results using biological data is ongoing.

Conclusion or Scope

This study has identified high-risk areas for T. solium in Laos using readily available census data. The multicriteria decision analysis method can rapidly produce sub-national risk maps in countries with available data. The application of census data allows for increased coverage and versatility compared to WHO's current risk mapping template that relies heavily on disease occurrence.

Acknowledgement

This research is funded by the Australian Centre for International Agricultural Research and a Murdoch University Strategic Scholarship.

Keywords: One Health; Taenia solium; Zoonosis; Neglected Tropical Diseases; Risk mapping

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Predictive risk models
Abstract No: 15094

A risk-based mutual insurance framework to generate national vulnerability indices for agro/bio-crime or agro/bio-terror events involving zoonotic disease agents

H. Morgan Scott*[1] ; Gizem Levent[2] ; Christopher Laine[1] ; Melissa Berquist[3] ; Miguel Gonzalez[4] ; Heather Simmons[5] ; Jimmy Tickel[5]
[1]Department of Veterinary Pathobiology/ Texas A&M University/ United States, [2]School of Veterinary Medicine/ Texas Tech University/ United States, [3]Inc./ IBio/ United States, [4]Organization/ BCarbon/ United States, [5]Institute for Infectious Animal Diseases/ Texas A&M AgriLife Research/ United States

Introduction and Objectives or Purpose

Intentional release of zoonotic disease pathogens that targets vulnerable animal and human populations constitutes agro/bio-crime or agro/bio-terrorism, respectively. Such action not only negatively impacts animal and human health, but may threaten peace and global health security and impose enormous economic costs on nations. We used the World Organisation for Animal Health (WOAH) quantitative risk assessment framework to generate an approach for developing vulnerability indices for 25 countries with high levels of data completeness against Brucella abortus (BA) and highly pathogenic avian influenza virus (HPAIv).

Methods

Variables to build release, exposure, preparedness, and resilience components of each country’s vulnerability index were generated from open-source databases generated by multiple international organizations and consisted of: 1) the number and density of the targeted populations, 2) availability of technical tools and the health services and disease control measures applied by each country, and 3) the political, economic, and research and development capabilities of each country. Component scores for each pathogen and country were calculated using three different index construction approaches. An overall vulnerability index for each country and pathogen was derived from the final component scores.

Results or Focus

The final component scores as well as the overall vulnerability scores obtained using three different methods showed highly consistent and correlated results; overall, principal components analysis yielded the greatest potential to discriminate differences among countries and regions. The framework may be readily modified by policymakers and used to improve risk management strategies based on reliable and widely available databases.

Conclusion or Scope

This risk-based mutual insurance scheme provides an expandable global framework for targeting and prioritizing capacity building investments and resource allocations in order to reduce vulnerabilities to zoonotic diseases and increase preparedness and resilience.

Acknowledgement

Support provided through “Building Resilience Against Agro-Crime and Agro-Terrorism”, coordinated by WOAH, FAO and INTERPOL and funded by the “Weapons Threat Reduction Program” of Global Affairs Canada.

Keywords: Vulnerability index; Agro/bio-crime or agro/bio-terrorism; Zoonotic disease; Resilience; Preparedness and response

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Risk assessment of emerging pathogens in animal models
Abstract No: 14871

The rat hepatitis E virus prevalence and associated factors in rodent population in Cambodia rural and urban settings.

Oudamdaniel YANNETH*[1] ; Veasna Duong[1] ; Erik Karlsson[1] ; Vibol Hul[1] ; Janin Nouhin[1] ; Thavry Hoem[1]
[1]Virology Unit/ Institut Pasteur du Cambodge/ Cambodia (□□□□□□□)

Introduction and Objectives or Purpose

The Hepatitis E infection is one of the neglected human pathogens which cause acute hepatitis and could clinically aggravate in immunocompromised patients. A new genotype of this Hepeviridae viral family, Orthohepevirus C genotype 1 (HEV-C1), emerged in Germany’s wild rats in 2009 and has been circulated in rodents globally since then, particularly in countries with poor sanitation. And the evidence of transmission to humans was observed in Hong Kong’s impaired immune response patients in 2018.

Methods

We conducted a cross-sectional study in three provinces in Cambodia from 2020 to 2022 in two seasons to assess the rat HEV prevalence and determine the potential factors associated with the infection in the murine family.

Results or Focus

Of the 750 caught rodents, after screening with the RT-PCR assay, the prevalence of infection was 1.8% (14/750), where 6 (0.8 %) and 8 (1 %) were found to be positive in dry and rainy seasons, respectively. This new HEV-C1 genotype is mainly detected in an urban setting, specifically in markets. We also discovered that rodent species, including Rattus rattus (Black rat) and Rattus norvegicus (Brown rat), are susceptible to HEV-C1 infection. However, the p-value is not significant after adjusting for other rodent characteristics. In addition, for the rodent population in Phnom Penh, the infection is more likely to occur in the Old Market with an OR (15.8 and 95% CI 2.21 – 329) compared to other markets.

Conclusion or Scope

The further approach should focus on developing a specific serological assay to detect the HEV-C1 in the human population to assess the virus circulation as it proved to be transmissible zoonotically. A genetic characterization study is also encouraged.

Keywords: Cambodia, Cross-sectional study, HEV-C1 infection, Rat HEV, RT-PCR assay.

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Risk assessment of emerging pathogens in animal models
Abstract No: 15124

QUALITATIVE RISK ASSESSMENT ADDRESSING THE RISK OF ZOONOTIC H5 HIGH PATHOGENICITY AVIAN INFLUENZA INTRODUCTION INTO CENTRAL AND SOUTH AMERICAS

Xavier ROCHE[1] ; Sophie Von Dobschuetz[1] ; Andres Gonzalez Serrano[2] ; Vanessa Max Kraus[2] ; Hernan Rojas[2] ; Gabriela Espejo[2] ; Baba Soumare[1] ; Madhur Dhingra[*1]
[1]Animal Health/ Food and Agriculture Organization/ Italy (Italia), [2]Animal Health/ FAO Regional Office for Latin America and the Caribbean/ Chile

Introduction and Objectives or Purpose

Since 2020, the world is facing an unprecedented H5 high pathogenicity avian influenza (HPAI) intercontinental wave affecting around 70 countries worldwide. Eighteen countries reported the disease for the first time ever. Outbreaks resulted in heavy economic losses for the poultry industry, and have jeopardized populations of endangered avifauna. Spillover to wild mammals and humans have been recorded, reminding about the zoonotic potential of such viruses. In November 2021, H5 HPAI was introduced into North America and by now established itself in wild bird populations of the region. Given the upcoming southwards bird migration throughout the Northern hemisphere autumn, FAO conducted a qualitative risk assessment addressing H5 HPAI introduction risk for Central and South America to provide countries/territories, most of which have never been affected by HPAI, with scientific evidence for HPAI preparedness advocacy.

Methods

The assessment was based on identification of main risk pathways, including informal/formal trade of live poultry and their products, fomites, and wild bird movements. A questionnaire was disseminated to Veterinary Services to collect data on HPAI risk factors and assess national capacities for HPAI surveillance, diagnosis, prevention, and control. Five levels from negligible to high were used to determine the likelihood of introduction, and a consequence assessment was conducted on potential impacts on the poultry value-chain, avifauna, and public health. The assessment also considered the level of uncertainty related to data availability, quality and quantity.

Results or Focus

The risk of H5 HPAI introduction into Central and South Americas is higher than it has never been in the past, considering wild bird migration movements starting in September and reaching peak influx in November, raising concerns for national and regional economies and public health.

Conclusion or Scope

FAO is using information from the assessment to provide targeted capacity building support to countries/territories for enhanced HPAI preparedness, prevention, and control.

Keywords: HPAI; americas; risk; assessment; zoonosis

Topic: One Health Science (OHS): Vaccines and Therapeutics for Emerging Infections: Enabling equitable access
Abstract No: 14768

VACCINE EQUITY IN COVID-19: A META-NARRATIVE REVIEW

Zheting Zhang*[1] ; Julia Borowicz*[2] ; Giskin Day[2] [3] ; Mariana Pinto Da Costa[4] [5]
[1]Lee Kong Chian School of Medicine/ Nanyang Technological University/ Singapore, [2]Imperial College School of Medicine/ Imperial College London/ United Kingdom, [3]Florence Nightingale Faculty of Nursing, Midwifery and Palliative Care/ King's College London/ United Kingdom, [4]Institute of Psychiatry, Psychology & Neuroscience/ King's College London/ United Kingdom, [5]Institute of Biomedical Sciences Abel Salazar/ University of Porto/ Portugal

Introduction and Objectives or Purpose

Throughout the COVID-19 pandemic, the topic of inequitable vaccine distribution has been widely discussed by academics, journalists, and policymakers. However, there is a lack of universal understanding of the concept of vaccine equity, and research into the perception of vaccine equity has been particularly neglected.

Methods

We conducted a meta-narrative review on COVID-19 vaccine equity according to the Realist And MEta-narrative Evidence Syntheses: Evolving Standards (RAMESES). We searched four databases—MEDLINE, Embase, CINAHL, and Web of Science—for peer-reviewed articles published between January 2020 and July 2021. We included English-language articles that addressed vaccine equity in the context of global COVID-19 vaccination.

Results or Focus

Of 1148 articles found in the search, 213 full-text articles were screened independently by two reviewers, and 26 articles were included. Five meta-narratives from literature across various research traditions were identified, contextualised, and discussed: Practical Frameworks for Vaccine Allocation; Global Governance; Vaccine Nationalism; Ethics and Morality; and Reparative Justice. The attitudes towards the concept of vaccine equity and the angles from which it was investigated differed between various research groups and kept changing within each meta-narrative as the COVID-19 pandemic evolved.

Conclusion or Scope

This study reviews the current debates on the different attitudes towards mechanisms of achieving vaccine equity in the existing global COVID-19 allocation frameworks. The lack of agreement on the meaning of the term 'equity' in the context of the COVID-19 pandemic has hindered the achievement of practical solutions. In the interests of global public health, it is crucial to reach a consensus on a definition of 'equity' in the face of scarce resources, prior to establishing a global resource allocation framework.

Acknowledgement

This review was funded by the Professor Jenny Higham Collaboration Grant, which promotes innovative cross-border pursuits between Imperial College School of Medicine, London, United Kingdom and Lee Kong Chian School of Medicine, Nanyang Technological University, Singapore.

Keywords: vaccine equity; COVID-19; vaccination; vaccines; health equity

Topic: One Health Science (OHS): Vaccines and Therapeutics for Emerging Infections: Enabling equitable access
Abstract No: 15191

COVID 19 VACCINE HESITANCY IN AFRICA: POLICY AND STARTEGY ISSUES.

Polydor Ngoy MUTOMBO*[1] ; Mosoka P. FALLAH*[1] ; Davison MUNODAWAFA*[2] ; Ahmed KABEL[3] ; David HOUETO[4] ; Oliver MWE-EMBA[5] ; Gladys BALANCE[6] ; Hans ONYA[7] ; Jean-Marie Ntumba KAYEMBE[8] ; Bartholomew AKANMORI[9]
[1]Centre for Naturopathic Medicine, Faculty of Health Sciences/ Southern Cross University/ Australia, [1]Saving Lives and Livelihoods/ AFRICA CDC/ Ethiopia, [2]Faculty of Medicine/ Midlands State University/ Zimbabwe, [3]School of Humanities and Social Sciences/ Al Akhawayn University / Morocco (المغرب), [4]School of Public Health/ University of Parakou/ Benin (Bénin), [5]School of Public Health/ University of Zambia / Zambia, [6]Gender Institute/ Midlands State University/ Zimbabwe, [7]Department of Public Health/ University of Limpopo/ South Africa, [8]Faculty of Medicine, Department of lung diseases/ University of Kinshasa/ Democratic Republic of the Congo [9]Vaccines/ WHO Regional Office for Africa/ Republic of the Congo

Introduction and Objectives or Purpose

In March 2020, COVID-19 was declared a global pandemic. Africa became the focus due to its vulnerabilities. The WHO measures to minimize transmission were adopted by all countries. However, the introduction of vaccines globally exposed Africa's weaknesses regarding vaccine access and vaccine hesitancy. Funds to purchase vaccines were scarce. Public knowledge about vaccine efficacy and effectiveness in preventing and controlling COVID-19 throughout Africa was limited. There was widely held negative views across Africa regarding vaccines, which arise from structural and systematic dynamics linked to historical medical research on vaccines from the colonial past. In addition, there has been a systemic failure by health officials to inform and educate the general population on the efficacy and effectiveness of vaccines in disease control and prevention. As multi-disciplinary researchers from Africa, we firmly argue that COVID-19 vaccine hesitancy is due to misinformation and disinformation driven by the social media and religious groups and worsened by a weak health system that cannot create public awareness or increase vaccine access. At the global level, vaccine diplomacy and donor dependency has led to suspicion that Africa is receiving vaccines that are not sanctioned by WHO. As a result, Africa is viewed as a testing ground for vaccines, which further fuels vaccine hesitancy. Africa's collective efforts through Africa Centers for Disease Control and Prevention (Africa CDC) should be reinforced. A mechanism managed by the Africa CDC to procure and manage COVID-19 vaccines premised on equity, justice and human rights has great potential to address vaccine access and hesitancy. Advocacy for COVID 19 vaccines should be through Africa CDC and WHO Regional Office for Africa and drawing lessons disease outbreaks such as Ebola. Concerted efforts are required to monitor and fake information about COVIID-19 and vaccines. Ultimately, Africa requires financial resources from both Governments and global partners.

Keywords: Hesitancy; Equity; access; vaccine nationalism; vaccine diplomacy; structural violence

Topic: One Health Science (OHS): Vaccines and Therapeutics for Emerging Infections: Novel vaccine technology
Abstract No: 14992

A new class of transmission-enhancing compounds: Lipids from mosquito saliva increase arbovirus infection at the bite site

Hacène MEDKOUR*[1] ; Lauryne Pruvost[1] ; Florian Rachenne[1] ; Felix Rey-Cadilhac[1] ; Dorothée Missé[1] ; Sébatien Nisole; Guillaume Marti; Justine Bertrand-Michel; Julien Pompon[1]
[1]Herault/ MIVEGEC, Univ. Montpellier, IRD, CNRS/ France

Introduction and Objectives or Purpose
Mosquito-borne flaviviruses infect half a billion people, kill 250,000 and cost US$ 10 billion yearly. These threats will expand geographically due to the expansion of mosquito vectors. However, despite the urgency, no therapy or control methods exist to prevent outbreaks. During mosquito bite, viruses are deposited within saliva in the epidermis and dermis. Infection of skin cells is required for systemic infection, making skin infection a key step in viral transmission. Previous studies have shown that mosquito saliva facilitates infection of skin cells and recently our team discovered that it contains extracellular vesicles (EV), which are rich in lipids. Here, we studied the roles of salivary EV-lipids on flavivirus transmission.

Methods
First, we developed a protocol to purify EV-lipids produced in an in vitro model (A. aegypti mosquito cells). Second, to estimate the impact of EV-lipids on dengue infection, we infected Huh7, primary skin fibroblasts and monocyte-derived dendritic cells with different amounts of EV-lipids. For all cell types, the infection increased in the presence of lipids. Third, to determine which lipid groups are involved, we fractioned the purified EV-lipids by solid phase extraction (SPE) and validated the group separation by mass spectrometry.

Results or Focus
We infected cells with the different fractions and we showed that phospholipids, cholesterols, and fatty acids are responsible for the enhanced infection. Overall, our results showed that salivary lipids increase dengue transmission to humans. There remain to determine the impact of EV-lipids on other flavivirus infections, what step of the viral cellular cycle (virus entry, translation, genome replication and assembly) is affected and how EV lipids influence infection.

Conclusion or Scope

After proteins, microbiota and nucleic acids were shown to be involved in saliva function, we discovered that salivary EV-lipids also play a role in transmission, revealing a new targetable class of compounds to block transmission.

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KIM RIVE, University of Montpellier

Keywords: Salivary EV-lipids, Mosquito, Flaviviruses, Dengue, transmission, new target

Topic: One Health Science (OHS): Vaccines and Therapeutics for Emerging Infections: Therapeutic antibodies
Abstract No: 14699

Third mRNA COVID-19 vaccine dose induces high NAb levels in older people and those with diabetes and chronic kidney disease.

Liyana Ahmad[1] ; Hazim Ghani[1] ; Hanisah Sharif[1] ; Saifuddien Bagol[2] ; Surita Taib[2] ; Chin Yee Shim[3] ; Justin Wong[4] ; Lin Naing[1] ; Linfa Wang[5] ; Anne Cunningham[*1]
[1]PAPRSB Institute of Health Sciences/ Universiti Brunei Darussalam/ Brunei, [2]Department of Laboratory Services/ Ministry of Health/ Brunei, [3]EVYD Research Private Limited/ EVYD Research Private Limited/ Singapore, [4]Disease Control Division/ Ministry of Health/ Brunei, [5]Programme in Emerging Infectious Disease/ Duke-NUS Medical School/ Singapore

Introduction and Objectives or Purpose

A population-based serological study to evaluate the immunogenicity of the vaccination programme in Brunei was performed to evaluate the levels of neutralizing antibodies (NAb) generated in response to homologous primary vaccination with either mRNA-1273, AZD1222, or BBIBP-CorV vaccines, plus a third booster dose of either mRNA vaccines (mRNA-1273 or BNT162b2), or BBIBP-CorV vaccines.

Methods

Adults without prior history of COVID-19 who had completed a two-dose primary homologous vaccination with either mRNA-1273, AZD1222 or BBIBP-CorV vaccines, or received a third booster dose of mRNA vaccine (mRNA-1273 or BNT162b2) or BBIBP-CorV were randomly recruited and stratified by gender and age. Their serum samples were collected between 2 to 6 weeks following their last dose of COVID-19 vaccine. NAb were measured by cPass™ SARS-CoV-2 surrogate virus-neutralization kit and assessed for comparative analyses across vaccine groups by adjusting for age, sex, ethnicity, pre-existing medical conditions and length of days following vaccination.

Results or Focus

A total of n=2713 individuals were recruited, n=1376 (50.7%) and n=1337 (49.3%) received two dose and three doses of COVID-19 vaccines respectively. A total of n=2640 (97.3%) individuals successfully seroconverted following vaccination. There was no difference in NAb levels by gender or ethnicity. Waning was observed by weeks 4 and 5 for AZD1222. Lower NAb were induced in older individuals (AZD1222, mRNA-1273; 1% reduction every 8 years). Waning was not observed up to 6 weeks following a third mRNA booster dose. There were no differences in NAb levels across age groups after boosting. Participants with diabetes mellitus and chronic kidney disease generated lower NAb in response to immunisation after two, but not three doses.

Conclusion or Scope

Boosting with an mRNA vaccine significantly improves levels of NAb specific to the ancestral SARS-CoV-2 strain. This is likely to be particularly important in older and vulnerable groups. Longer term durability warrants further investigation.

Acknowledgement
edited for typo correction

Keywords: COVID19, Vaccine, mRNA, booster, neutralising antibodies

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 15359

Healthy lives from sustainable food systems - Lessons learnt from the 2022 Uppsala Health Summit

Karin Artursson*[1]
[1]Dept of Biomedical Sciences and Veterinary Public Health/ National Veterinary Institute and Swedish University of Agricultural Sciences/ Sweden (Sverige)

Introduction and Objectives or Purpose

To provide healthy food for everyone is a huge challenge. To produce the food in a sustainable way is even more challenging. That is why this year´s Uppsala Health Summit focus on “Healthy lives from sustainable food systems”. Unfortunately, the number of under-nourished people in the world continues to increase, and the progress towards the Sustainable Development Goals is slow, ensuring access to safe, nutritious, and sufficient food for all people and eradicating all forms of malnutrition. Conflicts, climate shocks, low productivity and inefficient food supply chains push up the cost of nutritious foods and increase the unaffordability of healthy diets.

Methods

Uppsala Health Summit is a recurring international policy arena for dialogue on challenges for health and healthcare, and how we can overcome them. Personally invited decision-makers, opinion-makers and experts participate in active dialogue in thoroughly prepared workshops and plenum sessions.

Results or Focus

A Pre-conference report will be published during early autumn. This can be found at https://www.uppsalahealthsummit.se. During the 2022 Uppsala Health Summit, October 25-26, solutions for a more sustainable food production that produce healthy foods, affordable and accessible to everyone, will be presented and discussed with a One Health view. The outputs will be guidance and roadmaps to support such initiatives. Areas that will be highlighted during the summit are Sustainable animal production, Effects on health and Consumer behaviour. Food security and Food safety are among the aspects discussed. The perspective is From farm to fork!

Conclusion or Scope

Results and conclusions will be summarized in a Post conference report. The outcome will be presented at the meeting.

Keywords: Food security;Food safety;Health;Zoonoses;Antimicrobial resistance;

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15426

How a global genomics movement can address biosecurity threats

Phillip G. Febbo*[1] ; Michael Oberholzer[1]
[1]-/ Illumina/ United States

Introduction and Objectives or Purpose

The latest outbreak of Monkey Pox, Foot and Mouth Disease and the ongoing challenges with Tuberculosis in this region demonstrates and underscores the importance for the world to enhance its global biosecurity monitoring. With ongoing changes to our environment, climate, agricultural practices, and global trade, various biosecurity threats will continue to present challenges to the community, environment, and the world's economic prosperity.

Methods

Recent experience with the COVID19 pandemic highlighted an urgent need to strengthen global proactive pathogen discovery, monitoring and surveillance efforts to minimise the risk of future pandemics and zoonotic outbreaks that can have devastating global economic and social impact.

Results or Focus

Genomic sequencing technology has revolutionized medical research and has already started to improve patient care. One of the industry leaders will offer up their insights and perspectives on the value of accessible genomics technology as a new, emerging solution to novel pathogen discovery and surveillance of infectious disease.

Conclusion or Scope

The unprecedented collaboration among medical and scientific communities, we experienced during the COVID 19 pandemic, needs to continue. Health care providers and scientists around the world, from academia to biotech and pharmaceutical companies, must continue to share knowledge and work together to address the inevitable continuing biological threats that we face.

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 14874

MEDILABSECURE, ONE HEALTH NETWORK FOR THE PREVENTION OF VECTOR-BORNE DISEASES, THE SAHEL EXPERIENCE

Guillain Mikaty[1] ; Jean-Claude MANUGUERRA [1] ; Mohamed Abdellahi Bollahi[2] ; Miguel Angel Jiménez [3] ; Vincent Robert[4] ; Maria Grazia Dente[5] ; Guy Hendrickx[6] ; Oriana Rossi[7] ; Vanessa Lagal[*7] ; Maud Seguy[7]
[1]Cellule d’Intervention Biologique d’Urgence/ Institut Pasteur/ France, [2]Institut National de Recherche et Santé Publique/ Institut National de Recherche et Santé Publique/ Mauritania (موريتانيا), [3]Centro de Investigación en Sanidad Animal/ Instituto Nacional de Tecnologia Agraria y Alimentaria / Spain (España), [4]Infectious Diseases and Vectors : Ecology, Genetics, Evolution and Control/ French National Research Institute for Sustainable Development/ France, [5]National Center for Global Health / Italian National Institute of Health / Italy (Italia), [6]AVIA-GIS/ AVIA-GIS/ Belgium, [7]Direction Internationale/ Institut Pasteur/ France

Introduction and Objectives or Purpose

MediLabSecure (MLS) is a capacity-building project funded by the European Commission, coordinated by Institut Pasteur and implemented by European organisations for the benefit of 22 countries in the Mediterranean, Black Sea and Sahel regions. MLS gathers 114 multidisciplinary laboratories and health institutions to prevent and control vector-borne diseases.

Methods

MLS strategy is based on the evidence and experience gained in these years of activities, which support the integration of One Health in preparedness, surveillance and response against zoonotic arboviruses. Experts in human and animal virology, medical entomology, public and animal health, and geo-spatial modelling collaborate to provide trainings and guidance, conduct operational studies, to support the beneficiaries’ countries in case of local or cross-border outbreaks.

Results or Focus

Since its start in 2014, the project trained 1000 professionals through 29 workshops, 16 trainings and regional and global networking events. Sahel joined the network in 2018. Here, MLS focused on the Rift Valley Fever (RVF) that may cause human and animal health burden and severe economic loss. In 2020, Mauritania was hit by a large outbreak of RVF in animals and humans. The National Institute for Public Health Research of Nouakchott (INRSP), member of MLS, contacted the experts of the network for assistance. MLS contributed to the outbreak response with multisectoral technical and logistical support, providing reagents for molecular and serological diagnostics, and assistance in sequencing of the epidemic strains in human and animals. The experts, medical entomologists and human and animal virologists, advised on the decision flowchart for INRSP and on the risk mapping of the epidemic. MLS also helped to improve the sensibilization of breeding farmers on RVF risks and to activate the support of the World Organisation for Animal Health in North Africa.

Conclusion or Scope

This experience, as others carried out by MLS, provides guidance and strategies for One Health preparedness against arbovirus infections.

Acknowledgement

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Keywords: One Health; vector-borne diseases; arboviruses; outbreak

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15038

Enhancing preparedness through the integration of One Health approaches: the Anthrax case in Armenia

Claudia Robbiati[1] ; Alessia Milano[1] ; Silvia Declich[1] ; Paolo Calistri[2] ; Ombretta Pediconi[2] ; Laura Amato[2] ; Lusine Paronyan[3] ; Georgi Avetisyan[4] ; Maria Grazia Dente[*1]
[1]Center for Global Health/ Istituto Superiore di Sanità/ Italy (Italia), [2]COVEPI/ Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale"/ Italy (Italia), [3]Zoonotic and Parasitic Diseases Epidemiology / National Center for Disease Control and Prevention/ Armenia (□□□□□□□□), [4]Veterinary inspectorate/ Food Safety Inspection Body / Armenia (□□□□□□□□)

Introduction and Objectives or Purpose

Anthrax is endemic to Armenia and the country recently experienced two outbreaks of the cutaneous form. Ecosystems change, excessive exploitation of the territory, intermittent vaccination campaigns, weak health and animal surveillance systems, are among the most important drivers of Anthrax, which can exacerbate poverty and inequalities. Thus, One Health (OH), which promotes the collaboration among different sectors, can be a strategic approach especially in low resources settings. This study explored to what extent the OH approach was integrated within the response actions during the last Anthrax outbreak in Armenia.

Methods

We identified and discussed the priority areas to enhance OH preparedness in the Policy Brief "OH-based conceptual frameworks (OHCF) for comprehensive and coordinated prevention and preparedness plans addressing global health threats" and we developed a OHCF to address these priorities at national and international level.

We used the OHCF to assess, with a bottom-up process, aspects of the response to the Anthrax outbreak in Armenia that could have been enhanced by OH integration. Around 15 national stakeholders from Armenian ministries, research institutions, and laboratories from several relevant sectors were engaged over three participatory workshops from March to May 2022.

Results or Focus

The analysis pointed out the following aspects, which would have enhanced the response: greater involvement of the WHO-IHR national capacities; the availability of a multi-sectoral Anthrax preparedness plan and an integrated database; risk assessments involving the relevant sectors; multi-sectoral training and ad hoc research studies addressing also the socio-environmental drivers.

Conclusion or Scope

The OHCF is a useful tool to highlight weak aspects in the local preparedness system that could benefit from the integration of OH and it can be used to review actions taken at national level to reinforce preparedness capacity.

Acknowledgement
Study supported by MediLabSecure (European Commission/DEVCO: IFS/2018/402-247)

Keywords: One Health Preparedness; Anthrax; Armenia

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15058

HOW ARE ONE HEALTH PLANS FOR ZOONOSES ADDRESSING THEIR DRIVERS?

Alessia Milano*[1] ; Claudia Robbiati[1] ; Silvia Declich[1] ; Kevin Di Domenico[2] ; Laura Mancini[2] ; Flavia Riccardo[3] ; Gaia Scavia[4] ; Maria Grazia Dente[1]
[1]National center for global health/ Istituto Superiore di Sanità/ Italy (Italia), [2]Ecosystem and Health/ Istituto Superiore di Sanità/ Italy (Italia), [3]Infectious diseases/ Istituto Superiore di Sanità/ Italy (Italia), [4]Food safety, nutrition and veterinary public health/ Istituto Superiore di Sanità/ Italy (Italia)

Introduction and Objectives or Purpose

Drivers of zoonotic diseases, like improper animal husbandry and environmental transformations, need to be tackled to prevent, prepare, and respond to these threats. The One Health (OH) approach could support national and international strategies to address these drivers by involving different disciplines and stakeholders. We carried out a scoping review to investigate existing preparedness, response, and prevention plans with a OH approach, and we identified the plans and strategies that include drivers for zoonoses.

Methods

The methodology included five steps: elaboration of the research question; identification of peer-reviewed articles and grey literature documents published from January 1st, 2010, to June 14th, 2021; definition of criteria for the inclusion and analysis; charting of the information obtained; summarize and report the results. A framework consisting of three strategy areas was created to analyse the results related to drivers.

Results or Focus

A total of 1692 articles and 178 documents were identified from the peer-reviewed and the grey literature, while 95 articles and 118 documents met the inclusion criteria. 10 documents addressed zoonoses drivers. At governance level, sectors involved in an integrated approach for drivers surveillance and detection have to be actively engaged. At capacity building level, national and international plans highlight the importance of adequate zoonoses risk communication to inform the population. The need for training to recognize the drivers at the human-animal-environment interface is also emphasized. Data to identify drivers, including human behaviours and practices, potentially associated with spillovers and vulnerable hotspots need to be routinely collected.

Conclusion or Scope

The results obtained with this analysis underline the need to deepen and strengthen the operationalisation of activities to contrast potential drivers of zoonoses and include them in prevention and preparedness plans and strategies with a OH approach.

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Keywords: Drivers; Zoonoses; Plans; One Health

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Ensuring the fit of key One Health models and innovations and their implementation into health systems.
Abstract No: 14660

USE OF THE SMALLPOX AND MONKEYPOX VACCINE MVA FOR POST-EXPOSURE PROPHYLAXIS: A REVIEW

Florian Lienert*1 ; Heinz Weidenthaler2 ; Bernard Hoet1 ; Chris Chua*
1Medical Strategy/ Bavarian Nordic/ Switzerland (Schweiz), 2Medical Strategy/ Bavarian Nordic/ Germany (Deutschland)

Introduction and Objectives or Purpose

Traditional replicating smallpox vaccines can cause severe side effects. The non-replicating Modified Vaccinia Ankara (MVA) smallpox vaccine, which is also licensed for prevention of monkeypox in the U.S. and Canada, has a more favorable safety profile than replicating smallpox vaccines and is therefore ideally suited for pre-event vaccination. Given its approved dosing regimen of 2 doses over 4 weeks, it has however been questioned whether the immune response to MVA would be induced fast enough to also protect individuals in a post-exposure setting.

Methods
Here we review the available data on the induction of an immune response and the onset of protection after a single dose of MVA.

Results or Focus

Animal models have shown that a single dose of MVA can provide protection when administered before a challenge with an orthopoxvirus. This has been observed in mice challenged with a lethal dose of vaccinia virus and in non-human primates challenged with monkeypox virus. Compared to replicating smallpox vaccines, MVA induced a faster immune response and an earlier onset of protection. In clinical trials, a single dose of MVA induced comparable levels of vaccinia-neutralizing antibodies as a replicating smallpox vaccine and led to a robust memory response to a booster dose provided 2 years after primary immunization. MVA has also been studied in animal models that involved vaccination post an exposure to an orthopoxvirus. In these studies, MVA showed higher efficacy than replicating vaccines, likely because replication-competent viruses require sufficient time for antigen amplification and due to the higher dose of MVA that is safely tolerated.

Conclusion or Scope
In conclusion, the fast onset of a protective immune response after one dose of MVA and the limited data on the post-exposure efficacy of replicating smallpox vaccines support the use of MVA for offering protection to individuals in a post-exposure prophylaxis setting.

Keywords: smallpox; monkeypox; vaccine; MVA; post-exposure

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: One Health perspectives on bi-directional and indirect impacts on humans and animals
Abstract No: 15226

Economic impact of Rabies in Bangladesh through a One Health approach

Jinnat Ferdous*[1] [2] ; Ariful Islam[2] [3] ; Catherine Machalaba[2] ; Md. Ashiqur Rahman[1] [2]
[1]NA/ Institute of Epidemiology, Disease Control & Research, (IEDCR)/ Bangladesh (□□□□□□□□), [2]NA/ EcoHealth Alliance/ United States, [3]Centre for Integrative Ecology/ Deakin University/ Australia

Introduction and Objectives or Purpose

An estimated 1.6 million people suffer from animal bites, resulting in approximately 2,100 reported human rabies deaths annually in Bangladesh. Using a One Health lens, we aimed to estimate the cost associated with human and animal rabies cases in the country.

Methods

Between January-May 2019, we surveyed households of human rabies (n=6) and reported animal bite (n=127) cases from the Infectious Disease Hospital, Dhaka and four district general hospitals, farmers with rabies cases in livestock (n=125), and individuals (n=60) from markets representing the general population to understand impacts.

Results or Focus

63.0% of bite cases in humans and 95.7% of animal bite cases originated from dogs. The total costs per human clinical case and bite case were US $1,067.7, and US $33.4 respectively. Patients were absent from work for a mean of 2.8 days (0-53 days) whereas caregivers lost between 0-135 days. Of clinical cases and bite cases in humans, none received preventive measures and 9.8% (n=13) of patients' families sought help from a traditional healer which cost them US $1.19-$118.63. The average cost per animal case was US $4,146.4, 86% from production deprivation and 11.8% for mortality. Among the general population sampled, 63.3% were somewhat worried about getting rabies, though only 8.3% took preventive measures, with their mean cost of prevention US $54.81. Cost due to behavior change ranged from US $0-$14.24. National costs of bites and clinical cases were estimated at US $2,538,618 in humans and US $6,758,584 in animals, plus human productivity losses and avoidance costs totalling US $26 million.

Conclusion or Scope

This study generated the first national estimate of the economic impacts of rabies across sectors. As humans and animals are mostly infected by dogs, the cost-effectiveness of mass dog vaccination should be examined to inform policy planning and risk mitigation of rabies in Bangladesh.

Keywords: Rabies, economic loss, one health, survey, Bangladesh, policy

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Animal and human vaccines and other preventive interventions for pandemic preparedness: Costs, benefits and risks of animal vaccination
Abstract No: 14731

A PROGRESSIVE MANAGEMENT PATHWAY TO SUPPORT EFFECTIVE INTEGRATION INTO NATIONAL ACTION PLANS FOR ANTIMICROBIAL RESISTANCE OF FOOD AND AGRICULTURE SECTORS

Jieun Kim*[1] ; Koen Mintiens[1] ; Antonio Valcarce[1] ; Francesca Latronico[1] ; Junxia Song[1]
[1]CJW/NSAH/ Food and Agriculture Organization of the United Nations/ Italy (Italia)

Introduction and Objectives or Purpose

Antimicrobial resistance (AMR) is a global threat to health and development and requires a One Health approach. While 157 countries have developed National Action Plans on AMR (NAPs-AMR), only 32 countries implement them using effective monitoring and evaluation systems. In addition, the implementation gap of NAPs-AMR is related to a lack of governance incorporating all AMR-relevant sectors and funding. To overcome those barriers, we developed the Progressive Management Pathway for AMR (PMP-AMR), a practical guidance framework to monitor NAP-AMR implementation with a specific focus on the food and agriculture sectors.

Methods

PMP-AMR adopted the FAO’s stepwise approach, developed to control high-impact animal diseases like foot-and-mouth disease. The PMP-AMR proposes specific topics and activities which can be implemented by countries step-by-step to achieve optimal management of AMR. The topics and activities were identified through consultation with internal and external experts and grouped under focus areas (raising awareness, collecting evidence, enhancing governance, and enabling good practices) in alignment with the FAO Action Plan on AMR.

Results or Focus

The PMP-AMR approach allows countries to monitor the implementation of NAP-AMR especially incorporating the food and agriculture sectors into the multi-sectoral approach to address AMR. As of June 2022, twenty-three countries have used the PMP-AMR to assess their progress on AMR management and identify short- and medium-term actions to improve the level of implementation of their NAPs-AMR.

Conclusion or Scope

The PMP-AMR promotes an open discussion on AMR between the stakeholders while performing the self-assessment and identifying the short-term actions. The identified action has been an essential lever for recurring more resources to address AMR in the food and agriculture sectors. Therefore, countries can progress in the implementation of the NAPs-AMR with a One Health approach into actions by addressing the food and agriculture components.

Acknowledgement

Keywords: Antimirobial Resistance; AMR; National Action Plan; One Health approach; Progressive Management Pathway for AMR;

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Animal and human vaccines and other preventive interventions for pandemic preparedness: Costs, benefits and risks of animal vaccination: economics of vaccines in relation to antibiot
Abstract No: 14900

LEGAL BARRIERS TO THE “ONE HEALTH” APPROACH IN INDIA: PLACING ONE HEALTH APPROACH AT THE HEART OF COVID-19 RECOVERY

Kashish Aneja[*1 1] ; Rituparna Padhy[2] ; Katherine Ginsbach[1] ; Sam Halabi[1] ; Katie Gottschalk[1] ; Alison Durran[1]
[1]Law/ O’Neill institute for National and Global Health Law, Georgetown University/ United States, [1]Law/ Supreme Court of India/ India [2]Law/ National Law University, Odisha/ India

Introduction and Objectives or Purpose

The COVID-19 pandemic has highlighted glaring inadequacies in national legal preparedness and responses of low/lower-middle income countries (LMICs), which are further weakened by financial limitations. It has underscored the necessity of adopting an integrated approach towards sustainably balancing the health of people, animal and ecosystems and promoting One Health (OH).

Methods

Laws and policies on the COVID-19 Law Lab adopted by Asian countries during the pandemic are qualitatively reviewed. The Indian subcontinent in particular has witnessed significant OH-related policy changes during the ongoing pandemic. In May 2020, the Indian government’s Department of Biotechnology constituted a National Expert Group to promote multi-sectoral, transdisciplinary collaboration and cooperation for achieving an OH framework. Two states, Uttarakhand and Karnataka, have subsequently launched pilot programs from June 2022 to develop a national OH Framework. In 2022, the Ministry of Science and Technology also reported a list of OH initiatives “to evaluate the concept of one health for all living organisms including the invisible biota in soil that sustain our agricultural systems”.

Results or Focus

The federal structure in India has contributed to inconsistent regulation across states. Exacerbated by outdated public health legislations such as the Epidemic Diseases Act 1897, the incompatibility between health-related and environmental laws adversely affects the potential of an OH framework. As countries begin to review their legislative frameworks for pandemic preparedness, it is imperative to urgently address the regulatory gaps holistically by placing the OH at the heart of legal and policy reforms for controlling and preventing zoonotic diseases.

Conclusion or Scope

Legislations are vital for translating OH objectives into concrete, actionable and enforceable rights and duties. Lessons from analyzing the legal barriers to the OH approach in India will help address the complex regulatory challenges to the prevention of and effective legal response to zoonotic disease outbreaks, particularly in LMICs.

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Animal and human vaccines and other preventive interventions for pandemic preparedness: Costs, benefits and risks of animal vaccination: economics of vaccines in relation to antibiot
Abstract No: 15174

Sustained One Health practices for long-term control of Human African Trypanosomiasis infections in Uganda through economically viable strategies

Susan Welburn*[1] ; Charles Waiswa[1]
[1]Infection Medicine/ The University of Edinburgh and Zhejiang University / United Kingdom

Introduction and Objectives or Purpose

Human African Trypanosomiasis (HAT) is caused by trypanosome parasites transmitted by tsetse flies. Trypanosoma brucei rhodesiense HAT (rHAT) causes acute disease in East Africa and the primary reservoir for infection is domestic cattle. For control the source of infection must be eliminated from the cattle reservoir; cattle are long-term investments on which livelihoods depend and any disease control strategy must be cost-effective to farmers to be sustainable in the long-term.

Methods

Over 18% of cattle in south-eastern Uganda were shown infected with T. b. rhodesiense and treating 86% of cattle with a curative and prophylactic chemotherapeutic (i.e. parasite-killing, or ‘trypanocidal’) drug could prevent disease transmission. We have since shown that spraying only 25% cattle with inexpensive insecticide applied to only the legs and belly of cattle could sustainably prevent transmission.

Results or Focus

Stamp Out Sleeping Sickness PPP (SOS) oversaw treatment of 500,000 cattle (2006-2008) with trypanocidal drugs across 7 districts in Northern Uganda, resulting in 75% reduction of trypanosome prevalence and a 90% reduction in HAT cases. Monthly application of insecticide to cattle brought R0 <1, preventing rHAT transmission. In practice, treatment of only 25% village cattle offers sustained protection from both animal trypanosomiasis and rHAT and increased cattle productivity by USD30 per head adding USD98 per month household income.

Conclusion or Scope

rHAT is virtually eliminated as a public health problem in Uganda. A new national policy with the Coordinating Office for Control of Trypanosomiasis in Uganda mandates routine spraying of 25% cattle, delivered with the community. More than 1,000,000 cattle are treated annually, adding USD30,000,000 into impoverished communities.

Acknowledgement
SOS is one of the most successful examples of One Health in practice. Support from Department of International Development, UK, EU FP7, Ceva Sante Animale, IKARE, AVIA GIS and the Government of Uganda, COCTU and Makerere University have supported the sucesss of this long-term partnership.

Keywords: One Heath, Human African trypanosomiasis, control, economics

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Animal and human vaccines and other preventive interventions for pandemic preparedness: Optimal deployment and new strategies (e.g. oral vaccines) for vaccines
Abstract No: 14739

Seroprevalence of COVID-19 and vaccine immunogenicity in healthcare workers in Hong Kong: a longitudinal cohort study

Wey Wen Lim[*1] ; Samuel Cheng[1] ; Loretta Mak[1] ; Dennis K. M. Ip[1] ; Gabriel Leung[1 2] ; Benjamin Cowling[1 2] ; Malik Peiris[1]
[1]School of Public Health, Li Ka Shing Faculty of Medicine/ The University of Hong Kong/ Hong Kong (□□) [2]Laboratory of Data Discovery for Health Limited/ Hong Kong Science Park / Hong Kong (□□)

Introduction and Objectives or Purpose

COVID-19 is a potentially fatal acute respiratory disease that has caused great health and economic impact worldwide. The protection of health care workers (HCWs) is crucial to ensure patient safety and maintain a working healthcare system during a pandemic. An accurate assessment of the risk of infection and the effectiveness of public health measures in HCWs, including vaccination, are needed to support policy decisions surrounding public health measures in the community as well as infection control measures in healthcare settings.

Methods

We conducted a longitudinal cohort study with continuous follow-up and sequential blood samples collected at six-month intervals from June 2020 through to April 2021. Seroprevalence of COVID-19 every six months (Round 1 = May – November 2020, Round 2 = December – May 2021) was calculated as a percentage of samples that tested positive for anti-SARS-CoV-2 neutralising antibodies by plaque reduction neutralisation test (PRNT) collected during that period.

Results or Focus

Overall seroprevalence in Round 1 was estimated to be 0% with a 95% confidence interval of 0% to 0.50% despite heavy exposure to COVID-19 patients in our HCW cohort. In Round 2 the overall seroprevalence was slightly higher at 0.52% (95% CI 0.14, 1.32). Both the mRNA BNT162b2 and inactivated CoronaVac vaccines generated significant rises in antibody levels after the first and second doses among HCWs in our cohort.

Conclusion or Scope

The seroprevalence of COVID-19 in HCWs in Hong Kong was low during the first 1.5 years into the COVID-19 pandemic. Surveillance of emerging infectious diseases such as COVID-19 among longitudinal cohorts of HCWs can be used to monitor the health impact of evolving pandemics, and potential applications of such surveillance include the detection of emerging infectious diseases and the estimation of vaccine effectiveness among HCWs.

Acknowledgement

This study was supported by the Hong Kong Health and Medical Research Fund (grant no. COVID190119).

Keywords: COVID-19, seroprevalence, surveillance, vaccine immunogenicity, healthcare workers

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14751

COMBAT-AMR: Evidence-based cross-sectoral framework to assess antimicrobial resistance situation, needs and capacity

Angeline Ferdinand*[1] ; Callum McEwan[1] ; Chantel Lin[1] ; Kassandra Betham[1] ; Karishma Kandan[1] ; Barry Pugvea[2] ; Gilam Tamolsaian[2] ; Joanna McKenzie[3] ; Glenn Browning[4] ; James Gilkerson [4]
[1]Microbiological Diagnostic Unit Public Health Laboratory, Department of Microbiology and Immunology/ University of Melbourne/ Australia, [2]Health Emergencies/ Burnet Institute/ Australia, [3]School of Veterinary Science/ Massey University/ New Zealand, [4]Asia-Pacific Centre for Animal Health, Melbourne Veterinary School/ The University of Melbourne/ Australia

Introduction and Objectives or Purpose

Here we describe development and implementation of a purpose-built, cross-sectoral Antimicrobial Resistance (AMR) Situation and Needs Assessment Framework through the Combating the threat of AMR across Pacific Island Countries (COMBAT-AMR) program.

AMR is a growing threat in Pacific Island Countries (PICs). COMBAT-AMR is a capacity-building program to improve prevention and surveillance of AMR for human and animal health in PICs. To inform development of COMBAT-AMR activities, we designed and implemented a comprehensive AMR Situation and Needs Assessment Framework to review national-level and local policies and practices.

Methods

A rapid scoping review identified existing AMR situation assessment frameworks at the national level, and for the COMBAT-AMR program themes: Infection Prevention and Control, Antimicrobial Stewardship, Laboratory Capacity and Surveillance and Animal Health. Strengths and weaknesses of existing tools were identified, followed by an iterative process of tool development and refinement.

Tools were developed using REDCap and designed to be suitable for benchmarking and assessment. Piloting was undertaken across Australian hospitals and human and veterinary laboratory sites prior to implementation in participating PICs. Data ownership protocols were incorporated into the Framework, ensuring data custodianship remained with the collection site.

Results or Focus

The Framework was implemented across four countries, with subsequent analysis and reporting undertaken to identify capacity-building opportunities. Framework results formed the basis of program design, including training, updating treatment guidelines and SOPs, strengthening antimicrobial stewardship and strengthening multisectoral collaboration. The Framework has been integrated into program evaluation by enabling changes in key criteria to be tracked over time.

Conclusion or Scope

The Framework facilitated a systematic approach to workplan development, ensured program alignment with key national priorities, strengthened collaboration, and contributed to increased understanding and engagement from key stakeholders. The Framework is adaptable and available to other settings nationally and internationally.

Acknowledgement

COMBAT-AMR is funded by the Australian Department of Foreign Affairs and Trade Centre for Health Security.

Keywords: Situation assessment; Monitoring and evaluation; Program development; Cross-sectoral

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Animal and human vaccines and other preventive interventions for pandemic preparedness: Optimal deployment and new strategies (e.g. oral vaccines) for vaccines
Abstract No: 14868

INCIDENCE OF PERTUSSIS AMONG ADULTS AGED ≥50 YEARS IN AUSTRALIA

Jing Chen*[1] ; Rodney Pearce[2] ; Ken Chin[3] ; Adrienne Guignard[4] ; Leah-Anne Latorre[5] ; C Raina MacIntyre[6] ; Brittany Schoeninger[7] ; Giles Stratton[7] ; Sumitra Shantakumar[1]
[1]Epidemiology and Health Outcomes/ GSK/ Singapore, [2]General Practice/ Medical HQ Family Practice/ Australia, [3]Real World Evidence/ IQVIA/ Australia, [4]Vaccines R&D/ GSK/ Belgium, [5]Medical Affairs/ GSK/ Australia, [6]The Kirby Institute/ University of New South Wales/ Australia, [7]Real World Evidence/ IQVIA/ Australia

Introduction and Objectives or Purpose

In recent decades, a shift in distribution of pertussis cases towards older age groups has been reported in Australia. While pertussis is a notifiable disease in the National Notifiable Diseases Surveillance System (NNDSS), notification data are known to underestimate the number of diagnoses. This study aimed to estimate the incidence of pertussis among Australians ≥50 years in the primary care setting, including those with preexisting chronic obstructive pulmonary disease (COPD) or asthma.

Methods

A longitudinal retrospective observational study was carried out using the IQVIA general practitioner electronic medical record (EMR) database to identify patients ≥50 years diagnosed with pertussis in 2015–2019. Patients with preexisting COPD or asthma were identified based on diagnosis fields or prescribed pharmacological treatments. Incidence rates (IRs) of pertussis were reported per 100,000 persons.

Results or Focus

992 patients (mean age [95% confidence interval, CI]: 63.3 [62.7–63.9]) with pertussis were identified, of whom 283 had COPD/asthma. Pertussis IRs (95% CI) ranged from 57.6 (50.2–64.9) to 91.4 (84.1–98.7), compared with 24.3 to 56.9 as reported by the NNDSS. IRs were greater among females (70.7 [62.5–78.9] to 110.5 [102.3–118.7]) than males (41.6 [35.4–47.8] to 70.6 [64.3–76.8]) and were highest for the 50–64 years group. Patients with COPD/asthma had IRs ranging from 210.3 (195.8–224.9) to 325.2 (310.7–339.8), approximately four times higher than the overall ≥50 years population. This pattern was consistent across age groups.

Conclusion or Scope

These data suggest that Australians ≥50 years with COPD/asthma are substantially more likely to be diagnosed with pertussis versus those without. Risk was greatest among females, potentially due to grandparent caring roles. From a public health perspective, prioritising booster pertussis immunisation among Australians ≥50 years with pre-existing respiratory conditions may need to be considered.

Acknowledgement

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Keywords: Asthma; Chronic Obstructive Pulmonary Disease; Incidence; Pertussis; Vaccination

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Animal and human vaccines and other preventive interventions for pandemic preparedness: The impact of global vaccine inequity
Abstract No: 15213

ECONOMICS OF TAENIA SOLIUM CONTROL IN AN ENDEMIC AREA REVEALS A NEED FOR A PARADIGM SHIFT TOWARDS ONE HEALTH

Mwemezi Kabululu*[1] ; Helena Ngowi[2] ; Maria Vang Johansen[3] ; James Mlangwa[2] ; Enartus Mkupasi[2]
[1]Central Zone/ Tanzania Livestock Research Institute (TALIRI)/ Tanzania, United Republic of, [2]Department of Veterinary Medicine and Public Health/ Sokoine University of Agriculture/ Tanzania, United Republic of, [3]Independent/ Independent Researcher/ Denmark (Danmark)

Introduction and Objectives or Purpose

The zoonotic pork tapeworm, Taenia solium, is a parasite responsible for neurocysticercosis, the major cause of epilepsy in endemic areas. Pig vaccination with a vaccine - TSOL18, and chemotherapy using an anthelmintic - Oxfendazole (OFZ) are among the available control options. The tools have recently been evaluated in a field intervention trial in rural areas of Tanzania. This paper reports results of cost-benefit and cost-effectiveness analyses of the interventions, and implications for future control options in a One Health context.

Methods

An economic analysis was performed ex post, following a field trial to assess clinical effectiveness of an intervention using OFZ alone (T1 intervention), and another with a concurrent administration of OFZ and TSOL18 (T2 intervention). Capital and recurrent costs of intervention were determined. Intervention outcomes were valued in monetary and non-monetary terms. Benefit-cost ratios were estimated by dividing monetary benefits by intervention costs. Cost-effectiveness ratios (CERs) were computed as costs per averted zoonotic Disability-Adjusted Life Years (zDALY) - a modified metric that incorporates an animal loss equivalent.

Results or Focus

Monetary benefits were 10% and 6% of the costs of T1 and T2 interventions, respectively. Cost-effective ratios were estimated to be USD 980 and USD 1,720 for T1 and T2, respectively. Both CERs fell below the World Health Organization (WHO) threshold of three times the Gross Domestic Product per capita, hence the interventions were determined to be cost effective.

Conclusion or Scope

Although intervention costs outweighed monetary benefits, both interventions were cost effective. This means health benefits overrode financial benefits demonstrating that benefits of controlling T. solium in pigs accrue more to public health than to monetary gains of the pig farmers. These results underscore the importance of using a One Health approach in devising and implementing control strategies against T. solium.

Keywords: Taenia solium; control; cost-effectiveness; cost-benefit analysis; One Health

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Animal and human vaccines and other preventive interventions for pandemic preparedness: The need for transfer of technology and innovations in low resource settings
Abstract No: 15224

Understanding Linkages Between National One Health Platforms and Academia to Improve the One Health Workforce in Sub-Saharan Africa

Alice Stevenson*[1] ; Ava Sullivan[1] ; Elizabeth Alunguru[2] ; Milly Nattimba[2] ; Agnes Yawe[2] ; Anne Laudisoit[1] ; Stephanie Martinez[1] ; Irene Naigaga[2] ; Woutrina Smith[3] ; One Health Workforce - Next Generation Consortium [3]
[1]One Health/ EcoHealth Alliance/ United States, [2]One Health/ AFROHUN/ Uganda, [3]One Health Institute/ UC Davis/ United States

Introduction and Objectives or Purpose

National One Health platforms and academic institutions are both critical in building a competent, sustainable, and prepared One Health workforce. Even more critical is engagement and interaction between them to enhance training pipelines, identify demands for specific skills and competencies, and prioritize specific domains for pre-service education and in-service training. A literature review, a survey, and key informant interviews were conducted to understand and evaluate the current landscape of existing national One Health platforms, as well as the extent to which these platforms engage with universities and training institutions.

Methods

A rigorous review of country-level One Health workforce policy and planning evidence was conducted in six African countries. This review drew insights from various publicly available sources, including articles, reports, and policy documents. A survey was then circulated to stakeholders in academia, government ministries, and research organizations to capture practical insights and perceptions around national coordination platforms and their engagement with universities. Finally, a series of interviews was conducted with a subset of respondents who indicated a willingness for follow up and provided detailed responses in order to ground truth and expand upon survey results.

Results or Focus

The results indicated that all six countries have coordinating platforms at the national level with differing degrees of engagement with academia and that there is, overall, a strong interest in collaborating and transfering knowledge on One Health activities and innovations. They also shed light on various opportunities for improvement across the region, such as the need for formalized communication mechanisms, increased human resources, and sharing of technologies.

Conclusion or Scope

The literature review, survey, and interviews indicate that there are strengths, weaknesses, and opportunities that should be further explored, which have the potential to enhance One Health education, training pipelines, and the overall One Health workforce, thereby improving national and regional pandemic preparedness and overall health system capacity.

Acknowledgement

Keywords: Policy; Preparedness; Education; Coordination

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Animal and human vaccines and other preventive interventions for pandemic preparedness: The need for transfer of technology and innovations in low resource settings
Abstract No: 15363

ELECTRONIC-BASED INTEGRATED EPIDEMIOLOGICAL SURVEILLANCE IN MADAGASCAR: A CHALLENGE FOR THE IMPLEMENTATION OF THE ONE HEALTH PLATFORM

Mampîanina Randriambahoaka*[1] ; Rivomalala Randrianasolo[2] ; Hasina Jerson Razafindratsimba[1] ; Naltiana Rakotondrabe[3]
[1]Unité de Coordination des Projets/ Ministry of Public Health/ Madagascar (Madagasikara), [2]Direction de la Veille Sanitaire, de la Surveillance Epidémiologique et Riposte/ Ministry of Public Health/ Madagascar (Madagasikara), [3]Direction de la Santé Veterinaire/ Ministry of Agriculture and Livestock/ Madagascar (Madagasikara)

Introduction and Objectives or Purpose

Response to early epidemic outbreak is a determining factor of the impact of its burden to the country. It's known that electronic system is the best tools to reduce delay from detection to responses.

And sharing and having information for sectors is mandatory to well contain the outbreak. Thus, need for the establishment of One Health platform on e-surveillance.

The JEE of Madagascar's IHR capacity conducted in 2017 recommended improving the real-time surveillance network. The aim is to assesses the status and the best way to implement of integrated electronic surveillance (e-surveillance).

Methods

Since 2016, both public and animal health have functional e-surveillance but separately,

the common problem is the data transmission

Results or Focus

For animal health, Madagascar Animal Diseases Surveillance (MADSUR) has been set up with the support of the Surveillance Epidemiological and Alert Management (SEGA) network through the Epidemiological Surveillance and Investigation Network 3 (RSIE3) project.

By the end of 2021, more than 114 districts, and 250 sites are functional, and the 5-member countries of Commission of Indian Ocean (COI) are interconnected.

For Public Health, the DHIS 2 system has been implemented leaded by WHO. And more than 17 regions, and 67 districts with more than 1,650 health facilities using e-surveillance, i.e. 59% of the country's health facilities, the objective is reaching 90% coverage in 2024.

The average promptitude is 58%, the objective is reaching 80% in 2024, and the completeness is 80%.

Conclusion or Scope

The integration of public health, animal health and laboratory surveillance is very important for the successful functionality of the One Health platform. Excellent coordination between these stakeholders is the key to success

Acknowledgement

We thank our colleagues from DVSSER/MoH, DSV/MoAL who provided insight and expertise that greatly provided information and help, although they may have different interpretations/conclusions of this abstract

Keywords: IDSR, EIES, One Health, Challenge, Network

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Ensuring the fit of key One Health models and innovations and their implementation into health systems.
Abstract No: 14818

Targeting investments in One Health systems strengthening: A pilot from the African continent

Richard Suu-Ire*[1] ; Sarah Baum[2] ; Catherine Machalaba[2] ; Anne Laudisoit[2] ; William Karesh[2]
[1]School of Veterinary Medicine/ University of Ghana/ Ghana (Gaana), [2]Health and Policy/ EcoHealth Alliance/ United States

Introduction and Objectives or Purpose

Without guidance on how to target COVID-19 recovery investments, investments run the risk of duplicating resources; failing to fill chronic capacity gaps in public health, veterinary services, and environmental management and One Health coordination; and forgoing opportunities to generate environmental and health co-benefits. Specific entry points need to be identified to ensure investments are targeted and geared towards long-term preparedness, including for disease prevention and health protection.

Methods

Through the “Strategic Coordination to Strengthen AFRICOM One Health and Veterinary Programs for Global Health Engagement” project, we developed a One Health database of country-level data from over 30 publicly available datasets. Focusing on Africa, expert consultations ground-truthed available data and developed in-depth assessments of systems capacity in 5 regions and 11 countries, capturing aspects of One Health governance and multi-sectoral coordination platforms and disease management (surveillance, reporting, diagnostics, and vaccine availability). Disease case studies captured specific barriers to implementing One Health programs and policies as well as best practices. SWOT analyses (strengths, weaknesses, opportunities, and threats) for each country and region were generated to pinpoint entry points where investment and coordination could offer added value.

Results or Focus

There are stark regional variations in veterinary and human medical workforce capacity, with insufficient coverage where emerging infectious disease risk is higher and access to water, sanitation, and hygiene is more limited. Overall, the continent has a strong presence of One Health coordination mechanisms, particularly at national levels, and interest in One Health research. However, there are chronic gaps in animal and environmental health systems, including wildlife disease surveillance, sub-national laboratory capacity, and public sector veterinary workforce development in settings with key emerging disease risk interfaces and ongoing endemic disease burden.

Conclusion or Scope

Addressing chronic gaps in animal and environmental health system capacities must be a core part of strengthening One Health systems for resilient and long-term preparedness.

Keywords: Investment; Resilience; SWOT

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health:

Ensuring the fit of key One Health models and innovations and their implementation into health systems.
Abstract No: 14936

One-Health Initiatives by Department of Animal Husbandry and Dairying, Government of India

Dr Praveen Malik*[1] ; Dr Raj Kumar Singh[2] ; Dr Aruna Sharma[1] ; Dr Abhijit Kumar Jha[2] ; Dr Vijay Kumar Teotia[1] ; Dr Amit Kumar Tripathy[2] ; Dr Indrani Ghose[2] ; Dr Sindura Ganapathi[3] ; Dr Srivalli Krishnan[4] ; Dr Rahul Srivastava[5]
[1]Department of Animal Husbandry and Dairying/ Ministry of Fisheries, Animal Husbandry and Dairying, Government of India/ India, [2]Food and Agriculture Centre of Excellence (FACE)/ Confederation of Indian Industry/ India, [3]Government of India/ Office of the Principal Scientific Advisor to the Government of India/ India, [4]Global Development/ Bill and Melinda Gates Foundation (BMGF)/ India, [5]Public Private Partnership/ World Organisation for Animal Health (WOAH)/ France

Introduction and Objectives or Purpose

Besides zoonotic diseases, exotic animal diseases of economic significance like African Swine Fever do pose threats to food security, economy, and livelihood. Recognizing the challenges, Department of Animal Husbandry & Dairying (DAHD), Government of India took initiatives to address the emerging infections through One-Health approach wherein the focus of activities revolves around intersectoral coordination, capacity building, reporting, information sharing across sectors and outreach. Going beyond explaining One-Health concept to stakeholders, our focus has been directed on its implementation.

Methods

One Health Support Unit (OHSU) was established by DAHD with funding support from BMGF and CII as implementing agency. To pilot the proposed interventions, two states (Uttarakhand and Karnataka) were selected using various ranking indices including operational and non-operational parameters. The disease selection and prioritization was done using a questionnaire which was divided in five broad categories having 37 criteria. The interventions would use the priority diseases to assess the gaps and potential solutions.

Results or Focus

The interventions with the above referred aims would encompass the strengthening of field and diagnostic capacities, networking of laboratories networking, digital disease reporting and response and strengthening of biosafety and biosecurity in farm settings towards achieving “Predict-Prevent-Detect-Respond” doctrine. The strong data management can eventually be used for disease modelling, timely response and robust policy interventions. The training materials on these issues will be developed both for multisectoral professionals and public at large.

Conclusion or Scope

This program along with other DAHD initiatives like NDLM, doorstep delivery of veterinary services through MVUs, and nationwide vaccination program against critically important diseases and streamlining regulatory approval processes will pave the way towards better animal pandemic preparedness to handle any unknown infections in future. The pilots will help develop a national roadmap for improved animal health system for effective implementation of one health.

Keywords: One-Health; Predict-Prevent-Detect-Respond; NDLM; DAHD; Capacity-building; pilot; roadmap; biosafety

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Ensuring the fit of key One Health models and innovations and their implementation into health systems.
Abstract No: 15167

Sustaining health services during COVID19 pandemic: A case of Inter-sectoral collaboration & health system resilience from Ahmedabad, India

Sandul Yasobant*[1 2 3 4] ; Deepak Saxena[1 3] ; Hardi Thacker[1] ; Shruti Lekha K[1] ; Ravina Tadvi[1] ; Timo Falkenberg[2 4] ; Walter Bruchhausen[2 4]
[1]Center for One Health Education, Research & Development / Indian Institute of Public Health Gandhinagar/ India, [2]Global Health, Institute for Hygiene & Public Health / University Hospital Bonn/ Germany (Deutschland), [3]School of Epidemiology and Public Health/ Datta Megha Institute of Medical Sciences/ India, [4]One Health Graduate School, Center for Development Research/ University of Bonn/ Germany (Deutschland)

Introduction and Objectives or Purpose

The COVID-19 pandemic continues to pose severe challenges to health system resilience beyond the impact of the disease itself. Given the severe disruption of routine healthcare services, countries have developed and implemented strategies to mitigate their existing health system strengths. This research aimed to document how the multi-sectoral collaborations played a role in maintaining routine health services during the COVID-19 pandemic in a local health system in a Western city of India, Ahmedabad.

Methods

This study used a mixed method approach with quantitative and qualitative data collection and samples drawn from administrative (both health and non-health sectors), clinical (both public and private healthcare practitioners), and community levels (both COVID +ve and -ve mothers) during 2021-22. All potential sectors that collaborated and/or contributed to the health system's resilience were documented, and their collaboration pattern was explored, especially for the maternal and child health services. The quantitative data were analysed in STATA 14.1 and qualitative data were analysed in ATLAS.Ti 8.

Results or Focus

Different multi-sectoral collaborations were documented between health and non-health departments (like animal husbandry, fire, education, media, engineering, estate, and transport corporation) in Ahmedabad city for routine service delivery. The service delivery was hindered the most during the 1st wave and least during the 3rd wave. The services like two doses of TT and follow-up visits post-delivery were significantly reduced during 1st wave. Positive women availed of fewer services than negative mothers. Although there were multi-sectoral collaborations with different sectors, human resources management towards uninterrupted service delivery remained a challenge.

Conclusion or Scope

This study documented a classic case of multi-sectoral collaboration on maintaining the health system resilience through routine health service delivery during the COVID-19 pandemic. A similar kind of evidence is recommended to generate with respect to the diverse healthcare system, which will be vital for the pandemic preparedness plan in future.

Keywords: Health system, health services, pandemic, COVID-19, India

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Harmonisation of regulatory standards for pandemic response or research
Abstract No: 14793

Evaluation of the planning and performance of the “one health” platform with the OH-APP tool in Côte d’Ivoire

Aristide Dionkounda*[1] ; Serge Agbo[2] ; Sita Savané[3] ; Florence Kadjo[3] ; Alain Marc Kouadio[3] ; Youssouf Traoré[3] ; Daniel Cohn[1] ; Elodie Brandamir[1]
[1]TDDA (Tackling Deadly Diseases in Africa)/ DAI/ Ivory Coast [2]Global health/ Resolve to save lives/ Ivory Coast [3]Public Health/ INHP/ Ivory Coast

Introduction and Objectives or Purpose

Support the operationalisation of the “One Health” platform in Côte d’Ivoire through a self-evaluation of the platform’s organisational capacity and performance one year after the signing of the decree on the creation of the “One Health” Platform in 2019.

Methods

The assessment is carried out in December 2020 by national facilitators from different sectors of human, animal and environmental health and research trained in the OH-APP tool. The OH-APP incorporates two assessment components: the organisational capacity with 11 indicators and performance with 19 indicators. The assessment with the OH-APP tool is based on the degree of maturity (start, development, maturity and expansion). The OH-APP tool uses a participatory decision-making methodology. Participants discuss each measure to agree on the maturity level of the indicator.

Results or Focus

In general, the organisational capacity and organisational performance of the Platform have reached a Platform maturity level of “development”. However, the “development” level of organisational capacity is higher than that of organisational performance. Of the 11 organisational capacity indicators, 4 are at the “mature” level, 2 are at the “expanding” level and 5 are at the “developing” level. For the 19 organisational performance indicators, 3 have reached the “mature” level, 5 are “expanding”, 9 are “developing” and 2 are still at the “beginning” level. The status of gender is at the ‘mature’ level in terms of composition and inclusion, while it is at the ‘developing’ level in terms of preparation and planning of interventions and gender considerations when responding to events of unknown etiology.10 priority indicators were identified which were then used to develop the action plan matrix

Conclusion or Scope

Basic benchmarks for interventions and technical assistance have been established and a one-year roadmap for progress in the key priority areas identified by the One Health Platform was developed.

Acknowledgement

Côte d’Ivoire National One Health Plateforme

DAI Global Health

Keywords: Côte d’Ivoire; OH-APP;One Health

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Harmonisation of regulatory standards for pandemic response or research
Abstract No: 14935

Instituting a Multi-sectoral Collaboration for Public Health Emergency Preparedness and Response at a Point of Entry using a One-Health Paradigm.

Elizabeth Titilope Ajayi-Ogbe*[1] ; Samuel Alabi[1] ; Olaoluwa Akinloluwa[1] ; Olamide Pitan-Atolagbe[1] ; Abdullai Lawal[2] ; Onyekachi Nwitte-Eze[3] ; Juliet Hananiya[1] ; Geoffrey Okatubo[3]
[1]Integrated Response to Public Health Emergencies in Nigeria/ Pro-Health International/ Nigeria, [2]Port Health Services/ Federal Ministry of Health/ Nigeria, [3]Port Health Services/ Federal Ministry of Health/ Nigeria

Introduction and Objectives or Purpose

A key recommendation following Nigeria's WHO IHR Joint External Evaluation and action documented in the National Action Plans for Health Security, was institutionalizing all-hazards multisectoral, multi-disciplinary coordination and response mechanisms to public health events/emergencies through the One Health Approach. Pro-Health International (PHI) partnered with Port Health Services Federal Ministry of Health (PHS-FMOH) to facilitate the process of reviewing public health emergency preparedness plans at designated Points of Entry (POE) to reflect this approach. The POE is critical to mitigating PHEs/events due to the increase in traffic and trade.

Methods

PHI supported the PHS-FMOH at the Murtala Mohammed International Airport (MMA), to lead the review and operationalization of the MMA PHECP bringing the one-health paradigm into play. The response coordination and collaboration mechanism are incorporated and designed by a multi-sectoral and multi-stakeholder team who put into cognizance all areas of the one-health approach – human, animal, and the environment as all these may be affected in the advent of a public health event of international concern.

Results or Focus
Key stakeholders (human, animal, and environment - chemical, radiological, and/or nuclear), convergence, and interest points in all individual stakeholder plans were identified. The one-health multisectoral plan was anchored on these convergence points to ensure ownership and sustainable coordination between animals, humans, and the environment. This made the PHECP a multi-hazard document with clear terms of reference for the stakeholders.

Conclusion or Scope

A mechanism to promptly activate/mobilize human and capital resources from stakeholders across the different sectors for coordinating response to public health events/emergencies centered on the One Health Approach. This is suitable for countries with complex structures and limited independent funding for public health institutions.

_I would like to say thank you to the technical team and Leadership of PHI, PHS, and stakeholders at the MMA for their role and unwavering support in the success of the process.

Keywords: Multi-sectoral; All-hazards; Public Health Emergency Contingency Plan; One-Health; Public Health Emergency Preparedness and Response

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Harmonisation of regulatory standards for pandemic response or research
Abstract No: 15116

Using legislation to underpin a One Health approach to address antimicrobial resistance

Maarten Van der Heijden*[1] ; Carmen Bullón[2] ; Ambra Gobena[2] ; Camille Loi[3] ; Teemu Viinikainen, [2] ; Valeria Pasarin Linares [2] ; Li (Sara) Yingjing[2] ; Kelsey Galantich[3] ; Jorge Matheu Alvarez[1]
[1]Antimicrobial Resistance/ World Health Organization/ Switzerland (Schweiz), [2]Development Law Service of the FAO Legal Office/ Food and Agriculture Organization of the United Nations/ Italy (Italia), [3]Capacity-Building Department/ World Organisation for Animal Health/ France

Introduction and Objectives or Purpose

To introduce the Quadripartite One Health Legislative Assessment Tool for Antimicrobial Resistance (AMR) and illustrate how legislation can support One Health approach for governance solutions to address AMR.

Through extensive consultatiosn with legal and technical experts across disciplines, a team from the international organizations representing the AMR Quadripartite developed a Tool to facilitate the assessment of national legislation relevant for addressing AMR. The paper will be based on this experience and will incorporate a comparative review and analysis of legal doctrine, policy analysis and case studies from the field.

Results or Focus

The Tool assists countries in the identification of regulatory gaps, and enables the prioritization of solutions through legal reform, thereby improving the capacity of countries to curb AMR. The Tool facilitates the examination of a range of legislative instruments and governance arrangements at local, region/province and national levels. Adopting a One Health approach that integrates and sustainably balances the health of people, animals and ecosystems, this Tool targets key regulatory elements in (1) AMR governance (2); human health, (3) animal health and production, (4) food safety, (5) pesticide management, (6) plant health and (7) the environment. Cross-cutting themes and the need for multidisciplinary perspectives are emphasized to ensure multisectoral coordinated action against AMR. This Tool is currently being implemented in four countries prior to a wider rollout and implementation.

Conclusion or Scope

Legislation is often important or essential for many actions identified as a priority in National Actions Plans for AMR. A One Health approach to AMR requires a multidisciplinary response, among them multisectoral coordination mechanisms. In addition to bringing together a range of stakeholders as part of its development process, legislation formalizes and strengthens governance and accountability at local, regional and national levels within and across sectors and actors.

Acknowledgement

Funding was kindly provided by the funders of the Antimicrobial Resistance Multi-Partner Trust Fund.

Keywords: antimicrobial resistance; legislation; law; regulation; one health; governance; antibiotics; antimicrobials; human; animal; food safety; environment

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Harmonisation of regulatory standards for pandemic response or research
Abstract No: 15233

Regulation in the animal health system in Cambodia: opportunities to make progress towards One Health Objectives

Katherine Gilbert[1] ; Sreytouch Vong[*2] ; Suon Sothoeun[3] ; Has Phalmony[4] ; Justin McKinley[1] ; Barbara McPake[1]
[1]Health Systems, Governance and Financing / Nossal Institute for Global Health, School of Population and Global Health, University of Melbourne/ Australia, [2]Independent Consultant / One Health Researcher/ Cambodia (□□□□□□□), [3]General Directorate of Animal Health and Production/ Ministry of Agriculture Forestry and Fisheries/ Cambodia (□□□□□□□), [4]National Institute of Public Health/ Ministry of Health / Cambodia (□□□□□□□)

Introduction and Objectives or Purpose

Regulatory strategies can be used to strengthen animal health systems to achieve One Health objectives. This study aimed to explore constraints in the supply and demand of animal health system in Cambodia and to identify opportunities to use regulation to strengthen it, drawing on approaches used in governing the human health system.

Methods

We surveyed 1,528 smallholder livestock owners and 697 animal health workers on the supply and demand for veterinary services. We also interviewed 34 policymakers, livestock owners and animal health workers to elucidate the key issues. Data were analyzed using Stata and NVivo and interpreted at a collaborative workshop with officials from the animal health, human health and environment sectors in Cambodia held in April 2022. Ethics approval was received in Cambodia and Australia.

Results or Focus

Village Animal Health Workers (VAHWs) are the primary provider within the animal health system, especially for smallholders, yet regulatory action to ensure the accessibility, availability and quality of a package of clearly defined services that they should deliver is minimal, in contrast to the human health system. Provincial and district animal health offices hold increased responsibility for regulation of VAHW following recent decentralization reforms, but paused registration and pre- and in-service training, and other contact with VAHW, in recent years due to staffing and financial limitations.Some provincial and district offices provide VAHW with vaccines for cattle, but have limited oversight of service provision to different livestock types. Services are therefore predominantly demand driven and of variable coverage and quality, with limited information on services or diseases being gathered, collated, and acted upon.

Conclusion or Scope

The function of the VAWH within the system, including the nature and quality of services, could benefit from clear articulation in policy, and implementation through appropriate regulatory strategies, such as contracting, which has been used in the human health system.

Acknowledgement
FundIng: ACIAR, DFAT

Keywords: One Health Economics; Animal health system;

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: One Health perspectives on bi-directional and indirect impacts on humans and animals
Abstract No: 14924

THE POWER OF COLLABORATION: USING A ONE HEALTH APPROACH DURING THE U.S. GOVERNMENT RESPONSE TO COVID-19, UNITED STATES

Casey Barton Behravesh*[1] ; Kate Varela[1] ; Ann Carpenter[1] ; Natalie Wendling[1] ; Jonathan Sleeman[1] ; Ellen Hart[1 2] ; Jane Rooney[3] ; Steven Rekant[3] ; Laura Murrell[1] ; Ria Ghai[1]
[1]One Health Office/ U.S. Centers for Disease Control and Prevention (CDC)/ United States, [1]National Wildlife Health Center/ Department of the Interior/ United States [2]Center for Veterinary Medicine/ Food and Drug Administration/ United States [3]Animal and Plant Health Inspection Services (APHIS) / U.S. Department of Agriculture (USDA)/ United States

Introduction and Objectives or Purpose

In the United States, a formalized One Health coordination mechanism did not exist prior to the COVID-19 pandemic. In February 2020, CDC's One Health Office led the establishment of a federal coordination mechanism for One Health activities relevant to COVID-19, called the One Health Federal Interagency COVID-19 Coordination (OH-FICC) group. Here we describe OH-FICC function and outcomes that were instrumental in unifying U.S. government partners around One Health during the pandemic.

Methods

A One Health approach was used to identify U.S. officials from multiple departments and develop a flexible One Health coordination structure. OH-FICC leadership stood up five subgroups based on joint priorities which collaboratively developed resources and provided technical assistance. We assessed impact of the OH-FICC by analyzing metrics on joint resources and SARS-CoV-2 case/outbreak investigations, and by deploying a survey among OH-FICC members.

Results or Focus

As of June 2022, the OH-FICC includes approximately 150 officials from 23 federal agencies. Examples of coordinated OH-FICC One Health activities include joint field investigations; virtually supporting >300 One Health case investigations; developing surveillance infrastructure and diagnostic capacity; and establishing routine coordination calls. Overall, 18 jointly developed guidance and informational webpages were released with >19 million views. OH-FICC survey respondents reported increased quality (84%) and effectiveness (74%) of interagency coordination, expanded networks (90%), and more participation in cross-agency One Health activities (53%).

Conclusion or Scope

The OH-FICC is an example of an effective One Health interagency coordination structure. It facilitated harmonized U.S. government communication and enhanced surveillance, response, and research on zoonotic SARS-CoV-2. Because of increasing attention on One Health, in 2021, Congress asked CDC to lead interagency efforts to stand up a formalized One Health coordination mechanism that will strengthen One Health collaboration at the federal level. Lessons learned from the OH-FICC will be applied to future One Health coordination in the United States.

Acknowledgement

Authors thank OH-FICC members.

Keywords: Coordination mechanism; One Health; COVID-19; zoonotic diseases; interagency coordination

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health Strengthening Community Capacity
Abstract No: 14817

CONTINUOUS ADVOCACY AS A TOOL FOR ENHANCING THE IMPLEMENTATION OF THE NATIONAL ACTION PLAN FOR HEALTH SECURITY IN NIGERIA

Oguntola Ibukun*[1] ; Kemisola Agbaoye[1] ; Vivianne Ihekweazu[1] ; Beti Baiye[1]
[1]Prevent Epidemics Project/ Nigeria Health Watch/ Nigeria

Introduction and Objectives or Purpose

Nigeria is a signatory to the World Health Organisation (WHO) International Health Regulation (IHR) framework, This led to the use of the JEE to assess the country's IHR capacity in 2017 and again in 2019. Out of the JEE, a National Action Plan for Health Security (NAPHS) was developed to address the gaps in Nigeria's health security architecture. The implementation of the NAPHS has been challenging due to a variety of issues such as funding, lack of buy-in from other MDAs etc.

The project aimed to build public and policymaker awareness and demand for epidemic preparedness funding for the implementation of the NAPHS, through advocacy and communications.

Methods

We have been able to provide extensive support to technical leads for the implementation of NAPHS. We supported the IHR co-ordination technical area through the workshops with the NAPHS focal persons to discuss implementation status, gaps and ways forward, through advocacy to MDAs to include NAPHS activities in their budget, and to the public to increase knowledge and support for the NAPHS. We supported the development of the budgets for the year 2022 to ensure that NAPHS activities are included in MDA budgets.

Results or Focus

Support for the NAPHS significantly increased for the final year of the NAPHS, particularly within non-health MDAs such as the Federal Ministry of Agriculture and Rural Development, Federal Ministry of Environment and the Office of the National Security Adviser, etc which has led to increased implementation of the NAPHS in Nigeria.

Conclusion or Scope

Through the course of the Prevent Epidemics Project, we have successfully increased conversations around epidemic preparedness and have leveraged our social media platforms and advocacy activities to share key messages on improving health security in the country.

Acknowledgement
We would like to acknowledge the Nigeria CDC, Global Health Advocacy Incubator, LISDEL and BudgIT

Keywords: NAPHS; Funding; Advocacy; Implementation; One Health

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Surveillance
Abstract No: 14855

Operationalization of community-based one health surveillance-response Ethiopia: The case of Adadle district

Yahya Osman[*1 2] ; Jakob Zinsstag[1] ; Rahma Abtidon[2] ; Jan Hattendorf[1] ; Lisa Crump[1] ; Halane Wali Wali[3] ; Ahmed Mo'alin[4] ; Abdifatah Muhumed[1 2] ; Rea Tschopp[5]
[1]Epidemiology and public Health / swiss tropical and public health institute, Basel university/ Switzerland (Schweiz), [2]Medicine/ Jigjiga University, Ethiopia/ Ethiopia, [3]Epidemiology/ Adadle distric Health office/ Ethiopia, [4]Epidemiology / Adadle distric livestock office / Ethiopia, [5]Epidemiology and public health / Swiss tropical and public health institute , and Armauer Hansen Research Institute/ Switzerland (Schweiz)

Introduction and Objectives or Purpose

There is high risk of zoonotic diseases transmission between humans and animals in pastoral areas. However, the collaboration between sectors in disease surveillance and response in Ethiopia is weak.

Objective: To assess the feasibility of one health surveillance and response system (OHSRS) in Adadle district in order to introduce (OHSRS) in the surveillance system of Somali region (SRS).

Methods

Firstly, we have established one health surveillance and response unit (OHSRU) in the health office, which coordinate over all the surveillance response activities. Secondly, (community animal health workers (CAHWs), community health workers (CHWs), human and animal health staffs of the district and regional experts were trained together on zoonotic disease and unusual health events surveillance. Thirdly, inception workshop with stakeholders were held. Fourthly, to ensure the sustainability, community-based health insurance and CAHWs cost recovery mechanism were established. Finally, all public and animal health staffs including CAHWs and CHWs at different administration level were linked together.

Results or Focus

zoonotic diseases such as anthrax, brucellosis, RFV (suspected) and unknown camel zoonotic diseases were reported. Human and animal health information (HAHI) were successfully collected, analyzed and shared among sectors and professionals of different discipline at different level of administration. Joint intervention such as disease outbreak investigation, vaccination and community awareness creation (zoonotic disease) were conducted to prevent the spread of zoonotic diseases between humans and animals. However, improve public and veterinary services, technical barriers, cost effectiveness, data ethics, political commitment should be addressed to effectively operationalize OHSR in SRS and to scale it up to other parts of the country

Conclusion or Scope

OHSR is an important approach to detect and respond to zoonotic diseases earlier. Designing the OHSR using existing surveillance system, engaging communities and other relevant sectors using transdisciplinary process could contribute to sustainability of OHSR.

Acknowledgement

We are thankfull to JOHI and Biovision foundation for funding.

Keywords: Community_based; One health surveillance and response; zoonotic diseases; pastoralists; Ethiopia

Topic: Policy, Environment & Biosecurity (PEB): Science of Climate and Ecological Change of One Health: Climate change and the socio-ecological
Abstract No: 14896

A One Health perspective on brucellosis in East Africa

Joachim Otte*[3] ; Giuseppina Cinardi[3] ; Alessandra Falcucci[3] ; Orsolya Mikecz[3] ; Giuseppe Tempio[3] ; Dominik Wisser[3] ; Ugo Pica-Ciamarra[3]
[3]Animal Production and Health Division/ Food and Agriculture Organization of the United Nations (FAO)/ Italy (Italia)

Introduction and Objectives or Purpose

The One Health approach aims at achieving optimal health outcomes by recognizing the interconnection between people, animals and the environment in which they operate. This paper develops and presents an integrated model to estimate and map the impact of eliminating brucellosis (B. abortus and B. melitensis) in ruminants (cattle, sheep and goats and camels) on livestock production, public health and greenhouse gas (GHG) emissions in East Africa.

Methods

We relied upon FAO GIS data on livestock populations and productivity parameters by ruminant production system in East Africa. We assembled data on brucellosis sero-prevalence and impact in ruminant species and livestock keepers by location and production system. We developed a spatial distribution model for brucellosis. We recalibrated the FAO Global Assessment Environmental Model to assess the effects of brucellosis on livestock production and GHG emissions and added a component to assess its impact on human health.

Results or Focus

In East Africa, the overall impact of brucellosis varies by production system and level of sero-prevalence, which ranges from 2 to 24 percent in the various cattle production systems. Eliminating brucellosis in cattle would increase total protein production by 0.7 to 3.3 percent; at constant herd size, improved fertility and reduced losses of offspring result in a decrease in the amount and intensity of GHG emissions per ton of protein produced; between 150 and 220 thousand cases of clinical brucellosis would be avoided in livestock keepers with an additional, but unquantified, health benefit to consumers.

Conclusion or Scope

The integrated assessment of the returns of One Health investments in the livestock sector, as applied to brucellosis in East Africa, could facilitate cooperation and co-investments across different sectors and social domains for improved health, economic and environmental outcomes. We plan to refine and apply the integrated assessment model to other animal diseases and geographies.

Keywords: Brucelossis, East Africa, One Health, public health, environment

Topic: Policy, Environment & Biosecurity (PEB): Science of Climate and Ecological Change of One Health: Climate change and the socio-ecological
Abstract No: 14976

Unique Challenges for Indigenous and Northern Communities During COVID 19: Applying Lessons Learned to Climate Change

Katherine Ginsbach*[1] ; Kashish Aneja*[1] ; Francesca Nardi [1] ; Alison Durran*
[1]Center for Transformational Health Law / O'Neill Institute for National and Global Health Law/ United States

Introduction and Objectives or Purpose

COVID-19 has shown how the lack of infrastructure and preparedness results in overwhelming health systems and outcome disparities. Areas that are at higher risk for climate change and global warming faced unique challenges in responding to COVID-19. Isolated Arctic villages that rely on subsistence life, have no road access, no running water and no neighbors for miles were still hit by the coronavirus. These villages are also being disproportionately impacted by climate change, with water rising and displacing villages, the arctic sea ice melting, food becoming harder to source, and thawing of permafrost that exposes pathogens.

Methods

We examine the intersection of COVID-19 and climate policies for Indigenous and arctic villages. Through a One Health lens, we look at how the experiences with previous outbreaks, 1918 flu pandemic, recent anthrax outbreaks as well as climate mitigation policies, moving entire villages due to sea level rising can serve as a model for developing disease and disaster response legislation at the local, national, regional, and international level.

Results or Focus

Local, national, regional, and international frameworks include a variety of sectoral legislation that is relevant for the One Health approach to disease prevention and climate mitigation. An effective One Health integration requires a multifaceted approach when it comes to disease prevention and climate adaption for these remote villages. It will address the challenges and opportunities of setting up One Health institutional frameworks that can provide coordination among governance groups to ensure effective responses for increasing threats.

Conclusion or Scope

Arctic communities face unique challenges when it comes to emergency preparedness and response and as a result require unique solutions. A One Health framework can provide the guidance needed in establishing a robust multisectoral collaboration.

Keywords: Arctic Council; Climate Change; Pandemic Preparedness and Response; Indigenous Communities

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Public and Private policy and practice
Abstract No: 15057

Exchange and Coordination: Deficits of the Global One Health Movement

Ulrich Laaser[*1] ; Vesna Bjegovic-Mikanovic[2] ; Helmut Wenzel[3] ; Richard Seifman[4] ; Cheryl Stroud[5] ; Carter Craig[6] ; Bruce Kaplan[7] ; Laura Kahn[8] ; Rohini Roopnarine[9]
[1]School of Public Health/ University of Bielefeld/ Germany (Deutschland), [2]Institute of Social Medicione/ Faculty of Medicine/ Serbia (Србија), [3]Freelance/ Consultant/ Germany (Deutschland), [4]National Capital Area/ United Nations Association/ United States, [5]Lead office/ One Health Commission/ United States, [6]Pro bono team/ One Health Initiative/ United States, [7]Pro bono/ One Health Initiative/ United States, [8]Pro bono/ One Health Initiative/ United States, [9]Global Public Health/ St. Georgers University/ Grenada

Introduction and Objectives or Purpose

Current economic, social, and environmental trajectories within most world regions are unsustainable, whereas the One Health movement appears as a conglomeration with many different players and often uncoordinated actions. We explore the options to increase cooperation and systemic strategies to improve the impact on people and politics based on the OHHLEP definition of One Health.

Methods

Starting from the websites collected by the One Health Commission (OHC) and the One Health Initiative (OHI), we identified 291 websites of One Health organizations (as of 29 July 2022: 30 governmental, 135 academic, 126 non-profits) and searched for organization, transparency, and focus of work, using MAXQDA 2022 for a mixed-methods analysis.

Results or Focus

Looking at the organizations' websites, we found significant structural deficits: Although 63.2% refer to One Health in the organization's name and almost all list a task profile, concrete projects for the years 2021/2 seem rare or not reported, including publications and especially budgetary information. The kind and number of members are published only by 46.2%. We observed further dominance of US-based organizations, veterinarians, and physicians among the individuals named. The social sciences - sociology and economy in particular - are underrepresented.

Conclusion or Scope

The World Bank called already in 2010 for a permanent system of international One Health surveillance and response instead of 'prevailing temporary arrangements and uncoordinated duplication of efforts.' Bottom-up and top-down: coordinated action from both sides is essential to secure long-term success. Innovative ideas are often conceptualized bottom-up; supportive leadership carrying forward and stabilizing initiatives is mandatory to secure a long-term perspective and permanent progress. Therefore, we call for a global One Health Communications Alliance to enhance synergy and collaboration, administrated by an adjunct close to the UN Secretary-General in a "force multiplier role". This office may be inaugurated in a special session of the United Nations General Assembly on One Health.

Acknowledgement

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Keywords: One Health movement; globality; deficits; alliance

Topic: Policy, Environment & Biosecurity (PEB): Science of Climate and Ecological Change of One Health: Conservation and Restoration Ecology
Abstract No: 15082

The Watershed Interventions for Systems Health (WISH Fiji) project -- transforming place-based management within watersheds in Fiji.

Aaron Jenkins*[1]
[1]School of Public Health/ University of Sydney/ Australia

Introduction and Objectives or Purpose

Watersheds are coherent, ecologically representative units, offering opportunities for place-based interventions to transform systems health via preventative approaches that achieve co-benefits for public health and the environment.The Watershed Interventions for Systems Health in Fiji (WISH Fiji) project embraces participatory knowledge co-production and action-oriented research to identify risks, prioritize interventions and monitor responses.

Methods

We used screening filters and local knowledge to identify five watersheds for action with high incidence of water-related diseases (Fiji's “three plagues” of leptospirosis, typhoid, and dengue) and high risk to downstream environmental health. We reviewed literature to identify risk factors for each disease, identified overlaps with risks for downstream environmental impact, and designed nine instruments to assess baseline risk. Following community consultations to obtain free, prior, and informed consent, we enrolled 311 households across 29 communities in the study. We synthesized data to identify risks at the household, village, and broader landscape (i.e., watershed) level, and communicated to community water and resource management committees, local leaders to assist developing water safety and security plans.

Results or Focus

Two-hundred and twenty priority risk reduction actions were identified by local committees across eight main categories: personal hygiene; sanitation infrastructure; access to clean water; village drainage; livestock and waste management; land use practices; cross-sectoral coordination; health systems surveillance. We continue tracking co-implemented changes to factors that reduce risk of water-related disease and improve in-stream and downstream environmental conditions. Direct evaluation of public health impacts is limited by health system failure to geolocate confirmed cases of illness. To overcome this, we involve direct community participation in syndromic surveillance of symptoms associated with water-related diseases.

Conclusion or Scope

WISH Fiji is a systems model of cross-sectoral coordination, efficiently progressing many Sustainable Development Goals, but requires sustained investment in interventions across nested scales to realize full benefits, particularly for nature-based solutions that exhibit lagged responses.

Acknowledgement

26 coauthors

Keywords: Watershed ecology; Fiji; Typhoid ;Leptospirosis; Dengue

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Surveillance
Abstract No: 15086

Risk assessment of rodent-borne zoonoses in Qatar: a One-Health framework for future surveillance and intervention

Md Mazharul Islam[*1] ; Elmoubashar Farag[2] ; Devendra Bansal[2] ; Shariq Jaffrey[2] ; Mohammad Mahmudul Hassan[3] ; Muzzamil Atta[1] ; Abdulla Mohammad AlMarri[1] ; Abdulaziz Al-Zeyara[1] ; Hamad Al-Romaihi[2] ; Zilungile Mkhize-Kwitshana[4]
[1]Department of Animal Resources/ Ministry of Municipality/ Qatar (قطر), [2]Department of Public Health/ Ministry of Public Health/ Qatar (قطر), [3]Faculty of Veterinary Medicine/ Chattogram Veterinary and Animal Sciences University/ Bangladesh (□□□□□□□□), [4]Department of Medical Microbiology/ University of KwaZulu Natal/ South Africa

Introduction and Objectives or Purpose

Rodents are essential components of every terrestrial ecosystem. Besides several benefits, they are important sources of zoonoses. To prevent any rodent-related zoonoses epidemic in future, especially during FIFA world cup 2022, a study aimed to assess the risk of rodent-borne zoonotic pathogens at the human-animal-ecosystem interface in Qatar.

Methods

The study conducted several systematic reviews and tested 148 rodents trapped in different ecosystems of Qatar to understand rodent-borne zoonotic pathogens. Then a panel discussion was conducted with local, regional, and international experts to propose future surveillance and intervention plans.

Results or Focus

Three commensal rodents, including Mus musculus, Rattus norvegicus, and R. rattus have been identified, of which R. norvegicus is predominant in Qatar. Livestock and agricultural farms are the hotspots for rodent abundance. Eight species of helminths, ten species of protozoa, twenty-four species of bacteria, and four species of viruses were reported at the human-animal-environment interface, for which rodents can act as reservoirs or carriers. In addition, several vectors, such as fleas, ticks, mites, and mosquitos, were also identified. The expert panel stated that Qatar is at risk of rodent-related zoonotic pathogens by its internal farming practices, immigrant workers, importation of food and agricultural products, and international travelers. One Health approach could be a classical way to mitigate such risks. One Health framework (OHF) was proposed, and it will be working on rodent-borne pathogen surveillance and characterization, risk mapping, and prediction model preparation and intervention considering local socio-economic, cultural, and spiritual facets.

Conclusion or Scope

Qatar has previous success with the One Health approach in emerging disease research for outbreak investigation, surveillance, and early detection of diseases. A policy should go through (1) surveillance, monitoring, and evaluation; (2) set action thresholds; and (3) prevention and control. The OHF should be functional by formulating supportive legislation, allocating budget, and engaging relevant organizations and personnel.

Keywords: Rodent, zoonotic pathogens, risk assessment, One Health, Qatar

Topic: Policy, Environment & Biosecurity (PEB): Science of Climate and Ecological Change of One Health: Climate change and the socio-ecological
Abstract No: 15138

Health Professionals' and Pastoralists' Knowledge, Attitude, and Practice about Antimicrobial Resistance and Climate Change, Somali Region, Eastern Ethiopia: Qualitative Study.

Abdifatah Muktar Muhummed*[1 2] ; Andrea Kaiser-Grolimund[1] ; Yahya Maidane Osman[1] ; Gueladio Cisse[1] ; Jakob Zinsstag[1]
[1]Epidemiology and Public Health / Swiss Tropical and Public Health/ Switzerland (Schweiz) [2]Medicine and Health Science / Jigjiga University/ Ethiopia

Introduction and Objectives or Purpose

Despite the fact that AMR and climate change are among the most serious threats to the global health system and economy, many people around the world are unaware of their significant negative impact. Human behavior is the central plan to address AMR and climate change. This qualitative study aims to understand the knowledge, attitude, and practices on AMR and climate change of both pastoralists and health professionals in the Somali region, Ethiopia.

Methods

This qualitative research was carried out in three separate locations in the Somali region (Jigjiga, Gode, and Adadle). 44 in-depth interviews were conducted with health professionals in different health facilities in urban, semi-urban, and rural settings. Additionally, 12 focus group discussions with rural populations were conducted to understand their KAP towards antibiotics. A combination of content and thematic analysis was used to analyze the qualitative data.

Results or Focus

Except for doctors and pharmacists, the majority of other health professionals and communities had poor awareness of AMR and climate change. Conversely, after simple explanations of the term "climate change" the communities understood it better than health professionals. Self-medication is highly practiced according to the participants. Furthermore, both the health professionals and communities poorly understood the source and transmission path of AMR. Educating health professionals and communities, imposing legislative constraints on antibiotic purchases, and improving diagnostics in health facilities, could mitigate at least part of the problem. A few participants mentioned the relationship between climate change and antimicrobial resistance, despite different views of the participants.

Conclusion or Scope

The knowledge gap in AMR varied by profession rather than setting, while for climate change, the understanding differed by setting rather than profession. Thus, a transdisciplinary One Health research approach for further understanding of AMR and climate change in different stakeholders, as well as strategies to raise awareness of AMR and climate change to initiate behavioral change.

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health Strengthening Community Capacity
Abstract No: 15139

Learnings from One Health operationalizations in West Africa and Switzerland

Kathrin Heitz-Tokpa*[1] ; Nestor N'dri[1] ; Andrée Prisca Ndjoug Ndour[2] ; Kabiru Salami[3] ; Souleymane Taoré[2] ; Zakaria Keita[4] ; Oyeladun Okunromade[5] ; Kennedy Kwasi Addo[6] ; Jakob Zinsstag[7] ; Bassirou Bonfoh[1]
[1]Research and Development/ Centre Suisse de Recherches Scientifiques en Côte d'Ivoire/ Ivory Coast, [2]Public Health and Environment/ Ecole Inter-Etats des Sciences et Médecine Vétérinaires (EISMV)/ Senegal (Sénégal), [3]Department of Sociology/ University of Ibadan/ Nigeria, [4]Department of Education and Research in Public Health and Specialties/ Centre Universitaire de Recherche Clinique du point G/ Mali, [5]Department of Surveillance/ Nigeria Center for Disease Control/ Nigeria, [6]Bacteriology Department/ Noguchi Memorial Institute for Medical Research, University of Ghana/ Ghana (Gaana), [7]Department of Epidemiology and Public Health/ Swiss Tropical and Public Health Institute/ Switzerland (Schweiz)

Introduction and Objectives or Purpose

One Health has become a popular approach and its applications are numerous. This study's aim is to learn from existing implementations of the approach and to identify potentials, challenges and enabling factors of its operationalization in two health system contexts, in Switzerland and selected countries in West Africa.

Methods

Following a qualitative research design, the project identifies and describes One Health initiatives in the selected countries, Côte d'Ivoire, Ghana, Nigeria, Mali, Senegal and Switzerland. The selection of countries and people interviewed is based on expert knowledge, literature review and the snowball method. People who have participated in One Health initiatives have been interviewed on different steps of One Health implementation, multisectoral cooperation, financial management, training needs, the added value of the approach and future developments.

Results or Focus

Interviewees have stressed the importance of One Health as a principle but mentioned challenges in its operationalization. The multisectoral exchange is sometimes perceived as an additional task on top of the regular workload, making it occasionally difficult to schedule meetings. However, the work on common problems (such as AMR, Campylobacter infection, rabies) helps overcome the reluctance of collaborators. The transmission of meeting outcomes back into the different sectors by the representatives has been identified as another challenge. Champions who advocate for multisectoral collaboration are also key to keeping One Health initiatives going, as exchange platforms may not run well when a change of personnel occurs.

Conclusion or Scope

Since the COVID-19 pandemic, the need for information about working successfully at the human-animal-environmental interface has increased. Our analysis shows that existing institutions are sufficient to address health challenges if sectors cooperate more closely under the One Health framework. However, there is a need to better document the added value of multisectoral collaborations in existing operationalizations of One Health and to share learnings of different modes of cooperation at different levels.

Keywords: One Health; health system; multisectoral collaboration; operationalization; implementation

Topic: Policy, Environment & Biosecurity (PEB): Science of Climate and Ecological Change of One Health: Conservation and Restoration Ecology
Abstract No: 15238

REVITALIZATION OF THE RIVER AND ADJACENT ECOSYSTEMS AFFECTED BY THE COLLAPSE OF A TAILINGS DAM IN BRAZIL: A ONE-HEALTH PERSPECTIVE

Luan Ritchelle Dos Anjos*[1] ; Klaisy Christina Pettan-Brewer[2] ; Silvia Dantas Costa[3]
[1]Agroecological Technical Assistance / Fundação Renova/ Brazil (Brasil) [2]Department of Comparative Medicine/ University of Washington/ United States [3]Agroecological Technical Assistence/ Fundação Renova/ Brazil (Brasil)

Introduction and Objectives or Purpose

The rupture of Vale® and BHP Billiton® tailings dam in Brazil (2015), characterized the biggest environmental disaster in Brazilian history, compromising the water quality of the RIO DOCE – the river that gives its name to the hydrographic basin and supplies 230 municipalities and 3.6 million inhabitants plus a diversity of plants, domestic and wild animals. It is important to point out that 70% of the diseases treated by the Brazilian public health system are waterborne. In addition, there also has been a reduction in precipitation and distribution of rainfall over the water period in the same region, most likely a consequence of climate change, causing serious concern about water supply. One of the main causes of the scarcity of this resource is the low efficiency related to the reception of rainwater by the soil, resulting in lower water accumulation in groundwater and greater surface runoff.

Methods

In this context, the process of repairing the impact caused by the dam rupture has developed actions of conserving the water resources and increasing the infiltration of rainwater in soils and groundwater. The main tools involved in this process are: isolation of Permanent Preservation Areas from springs and watercourses; recovery of riparian forests with native forestry; construction of catchment structures called full boxes on the hills; terraces in the slopes; and recovery of degraded pasture areas, which constitute the main area of contribution to the springs.

Results or Focus

Therefore, these actions contribute to the revitalization of the river, both in quantity and quality, given the fact that the water coming from the production systems is contaminant-free, which substantially reduces the risk of contamination of the human and animal populations that depend from the water of the river.

Conclusion or Scope

The One Health concept is not only about diseases as it includes environmental and economic health and their close inter-linkages.

Acknowledgement

To Renova Foundation and the Organização Cooperativa de Agroecoligia (OCA) for their support.

Keywords: agroecology; climate change; planetary health, sustainability, water conservation,

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health Strengthening Community Capacity
Abstract No: 15374

BRIDGING THE GAP AND CATALYZING ENVIRONMENTAL INVOLVEMENT FOR ONE HEALTH: THE AFROHUN KENYA EXPERIENCE

Samuel Wanjohi*[1] ; Ronald Kimtai[1] ; Diana Muta[1] ; Eddy Mogoa[1] ; Tequiero Okumu[1]
[1]N/A/ Africa One Health University Network (AFROHUN) Kenya/ Kenya

Introduction and Objectives or Purpose

Despite it being a critical component in the epidemiological triad, the environmental dimension has been noted to the least established in the One Health framework.

In Kenya, involvement of the environmental sector in One Health initiatives was noted to be done in an ad hoc basis. Africa One Health University Network (AFROHUN) Kenya sought to change the narrative by promoting meaningful engagements and action from the environmental domain.

Methods

AFROHUN Kenya, with support from the USAID funded One Health Workforce Next Generation (OHW-NG) initiative, set out to establish a mutually beneficial relationship with environmental practitioners in Kenya. AFROHUN Kenya mapped and identified the relevant stakeholders, worked together to understand the system and issues at hand, and jointly engaged to develop a value creating and maximization partnership.

Results or Focus

AFROHUN Kenya collaborated with the Environment Institute of Kenya (EIK) for impact in various developments e.g., development of a One Health Policy Brief and customization of a curriculum on Antimicrobial Resistance (AMR), with a module on AMR and the Environment. EIK proposed a facilitator for the module for a subsequent five-day 1.5hours online training that was attended by an average of 40 participants from multiple fields including human, animal and environmental health, as well environmental and social sciences. EIK also offered CPD points for their members who attended various One Health capacity building sessions offered by AFROHUN Kenya, which the participants deemed very useful and applicable.

Conclusion or Scope

The engagements between AFROHUN Kenya and EIK highlighted the need and benefit of creating opportunities for promoting knowledge sharing, best practices, and involvement of the environment sector in One Health initiatives. Further, Environmental professionals were willing to engage on One Health issues and participate in enabling discussions on context-specific solutions to address the One Health challenges in Kenya and beyond. AFROHUN Kenya will continue to promote these discussions.

Keywords: Policy;Environment;Partnership;One Health

Topic: Policy, Environment & Biosecurity (PEB): Science of Climate and Ecological Change of One Health: Vector ecology
Abstract No: 15401

Ecological Changes and Zoonotic Malaria Transmission: a One Health Lens on Plasmodium knowlesi

Novra Sandi*[1 2] ; Haniena Diva[1]
[1]Preventive Medicine/ Center for Immunopathobiology, Preventive & Diagnostic Medicine/ Indonesia, [2]Geospatial Epidemiology/ Eijkman-Oxford Clinical Research Unit (EOCRU)/ Indonesia

Introduction and Objectives or Purpose

Knowlesi malaria is originally infects macaque as the primary host, which also infect human through mosquito bites. Although the disease has been found in SEA region in 1960s, knowlesi malaria cases only becoming a concern within the region only in the past three decades.

Methods

A qualitative method was conducted using literature review and in-depth interview with two key informants in vector control and malaria elimination program. Literature review was used to assess knowlesi malaria case prevalence in Indonesia from published scientific articles in English and/or Bahasa Indonesia. Key informants were interviewed to seek in-depth understanding of knowlesi malaria cases and prevention management in Indonesia from two perspectives (Ministry of Health and UNICEF).

Results or Focus

The result from literature review was reported that five provinces already confirmed to have knowlesi malaria. Approximately, 734 malaria knowlesi cases were identified in human from 2011-2015. The first case was identified in Aceh in 2011, even though it was recorded prior to that in 2010 there was one imported knowlesi malaria case to Australia from Indonesian Borneo. During 2013-2015, malaria knowlesi was identified in four new locations, including Central Kalimantan, South Kalimantan, North Sumatera, and Jambi. The result from key informant confirming that six from twelve species Anopheles leucosphyrus group namely An. leucosphyrus. An. latens, An. introlatus, An. balabacensis, An. dirus, An. cracens have been identified in five provinces in Indonesia. Another finding from key informant that Indonesia still does not include knowlesi malaria at the national level. The result of the program has been successfully controlling malaria cases, especially by Plasmodium vivax and Plasmodium falciparum. Despite that success, the increasing knowlesi malaria cases alarming concern for interrupting elimination program in specific area with confirmed cases. As the result of knowlesi malaria is not included in global malaria program, leading to unprioritized program at the national level.

Keywords: Ecological change; knowlesi malaria; malaria elimination program; One Health

Topic: Policy, Environment & Biosecurity (PEB): Science of Climate and Ecological Change of One Health: Rabies and dog
Abstract No: 15419

Mad dogs and sick monkeys: A co-production approach to understanding zoonoses in India

Abi Tamim Vanak*[1]
[1]-/ Ashoka Trust for Research in Ecology and the Envir/ India

Introduction and Objectives or Purpose

The combination of high biodiversity, human population density, and close proximity with domestic and wild animals makes India highly vulnerable to the threat of emerging and re-emerging zoonotic diseases. A OneHealth approach to surveillance, preparedness and control has been advocated for effectively tackling these threats. Here, I outline two examples of community-based OneHealth research initiatives that have helped generate novel insights into disease dynamics for rabies and Kyasanur forest disease in India, and highlight how this can be a useful template to operationalise OneHealth research in India.

Methods

Case 1: We used a citizen based reporting platform for passive surveillance of suspected canine rabies cases in Pune city, India. Positive samples were subjected to whole genome sequencing to better understand rabies dynamics in a large metropolitan area.

Case 2: We used a co-production approach to understand hazards and exposure of forest dwelling communities to Kyasanur forest disease (KFD) in Karnataka, India, and build spatial models of risk (ATREE Ethics Approval number: AAEC/101/2016 and IPH Study ID, IEC-FR/04/2017).

Results or Focus

In Pune city, we detected ~750 cases of canine rabies over a period of 4 years, indicating an ongoing enzootic event. Whole genome sequencing of 106 samples revealed co-circulation of two subtypes of the Arctic lineage of this virus.

For KFD, models combining forest metrics, livestock densities and elevation accurately predicted spatial patterns in human KFD cases (2014–2018), and new hotspots in 2019 indicating their value for spatial targeting of intervention. Landscapes at higher risk for human KFD contained diverse forest-plantation mosaics with high coverage of moist evergreen forest and plantation, high indigenous cattle density, and low coverage of dry deciduous forest. indicating their value for spatial targeting of intervention.

Conclusion or Scope

Citizen reporting and co-production were vital for: gathering outbreak data that reflected locations of exposure in the landscape; better understanding contextual socio-ecological risk factors; and tailoring the spatial grain and outputs to the scale of forest use, and public health interventions.

Keywords: Socio-ecological; neglected tropical disease; surveillance; OneHealth

Topic: Policy, Environment & Biosecurity (PEB): Science of Climate and Ecological Change of One Health: Vector ecology
Abstract No: 14714

Mapping the habitat suitability of the Asian longhorned tick in North America under current and future climate scenarios

Susan Cork*[1] ; Isabelle Couloigner[1] ; Jamyang Namgyal[1] ; Akysha Envik[1] ; Sylvia Checkley[1]
[1]Ecosystem & Public Health/ University of Calgary/ Canada

Introduction and Objectives or Purpose

The Asian longhorned tick (Haemaphysalis longicornis ALHT) is a vector for many pathogenic micro-organisms, of veterinary and public health importance, in its native range in East Asia. It is also a competent vector for Theileria orientalis Ikeda which resulted in livestock morbidity and mortality in its introduced range of Australia and New Zealand. In North America, this tick was first formally reported from sheep in New Jersey (USA) in 2017. It is currently found in 17 states in North Eastern (NE) USA. In this study we examined the current and future habitat suitability for the ALHT across North America and considered potential routes of entry into Canada.

Methods

Habitat suitability models were developed using a machine learning tool, MaxEnt, to predict where the ALHT could establish in North America, based on current presence locations, biotic and abiotic factors. Following discussions with climate change experts and entomologists, models were projected onto selected climate scenarios to examine future habitat suitability. A qualitative risk assessment (by soliciting expert opinions) was developed using methods established for import risk analysis, to identify likely routes of entry of this tick into Canada from the USA.

Results or Focus

Our best model predicted that the most suitable North American areas for geographic expansion are from Arkansas–South Carolina to the south of Quebec–Nova Scotia in the east, and from California to the coast of British Columbia in the west. Future habitat is likely to expand northwards under the selected climate change scenarios. Likely routes of entry into Canada include cross border movement of infested terrestrial wildlife and livestock, dog importations and the movement of migratory birds.

Conclusion or Scope

Enhanced tick surveillance is required to gain a better understanding of how this tick may spread into new areas. Biosecurity practices should be enhanced to mitigate the risk of introducing this tick to new areas.

Keywords: Habitat suitability modeling, Asian longhorned tick, risk assessment, climate change

Topic: Policy, Environment & Biosecurity (PEB): Science of Climate and Ecological Change of One Health: Climate change and the socio-ecological
Abstract No: 15000

CLIMATE CHANGE AND TICK-BORNE DISEASES: A ONE HEALTH APPROACH IN ALBERTA, BRITISH COLUMBIA AND SASKATCHEWAN, CANADA

Erin Fraser[*1 2] ; Stefan Iwasawa[1] ; Isabelle Couloigner[3] ; Muhammad Morshed[2 4] ; Andrew Cameron[5] ; Amanda Lang[6] ; Shaun Dergousoff[7] ; Sunny Mak[1] ; Sylvia Checkley[3] ; Susan Cork[3]
[1]Communicable Disease and Immunization Service/ British Columbia Centre for Disease Control/ Canada, [2]Faculty of Medicine/ University of British Columbia/ Canada, [3]Faculty of Veterinary Medicine/ University of Calgary / Canada, [4]Public Health Laboratory/ British Columbia Centre for Disease Control/ Canada, [5]Institute for Microbial Systems and Society/ University of Regina/ Canada, [6]Roy Romanow Provincial Laboratory/ Saskatchewan Health Authority/ Canada, [7]Lethbridge Research and Development Centre/ Agriculture and Agri-Food Canada/ Canada

Introduction and Objectives or Purpose

Climate change alters tick abundance, range expansion, and tick-borne disease risks for humans, domestic animals, and wildlife. Project aims are to: 1) improve tick and tick-borne disease surveillance; 2) develop data models to explore the impact of climate change on tick distribution and abundance; and 3) to enhance collaboration across disciplines and stakeholders in Canada's Western provinces.

Methods

This project engages One Health partners to collaborate on shared climate and tick-borne disease priorities. The project uses the following approaches: One Health networking and partnership development, cross-sectoral data mapping, enhancing One Health surveillance, improving laboratory diagnostics for tick-borne pathogen detection, developing regionally-specific, risk and habitat suitability maps under different climate scenarios, training future One Health professionals, and developing knowledge translation resources on ticks and tick-borne diseases.

Results or Focus

There is an urgent need for robust and regionally-specific surveillance systems and One Health collaboration to detect shifts in vector and pathogen distribution and communicate findings in a timely way to at-risk populations, health professionals, and policy makers. This project responds to evidence-, capacity-, and information-gaps for prediction, detection, and response to climate-driven changes of ticks and tick-borne pathogens in Western Canada.

Conclusion or Scope

This initiative contributes to adaptation actions in the Pan Canadian Framework on Clean Growth and Climate Change and addresses risks to people and animals from climate-sensitive, tick-borne diseases by improving surveillance, evidence-base for risk assessments, region-specific modelling, laboratory diagnostics, and knowledge resources for professionals and at-risk populations. The project demonstrates that a One Health approach to advance the capacity and evidence-base needs on tick-borne diseases and climate change is feasible, effective, and efficient.

Acknowledgement

Project collaborators: Theresa Burns, Katie Clow, Eleni Galanis, Camille Guillot, Emily Jenkins, Patrick Leighton, Cait Nelson, Nathanial Osgoode, Michael Otterstatter, David Patrick, Carl Ribble, Maarten Voordouw. Funding from the Public Health Agency of Canada.

Keywords: vector-borne diseases, climate change, One Health approach

Topic: Policy, Environment & Biosecurity (PEB): Science of Climate and Ecological Change of One Health: Vector ecology
Abstract No: 15173

Ecological foundation of Rift Valley Fever**

Max Korir*[1] ; Dr. Bett[1]
[1]Animal and Human Health/ ILRI/ Kenya

Introduction and Objectives or Purpose

Rift Valley fever (RVF) is a zoonotic disease caused by an RVF virus (RVFV) and occurs sporadically in sub-Saharan Africa and parts of the Middle East. Its epidemics cause far-reaching socioeconomic losses particularly among rural communities that rely on livestock. Epidemics occur after periods of above-normal precipitation and flooding, which provide good conditions for mosquitoes, biological vectors of the virus, to develop to high populations. We conducted an entomological survey during an RVF outbreak in four villages in Isiolo in 2020-2021 and analyzed it to determine factors that influenced mosquito abundance and distribution.

Methods

Mosquitoes were trapped using CDC light traps that were deployed in each site for 48 hours. Land cover data from the Landsat satellite imagery for the period 1990 to 2020 were analyzed using Open source QGIS software and the Google Earth Engine and used with other variables to generate ecological factors for RVF modeling in the target area. Data obtained from unmanned aerial vehicles (UAV) images at the time of sampling were utilized to calibrate Landsat images obtained in 2021. The semi-parametric generalized additive models were used to analyze the data with the number of mosquitoes per trap per day being used as an outcome variable. Two models were created with and without the UAV calibrated land cover classes. The dataset with the UAV-based land cover classification was used for discussion owing to its higher classification accuracy

Results or Focus

Factors that were significantly associated with mosquito abundance were normalized difference vegetation index (NDVI), grassland areas, land MNDWI, and curvature. There was also a significant negative correlation between NDVI and rainfall quantity. The analysis showed the possible cause of RVF being floods rather than rainfall

Conclusion or Scope

The model developed would be useful for predicting the spatial distribution of potential RVFV vector breeding sites in the region.

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health Strengthening Community Capacity
Abstract No: 15234

The UAF One Health Master’s Degree: Operationalizing One Health in the Circumpolar North

Hannah Robinson*[1] ; Arleigh Reynolds *[1] ; Kelsey Nicholson*[1] ; Laurie Meythaler-Mullins [1]
[1]UAF Center for One Health Research / University of Alaska Fairbanks / United States

Introduction and Objectives or Purpose

Many of the challenges that residents of the Circumpolar North we are facing reside in the realm of One Health such as: emerging zoonotic disease threats, food safety, security, and sovereignty, mental health, built infrastructure, biocontaminants, etc. Individuals who have a comprehensive understanding of One Health and an ability to utilize a community-centered, constructionist approach to problem-solving are required to create solutions for these challenges. UAF Center for One Health Research is recognized as a leader in educating these individuals.

Methods

The One Health Master’s Degree (OHM) combines training and hands-on practice. The program is an integration of science, culture, history, communication and more. Students explore how the health of people is connected to the health of animals and the environment — and how to work together to develop effective public health management plans that benefit communities. There are two concentrations, Biomedical and Community Advocacy. Students in each concentration work together starting at the community level and build outward to develop management solutions that address pressing One Health issues identified by the community.

Acknowledgement

University of Alaska Fairbanks

UAF College of Natural Sciences and Mathematics

UAF Center for One Health Research

Results or Focus

Graduates of the program are able to engage key stakeholders to develop and implement realistic management plans that can be implemented in communities across the Circumpolar North and beyond.

Conclusion or Scope

Our students have a comprehensive understanding of One Health and an ability to utilize a community-centered, constructionist approach to problem-solving and are emerging as leaders in the mitigation of issues such as climate change and ecological change.

Keywords: One Health; Education; Collaboration; Interdisciplinary; Community

Topic: Policy, Environment & Biosecurity (PEB): Science of Climate and Ecological Change of One Health: Conservation and Restoration Ecology
Abstract No: 15237

A One Health Approach to Protected and Conserved Areas in Liberia

Urias Goll*[1] ; Catherine Machalaba[2] ; James Desmond[3] ; Allison Bailey[4] ; Tara Hoda[4] ; Paula Prist[4]
[1]Conservation and Health/ EcoHealth Alliance/ Liberia, [2]Health and Policy/ EcoHealth Alliance/ United States, [3]LCRP/ Liberia Chimpanzee Rescue and Protection/ Liberia, [4]Conservation and Health/ EcoHealth Alliance/ United States

Introduction and Objectives or Purpose

The Guinean forest of West Africa is a biodiversity hotspot that provides vital ecosystem services to combat global climate change. Most endangered species and biodiverse habitats can be found in one of the 1,936 protected areas across the region, covering approximately 9.6 percent of West Africa. Liberia contains more than 40% of the remaining Upper Guinean forest, and has substantial mangrove ecosystems that contribute to food security, water quality, and protection against coastal flooding. At a large scale, these ecosystems and species are under threat from land conversion to agriculture, commercial and artisanal extractive industries, illegal and unsustainable wildlife trade, and coastal development.

Methods

Through the lens of the Conservation Works Liberia program, we present how a One Health approach is being applied to broaden awareness of the value of protected areas and harmonize the protected area establishment process, with an objective of increasing areas under protected or conserved status and strengthening the management of existing sites.

Results or Focus

We introduce the model of One Health Conservation Centers, which aim to drive sustainable tourism, promote environmental stewardship by local communities and national and international visitors, facilitate local use and ownership of biodiversity and health research, and promote conservation-compatible economic growth.

Conclusion or Scope

This work builds on Liberia's strong leadership on One Health, including through its National One Health Coordination Platform, increasing the contributions from forest stewardship, wildlife management, and protected area expertise and stakeholders, and reinforcing Liberia's climate commitments.

Acknowledgement

Liberia Conservation Works is a partnership between EcoHealth Alliance, Liberia Chimpanzee Rescue & Protection, Fauna and Flora International, Partners in Development, and Solimar International, working in close collaboration with the Liberia Forestry Development Authority. The program is enabled through the support of the United States Agency for International Development.

Keywords: Protected Areas; Conservation; Wildlife; Biodiversity; Tourism

Topic: Policy, Environment & Biosecurity (PEB): Science of Climate and Ecological
Change of One Health: Climate change and the socio-ecological
Abstract No: 14654

HOW RELEVANT IS 'GREENHOUSE GASES' GLOBAL WARMING CLIMATE CHANGE TO ONE HEALTH

Meer Ahmad Meera*[1]
[1]Health Research & Consultancy/ Meer Ahmad Healthcare Consultancy/ Malaysia

Introduction and Objectives or Purpose

Climate change involve 'human-induced global warming' on weather patterns' - caused by emission of 'greenhouse gases',CO2 and methane.

Climate change threaten population to food and water scarcity, increased flooding, additional diseases, and economic loss.

Current warming is 1.2 °C - increase in these impact expected as continue > 1.5 °C, possibly triggering 'tipping points'. Limiting warming to 1.5 °C is necessary.

Methods

Literature is retrieved following Google search, and existing literature reviewed.

Results or Focus

Controversy is in a outline.

Containing carbon dioxide emission's outlined in detail - reforestation, farming, carbon mineralization, bioenergy together carbon capture and storage (BECCS) and ocean-based strategy, beside existing carbon dioxide removal (CDR) methods. Energy source is talked over, beside Vehicle Emission Standard.

Heat dissipation require thought, beside manner atmospheric water dissolve streaming emitted CO2 through soil and rivers to sea, and CO2 escaping to space. Photosynthesis by land vegetation and sea phytoplankton in removing CO2, beside.Existing methods can remove about 10 gT of CO2 per year - can additionally prevent 59% of CO2 becoming emitted. Releasing captured CO2 in stratosphere is possible.

Control measures on emission within Law should be made mandatory by every nation and have mechanism, international (UN) agency monitoring.There is need to intensify research aimed at filling (knowledge) gap and correcting uncertainty.

Subsidization of CCS, CCU and CCUS should be given priority. Large-scale DAC deployment require speeding by increasing economical use and by policy incentive.

Several country have standard of vehicle emission – and, every country should adopt these.

Community education is necessary. Future energy efficiency should be encouraged. Public transportation should be used, beside prudent-commercialization of biofuels.

Conclusion or Scope

There is plenty controversy around 'green house global warming climate change, over whether really happening, what amount presently, cause, effect, whether action can or should be taken, and what action – and, whether cyclical phenomenon.

Keywords: Climate change, greenhouse gases, emerging diseases, bioenergy, carbon capture and storage (BECCS)

Rabies and dog

Abstract No: 14767

Integration of Rabies Management Information System (RabMIS) through One-Health Approach into the Rabies Prevention and Control Program of Agusan del Norte, Philippines: An Evaluation

Joseph Rizalyndo Dargantes[*1] ; Suporn Thongyuan[2] ; Flavie Goutard[3] ; Alan Dargantes[4] ; Jose Jr. Escarlos[4]
[1]Provincial Veterinary Office/ Provincial Government-Agusan del Norte, Philippines/ Philippines, [2]Faculty of Veterinary Medicine/ Kasetsart University/ Thailand (□□□), [3]Faculty of Veterinary Medicine / GREASE / CIRAD / Kasetsart University/ Thailand (□□□), [4]College of Veterinary Medicine/ Central Mindanao University/ Philippines

Introduction and Objectives or Purpose

Rabies Management Information System (RabMIS) is a coordinated information computer application run in a user-friendly software. RabMIS records, stores, and maintains a database that contains data on Rabies Prevention and Control Program. The system enhances the manual recording system of the rabies program with the comfort and ease of computer mouse and search buttons. The system incorporates image capture ability embedding photographs of the animal and its owner in printed records.

This research was carried out to evaluate the impact of the integration of RabMIS through One-Health Approach into the Rabies Prevention and Control Program in the Province of Agusan del Norte, southern Philippines.

Methods

Stakeholders in the province were surveyed through a personal interview and Focus Group Discussion (FGD), while existing rabies data and financial aspect of the program were assessed.

Results or Focus

Findings revealed that RabMIS users found the software handy, time-saving and reliable resulting in well-kept, orderly, readily accessible and easy-to-retrieve records. Majority of dog owners and animal bite patients considered RabMIS recording brief, concise and generates more credible and authentic printed records. In totality, the integration of RabMIS through One-Health Approach had increased dog registration, dog vaccination coverage and increased coordination among stakeholders. It also helped reduce human and animal rabies cases in the province. By generating funds, it was able to augment rabies program workforce, procure medical supplies and equipment and provide incentive to program implementers.

Conclusion or Scope

In conclusion, the integration of RABMIS through One-Health Approach has improved the rabies prevention and control program in the Province of Agusan del Norte, Philippines

Acknowledgement

The research was funded by GREASE (Gestion des Risques Emergents en Asie du Sud-Est) and the French Agricultural Research Centre for International Development (CIRAD)

Keywords: rabies control; recordkeeping; vaccination; One-Health; Agusan del Norte, Philippines

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health Strengthening Community Capacity
Abstract No: 14816

NEXT GENERATION ONE HEALTH PHILIPPINES: BUILDING DOMESTIC CAPACITY FOR TRANSDISCIPLINARY AND TRANSLATIONAL RESEARCH TO PREVENT THE NEXT PANDEMIC

Renzo Guinto*[1 2] ; Gail Co*[1] ; Jerome Mejarito*[1] ; Louella Asuncion*[1] ; Carlo Luayon*[1]
[1]Planetary and Global Health Program/ St. Luke's Medical Center College of Medicine - William H. Quasha Memorial/ Philippines,
[2]Planetary Health/ Sunway Centre for Planetary Health/ Malaysia

Introduction and Objectives or Purpose

The Philippines is a biodiversity hotspot and a major hub for the global wildlife trade, many of which are identified as carriers of zoonotic pathogens. With support from the International Alliance Against Health Risks in Wildlife Trade, the Planetary and Global Health Program of the St. Luke's Medical Center College of Medicine established the Next Generation One Health Philippines (NGOHP) Fellowship Program to strengthen domestic capacity for One Health research in tackling wildlife trade and biodiversity loss as drivers of infectious disease emergence.

Methods

This program will comprise a small cohort of professionals from diverse sociocultural and interdisciplinary backgrounds related to One Health, wildlife conservation, and zoonotic spillover prevention. They will participate in a year-long fellowship that begins with an online introductory course, followed by a workshop in collaborative research, leadership, advocacy, and communications. Supported by mentors and small grants, fellows will conduct transdisciplinary research on issues surrounding wildlife trade and zoonotic spillover prevention. To ensure immediate dissemination and translation of findings, fellows will participate in One Health dialogues with relevant stakeholders.

Results or Focus

Training a small group of professionals in the application of the One Health approach, especially in addressing issues surrounding wildlife trade and consumption in relation to emerging infectious diseases, will be the focus of this program. The Philippine context will be central to the discussions in the program, highlighting the interconnectedness of biodiversity and health.

Conclusion or Scope

Prevention of future pandemics entails the creation of a new cadre of emerging scholar-practitioners who are equipped to apply the One Health approach to navigate complex transdisciplinary and cross-sectoral spaces. Moving forward, sustained support from different sectors is critical to ensure the program's institutionalization and continuity in producing new One Health leaders. The knowledge products from the fellowship must also be made widely available to all learners in the country.

Keywords: One Health Education; training; fellowship; research, Philippines

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Surveillance
Abstract No: 14839

Automating a national communicable disease surveillance system in Brunei Darussalam: key steps and challenges

Mohammad Alikhan*[1] ; Justin Wong[1]
[1]Public Health Surveillance/ EVYD Technology/ Brunei

Introduction and Objectives or Purpose

Communicable disease surveillance is an important epidemiological tool to monitor the health of a population. Health jurisdictions design their surveillance system based on their specific objectives but generally is aimed at alert and early warning of outbreaks of notifiable diseases and new pathogens by monitoring of a set of epidemiological parameters. Here we describe the process and challenges of implementing a digital national communicable disease surveillance system in a high-income country. Prior to implementation, the process was largely fragmented with manual reporting required by clinicians and laboratory personnel leading to significant case ascertainment issues.

Methods

The key steps during implementation of the digital surveillance system are identified and described, namely: 1) User landscape assessment (mapping process flows, describing existing systems and reporting methods), 2) User engagement and requirement gathering, 3) Priority disease identification, 4) Enhancement of priority disease tools, 5) User optimization, 6) Monitoring and evaluation

Results or Focus

We leveraged on the existing Brunei Health Information System (a national electronic health record covering >95% of the population) and used machine learning to extract socio-demographic, laboratory and clinical information entered by BruHIMS systems users to feedback into a real-time digital dashboard with set warning levels for outbreaks based on the 5-year historical average of cases. Automating the extraction of clinical notes and laboratory reports has allowed the Ministry of Health to dispense with the manual-based, user-dependent reporting system.

Conclusion or Scope

The key to implementation is understanding the user journey and landscape. Continuous engagement with end users and addressing the needs for each priority disease is important in ensuring uptake. Challenges such as user engagement, timeliness and data accuracy were also identified. Enhancement of the digital surveillance system will be made to include antimicrobial resistant pathogens, priority zoonotic diseases and adopting one health principles by widening the user base to include the animal health sector.

Keywords: Surveillance, automation, Infectious diseases, National system, communicable diseases

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Public and Private policy and practice
Abstract No: 14872

A business perspective on One Health Lessons from the Egypt poultry sector

Amira Abdelnabi*[1] ; Lina Abdalla[1] ; Sherif Moubarak[2] ; Safaa Elfadaly[3] ; Zelalem Tadesse[1] ; Ahmed Saad[1] ; Ugo PicaCiamara*[4] ; Abdelhakim Ali; Mohamed Atia
[1]ECTAD, FAO Egypt/ Food and Agriculture Organization of the United Nations (FAO)/ Egypt, Arab Rep., [2]Department of Veterinary Hygiene and Management/ Faculty of Veterinary Medicine, Cairo University/ Egypt, Arab Rep., [3]Preventive Medicine/ General Organization for Veterinary Services (GOVS)/ Egypt, Arab Rep., [4]NSAL/ Food and Agriculture Organization (FAO), Rome/ Italy (Italia)

Introduction and Objectives or Purpose

A key step towards implementing the One Health approach in the livestock sector is the adoption of veterinary public health practices along the value chain. There is plenty of guidelines on practices that minimize the risk of pathogens spillover from animals to humans, but their application is limited. This paper presents a case study from Egypt: it demonstrates that integrating the technical and business dimensions in the provision of extension services to livestock farmers can support the wide adoption of veterinary public health practices.

Methods

We engaged broiler farmers in peri-urban areas of Egypt to discuss their business models. We found out that, every year, they throw about 39 million dead poultry in water and drainage canals, creating major public health risks for the populace. We facilitated a dialogue between broiler farmers and extension officers to co-create solutions that increased farmers' profits while at the same ensuring the proper disposal of dead poultry.

Results or Focus

Broiler farmers and extension officers concurred that composting dead poultry improves business profitability while minimizing public health risks. Composting is technically simple and requires minimal investment at farm level. Under the supervision of animal health officers, a number of farmers are making investments to compost their dead poultry, which is generating positive returns through applying or selling compost while minimizing pathogens spread into the environment. The government of Egypt and Egypt Poultry Association have expressed interest to scale up the practice of composting dead birds throughout the country.

Conclusion or Scope

Combining technical and business dimensions into the provision of extension services could be an effective way to ensure the wide adoption of veterinary public health practices, and hence support the adoption of the One Health approach in the livestock sector.

Keywords: Poultry sector; Composting; Public Health risk

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Public and Private policy and practice
Abstract No: 14915

Implementing One Health policies through public-private partnerships. A FAO Guidebook for livestock decision-makers

Amira Abdel Nabi[1] ; Lina Abdalla[1] ; Stephen Gikonyo[2] ; Martin Heilmann[3] ; Joy Kiplamai[2] ; Orsolya Mikecz[3] [4] ; Frank Mubiru[4] ; Gerald Nizeyimana[4] ; Ugo Pica-Ciamarra[3] ; Damian Tago Pacheco[*5]
[1]Emergency Centre for Transboundary Animal Diseases/ Food and Agriculture Organization of the United Nations (FAO)/ Egypt, Arab Rep. [2]Emergency Centre for Transboundary Animal Diseases/ Food and Agriculture Organization of the United Nations (FAO)/ Kenya [3]Animal Production and Health Division/ Food and Agriculture Organization of the United Nations (FAO)/ Italy (Italia) [4]Emergency Centre for Transboundary Animal Diseases/ Food and Agriculture Organization of the United Nations (FAO)/ Uganda [5]Regional Office for Asia and the Pacific/ Food and Agriculture Organization of the United Nations (FAO)/ Thailand (□□□)

Introduction and Objectives or Purpose

Over the past decades, low and middle-income countries have published numerous One Health related policies. Their operationalization, however, remains limited. This paper summarizes a FAO Guidebook for livestock decision-makers to engage private actors and successfully implement veterinary public-health policies that reduce public health risks along the livestock value chain.

Methods

We reviewed One Health related policies in Egypt, Kenya and Uganda, including overarching policy documents, laws and regulations. While comprehensive, these policies are poorly implemented. We engaged policy implementers – that is livestock farmers, processors, traders, public animal health officers from central and local governments and other stakeholders – in a co-creation process to identify a set of complementary and self-reinforcing public and private sector actions that facilitate compliance with the existing policy framework and contribute to the wide adoption of veterinary public health practices. As a result, in all three countries livestock stakeholders are currently making investments to adopt these practices.

Results or Focus

We summarized our experience in a Guidebook for livestock decision-makers. The Guidebook identifies five steps to implement One Health related policies: (i) Identification of veterinary public health practices as prioritized in existing policy documents. (ii) Evidence gathering on stakeholders' business models and their compliance with those practices. (iii) Evidence gathering on the human, financial and institutional capacity of local governments, which are responsible to implement policies. (iv) Participatory public-private dialogues to co-create solutions that facilitate the adoption of selected practices. (v) Experimentation, evaluation and scaling up of the co-created solutions.

Conclusion or Scope

The FAO Guidebook to implement One Health related policies provides guidance to national and local stakeholders to facilitate public-private dialogues that result in the wide adoption of veterinary public health practices along the livestock value chain. We plan to utilize the Guidebook in different geographies and build national and local capacity to utilize it.

Keywords: One Health, policy implementation, law enforcement, participatory process, local governments

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Public and Private policy and practice
Abstract No: 14933

Public-private co-creation of One Health practices : A pilot initiative in the Uganda poultry sector

Gerald Nizeyimana*[1] ; Willington Bessong[1] ; Martin Heilman[2] ; Ugo Pica-Ciamarra[2] ; Tabitha Kimani[3] ; Sarah Kyejjusa[4] ; Robert Mwebe[5] ; Betty Mbolanyi[6] ; Frank Mubiru[1]
[1]Emergency Centre for Transboundary Animal Diseases / Food and Agriculture Organization of the United Nations (FAO) -Uganda/ Food and Agriculture Organisation/ Uganda, [2]Animal Production and Health Division/ Animal Production and Health Division / Food and Agriculture Organization of the United Nations (FAO) / Italy (Italia)1/ Italy (Italia), [3]Emergency Centre for Transboundary Animal Diseases - Kenya/ Food and Agriculture Organization of the United Nations (FAO) / Kenya, [4]Entrepreneurship, incubation and Innovation Centre / Makerere University Business School/ Uganda, [5]Department of Animal Health/ Ministry of Agriculture Animal Industry and Fisheries/ Uganda, [6]Environmental Affairs/ Ministry of Water and Environment / Uganda

Introduction and Objectives or Purpose

Introduction and objective

While theories and discussions on the One Health approach abound, its implementation remains scattered and piecemeal. This paper presents a case study from Uganda where public and private actors co-created and implemented One Health practices along the poultry value chain, notably veterinary public health practices that minimize poultry-related risks to humans.

Methods

A key component of the One Health approach in the poultry sector is the adoption of good veterinary public health practices. This is achieved when public and private actors cooperate and create an enabling environment where their respective behaviors are complementary and self-reinforcing. We assessed the capacities and resources of the veterinary authorities in two Uganda peri-urban districts to deliver public goods and services, and the business models of poultry slaughter operators. We facilitated a dialogue between veterinary authorities and slaughterers to co-create solutions that increased the profitability of the slaughter facilities while ensuring proper slaughtering practices.

Results or Focus

Veterinary authorities and slaughterers agreed upon a list of minimal requirements to ensure hygiene and biosecurity during the slaughter process. Moreover, they developed indicators of compliance, which facilitated the inspection process and changed their perspective from an enforcing towards an enabling role. The veterinary authorities agreed to allow for progressive improvements, occasional audits and certification of slaughter facilities complying with an agreed threshold of practices. A number of slaughter facilities are currently making investments to comply with the agreed and jointly developed requirements, which is expected to enlarge their client base.

Conclusion or Scope

Adopting the One Health approach requires cooperation between sectors. Evidence-based dialogues, which take into account the incentives and capacities of public and private actors, can facilitate the identification of actionable solutions that reduce public health threats along the livestock value chain.

Keywords: One health, co-creation, public private partnerships, public health risks

Topic: Policy, Environment & Biosecurity (PEB): Science of Climate and Ecological Change of One Health: Rabies and dog
Abstract No: 15010

Development, feasibility and potential effectiveness of community-based continuous mass dog vaccination delivery strategies: lessons for optimization and replication

Christian Tetteh DUAMOR*[1] ; Katie Hampson; Felix Lankester; Ahmed Lugelo; Emmanuel Mpolya; Katharina Kreppel; Sarah Cleaveland; Sally Wyke
[1]Global Health/ Nelson Mandela African Institute of Science and Technology/ Tanzania, United Republic of

Introduction and Objectives or Purpose

Dog vaccination can eliminate rabies in dogs, but annual delivery strategies do not sustain vaccination coverage between campaigns. We describe the development of a community-based continuous mass dog vaccination (CBC-MDV) approach designed to improve and maintain vaccination coverage in Tanzania and examine the feasibility of delivering this approach as well as lessons for its optimization.

Methods

We developed three delivery strategies of CBC-MDV and tested them against the current annual vaccination strategy following the UK Medical Research Council's guidance: i) developing an evidence-based theoretical framework of intervention pathways and ii) piloting to test feasibility and inform optimization. For our process evaluation of CBC-MDV we collected data using non-participant observations, meeting reports and implementation audits and in-depth interviews, as well as household surveys of vaccination coverage to assess potential effectiveness. We analyzed qualitative data thematically and quantitative data descriptively.

Results or Focus

The final design included delivery by veterinary teams supported by village-level one health champions. In terms of feasibility, we found that less than half of CBC-MDV's components were implemented as planned. Fidelity of delivery was influenced by the strategy design, implementer availability and appreciation of value intervention components, and local environmental and socioeconomic events (e.g. elections, funerals, school cycles). CBC-MDV activities decreased sharply after initial campaigns, partly due to lack of supervision. Community engagement and involvement was not strong. Nonetheless, the CBC-MDV approaches achieved vaccination coverage above the critical threshold (40%) all-year-round. CBC-MDV components such as identifying vaccinated dogs, which village members work as one health champions and how provision of continuous vaccination is implemented need further optimization prior to scale up.

Conclusion or Scope

CBC-MDV is feasible to deliver and can achieve good vaccination coverage. Community involvement in the development of CBC-MDV, to better tailor components to contextual situations, and improved supervision of activities are likely to improve vaccination coverage in future.

Keywords: community-based, dog vaccination, process evaluation, rabies, One-Health.

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Surveillance
Abstract No: 15025

Electronic Surveillance Information Systems in Human, Animal and Environment Sectors to Support Integrated Disease Reporting: A One Health Policy Brief

Maureen Nabatanzi*[1] ; Immaculate Nabukenya[1] ; Ekwaro Obuku[1] ; Herbert Bakiika[1] ; Rodney Mugasha[1] ; Robert Mwebe; Esther Nambo; Immaculate Ayebazibwe; Emma Sam Arinaitwe; Mohammed Lamorde[1]
[1]Global Health Security/ Infectious Diseases Institute, Makerere College of Health Sciences, Kampala, Uganda/ Uganda

Introduction and Objectives or Purpose

Diseases involving humans, animals and the environment are increasing in Uganda yet surveillance information systems don't always enable prompt integrated detection and response across sectors. We recommend policy options for utilisation of electronic information systems in human, animal and environment sectors for integrated disease reporting and surveillance in Uganda.

Methods

During November 2020- April 2022, Ministries of Health, Animal/Wildlife held multi-sectoral workshops to assess electronic surveillance information systems in their sectors, identify gaps and propose interventions. In addition, an information systems specialist assessed these informaiton systems to propose options. Findings from these multiple approaches were triangulated with a literature review and synthesis and informed a policy brief on a One Health approach to electronic surveillance information systems.

Results or Focus

In human health, adopting electronic surveillance based on District Health Information System (DHIS2) improved weekly epidemiological data reporting from 42% in 2015 to 75% in 2021. In animal health, by 2022, 17% of 136 districts used the Event Mobile Application for event reporting. Syndromic-based district monthly epidemiological reporting was low (27% in 2022). Reliance on paper-based tools delayed data analysis and use across sectors. In environment health, the Water Information System was designed for internal management of water resources data and may not favor cross-sectoral information sharing. Subsequently, reporting for zoonoses and events of environment origin was sub-optimal across the One Health sectors. A One Health information system would have: offline SMS functionality, verification, online data integration, security, feedback, automated epidemiological analysis and large data capacity. DHIS2 is an easy to adapt web-based information software for integrated surveillance with these features.

Conclusion or Scope

In Uganda's animal and environment sectors, we recommend adapted systems based on DHIS2 for integrated elcetronic One Health surveillance. Findings from this policy brief can inform policy dialogues to adopt country spcific systems.

Acknowledgement
Uganda Ministries of Health, Animal/Wildlife and Environment

Keywords: Surveillance, Electronic, One Health, Integrated, Uganda

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Public and Private policy and practice
Abstract No: 15133

Indigenous One Health: aligning theory and reshaping praxis

Jessica Hernandez*[1] [1] ; Vickie Ramirez[1] ; Julianne Meisner[1] ; Michelle Polowitz[1] ; Peter Rabinowitz[1]
[1]Department of Environmental and Occupational Health Sciences/ Center for One Health Research/University of Washington/ United States [1]School of Science, Technology, Engineering, and Mathematics/ University of Washington Bothell/ United States

Introduction and Objectives or Purpose

The origins of One Health are credited to white male academics, however, worldviews which celebrate the interconnectedness of humans with nature predate these scholars within global Indigenous communities. Building on a series of think pieces on the relevance of landback, Indigenous sentinels networks, and Indigenous resistance to infectious disease transmission and climate change, we sought to explore how Indigenous knowledge and science has been appropriated and included within One Health. Characterizing how the One Health framework can be more positively viewed through the lens of Indigenous knowledge and better serve Indigenous communities is crucial for building an equitable future for One Health.

Methods

We conducted a review of the existing literature pertaining to the relationships, inclusion, and leadership of Indigenous peoples in One Health research. Additionally, we began semi-structured interviews of Indigenous Peoples of the Americas where participants reflected on the One Health model, oriented around the 4Rs of Indigenous research: respect, responsibility, reciprocity, and relevance. Interview transcripts were analyzed using thematic analysis methods.

Results or Focus

While studies referenced the need to incorporate Indigenous knowledge and science, few engaged Indigenous knowledge keepers beyond playing the role of key informants or as an access point to the communities. Interim findings indicate the 4Rs are a good starting place to orient the One Health framework within Indigenous knowledge, however the conceptual model (Figure) does not align with their worldviews. In particular, no defined lines separate humans, animals, and the environment.

Conclusion or Scope

Indigenizing One Health requires re-imagining conceptual models and engaging Indigenous communities as leaders. This includes a more nuanced version of the 4Rs framework to holistically characterize alignment between One Health and Indigenous worldviews, and must be adaptable as Indigenous knowledge is place-based and highly contextualized. Non-Indigenous scholars and practitioners must take care to avoid self-promotion and tokenization, or risk re-producing colonial power structures.

Keywords: Indigenous Knowledge; Indigenous One Health; Equity; Decolonisation; Inclusion; Indigenous health

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Public and Private policy and practice
Abstract No: 15207

EPISTEMOLOGY OF ONE HEALTH

Kristina Pelikan*[1] ; Monique Lechenne[1] ; Jakob Zinsstag[1]
[1]Epidemiology and Public Health/ Swiss Tropical and Public Health Institute/ Switzerland (Schweiz)

Introduction and Objectives or Purpose

One Health is understood here as the linkage of the health of humans, animals and their environment. Thus, One Health is always interdisciplinary. Increasingly it is also transdisciplinary, meaning the cooperation (integration) of academic researchers from different disciplines with non-academic actors, often between different cultures and languages, in co-creating new knowledge and theory to achieve a common goal for One Health. This creates incremental added value, insights that are not gained in interdisciplinary collaboration alone. One Health, as understood here, is based on a multi-epistemic approach with values and concepts manifested in language (embedded in various communicative practices and strategies), which contradicts the use of a common language. Even when using a lingua franca, so-called intralingual multilingualism occurs due to the different technical languages and dialects within a language: One Health is therefore always multilingual, which has also ethical implications.

Methods

This contribution will show how multiepistemic collaboration in One Health is linguistically verifiable through communication and consensual intercultural hermeneutics in One Health. A One Health ontology is created from multicultural worldviews expressed in different languages. We methodically follow an inductive approach oriented towards classical ontology. We anlayse qualitatively communication examples of different international and transdisciplinary projects in the field of One Health. This results in a multispecies ontology interrelating humans, animals and the environment. The structure of elements and relationships of One Health documented in an ontology, will serve as basis for the work on the epistemology of One Health. The methods used transdisciplinary and multiepistemic One Health approaches to gain knowledge and their evidence in communication should be better documented.

Conclusion or Scope

It will become apparent that only through strategically used multilingualism can the added value of transdisciplinary communication in the field of One Health be achieved.

Keywords: Transdisciplinarity, multilingualism, cooperation, multi-epistemic

Topic: Policy, Environment & Biosecurity (PEB): Science of Climate and Ecological Change of One Health: Vector ecology
Abstract No: 15239

EXPLORING INFECTIOUS ORGANISMS ASSOCIATED WITH WILD MEAT

Georgia Moloney [*1] ; Philippe Gaubert[3 4] ; Sophie Gryseels[1 2] ; Erik Verheyen[1 2] ; Anne-Lise Chaber[1]
[1]School of Animal and Veterinary Sciences/ The University of Adelaide/ Australia, [3]Laboratoire Evolution et Diversité Biologique (EDB), IRD/CNRS/UPS/ Université Toulouse III Paul Sabatier / France [4]Centro Interdisciplinar de Investigação Marinha e Ambiental (CIIMAR)/ Universidade do Porto/ Portugal [1]Evolutionary Ecology group, Department Biology/ University of Antwerp/ Belgium [2]OD Taxonomy and Phylogeny/ Royal Belgian Institute of Natural Sciences/ Belgium

Introduction and Objectives or Purpose

The wild meat trade poses a threat to public health as it facilitates the spillover of zoonotic pathogens through high-risk activities such as hunting, preparation, trade and consumption of wild meat. However, despite the sanitary risks and association with marking epidemics including SARS, Ebola and COVID-19, the global wild meat trade continues to thrive.

Methods

To summarise the evidence available, primary literature published between 2000 and 2022 was systematically assessed for evidence of zoonotic pathogens or other public health risks detected in samples directly from wild meat, from animals hunted for wild meat, or from humans demonstrating exposure through high-risk activities.

Results or Focus

Within the 97 articles analysed, 115 pathogen genera (15 viruses, 40 bacteria, 55 parasites, five fungi) were detected in 176 wild meat species from 32 countries. The wild meat species identified included mammals (43 Chiroptera, 39 Primates, 39 Artiodactyla, 18 Rodentia, 16 Carnivora, five Lagomorpha, two Perissodactyla, two Pholidota, one Cingulata, one Eulipotyphla, one Tubulidentata, one Proboscidea), reptiles (five Squamata, one Crocodilia) and aves (two Galliformes). Most pathogen genera reported have demonstrated zoonotic potential (66%), function as vectors (10%), or could potentially contribute to human disease. Human cases (13 viral, four bacterial, one parasitic) were also documented in association with high-risk activities. Most studies employed a targeted approach to evaluate pathogen presence (i.e. PCR; n = 61) or exposure (i.e. ELISA; n = 19), whereas only seven studies employed non-selective metabarcoding techniques.

Conclusion or Scope

Infectious organisms associated with wild meat are highlighted through this review and should be used to guide policy development. However, the common use of a selected set of targeted detection assays likely bias the exploration of pathogen diversity, therefore potentially preventing the discovery of ‘disease x’. The global health risk demonstrated should make the illegal wild meat trade a priority for law enforcement agencies and future research.

Keywords: Biosecurity; Hunting; Public health; Wild meat; Zoonoses

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health Strengthening Community Capacity
Abstract No: 15307

Strengthen local governance for preventing and mitigating global crises

Sergio Guerrero-Sanchez*[1] ; Liesbeth Frias[2]
[1]Centre for Applied One Health Research and Policy Advice/ City University of Hong Kong/ Hong Kong (□□), [2]Asian School of the Environment/ Nanyang Technological University/ Singapore

Introduction and Objectives or Purpose

Deforestation and land conversion have dramatic consequences to biodiversity and disease emergence, and they are also deep-rooted in historical forces involved in environmental injustice. Global guidelines tackling global crises approach these problems using top-down policies, which often fail to match local needs and priorities, and are rarely evaluated for local suitability, implications, and impacts. Top-down policies commonly serve the needs of the Global North and lack consideration for the local context, while offering escape routes to more privileged sectors, and creating a climate of mistrust unfavourable for global negotiations.

Methods

Motivated by the IBPES workshop report on biodiversity and pandemics published in 2020, we reflect on how drivers of zoonotic disease emergence are linked to historical injustices and how global initiatives tackling global crises are prone to reproducing colonial structures.

Results or Focus

We discuss the importance of horizontal collaborations that acknowledge local governance as a basic strategy to address local needs while contributing to global solutions. We highlight a few successful examples of local governance strengthening through horizontal and interdisciplinary collaborations, and show how supporting local solutions can build resilience against global crises.

Conclusion or Scope

There is a need for a paradigm shift, when addressing global crises, where local actors have stronger voices in the discussion for solutions. Pandemics cannot be prevented and global warming cannot be reduced by carbon markets alone. However, both have become part of political agendas with no real benefits to society. We need to start thinking about strategies for mitigation and resilience, which will only succeed through horizontal conversations where Global South actors take the lead. By doing so, prevention might come along.

Keywords: Pandemics prevention, IPBES, Global South, Local governance, Resilience

Topic: Policy, Environment & Biosecurity (PEB): Science of Climate and Ecological Change of One Health: Rabies and dog
Abstract No: 15364

Rabies Prevention and Control in South-East Asia – application of One Health approach

Ronello Abila*[1] ; Kinley Choden[1]
[1]Sub-Regional Representation for South-East Asia/ World Organisation for Animal Health/ Thailand (□□□)

Introduction and Objectives or Purpose

Rabies remains endemic in most parts in South-East Asia, however there are few countries (Brunei and Singapore) that remain free but are in increasing risks of incursion. The ASEAN Member States with the support of the Tripartite has developed the ASEAN Rabies Elimination Strategy (ARES) which is anchored on four pillars : Socio-cultural (S), Technical (T), Organizational (O) and Political (P). Key in the implementation of ARES is the Organization pillar which espouses the setting up of One Health coordination mechanisms from the national down to community level with involvement not only of the medical and veterinary sectors, but also the various stakeholders.

Methods

Through a series of workshops involving both the public health (AEGCD) and animal health (ASWGL) sectors of ASEAN from 2012 to 2014, the ARES was developed and endorsed by the ASEAN Ministers of Health (AHHM) and ASEAN Minsters of Agriculture (AMAF) in 2014. In 2015, the ASEAN MS with support from the Tripartite developed the ARES Implementation Plan, and in December 2018 a workshop was held in Hanoi, Vietnam to review ASEAN MS implementation of ARES. A new workplan was developed to improve its implementation rabies control and prevention in ASEAN.

Results or Focus

Then ARES four pillars of STOP has been effective in assisting countries in updating their national rabies strategies. This was recognise globally with the Tripartite adopting it globally and adding one more pillar on resources (R), making the STOP-R. The Philippines, one of the first country to align its national rabies strategy with ARES , and later with global STOP-R, got an endorsement of their National Rabies Strategy from the WOAH in May 2021.

In consultation with ASEAN Secretariat and Member States in 2020 and 2021, it was agreed to revise and update the ARES. The ASEAN Sectoral Working Group for livestock (ASWGL) during its meeting in June 2022 has requested WOAH to support ASEAN in revising then ARES and endorsed the process for its revision. An ASEAN technical working group was organised to work collaboratively with WOAH in the revision of the ARES.

Conclusion or Scope

COVID-19 pandemic has greatly affected the momentum of rabies control activities in most countries in South-East. There is a need to increase advocacy and bring back rabies control in the priorities of the ASEAN MS. With revision of the ARES, and its eventual endorsement by both AHHM and AMAF will hopefully bring back that momentum.

Acknowledgement
We thank the Members and other stakeholders for continuous support.

Keywords: rabies; prevention and control; one health

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Monitoring One health Determinants
Abstract No: 15003

Assessment of integrated health of human, animal and environment: a holistic and stratified analysis based on global One Health index

Shizhu Li[1 2] ; GUO Zhaoyu[*1] ; Jiaxin Feng[1] ; Jin Chen[1] ; Lin Ai[1] ; Jingshu Liu[2] ; Xiaoxi Zhang[2] ; Chunli Cao[1] ; Jing Xu[1] ; Xiaonong Zhou[1 2] ; Shang Xia; Jingbo Xue[1]
[1]National Institute of Parasitic Diseases/ Chinese Center for Disease Control and Prevention/ China (□□), [2] School of Global Health/ Shanghai Jiao Tong University School of Medicine/ China (□□)

Introduction and Objectives or Purpose

As part of the global One Health index, the global One Health Intrinsic Drivers index (GOH-IDI) is a framework for evaluating the baseline conditions of human health, environmental health, and animal health. This study aim to provides a potential policy assessment tool for policy makers to help them better understand what can be enhanced in the future. This study is to assess the global performance in terms of GOH-IDI, analysis the difference under the world bank regional classification, and evauate the relationship between GOH-IDI and national economic levels.

Methods

The raw data among 146 countries worldwide were collected from authoritative databases and official reports in November 2021.The spatial and classificatory distribution of GOH-IDI were evaluated and identified by descriptive statistic analysis, data visualisations and shaping, Shapiro normality test and ridge map. The GOH-IDI was divided into five levels in the form of heat maps and visualised with regular heat maps and global maps. The differences under the world bank regional classification are analysed. The relationship between GOH-IDI and gross national income per capita was assessed using quadratic regression model. World Bank country classifications by income level are used to evaluate the differences in GOH-IDI performance between countries of various economic levels.

Results or Focus

We evaluated the performance of One Health Intrinsic Driver in 146 countries. The mean (SD) score of GOH-IDI is 52.58 (5.30). Gross national income per capita was moderately correlated with GOH-IDI($r= 0.744$, $P<0.001$). High-income countries (HICs) and other economic levels are statistically different from each other($P<0.001$).

Conclusion or Scope

The GOH-IDI is a crucial tool to evaluate the situation of One Health. There are inter-regional differences in GOH-IDI significantly at the worldwide level. GOH-IDI facilitates researchers' understanding of the multidimensional situation in each country and invests more attention in scientific questions that need to be addressed urgently.

Keywords: One Health; Evaluation framework; Economic disparities; Global One Health index

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Legal responses to one health and health inequalities
Abstract No: 15099

Strengthening the International Health Regulations through a One Health Approach

Katherine Ginsbach*[1] ; Stefania Negri [4] ; David Sherman[3] ; Kelsey Galantich[3] ; Carmen Bullon[2] ; Alison Durran [1]
[1]Center for Transformational Health Law / O'Neill Institute for National and Global Health Law/ United States [4]International Law / UNISA School of Law / Italy (Italia) [3]Capacity Building Department / The World Organisation for Animal Health / France [2]FAO Development Law Service / Food and Agriculture Organization of the United Nations/ Italy (Italia)

Introduction and Objectives or Purpose

The COVID-19 pandemic demonstrated the critical need for an enhanced multisectoral and multi-institutional collaboration overcoming silos approaches, including the IHR. While the global community has been responding to COVID-19 through a multisectoral approach, the IHR contains no specific reference to the intersection between human and animal health or to the One Health approach. Member States must amend the IHRs to not only respond to novel pathogens, but also to anticipate those threats, including AMR and zoonotic disease spillovers.

Methods

Conducting an analysis of the legal solutions to identify opportunities to reframe/amend the IHRs to strengthen a One Health preparedness and response platform, including examples of how amending Articles 5, 14 and 57 of the IHR could strengthen a One Health framework. This includes more institutional forms of cooperation of the regulatory frameworks to prevent zoonotic spillovers and strengthen surveillance and response.

Results or Focus

A broad collaboration has been underway to address this for several years. The Tripartite, collaboration between the FAO, the WOAH, and the WHO has since 2010, now Quadripartite Cooperation with the addition of UNEP in March 2022, is one of the most significant high-level initiatives to strengthen the adoption of the One Health approach to human, animal, and environmental health. Rooting these collaborations in international legal frameworks will strengthen the cooperation's work on prevention, response, and sharing data and information.

Conclusion or Scope

Many existing threats to human health, including zoonotic diseases, food borne diseases, chemical events, radiological events, and antimicrobial resistance are complex and require a multisectoral and multistakeholder approach. Member States must ground the IHRs to serve as a trusted, legitimate global reference for public, private, and civil society organizations around the world as they consider how to trigger their disease surveillance and response. This grounding of the IHR will help to facilitate communication, coordination, surveillance, preparedness, and response among sectors.

Keywords: International Health Regulations; One Health; Prevention and Response; Legal Preparedness; Quadripartite Cooperation

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Biosecurity concerns and One Health
Abstract No: 15361

Understanding illegal wild meat markets and associated health risks in target EU countries

Anne-Lise Chaber*[1] ; Philippe Gaubert[1] ; Sophie Gombeer[2] ; Sophie Gryseels[2] ; Sandrella Morrison[3] ; Casimir Nebesse[4] ; Erik Verheyen[2]
[1]Pathobiology and Population Health/ University of Adelaide/ Australia, [1]Laboratory of Evolution and Biological Diversity / University Paul Sabatier/ France, [2]Taxonomy and Phylogeny/ Royal Belgian Institute of Natural Sciences / Belgium, [3]University Medical Center / University of Utrecht/ Netherlands [4]Centre de Surveillance de la Biodiversité/ University of Kisangani/ Congo, Democ. Republic of the

Introduction and Objectives or Purpose

Wild meat consumption and trade in the tropics, together with international wild meat exportation, are increasing in frequency due to the growing demand from urban centers worldwide. The trade of wild meat has a major impact on both the conservation of hunted species and public health, connecting the source countries with those that import this meat illegally. Alarmingly, many of the pathogens associated with wild meat have the potential to cause severe consequences for human health, economy, livestock and trade.

Methods

Our project carried out in 2021-2022 reports on market surveys in Europe, with an “on-the-ground” focus on French markets, lab-based identifications of pathogens conveyed by analyzing wild meat potentially entering Europe and lab-based identifications of the traded species of high conservation concern through DNA-typing of the wild meat.

Results or Focus

Overall, this study demonstrates that the African diaspora reports a high willingness to pay for wild meat in Europe, with no indication that there is a generational shift away from this consumption. In line with previous studies, mammals made the majority of the 513 wild meat samples collected in the European and African markets with rodents and artiodactyls being the most abundant. We uncovered a diversity of viruses and bacteria from wild meat specimens using unbiased sequencing technologies. Viruses were detected in over half of the investigated sample pools, belonging to 16 different virus strains from 7 different virus families. A total of 1,421 genera of bacteria could be identified.

Conclusion or Scope

We stress the urgency of appropriate training and adequate collaboration between health, biosecurity, trade, and environmental protection agencies at national and international levels. The wildlife trade will continue to generate major human pandemics without appropriate law enforcement strategies. We urge decision-makers to articulate international treaties, actions, and sanctions to preserve global health.

Acknowledgement
We thank WWF for funding this study.

Keywords: Wild meat, International Trade, European markets, Biosecurity, Public Health

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Biosecurity and zoonotic spill over
Abstract No: 14766

WildHealthNet: A One Health approach to sustainable wildlife health surveillance

Sarah Olson*[2]
[2]Health Program/ Wildlife Conservation Society/ United States

Introduction and Objectives or Purpose

Wildlife and their interfaces with people and livestock are essential surveillance targets to monitor the effects of environmental changes on biodiversity and the emergence of new pathogens affecting wildlife, livestock, and human health. However, unbalanced investments in One Health have neglected wildlife health surveillance at national and global scales, particularly in lower and middle income countries (LMICs) where previous efforts have been limited in scope and duration.

Methods

Building on decades of wildlife health work, and close relationships with environmental sector and One Health partners in over 60 countries, the Wildlife Conservation Society (WCS) has been developing and implementing WildHealthNet, a new locally-scaled multi-pronged One Health approach to establish wildlife health surveillance in LMICs. WildHealthNet utilizes existing capacity in the environmental, animal, and public health sectors, and focuses on iterative field implementation and policy development (WildHealthBuild), capacity building (WildHealthSkills), data collection and management systems (WildHealthTech), and supports management actions (WildHealthRespond).

Results or Focus

WildHealthNet has been piloted in Cambodia, Lao PDR, and Viet Nam to support the development of national wildlife health surveillance systems. Networks included protected area rangers, wildlife rescue centers, livestock and human health sector staff and laboratories, and community members. Surveillance activities detected outbreaks of H5N1 highly pathogenic avian influenza in wild birds, African swine fever in wild boar (Sus scrofa), Lumpy skin disease in banteng (Bos javanicus), and other priority endemic zoonotic pathogens. In Cambodia and Lao PDR, national plans for wildlife disease surveillance are being signed by governments.

Conclusion or Scope

Cross-sectoral and trans-disciplinary approaches are needed to implement effective and sustainable wildlife health surveillance systems at global scale. WildHealthNet responds to the global needs for wildlife health surveillance and supports the OIE Wildlife Health Framework objectives, but will require further investments and a consortium approach, where key global stakeholders coordinate and align into a coherent workflow.

Acknowledgement

Co-authors: Mathieu Pruvot[1,2], Emily Denstedt[3], Alice Latinne[4], Alice Porco[5], Diego Montecino-Latorre, Kongsy Khammavong[3], Phonesavanh Milavong[3], Souchinda Phouangsouvanh[3], Manoly Sisavanh[3], Nguyen Thi Thanh Nga[4], Pham Thi Bich Ngoc[4], Vo Duy Thanh[4], Sokha Chea[5], Sreyem Sours[5], Phouvong Phommachanh[6], Watthana Theppangna[6], Sithong Phiphakhavong[6], Chhuon Vanna[7], Kry Masphal[7], Tum Sothyra[8], Sorn San[9], Hong Chamnan[10], Pham Thanh Long[11], Nguyen Thi Diep[11], Vu Trong Duoc[12], Patrick Zimmer[13], Kevin Brown[13], & Amanda E. Fine[1]

1. Wildlife Conservation Society, Health Program, Bronx, NY, USA
2. University of Calgary, Faculty of Veterinary Medicine, Calgary, AB, Canada
3. Wildlife Conservation Society, Lao PDR Country Program, Vientiane, Lao PDR
4. Wildlife Conservation Society, Viet Nam Country Program, Hanoi, Viet Nam
5. Wildlife Conservation Society, Cambodia Country Program, Phnom Penh, Cambodia
6. National Animal Health Laboratory, Department of Livestock and Fisheries, Vientiane, Lao PDR
7. Department of Wildlife and Biodiversity, Forestry Administration, Phnom Penh, Cambodia
8. National Animal Health and Production Research Institute, Phnom Penh, Cambodia
9. General Directorate of Animal Health and Production, Phnom Penh, Cambodia
10. General Department of Administration for Nature Conservation and Protection, Phnom Penh, Cambodia
11. Department of Animal Health, Ministry of Agriculture and Rural Development, Hanoi, Viet Nam
12. National Institute of Hygiene and Epidemiology, Hanoi, Viet Nam
13. Canadian Wildlife Health Cooperative, Saskatoon, SK, Canada

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Biosecurity and zoonotic spill over
Abstract No: 14781

Wildlife and zoonotic disease risk management in China: examine gaps and One Health opportunities in scopes, mandates, and monitoring systems

Hongying Li*[1] ; Yufei Chen[1] ; Catherine Machalaba[1] ; Hao Tang[2] ; Aleksei Chmura[1] ; Mark Fielder[5] ; Peter Daszak[1]
[1]Research/ EcoHealth Alilance/ United States, [1]Research/ The Wildlife Hospital/ New Zealand [2]Research/ Harry Butler Institute, Murdoch University/ Australia [5]School of Life Sciences/ Kingston University/ United Kingdom

Introduction and Objectives or Purpose

The utilization of wild animals for commercial trade, farming, and captivity in China represents a critical zoonotic spillover pathway with a systematic pattern of human-animal contact. We review current systems for zoonotic disease monitoring, analyze the species coverage against known zoonotic disease sources, and present focus areas for further attention to strengthening cross-sectoral prevention and preparedness measures.

Methods

This study reviewed the current laws and regulations, government reports and policy documents, and existing literature on zoonotic disease preparedness and prevention across the forestry, agriculture, and public health authorities in China to identify coverage areas and gaps.

Results or Focus

Fifty-five known zoonotic diseases (59 pathogens) are routinely monitored under a multi-sectoral system among humans and domestic and wild animals in China. These diseases have been detected in a variety of animals, most of which are transmitted between humans and animals via direct or indirect contact and vectors. However, this current monitoring system covers a limited scope of disease threats and animal host species, the governance of wild animal protection and utilization, and limited knowledge about wild animal trade value chains present challenges for zoonotic disease risk assessment and monitoring and affect the completeness of mandates and enforcement.

Conclusion or Scope

A coordinating and collaborative One Health approach among different stakeholders is required to effectively monitor and manage disease emergence and transmission risks in the animal value chains. Moreover, pathogen surveillance among wild animal hosts and human populations outside the routine monitoring system will fill the data gaps and improve our understanding of future emerging zoonotic threats to prevent disease.

Acknowledgement

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Keywords: China; Emerging infectious disease; Governance; Monitoring; Wild animal; Zoonotic disease

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Monitoring One health Determinants
Abstract No: 15092

Identifying future global hotspots of deforestation and biodiversity loss to inform One Health risk

Abhishek Chaudhary*[1]
[1]Environmental Engineering and Management/ Indian Institute of Technology (IIT) Kanpur/ India

Introduction and Objectives or Purpose

To reduce the risk of future pandemics, efficient forward-looking mitigation measures are needed to halt deforestation and global biodiversity decline. Here we aim to identify world regions where a high amount of deforestation and consequent biodiversity loss is expected to take in place in future under different climate change and socio-economic scenarios.

Methods

We link six future (years 2050 and 2100) global gridded maps (0.25° × 0.25° resolution) available from the land use harmonization (LUH) database, representing alternative concentration pathways (RCP) and shared socio-economic pathways (SSPs), with the countryside species–area relationship model to project the future land use change and consequent species extinctions and phylogenetic diversity loss (in million years) for mammals, birds, and amphibians in each of the 804 terrestrial ecoregions and 176 countries and compare them with the current (1900–2015) and past (850–1900) rates of biodiversity loss.

Results or Focus

Future land-use changes are projected to commit an additional 209–818 endemic species and 1190–4402 million years of evolutionary history to extinction by 2100 depending upon the scenario with highest diversity loss projected for amphibians. We found that the most aggressive climate mitigation scenario (RCP2.6 SSP-1), representing a world shifting towards a radically more sustainable path, including increasing crop yields, reduced meat production, and reduced tropical deforestation coupled with high trade, projects the lowest land use change driven global biodiversity loss and thus a global momentum towards its adoption can improve One Health.

Conclusion or Scope

Future species extinctions and zoonotic disease spillover risk could potentially be reduced if habitat preservation is incorporated into national development plans, especially for biodiverse, low-income countries such as Indonesia, Madagascar, Tanzania, Philippines, and The Democratic Republic of Congo that are otherwise projected to suffer a high number of land use change driven extinctions under all scenarios.

Acknowledgement

We acknowledge the Initiation Grant of IIT Kanpur, India (project number 2018386).

Keywords: One Health; Biodiversity loss; Deforestation; Land use change; Future economic scenarios

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Legal responses to one health and health inequalities
Abstract No: 15004

Establishment of an indicator framework for Global One Health Intrinsic Drivers index based on the Grounded Theory

Shizhu Li; Jiaxin Feng*; Zhaoyu Guo; Jin Chen; Lin Ai; Jingshu Liu; Xiaoxi Zhang; Chunli Cao; Jing Xu; Shang Xia; Xiaonong Zhou; Shizhu Li

Introduction and Objectives or Purpose

One Health has become a global consensus to deal with complex health problems. However, the development process of One Health practice in various countries is still relatively slow, and there is a lack of systematic evaluation index. The purpose of this study was to establish an indicator framework for global One Health Intrinsic Drivers index (GOH-IDI) to evaluate human, animal and environmental health development process globally.

Methods

First, 82 studies were deeply analyzed by a grounded theory method to establish an indicator framework, which was composed of three first-level indicators, 19 second-level indicators, and 79 third-level indicators. Then, through semi-structured interviews with 28 health-related experts, the indicators were further integrated and simplified according to the inclusion criteria of the indicators. Finally, a fuzzy analytical hierarchy process was used to assign weights to the indicators, thus, forming the evaluation indicator framework of human, animal and environmental health development process.

Results or Focus

An indicator framework for GOH-IDI was formed consisting of three first-level indicators, 15 second-level indicators and 61 third-level indicators. There were six second-level indicators for Human Health, of which “Reproductive, Maternal, New-born, and Child Health” had the highest weight (20.63%) and “Health Risk” had the lowest weight (13.01%). There were four second-level indicators for Animal Health, of which “Animal Epidemic Disease” had the highest weight (31.87%) and “Animal Nutritional Status” had the lowest weight (17.36%). Five second-level indicators were set under Environmental Health, among which, “Air Quality and Climate Change” had the highest weight (23.82%) and “Hazardous Chemicals” had the lowest weight (17.52%).

Conclusion or Scope

An indicator framework for GOH-IDI was established in this study. The indicators were universal, balanced, and scientific, and established a tool for scientifically measuring the development level of human, animal and environmental health in different regions globally.

Acknowledgement

Shang Xia also participated in the study as an author.

Keywords: Global One Health; Intrinsic Drivers index; Indicators; Grounded theory; Fuzzy analytical hierarchy process

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Monitoring One health Determinants
Abstract No: 15012

The Approaching Pilot for One Health Governance Index

Odel Li*[1]
[1]China CDC / Shanghai Legislative Research Institute/ China CDC / Shanghai Municipal People's Congress/ China (□□)

Introduction and Objectives or Purpose

One Health approach advocates to realize the best health and harmonious symbiosis of human, animal and natural environment through cross-border, multi-sectoral and interdisciplinary cooperation. The good governance model is the leading factor for the performance of One Health governance. In order to tackle the complex problems in the One Health governance at global level, the variation of One Health governance in different countries were analyzed by a set of indicators of assessing specific governance capacity within the One Health system.

Methods

The data to calculate OHGI was quoted from various database sources, including from the Food and Agriculture Organization (FAO), the World Health Organization (WHO), the World Organization for Animal Health (OIE), and official health-related institutions of various countries. A total of 17 indicators at three levels, including 8 indicator, 19 sub-indicators, were employed in the OHGI system to comprehensively evaluate the capacity of OHGI in 146 countries.

Results or Focus

Among the 146 countries scored in OHGI system, the average score for all countries was 34.11. The countries with higher OHGI scores largely come from Europe and Central Asia, East Asia and the Pacific and North America, while countries with the lower OHGI scores are almost from Sub-Saharan Africa. Six countries scored more than 65 points, indicating that these countries are relatively mature in most aspects of One Health governance.

Conclusion or Scope

Good governance on One health is an important indicator to measure One Health governance capacity. The political stability, the level of rule of law and economic conditions in different regions are significantly correlated with the One Health governance capacity. Actions need to be taken urgently to close the gap of One Health governance between different regions.

Acknowledgement

We specially thank experts from the World Health Organization, the Food and Agriculture Organization of the United Nation, The World Bank, and universities or institutions.

Keywords: One Health, Governance, Developed countries, Developing countries, Rule of law

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Biosecurity and zoonotic spill over
Abstract No: 14671

ZOONOTIC EMERGING INFECTIOUS DISEASE PRESENCE IN CONFLICT ZONES AND THE PREPAREDNESS OF HUMANITARIAN ACTIONS

Tristán Learoyd*[1] ; John Pittman[2]
[1]Global Medical Affairs/ Emergent/ United Kingdom, [2]Global Medical Affairs/ Emergent/ United States

Introduction and Objectives or Purpose

Infection control in humanitarian situations is dictated to by emergency nature, environment, population vulnerability, and social de-stabilization. Consequently, health advice must be clear and actions expeditious. This research assessed humanitarian approaches to mitigating emerging zoonotic infectious diseases (EIDs) without an effective medical countermeasure (MCM).

Methods

International Committee of the Red Cross (ICRC) activity in zones of military conflict was registered as of February 12, 2022. Using data from the Centers for Disease Control and Prevention (CDC), the activity areas were correlated to epidemiological reports of zoonotic disease from January 1, 2012, to February 12, 2022, to determine risk. All epidemiological reports on diseases with an approved MCM were then excluded to enhance vulnerability. The zoonotic disease identified were reviewed within the emergency public health guidelines from ICRC-Johns Hopkins, Oxfam, Sphere, United Nations High Commissioner for Refugees (UNHCR), and the World Health Organization (WHO).

Results or Focus

As of February 12, 2022, the ICRC was active in conflict zones of 20 countries. In these areas, 25 viral diseases without an approved MCM were identified; 23 had a zoonotic and One Health implication, transmitted by multiple vectors with the potential to bypass stringent humanitarian water, sanitation, and hygiene (WASH) controls. Additionally, seven of the zoonotic viral diseases exhibited interhuman transmission with two capable of aerosol transmission.

Conclusion or Scope

The appraised humanitarian guidance had little mention of methods of vector control beyond simple barrier methods. Pest control guidance and animal husbandry advice was lacking, differential diagnosis between hemorrhagic fevers or diseases transmitted by mosquitoes was limited, with minimal mention of appropriate triage. The inclusion of vector considerations of One Health approaches and associated Susceptible-Infected-Recovered (SIR) Modeling would better inform humanitarian responders on how to prepare for zoonotic threats and reduce disease burdens in migratory and vulnerable populations.

Keywords: Humanitarian; conflict; zoonotic disease; preparedness; vectors

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Legal responses to one health and health inequalities
Abstract No: 15172

Equitable Access to Vaccines: The Role of Intellectual Property Licensing and Technology Transfer Agreements

Ayelet Berman *1
1Centre for International Law / National University of Singapore / Singapore

Introduction and Objectives or Purpose

Covid-19 vaccines were developed at an astounding speed, yet low- and middle-income countries (LMICs) have had to wait longer to receive them. As intellectual property (IP) legal protections prohibit the copying of new vaccines, critics have blamed IP rules for this delay. Indeed, at the WTO, there have been discussions over a TRIPS waiver.

Many experts argue, however, that waiving IP protections alone would not achieve the desired goal. Rather, the main bottleneck in LMICs is the lack of production capacities, including specialized facilities, technical know-how and trained staff. In his book “How to Prevent the Next Pandemic”, Bill Gates makes the case that the conclusion of technology transfer agreements between vaccine developers and LMIC manufacturers is key to any future vaccine global strategy.

During Covid-19 only few vaccine developers and LMIC manufacturers concluded such agreements. Three prominent examples are AstraZeneca’s agreements, such as with Fiocruz (Brazil), Novavax’s agreement with the Serum Institute (India), and Johnson & Johnson’s agreements with manufacturers in India and South Africa.

Against this background, the first objective of this study is to study these cases and to examine how and why they were concluded, and whether they have been effective in speeding up production and access. The second objective is to draw lessons from these experiences for a future regional or global vaccine strategy.

Methods
Desk research and interviews.

Results or Focus

The paper will derive insights for the development of new international best practices on IP and technology transfer. Such best practices could be considered in the context of WHO pandemic treaty negotiations, or by other regional or international initiatives, such as CEPI.

Conclusion or Scope

There is a need to adopt international or regional best practices on IP and technology transfer.

Acknowledgement
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Keywords: vaccines, intellectual property, technology transfer, low and middle income countries, best practices

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Legal responses to one health and health inequalities
Abstract No: 15210

Global and regional governance of One Health and implications for Global Health Security

Olaa Mohamed-Ahmed[1] ; Azza Elnaiem[2] ; Alimuddin Zumla[3 4] ; David Heymann[5 6] ; Richard Kock[5] ; Osman Dar[*1 5]
[1]Global Operations/ UK Health Security Agency/ United Kingdom, [2]Public Health Specialty Training Programme/ Health Education England North West London/ United Kingdom, [3]Department of Infection/ University College London/ United Kingdom, [4]NIHR Biomedical Research Centre/ UCL Hospitals NHS Foundation Trust/ United Kingdom, [5]Global Health Programme/ Chatham House/ United Kingdom, [6]Infectious Disease Epidemiology/ London School of Hygiene & Tropical Medicine/ United Kingdom

Introduction and Objectives or Purpose

The apparent failure of global health security to prevent or prepare for the COVID-19 pandemic has highlighted the need for closer cooperation between human, animal (domestic and wildlife) and environmental health sectors. However, the vast number of institutions, processes, regulatory frameworks and legal instruments with a direct and indirect role in the global governance of One Health, has led to a fragmented global multilateral health security architecture.

Methods

We used a grounded theory approach to identify and evaluate the structures and processes underpinning the global and regional governance of One Health, with a focus on legal and financial frameworks.

Results or Focus

We explore four challenges: first, the sectoral, professional and institutional silos and tensions existing between human, animal and environmental health; second, the challenge which the international legal system, state sovereignty and existing legal instruments pose for the governance of One Health; third, the power dynamics, and asymmetry in power, between countries represented in multilateral institutions and its impact on priority-setting; fourth, the current financing mechanisms which predominantly focus on response to crises, and the chronic underinvestment for epidemic and emergency prevention, mitigation and preparedness activities. We illustrate the global and regional dimensions to these challenges and how they relate to national needs and priorities, through three case studies on compulsory licensing, the governance of water resources in the Lake Chad basin and the desert locust infestation in East Africa. Finally, we propose 12 recommendations for the global community to address these challenges.

Conclusion or Scope

Despite its broad and holistic agenda, One Health continues to be dominated by human and domestic animal health experts. Significant efforts must be made to address the socioecological drivers of health emergencies. These drivers include climate change, biodiversity loss and land use change and therefore require investment, capacity building and integration of other sectors and professionals beyond health.

Keywords: governance; one health; zoonoses; global health security; international law

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Monitoring One health Determinants
Abstract No: 15163

GLOBAL MONITORING OF UPSTREAM DETERMINANTS ACROSS THE STEEP PILLARS FOR HEALTH EMERGENCIES

Prativa Baral*[1] ; Dr. Tim Evans[2] ; Kathleen Clark[3] ; Emily Magurno[3]
[1]International Health/ Johns Hopkins Bloomberg School of Public Health/ United States, [2]School of Population and Global Health/ McGill University/ Canada, [3]Bloomberg School of Public Health/ Johns Hopkins University/ United States

Introduction and Objectives or Purpose

The devastating consequences of COVID-19 have shed light on the multi-faceted dynamics of infectious threats that defy overly simplistic and narrow conceptions of risk and countermeasures that focus exclusively on response. Our current approach to global preparedness overlooks structural “upstream” forces that cross social, technological, economic, environmental, and political (STEEP) domains that shape health and wellbeing. This project identifies key upstream variables and their measurable indicators for global monitoring across STEEP and the four dimensions of risk: prevention, preparedness, response, and recovery (PPRR).

Methods

Using the social determinants of health (SDH), PPPR, and STEEP frameworks, our methodology employs a four-pronged approach:

- a two-step review process of the literature consisting of literature scans and five rapid scoping reviews for each STEEP pillar;
- identification of key upstream determinants and measurable indicators by assessing existing COVID-19 models;
- consultative exercises with experts through a Delphi process; and
- triangulation and triaging of indicators towards a “clean fifteen”: a narrow set of 15 baseline indicators (proxies for upstream factors) for immediate global monitoring that bear on risk.

Results or Focus

Our findings include a list of non-exhaustive but key upstream determinants (n=40) as well as associated indicators (n=300+) that drive risk at varying rates across STEEP. Inequity has emerged as a significant variable that exacerbates risk of health emergencies. The final 15 indicators, selected for immediate monitoring, emerged as important proxies for the following upstream determinants:

-Social: social inequity, individualism, global connectedness;

-Technological: social media and misinformation, digital connectivity, biomedical innovations;

-Economic: economic development, economic inequality, social program financing;

-Environmental: climate change, agricultural and farming practices, built environment;

-Political: governance, public trust, conflict, instability & violence.

Conclusion or Scope

Investing in monitoring of structural upstream factors (especially if difficult to measure, such as inequity) is vital to further our understanding of risk, and implement an effective global surveillance architecture.

Acknowledgement Our sincerest thanks to GPMB.

Keywords: inequity; pandemic preparedness; risk assessment; upstream factors

Poster Abstracts

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: Genomic data linking transmission between the different reservoirs
Abstract No: 14707

The genomic epidemiology of hypervirulent Klebsiella pneumoniae causing bloodstream infections in Vietnam between 2010 and 2020

Duy Pham*[1] ; Quynh Nguyen[1] ; To Nguyen[1] ; Dung Tran[1] ; Phat Voong[1] ; Tuyen Ha[1] ; Trang Nguyen[1] ; Lan Nguyen[2] ; Phuong Nguyen[2] ; Ngan Le[2]
[1]Molecular Epidemiology/ Oxford University Clinical Research Unit/ Vietnam (Việt Nam), [2]Microbiology/ Hospital for Tropical Diseases/ Vietnam (Việt Nam)

Introduction and Objectives or Purpose

Klebsiella pneumoniae (Kp) is one of the leading causes of bloodstream infections (BSIs) globally, associated with significant mortality. There are two distinct pathotypes of Kp: the classical Kp and the hypervirulent Kp (hvKp). HvKp is typically associated with severe community-acquired infections and a hypermucoid phenotype. Although hvKp isolates are often antimicrobial sensitive, the emergence of multidrug-resistant hypervirulent Kp poses a serious global health threat. The circulation, antimicrobial resistance (AMR) and genetic diversity of hvKp in endemic settings are generally understudied. This study aimed to reveal the epidemiology and population genetics of hvKp causing BSIs in Vietnam.

Methods

Realtime-PCR targeting four virulence genes (iucA,rmpA,rpmA2,iroB) was used to screen for hvKp isolates from a collection of 700 Kp BSI isolates at Hospital for Tropical Diseases in HCMC, Vietnam between 2010 and 2020. 109 hvKp isolates were identified and genome-sequenced. SNPs were identified using RedDog pipeline and phylogenetic tree was reconstructed using IQ-TREE. MLST, virulence/AMR genes, O and K antigens were identified using Kleborate and Kaptive.

Results or Focus

Our genomic analyses confirmed that all hvKp isolates carried at least two virulence genes including iucA. We identified 17 sequence types (STs), of which ST23 (56.7%), ST65 (9.3%), ST86 (8.2%) were most dominant. Hypervirulent phenotype was not restricted to K. pneumoniae, but also identified in other Klebsiella species. K1 (55.7%) and K2 (22.7%) capsular types were predominant, followed by K20/K54/K5/K16/K5/K15. Most hvKp isolates were susceptible to antibiotics; however, ESBL-producing hvKp were detected within ST23, ST65 and ST268. Phylogenetic analysis revealed multiple introductions of hvKp ST23 followed by endemic circulation.

Conclusion or Scope

In conclusion, we found a high prevalence of hvKp causing BSIs in Vietnam. ST23 (K1) was predominant; however, hvKp exhibiting diverse genotypes/capsular types were evident. ESBL-producing hvKp isolates were detected. Routine surveillance and tracking the emergence of AMR in hvKp are crucial to inform effective control measures and treatment.

Keywords: Hypervirulent Klebsiella pneumoniae; ST23; hypermucoid ; bloodstream infections; Vietnam;

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: Genomic data linking transmission between the different reservoirs
Abstract No: 15112

ANTIMICROBIAL RESISTANCE IN AGROECOSYSTEM: A MIXED-METHOD STUDY FROM ONE HEALTH PERSPECTIVE IN AHMEDABAD, INDIA

Kalpana Pachillu*[1] ; Christiane Schreiber[2] ; Timo Falkenberg[1 2] ; Sandul Yasobant [1 3 4] ; Deepak Saxena[4]
[1]One Health Graduate School/ Center for Development Research (ZEF), University of Bonn/ Germany (Deutschland), [2]GeoHealth Centre/ Institute for Hygiene and Public Health, University of Bonn Medical Center / Germany (Deutschland), [3]Global Health/ Institute for Hygiene and Public Health, University of Bonn Medical Center/ Germany (Deutschland), [4]Center for One Health Education, Research & Development (COHERD)/ Indian Institute of Public Health Gandhinagar, / India

Introduction and Objectives or Purpose

Antimicrobial resistance (AMR) possesses a multidimensional (social, economic, and environmental) challenge encompassing the food production system, influencing human and animal health. The One Health concept captures this scope by providing an avenue for the inextricable linkage and interdependence involving the health of people, animals, and the environment. Antibiotics, antibiotic residues, antibiotic-resistant bacteria (ARB), and related AMR genes (ARGs) are assumed to present in the natural environment and disseminate resistance to fresh produce/vegetables and thus to human health upon consumption. The spread and transmission of AMR, including the environment discussed intensively, and pathways and routes have been mapped, emphasizing the importance of integrating the environment in risks of AMR transmission. Therefore, this study aims to investigate the role of vegetables in the spread of AMR through an agroecosystem exploration from a One Health perspective in Ahmedabad, India.

Methods

The proposed study adopts a mixed-method approach. First, a systematic review to document the prevalence of ARB and ARGs on fresh produce in South Asia; second, agriculture farmland surveys to collect the general agriculture farming practices and the data on common vegetables consumed raw by the farm-dependent households. Third, using standard microbiological and molecular methods, the vegetable and soil samples analysis for the presence or absence of ARB and ARGs.

Results or Focus

A mixed-method approach from the One Health lens to understand the spread of ARB/ARGs through the agroecosystem in India.

Conclusion or Scope

This unique study attempts to provide an insight into the current state of ARB/ARGs contamination of fresh produce/vegetables and assists in identifying the relevant strategies for effective control and prevention of the spread of AMR. There is immense scope to conduct a similar type of mixed-method study to explore the AMR transmission across species from the One Health perspective in the global south.

Keywords: Antimicrobial resistance, antibiotic-resistant bacteria, antibiotic-resistant genes, vegetables, fresh produce, agroecosystem, one health

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: Genomic data linking transmission between the different reservoirs
Abstract No: 15222

The antimicrobial resistance profile of non-typhoidal Salmonella (NTS) detected within households in Malawi

Catherine Wilson*[1 2 1] ; Yohane Diness[2] ; Oscar Kanjerwa[2] ; John Nyangu[2] ; Patricia Duncan[2] ; Nicholas Feasey[2 3] ; Nicholas Thomson[1] ; Gina Pinchbeck[1] ; Eric Fèvre[1 4] ; Patrick Musicha[2 1]
[1]IVES/ University of Liverpool/ United Kingdom [2]Kamuzu University of Health Sciences/ Malawi-Liverpool Wellcome Research Programme/ Malawi [1]Pathogens and Microbes/ Wellcome Trust Sanger Institute/ United Kingdom [3]Department of Clinical Sciences/ Liverpool School of Tropical Medicine/ United Kingdom [4]Animal and human health/ International Livestock Research Institute/ Kenya

Introduction and Objectives or Purpose

This study describes the phenotypic and genotypic antimicrobial resistance profile of non-typhoidal Salmonella detected within stool of healthy humans, animals and environmental samples at households in Malawi.

Methods

Stool was collected from humans and animals at 30 households within two study sites in Malawi at three time points between November 2018-December 2019. Samples were collected from humans, animals (poultry, livestock, domestic animals, peri-domestic wildlife) and environmental swabs taken.

Selective bacterial culture and qPCR analysis were carried out. PCR positive samples underwent whole genome sequencing (WGS) and phenotypic antimicrobial susceptibility testing (AST) using the disc diffusion method to nalidixic acid, chloramphenicol, tetracycline, streptomycin, cefpodoxime and ampicillin. Genotypic analysis of AMR determinants was carried out using AMRFinderPlus.

Results or Focus

Selective culture was carried out on 2,080 samples. 234 samples were positive for NTS following qPCR (11.2% positivity).

Phenotypic AST demonstrated 294/838(35.1%) isolates were fully susceptible to all antimicrobials tested. 373/838(44.5%) were resistant to 1 antimicrobial. 29/838(3.5%) isolates were multidrug resistant. There was minimal associations of phenotypic AMR profile to host category or species.

Genotypic investigation showed four different AMR determinants within 47 genomes in the dataset of 227 genomes (20.7%). No genomes contained more than 1 AMR determinant, 180 genomes (79.3%) contained no AMR determinants. The most common AMR gene was fosA7(36/227, 15.9%). Three genomes contained a variant of fosA7; fosA7.7. Four qnrB19 genes were found to be located on plasmid contigs. The plasmids carrying the qnrB19 genes are identified as rep cluster 2355, all within S. Typhimurium ST19. Four nonsynonymous mutations of gyrB were detected in four genomes, on chromosomal contigs of S. Typhimurium ST19.

Conclusion or Scope

Encouragingly, low levels of phenotypic and genotypic antimicrobial resistance are currently detected within NTS isolates from humans, animals and the environment from households in Malawi.

Acknowledgement

Many thanks to the participants for taking part in this study.

Keywords: Salmonella, AMR, phenotypic, genotypic

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: Genomic data linking transmission between the different reservoirs
Abstract No: 15263

Transmission of Extended-spectrum β-lactamase (ESBL) in Singapore is mainly mediated by ISEcp1-CTX-M-WbuC-like conserved gene cluster

Yang Zhong*[1] [2] ; Jocelyn, Qi Min Teo[3] ; Siyao Guo[1] ; Joergen Schlundt[1] ; Rick,Twee Hee Ong[4] ; Lay Hoon Kwa[3]
[1]School of Chemistry, Chemical Engineering and Biotechnology/ Nanyang Technological University/ Singapore, [2]Department of Translational Clinical research/ Singapore General Hospital/ Singapore, [3]Pharmacy-Inpatient / Singapore General Hospital/ Singapore, [4]Saw Swee Hock School of Public Health/ National University of Singapore/ Singapore

Introduction and Objectives or Purpose

Extended-spectrum β-lactamase (ESBL) -producing Enterobacteriaceae are emerging globally in causing community-acquired infections and are widely found in all "One Health" sectors. The isolation and genomic characterization of ESBL-producing Enterobacteriaceae have been done in humans, food, wild animal, and aquatic environment in Singapore. However, few studies have pooled their whole genome sequencing (WGS) data together and investigated them from a "One Health" perspective. Therefore, the objectives of this study are 1) characterization of ESBL-producing Enterobacteriaceae with bioinformatic approaches and understanding the genomic relatedness of organisms from different sources. 2) finding the conserved gene cluster circling in all One Health sectors, mediating ESBL transmission in Singapore.

Methods

The WGS data from eight published studies performed between 2010 to 2019 in Singapore covering food, animal, humans and the environment were pooled together and subjected to in silico typing, phylogenetic analysis, mobile genetic elements (MGEs) and acquired resistance genes (ARGs) annotation. All the analyses were performed with relevant R packages and databases, including ResFinder, plasmidFinder, ISFinder et al.

Results or Focus

In total, 641 strains were included in the WGS analysis. Phylogenetic analysis has revealed a distinguishable sequence type (ST) distribution among different sources. Eight beta-lactamase genes were shared by all "One Health" sectors. CTX-M-15 (proportion ~ 33%) and CTX-M-55 (proportion ~14%) were the most prevalent ESBL gene in humans and non-human sources, respectively. They are both located on a conserved ISEcp1-CTX-M-WbuC-like cluster which can be mobile between sources and species.

Conclusion or Scope

In summary, ESBL-producing strains show limited similarity among different sources. However, from a gene-based perspective, the non-human sources are reservoirs for CTX-M ESBLs, which are mobilized on the ISEcp1-CTX-M-WbuC-like cluster. This cluster can be used as a genetic indicator to monitor resistance transmission within and between sources, including humans.

Acknowledgement

Singapore General Hospital, Nanyang Technological University and National University of Singapore supported this study.

Keywords: ESBL, WGS, CTX-M

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: Genomic data linking transmission between the different reservoirs
Abstract No: 15366

Genetic Environment of blaTEM-1 in Global Salmonella Typhi

NARONG NUANMUANG*[1] ; Frank M. Aarestrup[1] ; Pimlapas Leekitcharoenphon[1]
[1]National Food Institute/ Research Group for Genomic Epidemiology/ Denmark (Danmark)

Introduction and Objectives or Purpose

Salmonella Typhi (S. Typhi) causes typhoid fever, a significant healthcare concern in humans. Antimicrobial resistance in S. Typhi challenges therapeutic treatment. The global reports showed that bla_{TEM-1} was the most common beta-lactam resistance gene in Salmonella enterica. The objective of this study was to investigate the genetic environment of bla_{TEM-1} to gain understanding about gene arrangements and its dissemination.

Methods

We downloaded global Salmonella metadata from NCBI Pathogen Detection project with screened antimicrobial resistance genes (AMRPlusFinder). From metadata, we selected S. Typhi that carried bla_{TEM-1} gene and the raw data (n=2,476) of S. Typhi were downloaded and assembled with bioinformatic tools. SISTR for confirming serovar, MLST for finding ST-type, PlasmidFinder for finding plasmids, and MobileElementFinder for finding mobile genetic elements were used. Then, the genomic context of bla_{TEM-1} was analyzed with Frankophile.

Results or Focus

S. Typhi was mostly isolated from humans (63.3%) and unidentified sources (36.4%). All S. Typhi were divided into 2 common ST-types, ST-1 (87.8%) and ST-2 (11.9%). The most common resistance determinant profile was aph(3'')-Ib,aph(6)-Id,bla_{TEM-1},catA1,dfrA7,gyrA_S83F,sul1,sul2 (25.7%). The common plasmid replicons were IncHI1B (27.0%), IncHI1A (26.9%), IncFIB(pHCM2) (16.4%) and IncFIA(HI1)(7.7%). We found several mobile genetic elements-MITEEc1 (100%), ISSen6 (99.9%), ISSty2 (99.9%,) and IS26 (88.4%). When focusing on genetic environment of bla_{TEM-1} gene, there were 5 main patterns of bla_{TEM-1} arrangement: (1) tnpR+bla_{TEM-1}+hns (2) tnpR+bla_{TEM-1}+sul2 (3) (ISEcp1)+tnpR+bla_{TEM-1}+ aph(3'')−Ib+aph(6)−Id, (4) tnpR+bla_{TEM-1}+tetR and (5) IS26+tnpR+bla_{TEM-1}+IS26

Conclusion or Scope

Our results indicated that bla_{TEM-1} gene in S. Typhi could be found in various arrangements. At least two Insertion sequences (ISEcp1 and IS26) are involved in dissemination of this gene in S. Typhi affecting beta-lactam resistance worldwide.

Acknowledgement

The authors would like to thank the Center for Genomic Epidemiology, Technical University of Denmark, for supporting bioinformatic analysis and suggestions.

Keywords: Salmonella Typhi, blaTEM-1, genetic environment

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: Genomic data linking transmission between the different reservoirs
Abstract No: 15393

High-throughput single-cell metagenomic sequencing of microbial community in sewage and pig feces for antimicrobial resistance surveillance

Meilee Ling*[1] ; Judit Szarvas[1] ; Baptiste Avot[1] ; Patrick Munk [1] ; Saria Otani[1] ; Frank M. Aarestrup [1]
[1]National Institute of Food/ Technical University of Denmark/ Denmark (Danmark)

Introduction and Objectives or Purpose

Metagenomic sequencing has been utilized for surveillance of global antimicrobial resistance (AMR) gene dissemination in sewage and pig feces, thus enabling real-time monitoring of the AMR load in a country. Single-cell metagenomic sequencing is a powerful complementary approach to shotgun metagenomic approach due to the bottlenecks of metagenomic sequencing, such as difficulties to separate contigs belonging to closely related organism. Here we used microfluidics to obtain high-throughput single cell metagenomic sequencing within complex matrixes fsuch as sewage and pig feces.

Methods

In our study, we obtained 1738 single-cell amplified genome (SAG) library with at least 1e+5 reads per cell in deep sequencing and with 7971 SAG library with at least 1e+4 reads per cell in shallow sequencing.

Results or Focus

We are currently exploring the possibilities and limitation of different computational methods and analyses on the single cell metagenomics data in order to (i) link AMR genes to single cells within the sewage and fecal samples, (ii) investigate the possibility of obtaining intra-species diversity within microbiomes, (iii) identify AMR genes that are related to horizontal gene transfer in the single amplified genomes (SAGs) and (iv) building a database of dark matter from the sewage and pig feces sample. This will allow for more comprehensive microbiome analyses to identify individual bacterial strains that are potential major players in AMR emergence and distributions in complex matrices,

Conclusion or Scope

We presented possible computational methods to reveal strain-resolved phylogenies and direct link of AMR genes to single bacteria cell using SAGs data. Few challenges remain in the analysis and interpretation of single-cell meta genomics data. For example, uneven sequence coverage due to multiple displacement amplification(MDA), possible contamination with doublet cells, and the genome assembly of different data that can be obtained through deep sequencing of a few cells vs shallow sequencing of many cells within a sample.

Keywords: Single cell metagenomic sequencing, AMR

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: Plasmid-mediated resistance
Abstract No: 15170

Investigation of Escherichia coli isolates from pigs and humans in Lao PDR for colistin resistance

Vilaiphone Phomsisavath[*1] ; Vilada Chansamouth[1,2] ; Tamalee Roberts[1,3] ; Matthew T Robinson[1,3] ; Manivanh Vongsouvath[1,2] ; Watthana Theppangna[4] ; Peter Christensen[5] ; Stuart Blacksell[1,3,5] ; Mayfong Mayxay[1,3,6] ; Elizabeth A Ashley[1,3]
[1]Mahosot Hospital/ Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit/ Lao People's Democ. Rep., [2]Mahosot Hospital/ Microbiology Laboratory/ Lao People's Democ. Rep., [3]University of Oxford/ Centre for Tropical Medicine and Global Health/ United Kingdom, [4]Department of Lifestocks and Fisheries/ National Animal Health Laboratory/ Lao People's Democ. Rep., [5]Faculty of Tropical Medicine, Mahidol University/ Mahidol Oxford Tropical Medicine Research Unit/ Thailand (□□□), [6]University of Health Sciences/ Institute of Research and Education Development/ Lao People's Democ. Rep.

Introduction and Objectives or Purpose

Antimicrobial resistance (AMR) is a significant public health threat that should be tackled using One Health approach. Colistin is not available in Laos to treat human infections, only for animal treatment. The first report of colistin-resistant E.coli in human in Laos was in 2012, possibly acquired by horizontal transmission from a pig. However, it is unknown when colistin resistance in E.coli emerged and what the proportion of invasive isolates in humans is. Therefore, this study seeks to investigate colistin-resistant Escherichia coli, determine the prevalence, characterize antimicrobial susceptibility, and detect their genes from pigs and humans in Laos.

Methods

To investigate this, between August and November 2022, we will study up to 1900 samples from pigs and humans in Laos. Rectal swabs from approximately 900 domestic pigs and 1000 stored E.coli isolates from blood cultures from patients from all over Laos admitted to Mahosot Hospital between 2000 to 2022 will be included. Potential colistin-resistant E.coli isolates will be identified using selective colistin chromogenic agar. The minimal inhibitory concentration will be calculated for all isolates that grow on the selective agar using microbroth dilution (ComASP™ Colistin, Liofilchem®) following EUCAST guidelines. The clinical breakpoint for defining colistin resistance will be >2 mg/liter. Isolates will also be tested by Real-Time Polymerase Chain Reaction to detect plasmid-mediated genes (mcr-1, mcr-2, mcr-3).

Results or Focus

We will present data on colistin-resistant E.coli in humans and pigs in Laos from representative regions of the country and describe when colistin resistance in clinical invasive isolates emerged. Demographic and geographic results will be analyzed to show trends and risk factors for resistance.

Conclusion or Scope

Results will provide evidence of a link between colistin use in animals and invasive human infection and may inform policies for antibiotic usage both in the human and animal sectors.

Acknowledgement

Keywords: Colistin resistance; E.coli; Laos; One Health; antimicrobial resistance

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 14673

Detection of MDR/ESBL Salmonella and Campybalocter spp in poultry and Domestic Pigeons in North-central Nigeria: The One Health implication

Aliyu Haruna*[1]
[1]Life Sciences/ Africa Center of Excellence for Mycotoxin and Food Safety (ACEMFS) Federal University of Technology, Minna, Niger State/ Nigeria

Introduction and Objectives or Purpose

Salmonella and Campylobacter infection are the leading global burden foodborne diseases. In 2010, WHO estimated 78 million illnesses and 59,153 deaths in humans to be associated with foodborne non-typhoidal S. enterica, while food-borne Campylobacter spp. caused more than 95 million illnesses and 21,374 deaths in humans. poultry meat has been identified as one of the most important food vehicles for non-typhoidal Salmonella spp. and Campylobacter spp. This study investigated the presence of Salmonella and Campylobacter species in commercial poultry and domestic pigeon.

Methods

A cross-sectional study was conducted in North-central Nigeria. We collected 192 pigeons and 121 chicken cloacal swab samples and analyzed using standard bacteriological methods. Polymerase Chain Reaction (PCR) was used to detect Salmonella invA virulence gene presence. Antibiotic susceptibility profiling for multidrug resistance isolates was performed using Kirby-Bauer disk diffusion method. ESBLs genes were determined using multiplex PCR.

Results or Focus

Multidrug resistance was observed in 100% Salmonella and Campylobacter isolates, all with multiple antibiotic resistance index of ≥ 0.20. Resistance profiles of MDR Salmonella species ranged from 7 to 20 antibiotics. One isolate was resistant to the highest number of antibiotics and was sensitive to imipenem, fosfomycin, and nitrofurantoin. invA virulence and ESBL genes: blaTEM and blaSHV were detected in Salmonella isolates. MDR and ESBL-Salmonella and Campylobacter isolates were detected in chickens from commercial birds.

Conclusion or Scope

Inappropriate antibiotic usage and poor biosecurity measures were observed. Health education of the farmers on antimicrobial stewardship should be promoted. One Health approach, a multidisciplinary concept, should be adopted for control and prevention through surveillance and antibiotic susceptibility profiles monitoring of MDR Campylobacter, Salmonella strains emergence and spread along human-poultry-environment interface. This will assure food safety, food security, public and environmental health.

Acknowledgement

Poultry attendants that assisted in samples collection

Keywords: Antimicrobial resistance, poultry, pigeon

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 14716

Prevalence of carbapenem resistance and its potential association with antimicrobial use in humans and animals in rural communities in Vietnam

Yen Nguyen Thi Phuong*[1 2] ; Nhung Nguyen Thi[1] ; Phu Doan Hoang[1 3] ; Dung Nguyen Thi Thuy[1 3] ; Van Nguyen Thi Bich[1] ; Kiet Bach Tuan[4] ; Mattias Larsson [5] ; Quynh Nguyen Pham Nhu[1] ; Duy Pham Thanh[1] ; Juan Carrique-Mass[1 6]
[1]ViParc/ Oxford University Clinical Research Unit (OUCRU)/ Vietnam (Việt Nam), [2]Microbiology/ University of Science/ Vietnam (Việt Nam), [3]Faculty of Animal Science and Veterinary Medicine/ Nong Lam University/ Vietnam (Việt Nam), [4]Animal/ Sub-Department of Animal Health, Production and Aquaculture/ Vietnam (Việt Nam), [5]Global Public Health/ Karolinska Institute/ Sweden (Sverige), [6]Centre for Tropical Medicine and Global Health/ Oxford University/ United Kingdom

Introduction and Objectives or Purpose

Background

Vietnam is a hotspot for antimicrobial resistance; however, little is known on the prevalence of carriage of carbapenem resistance in non-hospitalized humans and in animals. Carbapenem-resistant Enterobacteriaceae (CRE), particularly Escherichia coli (CREC) and Klebsiella pneumoniae (CRKP) and also Acinetobacter baumannii (CRAB) are emerging threats worldwide.

Purpose

(1) Investigate the prevalence of carriage of carbapenem-resistant bacteria among livestock and in-contact humans in the Mekong Delta (Vietnam) and its potential relationship with antimicrobial use; and (2) the genetic determinants of carbapenem resistance in CREC/CRKP/CRAB in this area.

Methods

Methods

Samples were collected from humans (n=652), chickens (n=237), ducks (n=150) and pigs (n=143) in 400 small-scale farms in the Mekong Delta of Vietnam. Samples (rectal swabs, faecal swabs) were investigated for carriage of CRE/CRAB and were further characterized phenotypically and genotypically.

Results or Focus

Results

The prevalence of CRE isolates in human rectal swabs was 0.6%, including 4 CREC and 1 CRKP. One pig was infected with CREC (prevalence 0.7%). CRAB was isolated from chickens (n=4) (prevalence 2.1%) and one duck (prevalence 0.7%). CRKP was isolated from a human who was also colonized with CREC. The CRKP strain (ST16), from a participant with pneumonia under antimicrobial treatment, genetically clustered with clinical strains isolated in a hospital outbreak in southern Vietnam. The prevalence of CRE was higher among humans that had used antimicrobials within 90 days of the sampling date than those had not (4.2% versus 0.2%) ($P=0.005$). All CRE/CRAB strains were MDR, although they were susceptible to colistin and neomycin. The carbapenemase genes identified in study strains were bla_{NDM} and bla_{OXA}.

Conclusion or Scope

Conclusions

The finding of a CRKP strain clustering with previous hospital outbreak raises concerns about potential transmission of carbapenem-resistant organisms from hospital to community settings or vice-versa.

Keywords: Carbapenem resistant; Escherichia coli; Klebsiella pneumoniae; Acinetobacter baumannii

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 14747

PROMOTION OF SAFE-FOOD TO CONSUMERS OF MILK AND DAIRY PRODUCTS AT KIBAHA TOWN COUNCIL (KTC) – TANZANIA

Damas Theobald Msaki*[1] ; Sigrid Agenas[2]
[1]Planning, Monitoring and Evaluation/ Kibaha Education Centre/ Tanzania, United Republic of, [2]Department of Animal Nutrition and Management/ Swedish University of Agricultural Sciences (SLU)/ Sweden (Sverige)

Introduction and Objectives or Purpose

A cross-sectional baseline survey was conducted at Kibaha Town Council (KTC), Pwani Region (Tanzania), to assess awareness and practices of smallholder dairy producers towards antimicrobial use (AMU), a major cause of food-borne antimicrobial resistance (AMR) in the livestock production systems. The aim was to improve consumers' confidence towards consumption of milk and other dairy products.

Methods

Quantitative data were collected from a total of 30 randomly selected respondents from a sampling frame of households keeping dairy cattle in 3 administrative wards of Tumbi, Picha ya Ndege and Maili-Moja. Structured questionnaire was administered through face to face conversation between the interviewer and the interviewees. Six other respondents participated in the Focus Group Discussions (FGDs) for qualitative data collection. The quantitative data were analysed using the statistical package for social science (SPSS, Version 16) and MS Office Excel 2010 for window packages.

Results or Focus

There were more male respondents (63.3%) than female whereas the level of education was primary (46.7%), secondary (33.3%) and tertiary level for remaining 20%. About 76.6% of them were using antimicrobials to treat lactating dairy cows, mainly Oxytetracycline (OTC 20%), Penicillin and Peni-Strep. About half of male respondents (53.3%) used antimicrobials compared to female (23.3%). Respondents with tertiary education rarely administered antimicrobials themselves. The common diseases being treated were diarrhea (46.7%), mastitis (43.3%) and respiratory diseases (36.7%). A proportion of milk from animals treated with antimicrobials was fed to calves (33.3%), sold to milk collection centres (26.7%) where it goes through normal value chain, fed to other animals (26.7%) and little was consumed by the family at home (6.7%).

Conclusion or Scope

In conclusion, the dairy producers administer antimicrobials themselves even when the animals are being milked and thereby, posing health challenges among the milk consumers. We advise dairy producers to avoid the unnecessary AMU.

Acknowledgement
Authors acknoweledge the SIDA's support through ITP programme.

Keywords: Antimicrobials; lactating; smallholder; dairy; mastitis

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 14759

Expert consensus on use of high importance antimicrobials in animals

Anna Sri*[1 2] ; Laura Hardefeldt[1 2] ; Kirsten Bailey[1 2] ; James Gilkerson[1 2] ; Glenn Browning[1 2]
[1]University of Melbourne/ Asia Pacific Centre for Animal Health/ Australia, [2]University of Melbourne/ Faculty of Veterinary and Agricultural Sciences/ Australia

Introduction and Objectives or Purpose

This study aims to develop expert consensus across veterinary and medical fields on the circumstances under which antimicrobials with high importance to human health can be used in animals. This will help guide future policy direction to reduce the development of antimicrobial resistance.

Methods

This study used the Delphi method to develop consensus. Three online surveys were distributed over seven months to pre-selected participants from Australia and overseas who were considered experts in relation to antimicrobial stewardship, antibiotic resistance, or a related discipline, for example, infection prevention, microbiology, or public health. The initial response rate was 38% (n=45). Subsequent surveys presented a summary of responses where there was not consensus and asked participants to re-evaluate their response with the aim of building consensus.

Results or Focus

Consensus was reached on several items including which antimicrobial importance rating system should be used, the use of prescribing guidelines, and the role of culture and susceptibility testing. It was agreed that if high importance antimicrobials are used, certain parameters including justification must be recorded and use of high importance antimicrobials not registered for use in animals must be reported for surveillance and auditing purposes. Consensus was not reached on whether use should be allowed in critically ill animals or after treatment failure if no culture and sensitivity testing had been performed.

Conclusion or Scope

Achieving consensus on these items means countries, particularly Australia, can use this evidence to implement policy changes and provide targetted education and other supports for antimicrobial stewardship, with increased confidence. Even among experts, there are differing views about the circumstances in which high importance antimicrobials can be used in animals.

Acknowledgement

Thank-you to all the experts who participated in this consenus-building process.

Keywords: stewardship; antimicrobial resistance; critically important antimicrobials; restrictions; rating system

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 14887

Utility of oligodeoxynucleotides containing CpG motifs as an alternative to antibiotics against Escherichia coli and Salmonella infections in broiler chickens

Susantha Gomis*[1] ; Thushari Gunawardana[1] ; Kalhari Goonewardene[1] ; Khawaja Ahmed[1] ; Shelly Popowich[1] ; Suresh Tikoo
[1]Veterinary Pathology/ Western College of Veterinary Medicine, University of Saskatchewan/ Canada

Introduction and Objectives or Purpose

Antimicrobials have been used in feeds in sub-therapeutic doses in food animal species for many decades to enhance feed efficiency, promote growth, and improve animals' health. The poultry industry needs alternatives to antibiotics as there are growing public concerns about the emergence of antimicrobial resistance owing to antimicrobial use. We have reported that the administration of synthetic DNA containing CpG motifs (CpG-ODN) can protect against bacterial pathogens such as E. coli and S. typhimurium infections in chickens. The objective of this study was to compare the immunoprotective effects of CpG-ODN against Escherichia coli infection versus commonly used therapeutic antibiotics.

Methods

Day-old broiler chicks were divided into five groups. The chicks in group 1 received a single dose of CpG-ODN by the intramuscular route on day four (D4) post-hatch (PH). The group 3 chicks received tetracycline antibiotics during D9-D13 in drinking water, and the group 4 chicks got sodium sulfamethazine on D9, D10, D15 post-hatch in drinking water, and the group 5 chicks were administered saline D4 PH. We challenged all the groups with E. coli (1×10^5 or 1×10^6 cfu/bird) on D8 post-hatch through the subcutaneous route.

Results or Focus

Our data demonstrated that the CpG-ODNs protect neonatal broiler chickens against lethal E. coli septicemia like the tetracycline or sodium sulfamethazine. The flow cytometry analysis revealed enrichment of immune cells in the CpG-ODN group and a marked decrease in macrophages and T-cell numbers in antibiotics treated groups indicating immunosuppressive effects. Our data showed that like therapeutic antibiotics, CpG-ODNs reduced clinical signs, decreased bacterial loads, and induced protection in chicks against E. coli septicemia. Unlike therapeutic antibiotics-induced immunosuppressive effects, CpG-ODN caused immune enrichment by increasing chicken immune cells recruitment.

Conclusion or Scope

Furthermore, this study highlights that although therapeutic antibiotics can treat bacterial infections, the ensuing immunosuppressive effects may negatively impact the overall chicken health.

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 14973

MULTIDRUG-RESISTANT SALMONELLA ENTERICA SEROTYPE KENTUCKY ST198 IS WIDELY DISTRIBUTED ACROSS POULTRY FARMS IN NIGERIA

Roderick Card[1] ; Idowu Fagbamila[*3] ; Thomas Chisnall[1] ; Carmen Losasso[1] ; Lisa Barco[1]
[1]Department of Bacteriology/ Animal and Plant Health Agency/ United Kingdom [3]Bacterial Research Division/ National Veterinary Research Institute/ Nigeria [1]Department of Food Safety/ Istituto Zooprofilattico Sperimentale delle Venezie/ Italy (Italia)

Introduction and Objectives or Purpose

Multidrug-resistant foodborne pathogens such as Salmonella spp. present a significant risk to public health. The globally distributed Salmonella ser Kentucky ST198 lineage is associated with multidrug-resistance to key antimicrobials, including ciprofloxacin, and constitutes an ongoing risk to public health worldwide. Although ST198 has been reported in Nigeria there is limited information on its distribution and diversity.

Methods

Sixty-six Salmonella Kentucky ST198 isolates collected from 40 poultry layer farms in ten Nigerian States were investigated. Antimicrobial susceptibility testing was conducted by broth microdilution for 14 antimicrobials and interpreted using EUCAST ECOFF values. Whole-genome sequencing was undertaken on 59 isolates to identify AMR genotypes, assess phylogenetic relatedness based on core genome Single Nucleotide Polymorphisms, and compare to published genomes.

Results or Focus

All isolates were resistant to nalidixic acid and ciprofloxacin, due to point mutations in the quinolone-resistance-determining regions of gyrA and parC. Six isolates additionally harboured a qnr gene. Most isolates (62/66) were multidrug resistant, and the most frequent combination was resistance to nalidixic acid, ciprofloxacin, tetracycline, sulfamethoxazole, and gentamicin. These isolates harboured the AMR genes tet(A), sul1, and aac(3)-Id. Nine isolates were resistant to chloramphenicol, correlating with the presence of floR or cmlA1. The phylogenetic tree indicated the presence of multiple sub-lineages, with relatedness to different published genomes.

Conclusion or Scope

The presence of Salmonella Kentucky ST198 in poultry farms presents an ongoing risk to public health as poultry are a common source of human infection, multidrug-resistance is associated with more serious disease, and ciprofloxacin resistant Salmonella meet WHO criteria for priority pathogens. Multidrug-resistant ST198 was widely distributed in Nigerian laying hen farms and the different sub-lineages were present in many states, but with no clear geographical clustering. These data may indicate multiple introductions of ST198 into farms in Nigeria. Strengthened food safety awareness and on-farm mitigation measures can contribute to risk reduction.

Acknowledgement

Fleming Fund

Keywords: Salmonella Kentucky; multidrug-resistance; AMR; poultry; ST198

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 15033

Molecular Detection of Tetracycline Resistance tetA, tetB, tetC, and tetD Gene in Multi-drug-Resistant Escherichia coli Isolated from Broiler Meat

Mohammad Mahmudul Hassan[*1 2] ; Gazi Sofiul Alam[2] ; Md. Ahaduzzaman[2] ; Chandan Nath[2] ; Hamida Khanam[2] ; Shahneaz Ali Khan[2] ; Ariful Islam[3] ; Ricardo J. Soares Magalhães[1] ; Rowland Cobbold[1]
[1]School of Veterinary Science/ The University of Queensland/ Australia, [2]Faculty of Veterinary Medicine/ Chattogram Veterinary and Animal Sciences University/ Bangladesh (□□□□□□□□), [3]IEDCR/ EcoHealth Alliance / Bangladesh (□□□□□□□□)

Introduction and Objectives or Purpose

Escherichia coli is a versatile commensal that resides in the gastrointestinal tracts of poultry and can contaminate poultry, especially meat during processing. Multidrug-resistant (MDR) Escherichia coli is a growing concern worldwide. This study estimated the prevalence of MDR E. coli and their tetracycline resistance genes in broiler meat obtained from Live Bird Markets (LBM) and Super Shops (SS) in Chattogram, Bangladesh.

Methods

405 samples were collected from LBMs and SSs consisting of muscle (n=215) and liver (n=190). Isolated E. coli were screened against eight antimicrobials of seven different unrelated groups using the disc diffusion technique. PCR was used to investigate tetracycline-resistant isolates for the presence of tetA, tetB, tetC, and tetD genes.

Results or Focus

229 (56.54%; 95% CI 51.56% - 61.43%) samples were found positive with E. coli. Antimicrobial resistance profiling showed the highest resistance against sulphamethoxazole trimethoprim 88.65% (95% CI 83.81% - 92.45%) followed by tetracycline 86.90% (95% CI 81.82% - 90.92%), ampicillin 82.53% (95% CI 76.99% - 87.22%), and ciprofloxacin 60.70% (95% CI 54.04%- 67.06%). E. coli isolates were also variably resistant to Cephalexin 37.12% (95% CI 30.85 - 43.73%), Gentamycin 32.31% (95% CI 26.30 - 38.79%) and colistin sulfate 20.52% (95% CI 15.49% - 26.34 %). Most (84.4%: 95% CI 78.62% - 89.16%) of the tetracycline resistance isolates encoded tetA.

Conclusion or Scope

This study revealed significant contamination of broiler meat with multidrug resistance E. col. Findings related to tetracycline resistance are particularly pertinent to Bangladesh and would aid in reducing the growing risks of broiler-associated pathogens. Appropriate control measures should be developed and implemented involving the rational use of antimicrobials in poultry farming systems to mitigate the risk of this multidrug resistance zoonotic pathogen from foods of animal origin to protect public health.

Acknowledgement

We acknowledge CVASU and BANBEIS for providing approval and research funds.

Keywords: poultry meat, AMR, Escherichia coli, tetracycline resistance, food safety

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 15048

Modelling the impact of antimicrobials on the chicken gut microbiome and the dynamics of resistance genes

Sophie Hedges*[1] ; Ludovic Pelligand[1] ; Guillaume Fournié[2] ; Damer Blake[2] ; José Lourenço[3] ; Francesco Pinotti[3]
[1]Comparative Biomedical Sciences/ Royal Veterinary College/ United Kingdom [2]Pathobiology and Population Sciences/ Royal Veterinary College/ United Kingdom [3]Department of Biology/ University of Oxford/ United Kingdom

Introduction and Objectives or Purpose

Antimicrobials, such as colistin, have been used globally in livestock production and an increase in the prevalence of mediated colistin resistance (mcr) genes in both animals and humans has led to its ban in some countries, including China. Paralleled to this, the consumption of chicken meat has increased considerably. Using a modelling approach, this study aims to assess the transmission dynamics of colistin-resistant and susceptible strains of E. coli within chicken flocks in South and South-East Asia and how it is impacted using antimicrobials.

Methods

Multi-strain compartmental models were developed to simulate the dynamics of colistin-resistant and susceptible strains of E. coli within a chicken flock, with and without antimicrobial administration. They allowed for co-infection of chickens by multiple strains. Two different bacterial transmission routes were considered: direct contact and mediation through the environment. Transmission parameters were estimated by fitting the model to in vivo experimental infection data using a Bayesian Markov Chain Monte Carlo framework.

Results or Focus

The parameterised model will then be adapted to production in South-East Asia, based on antimicrobial usage estimated through questionnaire-based surveys. Model predictions will be compared to results from field samples and the sequencing of chicken gut microbiome.

Conclusion or Scope

The timing, duration, and dose of antimicrobial administration impacts on the dynamics of resistance genes throughout a production cycle - understanding these is crucial to help policy surrounding their use. Based on experimental data, in the absence of colistin there are levels of resistance which could be mediated through co-selection with other AMDs.

Keywords: antibiotic resistance; poultry; LCMS; mathematical modelling; disease

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 15135

Epidemiology of Multidrug-resistant Escherichia coli and associated genes Isolated from Commercial Broiler chicken in Bangladesh: implications for One Health surveillance in high-risk communities

Mohammad Mahmudul Hassan[*1 2] ; Chandan Nath[2] ; Md Kaisar Rahman[1] ; Hamida Khanam[2] ; Md Mazharul Islam[2] ; Babafela Awosile[1] ; Ariful Islam[3] ; Ricardo J. Soares Magalhães[1]
[1]School of Veterinary Science/ The University of Queensland/ Australia, [2]Faculty of Veterinary Medicine/ Chattogram Veterinary and Animal Sciences University/ Bangladesh (□□□□□□□□) [1]School of Veterinary Medicine/ Texas Tech University/ United States [2]Department of Animal Resources/ Ministry of Municipality and Environment/ Qatar (قطر) [3]IEDCR/ EcoHealth Alliance / Bangladesh (□□□□□□□□)

Introduction and Objectives or Purpose

Antimicrobial resistance (AMR) or multidrug resistance (MDR) is an “invisible pandemic”. In Bangladesh, Escherichia coli (E. coli) is poultry’s most common pathogen, and antimicrobials are used indiscriminately either as growth promoters or as treatment, which increases the possibility of the emergence of AMR. The study aimed to determine the prevalence of AMR/MDR and selected resistant genes of E. coli circulating in commercial broiler chickens.

Methods

We collected 1,200 fecal swabs from 240 commercial broiler chicken farms (24 sub-district within eight of the 64 districts) between 2019 and 2020. Standard bacteriological (culture) and followed by PCR were done to identify the E coli. CS test of 10 antimicrobials was done to detect the AMR. We screened AMR genes (tetA, tetB, tetC and tetD, bla$_{TEM,}$ SulI and SulII) in E. coli isolates using PCR.

Results or Focus

The overall prevalence of E. coli in broiler chicken was 72.1% (95% CI: 69.4-74.6). The resistance pattern across ten antimicrobials varied from 47.30 to 69.10% and most frequently to Gentamycin (69.10%), followed by Enrofloxacin (63.40%), Amikacin (61.3%), Ampicillin (61%), and Nitrofurantoin (59.80%). Among AMR isolates, 99.5% were MDR (resistant against at least 3 groups). Resistance to 6 drugs or 5 drugs was 43% and 41%, respectively. The proportion of resistant gene among E. coli isolates was higher in tetA (74.6%; 95% CI: 71.5-77.4), followed by sulII (61.4%; 95% CI: 58.0-64.6), blaTEM (58.3%; 95% CI:54.8-61.5), tetB (34.2%; 95% CI: 31.1-37.5), sulI (22.7% 95% CI: 19.9-25.6), tetC (5.7%; 95% CI:4.4-7.6), and tetD (3.1%; 95%CI: 2.1-4.6).

Conclusion or Scope

We detect a higher prevalence of E. coli in broiler farms. Among the AMR isolates, a higher prevalence of MDR E. coli was detected compared to previous studies. Our findings suggest the circulation of E. coli with several resistant genes in broiler chickens.

Acknowledgement

We acknowledge CVASU, BANBEIS and QAOHS for providing approval and research funds

Keywords: MDR; E coli; Gene; broiler; commercial farms; Bangladesh

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 15311

: Prevalence and risk factors for MRSA in milk at consumable level: Evidence from Indigenous Livestock Keepers' Community of India

Krupali Patel*[1 2] ; Dr. Timo Falkenburg[1 3] ; Professor Deepak Saxena[4] ; Professor Thomas Kistemann[1 3]
[1]ZEF C/ Center for Development Research, University of Bonn, Germany/ Germany (Deutschland), [2]Public Health/ Parul Institute of Pubic Health/ India, [3]GeoHealth Center/ Institute of Hygiene and Public Health/ Germany (Deutschland), [4]Epidemiology/ Indian Institute of Public Health Gandhinagar/ India

Introduction and Objectives or Purpose
Various studies provide evidence of the presence of MRSA in milk however main focus was either on bulk or raw milk directly from the udder. In Indian culture, milk is usually stored in steel utensils irrespective of refrigerator and milk type (pasteurized or raw) which indicates milk comes in contact with the different surface environments before consumption. Thus, this study aimed to check the prevalence and risk factors for MRSA in the milk of indigenous urban livestock keepers' communities.

Methods
A longitudinal Study design with a quantitative Household (HH) survey and microbiological surveillance was applied. We collected data on social demographics, environmental-animal hygiene, and human hospital contacts in the HH survey whereas microbiological surveillance included human nasal samples, indoor-outdoor HHs' surface samples, and milk samples from their utensils. All the microbiological samples were collected three times a year including some of the HH survey indicators. Almost 2800 samples were collected from January to September 2019 from 286 HHs of the Livestock keepers' community of Ahmedabad city. The samples were tested for Staphylococcus Aureus and Coagulase Negative Staphylococcus Aureus (CoNS) with Methicillin Resistance. The microbiological and HH data were analyzed to find out the prevalence and risk factors by using STATA16.

Results or Focus

The overall period prevalence of MRSA among humans, on indoor-outdoor surfaces, and in milk at consumable level was found at 32 per 1000 human population, 37 & 19 per 1000 HHs indoor & outdoor environment,s and 317 per 1000 HHs' milk at consumable level samples. Surprisingly, the risk of MRSA in milk during monsoon increased if HH had the human CoNS contamination in winter with OR 2.9 (CI 1.15- 7.35) for winter OR 4.8 (CI1.82-12.78) for summer. The study also provides some weak evidence on the relationship between environmental CoNS contamination and MRSA in Milk.

Conclusion or Scope
The present study drives the attention towards the complex nexus of horizontal transmission of MRSA pathogens in the One Health context.

Keywords: Milk at consumable level, MRSA, CoNS, One Health

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 15354

IMPROVING INFECTION PREVENTION CONTROL - WATER SANITATION AND HYGIENE (IPC-WASH) TO COMBAT INDONESIAN ANTIMICROBIAL RESISTANCE IN POULTRY FARMS.

Arief Wicaksono[1] ; Alfred Kompudu[*2] ; Yunita Widayati[1] ; Imas Yuyun[1] ; Nuryani Zainuddin[1] ; Erianto Nugroho[2] ; Gunawan Budi Utomo[2] ; Farida C. Zenal[2] ; Luuk Schoonman[2]
[1]Directorate of Animal Health Services/ Directorate General of Livestock and Animal Health Services, Ministry of Agriculture, Indonesia/ Indonesia, [2]Emergency Centre for Transboundary Animal Diseases/ Food and Agriculture Organization of the United Nations./ Indonesia

Introduction and Objectives or Purpose

Antimicrobial resistance (AMR) control through multi-sectoral approaches on infection prevention and improved antimicrobial stewardship is implemented in Indonesia. Collaborative wprk of the tripartite organizations (FAO, WHO and WOAH) updated the IPC-WASH instrument in the animal health sector by adopting WHO’s Infection Prevention and Control Assesment Framework and combining it with FAO’s Layer Farm Assesment Tools. The instrument was reviewed by the Ministry of Health, Ministry of Agriculture, and professional organizations, demonstrating a strong One Health collaboration between government and professional organizations in Indonesia.

Methods

Sixteen government Veterinary Service Officers (VSO) from Karanganyar, Boyolali, Blitar and Malang districts were trained- on the newly updated tool. The VSO used this tool to conduct an assesment in 160 farms consisting of 40 poultry farms per district.

Results or Focus

IPC implementation in poultry farms, including biosecurity, cleaning and disinfection, waste management, etc., reach up to 77% in Karanganyar, 72% in Boyolali, 68% in Blitar and 54% in Malang, but not all farmers follow written guidelines. Overall, 70% of the farmers replied receiving technucal training either from private sector advisors or government extension officers. A surveillance program with acces to laboratory capacity for disease diagnostics, antimicrobial susceptibility testing and monitoring common diseases that require antimicrobial treatments was reported by 69% of farmers in Karanganyar and Blitar districts, 57% in Boyolali and 50% in Malang. A total of 67% of all farmers expressed to carry out routine monitoring and audit of the implementation IPC-WASH. Adequate handling of water, sanitation, hygiene, sufficient power supply and good zooning was observed in respectively 82%, 69%, 78%, and 67% in Karanganyar, Boyolali, Blitar and Malang farms. Workload, staffing, and occupancy in all farms met the required standards.

Conclusion or Scope

The amended WHO assesment tool and the One Healh approach are applicable and useful to improve IPC-WASH implementation in poultry farms.

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 15376

Emergence of multidrug resistant Streptococcus suis in pig farms in Yangon Myanmar

Thanh Nguyen[*1] ; Hoa Ngo Thi[1] ; A. W. Dan Tucker[2] ; Aung Zaw Moe[3] ; Thiri Su Wai[3] ; Chieu Tran Thi Bich[1]
[1]Zoonoses/ Oxford University Clinical Research Unit, Hospital for Tropical Diseases/ Vietnam (Việt Nam), [2]Department of Veterinary Medicine/ University of Cambridge/ United Kingdom, [3]Veterinary Medicine and Disease Control Division/ Livestock Breeding and Veterinary Department, Ministry of Agriculture, Livestock and Irrigation/ Myanmar (Burma) (□□□□□□)

Introduction and Objectives or Purpose

Occupational exposure and consuming “high risk” port products were identified as top risk factors for Streptococcus suis (S. suis) infection in countries of Southeast Asia. In Myanmar, pig production system was rapidly developed in the recent years. This development was associated with increased antibiotic usage but not the improvement of hygiene practices. Thus, high risks of zoonotic and AMR transmission were predicted for current pig production system. This study aims to investigate the prevalence of S. suis and its AMR phenotypes across pig production chain in Yangon Myanmar

Methods

S. suis strains were isolated from pig farm, slaughterhouse and retail market samples in Yangon using standard microbiological approaches and MALDI-TOF MS. Antimicrobials susceptibility tests were performed with disk diffusion method following CLSI guidelines. Statistical analyses were performed with GraphPad Prism.

Results or Focus

S. suis was detected in 53.4% (n=465), 6.2% (n=307) and 0.74% (n=135) samples collected from farms, slaughterhouses and retail markets respectively (Fig. 1A-B). At the strain level, prevalence of AMR against twelve tested antibiotics were determined as following: 85%-100% for older antibiotics (Tetracycline, Clindamycin and Penicillin), 40%-60% for old antibiotics (Chloramphenicol, Trimethoprim sulfamethoxazole, Erythromycin and Enrofloxacin), 4.7%-16% for new antibiotics (Rifampin, Ceftiofur and Florfenicol) (Fig 1.C). Prevalence of AMR against some highest priority antibiotics (HP-CIAs) including Levofloxacin and Ceftriaxone were dramatically high, being 41% and 77% respectively. MDR were found in more than 95% collected strains. Prevalence of most AMR and MDR phenotypes were found to significantly associate with farming intensification and later sampling period (Fig 1.D).

Figure here: http://figshare.com/s/36ace7cd91c3e834db27

Conclusion or Scope

The presence of S. suis was detected in high percentage of samples from pig farms. But this was low in samples from slaughterhouses and retail markets. For collected S. suis strains, MDR and AMR against many HP-CIAs were found at very high prevalence and associated with higher farming intensifications and later sampling periods.

Acknowledgement

N/A

Keywords: Streptococcus suis, antibiotic resistance, AMR, swine zoonotic pathogen

Topic: Antimicrobial Resistance (AMR): AMR interaction and transmission drivers between reservoirs in humans, animals, food and the environment: The impact of human-animal interaction on AMR transmission
Abstract No: 15377

Survey of knowledge, attitudes and practices about AMR and AMU among poultry farmers in Bhutan

Pema Tshewang[*1] ; Glenn Browning[2] ; James Gilkenson[1] ; Mauricio Coppo[2] ; Sherub Phuntsho[1] ; Chendu Dorji[1] ; Ugyen Namgyel[1] ; Puspa Sharma[1]
[1]National Veterinary Hospital/ Department of Livestock/ Bhutan (□□□□□), [2]Veterinary Biosciences/ University of Melbourne/ Australia

Introduction and Objectives or Purpose

The irrational use of antimicrobials in animals can contribute to AMR in not just animals but also humans through spill over. Farmers' knowledge and attitude towards AMR and AMU can play an important role in influencing use on their farms. In Bhutan, the knowledge, attitudes and practices of farmers about AMR and AMU has never been studied.

Methods

We conducted a survey amongst poultry farmers to assess their knowledge, attitudes and practices, along with other factors that may influence their outlook towards AMR and AMU. A total of 420 poultry farmers from across the country completed the structured questionnaire.

Results or Focus

While 65% of the farmers had heard about AMR, only 36% were aware of the withdrawal period for antimicrobials. Only 18% of the farmers said meat from animals treated with antimicrobials should not be consumed, 88% said completion of an antimicrobial course was important. A total of 94% of the farmers obtained their feed from local feed mills, which are regulated. A total of 89% of farmers agreed that good management and biosecurity measures would prevent disease outbreaks and the need for antimicrobial use.

The majority of farmers (96%) consulted animal health centres for treatment and obtained their medicines from the animal health centres (77%). Only 0.04 % of the farmers they obtained antimicrobials for use on the farm from across the border. More than half the respondents were also trained to vaccinate their birds themselves.

A total of 69% of the farmers used antimicrobials to treat sick animals, but only 12% of the farmers used antimicrobials to treat targeted sick birds, while 88 % of the farmers treated the entire flock.

Conclusion or Scope

While Bhutanese farmers are dependent on livestock offices for treatment and medicines, training programs could be developed to improve their understanding on AMR and AMU.

Acknowledgement

Fleming Fund

University of Melbourne

Keywords: AMR, AMU, knowledege, attitudes, prctices

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Environmental AMR monitoring
Abstract No: 14744

GENOMIC EPIDEMIOLOGY OF NOSOCOMIAL CARBAPENEMASE-PRODUCING CITROBACTER FREUNDII IN SEWERAGE SYSTEMS IN HELSINKI METROPOLITAN AREA, FINLAND

Viivi Heljanko*[1] ; Venla Johansson[1] ; Kati Räisänen[2] ; Veli-Jukka Anttila[3] ; Outi Lyytikäinen[2] ; Kirsi-Maarit Lehto[4] ; Anssi Lipponen[5] ; Sami Oikarinen[4] ; Tarja Pitkänen[1 5] ; Annamari Heikinheimo[1 6]
[1]Department of Food Hygiene and Environmental Health, Faculty of Veterinary Medicine/ University of Helsinki/ Finland (Suomi), [2]Department of Health Security, Helsinki/ Finnish Institute for Health and Welfare / Finland (Suomi), [3]Inflammation center and University of Helsinki/ Helsinki University Hospital/ Finland (Suomi), [4]Faculty of Medicine and Health Technology/ Tampere University/ Finland (Suomi), [5]Department of Health Security, Kuopio/ Finnish Institute for Health and Welfare/ Finland (Suomi), [6]Microbiology unit/ Finnish Food Authority/ Finland (Suomi)

Introduction and Objectives or Purpose

Antimicrobial resistance (AMR) is a major global public health threat. Multi-drug resistance is also emerging in Citrobacter freundii, the third most common Carbapenemase-producing Enterobacteriaceae in Finland. Recent studies have proposed the benefits of wastewater-based surveillance (WBS) of infectious agents and their AMR. We performed a genomic comparison of C. freundii isolates from wastewater treatment plant (WWTP), hospital sinks and toilets (HST), and clinical isolates to uncover whether the clinically relevant C. freundii isolates are identified by WBS.

Methods

Carbapenemase-producing C. freundii was isolated from WWTP and HST in Helsinki, Finland, in 2021 by using selective culturing. Species confirmation and antimicrobial susceptibility testing were done with MALDI-TOF, disk diffusion, and broth microdilution method. Isolates were sequenced and sequence types (ST) and AMR genes were determined. Ad-hoc core genome multilocus sequence typing (cgMLST) was conducted to compare the sequences from WWTP and HST to clinical C. freundii isolates from three clusters in Finland from 2016 to 2020.

Results or Focus

Altogether 12 bla_{KPC-2}-carrying (ST8) and five bla_{VIM-1}-carrying (ST421) C. freundii from WWTP and 15 bla_{KPC-2}-carrying C. freundii from HST (ST18; n=8, ST8; n=4, and ST396; n=3) were identified. According to cgMLST six WWTP isolates clustered with four HST isolates and eight HST isolates with 15 clinical isolates (<10 allele difference). Clustering was not observed between WWTP and clinical isolates.

Conclusion or Scope

Clinical isolates clustering with HST isolates supports previous findings of clinically relevant strains persisting in HST. Close relations between some WWTP and HST isolates were observed, indicating a possible persistence of these strains throughout the sewerage system. Future research is needed to better understand the genomic epidemiology and persistence of Carbapenemase-producing C. freundii in sewerage systems and the applicability of WBS in observing the clinical infectious agents circulating in the community.

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Keywords: Antimicrobial resistance, Citrobacter freundii, Carbapenemase-producing Enterobacteriaceae, Wastewater surveillance

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Environmental AMR monitoring
Abstract No: 14867

Integrating ‘One Health Approach’ across different sectors of Bangladesh to prevent Antimicrobial Resistance (AMR)

Roksana Hoque*[1] ; Mohammad Monjurul Karim[2]
[1]IDP/ IDP/ Bangladesh (□□□□□□□□), [2]CDD/ CDD/ Bangladesh (□□□□□□□□)

Introduction and Objectives or Purpose

Antimicrobial resistance (AMR) is a growing problem worldwide. AMR is particularly important for the LMICs like Bangladesh due to the high burden of infectious disease in humans, and animals and the irrational use of antibiotics for their treatment. Dispensing of these antimicrobials in the environment causes environmental contamination including the plants, vegetables, etc, ultimately propagating AMR. This study aims to identify and recommend the scope of integrating ‘One Health Approach’ across different sectors of Bangladesh to prevent Antimicrobial Resistance (AMR)

Methods

The study was conducted using a systematic review, considering both quantitative and qualitative literature. Peer-reviewed literature was searched from Google Scholar, Pubmed, and Biomed Central databases in human, animal, and environment sectors from January 2022-May 2022. ‘Mixed studies review’ method was used for synthesizing evidence from different studies.

Results or Focus

Total 10 articles were selected considering the inclusion criteria, that discussed the ‘one health approach’ & ‘antimicrobial resistance (AMR)’ across the different sectors of Bangladesh. Findings of the studies identified 3 stakeholder groups, consumers, practitioners, and medicine sellers 3 prime facilities are hospitals, education institutes (schools, colleges, universities), and research institutes, where one health approach can be integrated. Tailored awareness-building need to start from the science book of the school for the school, college students including the consumers, and precise prescription and dispensing guideline need to be introduced for human, veterinary hospitals, and doctors (human, animal) with proper enforcement and monitoring system. Pharmaceutical companies need to have an ‘Effluent Treatment Plant (ETP)’, which are producing antimicrobials. Antimicrobial stewardship needs to be taught and promote in animal, human and environmental including agricultural sectors.

Conclusion or Scope

Use of ‘One Health Approach’ across different sectors (human, environment, animal) and engagement of the key stakeholders from all these sectors and their mutual collaboration including monitoring can reduce AMR in Bangladesh.

Keywords: One Health Approach ; Antimicrobial Resistance

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Environmental AMR monitoring
Abstract No: 14880

DRUG RESISTANT ENVIRONMENTAL MYCOBACTERIA ISOLATED FROM SUSPECTED TUBERCULOSIS PATIENTS IN WEST AND CENTRAL AFRICA

Pokam Thumamo David Benjamin*[1] ; Dorothy Yeboah-Manu[2] ; Stephen Ofori[2] ; Guemdjom Prisca[3] ; Teyim Pride[4] ; Yangkam Yhiler[5] ; Djuikoue Ingrid[6] ; Daniel Amiteye[7] ; Asuquo Anne[8]
[1]Medical Laboratory Science/ University of Buea/ Cameroon (Cameroun), [2]Bacteriology/ Noguchi Memorial Institute for Medical Research, University of Ghana/ Ghana (Gaana), [3]Public Health/ University of Buea/ Cameroon (Cameroun), [4]Ministry of Health/ Douala Tuberculosis Reference Laboratory/ Cameroon (Cameroun), [5]Allied Health/ Biaka University Institute/ Cameroon (Cameroun), [6]Microbiology/ Université des Montagnes/ Cameroon (Cameroun), [7]Biomedical Engineering/ All Nations University / Ghana (Gaana), [8]Medical Laboratory Science/ University of Calabar/ Nigeria

Introduction and Objectives or Purpose

The environmental mycobacteria (EM) also known as nontuberculous or atypical mycobacteria are group of human, animal, and bird pathogens. They have a serious impact on the morbidity and mortality of humans. Their identification/differentiation from Mycobacterium tuberculosis complex (MTBC) responsible for tuberculosis (TB) is crucial for case management with the appropriate drugs. This study was carried out in three West/Central African countries to understand EM associated with pulmonary TB in the sub-region.

Methods

A collection of 503 isolates (202 from Nigeria, 158 from Cameroon and 143 from Ghana) obtained from culture on Lowenstein–Jensen medium or Middlebrook 7H9 broth were analyzed. The isolates were tested for drug susceptibility using the indirect proportion method on solid media or BACTEC MGIT 960 and GeneXpert. MTBC were confirmed by detection of the marker IS6110. All IS6110-negative isolates were identified by hsp65 gene amplification, DNA sequencing and blast analysis.

Results or Focus

The prevalence of EM was 16/503 (3.2%) distributed in each country as 2/202 (1%) in Nigeria, 2/158 (1.3%) in Cameroon and 12/143 (8.4%) in Ghana. Of these 16 isolates, 5 (31.3%) were M. fortuitum, 2 (12.5%) M. intracellulare, 2 (12.5%) M. engbaekii and 1(6.3%) each of M. colombiense, M. gordonae, M. avium, M. paraense, M. peregrinum. EM and MTBC distribution across the age groups (p=0.999) and gender (p=0.393) was not significant. Eight (57.1%) of the 14 previously treated patients harboured EM (OR, 0.21, 95%CI, 0.06 – 0.77, p= 0.021). Isoniazid [6/16 (37.5%)] and Rifampicin [4/11 (36.4%)] showed the highest drug resistance among the EM isolates, with M. engbaekii, M. fortuitum and M. intracellulare being multi-drug resistant.

Conclusion or Scope

EM were mostly found among individuals with unsuccessful treatment. Distinction of EM from MTBC in patients presenting with TB symptoms using rapid molecular tools is necessary for appropriate case management, as most are resistant to the routine first line antimycobacterials.

Acknowledgement

To L. Lawson

Keywords: EM; multi-drug resistance; Sequencing; Retreatment patients; Gulf of Guinea - Africa.

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Environmental AMR monitoring
Abstract No: 14994

OCCURRENCE, PREDISPOSING RISK FACTORS AND ANTIBIOGRAM OF EXTENDED BETA LACTAMASE PRODUCING Salmonella IN Oreochromis niloticus FROM FISH FARMS AND RIVERS IN IBADAN, NIGERIA

Victoria Adetunji*[1] ; Leah O. Esuola, [1]
[1]Department of Veterinary Public Health and Preventive Medicine/ University of Ibadan, Nigeria/ Nigeria

Introduction and Objectives or Purpose

Fish has been reported to be capable of harbouring Salmonella. Extended spectrum beta-lactamase (ESBL) producing Salmonella could spread from farm animals to humans through the food chain. Few studies have been carried out on the prevalence of ESBL producing Salmonella spp. in tilapia (Oreochromis niloticus) fish in Ibadan. We investigated the occurrence and antibiogram of ESBL -producing Salmonella spp from Tilapia fish in Ibadan, Nigeria.

Methods

Fish samples were collected from two cultured farms and two rivers. Fish muscle and water samples were processed for isolation of Salmonella using selective media, followed by conventional biochemical tests and serological confirmation, using Antiserum Salmonella Polyvalent-O. Antibiogram and ESBL production of isolates was determined by disc diffusion. Data on predisposing risk factors were collected using a structured questionnaire through a face-to-face interview.

Results or Focus

Overall prevalence of Salmonella was 9 (12.5%) and only 2 (2.8%) was ESBL-Salmonella spp. All the Salmonella isolates are multidrug resistant and showed 100% resistance to ampicillin, tetraxycline and ciprofloxacin. Education reduced the likelihood of Salmonella contamination by 40% [OR 0.6; 95%CI; 1.300-2.212] while method of sewage disposal increased likelihood of Salmonella contamination by about 22% [OR1.22; 95%CI; 0.389-4.203].

Conclusion or Scope

The presence of multidrug resistant ESBL- Salmonella spp was established in Tilapia fish in Ibadan. Appropriate sewage disposal and judicious use of antibiotics in fish production is recommended.

Acknowledgement

We acknowledge the data clerks and laboratory assistants for their dedication during the field data collection and laboratory activities.

Keywords: ESBL- Salmonella; Multidrug resistance; Tilapia fish; Risk factors

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Environmental AMR monitoring
Abstract No: 15093

Water-based AMR detection in peri-urban Ghana (a SORMAS-WOPPA project)

Sylvia Dreyer*[1] ; Timo Homeier-Bachmann[2] ; Eugene Adade[3] ; Martin Beer[4] ; Tobias Busche[5] ; Klaas Dietze[1] ; Juliane Dörrbecker[6] ; Julia Hassa[5] ; Dirk Höper[4] ; Jörn Kalinowski[5]
[1]Institute of International Animal Health/ One Health/ Friedrich-Loeffler-Institut/ Germany (Deutschland), [2]Institute of Epidemiology/ Friedrich-Loeffler-Institut/ Germany (Deutschland), [3]Kumasi Centre of Collaborative Research in Tropical Medicine/ Kwame Nkrumah University of Science and Technology/ Ghana (Gaana), [4]Institute of Diagnostic Virology/ Friedrich-Loeffler-Institut/ Germany (Deutschland), [5]Center for Biotechnology (CeBiTec)/ Bielefeld University/ Germany (Deutschland), [6]Department of Epidemiology/ Helmholtz Centre for Infection Research/ Germany (Deutschland)

Introduction and Objectives or Purpose

In LICs, humans and animals frequently share water sources. This provides ample opportunity for the accumulation and spill-over of pathogenic bacteria, including resistant ones with high virulence properties. Within the One Health framework, monitoring of the regional water microbiome and its resistome may help to identify lead antibiotic-resistant (AMR) pathogens and the early detection of hotspots preventing disease outbreaks at the human-animal-environmental interface.

Our study aims to provide data on the regional bacterial diversity and AMR in water samples collected in Kumasi, Ghana.

Methods

10 water sources in Kumasi, Ghana, were sampled once a week over a period of 7 weeks. Samples were transported to the laboratory, and bacteria were obtained through water filtering and downstream analysis. Subsequently, bacteria were subjected to amplicon-based high-throughput sequencing of the 16S rRNA gene (microbiome) in combination with culturing for pheno- and genotypic profiling of AMR Enterobacterales including whole-genome sequencing (WGS).

Results or Focus

Each water source had its unique microbiome profile that was subject to temporal changes. 92 % (69 of 75) of the samples were positive for AMR Enterobacterales. From these, we isolated DNA and applied WGS resulting in five Enterobacter cloacae, 86 Escherichia coli, 30 Klebsiella spp. and one Pseudomonas aeruginosa. Our collection included representatives of international high-risk clonal lineages such as Escherichia coli sequence type (ST)131, 410, 648 and Klebsiella pneumoniae ST307 known to combine high-level AMR and virulence with the potential to infect humans and animals. Additionally, we detected bla_{NDM-5} and bla_{OXA-48} genes that confer resistance to last-resort carbapenems.

Conclusion or Scope

Our results highlight the importance of addressing the human-animal-environmental interface to monitor AMR pathogens and microbiome dynamics within a given ecosystem. The data will be used to establish an early warning system for microbial contamination of water for humans and animals in Ghana.

Acknowledgement

Funded by Helmholtz Initialization and Networking Fund for Infection Research Greifswald

Keywords: AMR, Ghana, microbiome, one health

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Environmental AMR monitoring
Abstract No: 15165

Antimicrobial resistance monitoring of water environment: isolation of first lytic bacteriophage from the Kinoya sewage treatment plant in the Fiji Islands

Vincent Lal*[1] ; Preeti Nand[2] ; Natasha Just-Poinapen[3] ; Walter Okelo[4] ; Barbara Drigo[5] ; Erica Donner[5]
[1]The Institute of Applied Sciences/ The University of the South Pacific/ Fiji, [2]SPC/ Pacific Community/ Fiji, [3]Independent Researcher/ Independent Researcher/ Netherlands, [4]CSIRO/ Commonwealth Scientific and Industrial Research Organisation / Australia, [5]Future Industries Institute/ University of South Australia/ Australia

Introduction and Objectives or Purpose

In Pacific Island Countries there are limited to no information on AMR hotspots in water environment as well as removal efficiencies of domestic wastewater infrastructure. There is a lack of standardized methods for sampling and quantification of antibiotic resistant bacteria and antibiotic resistance genes as well as lack of analytical capacity to provide environmental surveillance that could contribute towards the protection of human, animal and ecosystem health. The use of bacteriophage has potential to control bacterial diseases and reduce current dependency on the use of antibiotics. The present study utilized a range of analytical tools to isolate and identify bacteriophage from urban sewage in Fiji.

Methods

Standardized methods were used to isolate NZRM E. coli 916 and NZRM S. aureus 917 lytic phage. The NZRM E. coli 916 reference culture, was used in the validation of the methodology.

Results or Focus

The isolation of the NZRM S. aureus 917 lytic phage was challenging, it was successfully isolated from clarifier with stagnant wastewater. Enrichment technique and direct plating were used for phase isolation. To determine whether the putative plaques are due to phage a spot test was carried out and three rounds of plaque purification was done in order to obtain pure lysate of the phage. Transmission Electron Microscopy was used for identification of bacteriophage.

Conclusion or Scope

To the best of our knowledge, this is the first lytic phase isolates reported from Fiji. We suggest the development and use of standardized methods for environmental sampling to enable comparable and validated data to be collected, analyzed and shared for the surveillance of AMR in Fiji. Use of genome sequencing is recommended for confirmation.

Acknowledgement

Our thanks to the Australian Government, CSIRO for providing funding for this research. Special thanks to the University of the South Australia for analysis of samples from Fiji for TEM and gene sequencing.

Keywords: Antimicrobial resistance; environment; Fiji; Wastewater; Phage

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Environmental AMR monitoring
Abstract No: 15166

Microbial Contamination in Healthcare Facilities: Reflection from Water Sanitation and Hygiene Assessment in India

Deepak Saxena*[1 2] ; Poonam Trivedi[1] ; Pachillu Kalpana[3] ; Priya Bhavsar[1] ; Krupali Patel[4] ; Sandul Yasobant[1 5 3 2]
[1]Department of Public Health Science/ Indian Institute of Public Health Gandhinagar/ India, [2]School of Epidemiology & Public Health / Datta Meghe Institute of Medical Sciences/ India, [3]Center for Development Research / University of Bonn/ Germany (Deutschland), [4]Parul Institute of Public Health / Parul University/ India, [5]Global Health, Institute for Hygiene & Public Health / University Hospital Bonn/ Germany (Deutschland)

Introduction and Objectives or Purpose

Water, sanitation, and hygiene (WASH) services are integral components of one health as it is vital for the optimal health of humans and animals and for maintaining a healthy environment. Even after including the provision of WASH services to all in Sustainable Development Goals globally, many countries and healthcare facilities (HCFs) lack in achieving essential services. Thus, this study aims to assess the WASH status with respect to the anti-microbial resistance in two Indian states, Assam & Gujarat, in 2019-2021.

Methods

The cross-sectional study was conducted in two different states of India i.e. Gujarat and Assam. A total of 10 HCFs from Gujarat and 60 from Assam were assessed in this study. In addition to the WASH assessment, microbiological swab samples were also collected from various pre-decided environmental surfaces of the maternity ward, labour rooms and cleaning materials. A total of 251 environmental samples were collected from Gujarat and 1182 from Assam.

Results or Focus

The findings of the microbiological surveillance shows, 31.1% and 69.7% of collected samples were contaminated with the microorganisms in Gujarat and Assam, respectively. In both, states, cleaning mops were found mostly contaminated, followed by the maternity wards beds. Apart from this In Gujarat, acinetobacter speccies, staphylococcus species, pseudomonas species, pseudomonas aeruginosa, klebsiella species and E.coli were found while in Assam staphylococcus species, bacillus subtilis, bacillus megaterium, pseudomonas aeruginosa, klebsiella species and E.coli were found.

Conclusion or Scope

WASH is one of the important components to maintaining infection prevention and control at HCFs still neglected most of the time, and very little attention is given to the microbiological surveillance of the environmental surfaces of the HCFs. Currently, only visual assessment is used for hygiene assessment, which is not a proxy for safety.

Keywords: WASH, AMR, HCF, India

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Environmental AMR monitoring
Abstract No: 15225

Extended-Spectrum Beta Lactamase E. coli not detected in recreational beach waters in Singapore

Han Bin Pek[1] ; Sharain Abdul Kadir[*1] ; Sathish Arivalan[1] ; Sheereen Osman[1] ; Roslinda Mohamed[1] ; Lee Ching Ng[1 2] ; Judith Chui Ching Wong[1] ; Sophie Octavia[1 3]
[1]Environmental Health Institute/ National Environment Agency/ Singapore, [2]School of Biological Sciences/ Nanyang Technological University/ Singapore, [3]School of Biotechnology and Biomolecular Sciences/ University of New South Wales/ Australia

Introduction and Objectives or Purpose

Extended spectrum beta-lactamase Escherichia coli (ESBL-EC) has been selected by the World Health Organisation as an indicator for integrated multi-sectoral antimicrobial resistance (AMR) surveillance for monitoring its prevalence and trend globally. However, there have been limited studies on the prevalence of ESBL-EC in non-clinical settings in Singapore even though snapshot studies reveal its presence in wild birds, reservoirs and aquaculture sites. To understand the AMR burden in recreational beach water, a study was conducted where a total of 90 water samples from 6 different recreational beaches across Singapore were collected over three different time periods.

Methods

Enumeration of total E. coli in the water samples according to the APHA 9223 B & H standard method.

Results or Focus

Our results showed that only 28/90 (31.3%) samples had E. coli. E. coli counts ranged from 1 to 80 CFU/100 ml which were within limits of US EPA and EU guidelines for recreational waters. Direct screening using CHROMID ESBL agar as well as LB broth supplemented with ceftriaxone showed that there were no ESBL-EC in the collected water samples.

Conclusion or Scope

The absence of ESBL-EC in recreational beach water highlights Singapore's effort in safeguarding the coastal water environment through good management of trade effluents and discharges. With increased visitorship at these beaches, future screening of the presence and prevalence of ESBL-EC will provide timely risk assessment of exposure to ESBL-EC. These findings contribute to Singapore's integrated One-Health surveillance efforts.

Acknowledgement

This study was supported by Reinvestment Fund: Integrated Programme to Combat Antimicrobial Resistance in the Environment Sector

Keywords: ESBL E. coli, AMR, one health, environment

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Environmental AMR monitoring
Abstract No: 15228

Antimicrobial resistant bacteria in coastal water and linked waterways

Han Bin Pek[1] ; Sharain Abdul Kadir[1] ; Sheereen Osman[1] ; Roslinda Mohamed[1] ; Haikal Ismail[1] ; Graziel Garbo[1] ; Luhua You[1] ; Karina Yew-Hoong Gin[1 2] ; Lee Ching Ng[1 2] ; Sophie Octavia[*1 3] ; Judith Chui Ching Wong[1]
[1]Environmental Health Institute/ National Environment Agency/ Singapore, [1]Department of Civil and Environmental Engineering/ National University of Singapore/ Singapore [2]E2S2-CREATE, NUS Environmental Research Institute/ National University of Singapore/ Singapore [2]School of Biological Sciences/ Nanyang Technological University/ Singapore [3]School of Biotechnology and Biomolecular Sciences/ University of New South Wales/ Australia

Introduction and Objectives or Purpose

Environment may act a transmission pathway and reservoir for antimicrobial resistance (AMR) genes and AMR bacteria (ARB). In Singapore, AMR surveillance efforts in the environment have largely focused on analysing the presence of chemicals or antibiotic resistance genes in selected waterways, reservoirs and coastal environments. Despite detection of higher AMRs in waterbodies from urbanised areas, there is limited understanding on their baseline levels in the water environment and the possible contamination sources.

Methods

In this study, water samples were collected from 28 coastal sites and 34 waterway sites, representing four different land-uses, namely agricultural, recreational, residential and industrial. Samples were collected from two different sampling periods, inter-monsoon (October 2021) and northeast monsoon (March 2022) seasons. Four different bacterial species, E. coli, Klebsiella spp., Pseudomonas aeruginosa and Enterococcus spp. were enumerated according to the APHA standards.

Results or Focus

Lower bacterial counts were observed in coastal samples when compared to those from waterways, as expected. All samples from recreational coastal sites were below the limit for Enterococcus spp. (WHO guideline 200 CFU/100 ml) and E. coli (US EPA guideline 126 CFU/100 ml). Among land use types, higher bacterial counts were observed for waterway and coastal water samples from agricultural and industrial areas. Similarly, concentrations of different chemicals, which were detected using LC-MS-MS, may be correlated with different land uses.

Conclusion or Scope

The findings from this study provide scientific evidence that different land uses resulted in the different prevalence of the bacterial species of interest. Further molecular and phenotypic characterisations are being carried out to determine their resistance profiles and the presence of genes contributing to AMR.

Acknowledgement

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Keywords: AMR; one health; E. coli; Klebsiella; Pseudomonas aeruginosa; Enterococcus

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14672

Adequacy of cation-adjusted Mueller-Hinton broth as an alternative culture medium for antimicrobial susceptibility testing of Brucella melitensis

Tara Wahab*[1] ; Alina Tscherne[2] ; Sabine Zange[2] ; Daniela Jacob[3] ; Antonio Fasanella[4] ; Wojciech Iwaniak[5] ; Ana Pelerito[6] ; Susanne Thomann[7] ; Mandy Elschner[8] ; Siri L. Feruglio[9] ; Tone Johansen[9] ; Talar Boskani[1] ; Roland Grunow[3] ; Enrico Georgi[2] ; Lothar Zöller[2] ; Marcin Weiner[5] ; Agnieszka Kedrak-Jablonska[5] ; Judit Henczko[10] ; Christin Hinz[2] ; Viviana Manzulli[4] ; Maria Sofia Núncio[6] ; Krzysztof Szulowski[5] ; Herbert Tomaso[8]
[1]Microbiology/ Public health agency of Sweden/ Sweden (Sverige), [2]Central Diagnostic Unit/ Bundeswehr Institute of Microbiology/ Germany (Deutschland), [3]Centre for Biological Threats and Special Pathogens (ZBS 2)/ Robert Koch-Institute/ Germany (Deutschland), [4]Istituto Zooprofilattico Sperimentale della Puglia e della Basilicata/ Istituto Zooprofilattico Sperimentale della Puglia e della Basilicata/ Italy (Italia), [5]National Veterinary Research Institute/ National Veterinary Research Institute, Pulawy, Poland/ Poland (Polska), [6]National Institute of Health/ National Institute of Health/ Portugal, [7]Spiez Laboratory/ Spiez Laboratory, Spiez, Switzerland/ Swaziland, [8]Friedrich-Löffler-Institut/ Friedrich-Löffler-Institut/ Germany (Deutschland), [9]Norwegian Institute of Public Health/ Norwegian Institute of Public Health/ Norway (Norge), [10]National Center for Epidemiology/ National Center for Epidemiology/ Hungary (Magyarország)

Introduction and Objectives or Purpose

Introduction: Brucellosis, mainly caused by Brucella melitensis (Bm), is associated with a high risk of chronification and relapses. Up to now, treatment failures are not associated with antimicrobial resistance and because of biosafety reason, many laboratories neglect antimicrobial susceptibility testing (AST) of Bm. The lack of standards are a hamper to perform AST and therefore standards are needed. In the Clinical and Laboratory Standards Institute (CLSI) guideline M45 broth microdilution (BMD) is suggested for AST of Brucella spp. and therein breakpoints are available for all relevant substances, except rifampin, which is one of the recommended drugs for treatment of brucellosis. The recommended culture medium is Brucella broth (BB) due to the fastidious growth of the agent.

The European laboratory Joint Action EMERGE (Efficient Response to Highly Dangerous and Emerging Pathogens at EU level), consists of laboratories that are specialized in highly pathogenic microorganisms in their respective countries. One of the EMERGE working groups aimed at the development of a suitable method for AST of Bm and has identified pitfalls in the CLSI method that might be due to the selected culture medium. For rifampin and trimethoprim/sulfamethoxazole (SXT) the minimal inhibitory concentration (MIC) values cluster around the presently used breakpoints and several probably “false resistant” MIC values can be observed.

Methods

Material and Methods:BMD MIC values and growth curves obtained using different culture media were compared to BB and were obtained at different time points to identify an alternative. BMD using BB and CAMHB, respectively, was compared to the gold standard (agardilution) using one clinical and one Bm reference strain. BMD using CAMHB and BB in parallel was evaluated with 30 Bm clinical isolates. An inter-laboratory validation was performed at nine partner sites using CAMHB and BB in parallel. Ten replicates were performed per site using the identical clinical Bm isolate.

Results or Focus

Results and conclusion: CAMHB is applicable for BMD of Bm. Bm shows acceptable growth in CAMHB and the culture medium leads to significant lower MIC values for SXT (four log2 dilution steps). Nevertheless, the reading of the BMD of Bm is tricky and reveals to be even more difficult using CAMHB due to slightly reduced growth. This effect leads to higher variations in the inter-laboratory validation. We adapted SOP to describe the procedure for testing the antimicrobial susceptibility of Brucella spp. using broth microdilution method.

Conclusion or Scope

This SOP is now applied in interlaboratory proficiency testing during the ongoing Joint Action SHARP (Strengthened International HeAlth Regulations and Preparedness) and there the method is applied on at least 25 isolates of Bm.

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14708

Telling the truth about antibiotic use behaviors

Elaine Lum*[1] ; Alex Cook[2] ; Suhana Solhan[3] ; Jassie Ling[4] ; Eng Sing Lee[5 6] ; Tricia Chang[5] ; Lian Leng Low[7] ; Ngiap Chuan Tan[8] ; Li Yang Hsu[2] ; Tau Hong Lee[9]

[1]Health Services & Systems Research/ Duke-NUS Medical School/ Singapore, [2]Saw Swee Hock School of Public Health/ National University of Singapore/ Singapore, [3]Communicable Diseases, Preventive Health Programmes/ Health Promotion Board/ Singapore, [4]Corporate Marketing — Marketing Preventive Health/ Health Promotion Board/ Singapore, [5]National Healthcare Group Polyclinics/ National Healthcare Group/ Singapore, [6]Lee Kong Chian School of Medicine/ Nanyang Technological University/ Singapore, [7]SingHealth Office of Regional Health/ SingHealth/ Singapore, [8]SingHealth Polyclinics/ SingHealth/ Singapore, [9]Antimicrobial Resistance Coordinating Office/ National Centre for Infectious Diseases/ Singapore

Introduction and Objectives or Purpose

Antibiotic consumption, whether appropriate or otherwise, drives antibiotic resistance. Inappropriate behaviours around antibiotic use amongst consumers are well-documented. However, the true prevalence of such behaviors is difficult to quantify robustly. We aimed to estimate the prevalence of inappropriate behaviors around antibiotic use via a novel survey method which incentivizes truth-telling.

Methods

We designed an online anonymous survey for the general population, of ten inappropriate behaviors informed by the literature. The survey incentivizes truth-telling using the Bayesian truth serum, a method that has been successfully used to robustly quantify undesirable practices in education and research settings. Participants were recruited via paid ads in Facebook. Data analysis followed the Bayesian truth serum method.

Results or Focus

A total of 697 Singapore residents completed the survey. Participant characteristics are as follows: 61.4% were women, mean age 35 years old (SD: 12.1, range 21-78), and 63.8% received tertiary education. Prevalence estimates for five inappropriate behaviors were between two to four times higher than a previous local study which used self-reporting: (a) reject the doctor's decision that they don't need antibiotics to get better (29%), (b) will go to another doctor to get antibiotics if the first doctor did not give them antibiotics (20%), (c) keep a stock of antibiotics at home just in case they need it (43%), (d) take leftover antibiotics to treat the illness themselves without going to the doctor (38%), (e) give antibiotics to family or friends who are sick to treat their illness without going to the doctor (29%).

Conclusion or Scope

The Bayesian truth serum revealed higher estimates for inappropriate behaviours around antibiotic use compared to self-reporting. General population surveys using this method may be useful for gauging effectiveness of public campaigns on mitigating antimicrobial resistance.

Acknowledgement

Additional Co-authors: Angela Chow, Tan Tock Seng Hospital, Singapore; Katie Page, Centre for Health Economics Research and Evaluation, University of Technology Sydney, New South Wales, Australia; Nicholas Graves, Health Services & Systems Research, Duke-NUS Medical School, Singapore.

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Keywords: Antimicrobial resistance; prevalence estimates; consumer behavior.

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14726

Veterinary drug use by livestock farmers in Cameroon: A One Health approach to evaluate the human health implications

Ronald Vougat Ngom*[1] ; Harquin Foyet[2] ; Mark Moritz[3] ; Wilson Rumbeiha[4] ; Roland Ziebe[5] ; Andre Zoli[6] ; Rebecca Garabed[7]
[1]Department of Animal Production/ School of Veterinary Medicine and Sciences, University of Ngaoundéré/ Cameroon (Cameroun), [2]Department of Biological Sciences/ Faculty of Sciences, University of Maroua/ Cameroon (Cameroun), [3]Department of Anthropology/ Ohio State University/ United States, [4]Department of Molecular Biosciences/ School of Veterinary Medicine, University of California / United States, [5]Agriculture, Livestock and by-products/ National Advanced School of Engineering, University of Maroua/ Cameroon (Cameroun), [6]Department of Reproduction and Biotechnology/ School of Veterinary Medicine and Sciences, University of Ngaoundéré/ Cameroon (Cameroun), [7]Department of Veterinary Preventive Medicine/ Ohio State University/ United States

Introduction and Objectives or Purpose

In Cameroon, where livestock is an important sector of the national economy, infectious animal diseases constitute a major constraint to livestock production. To improve their yields, the majority of herders extensively use veterinary drugs which can result in resistant bacteria. By using a One Health approach, this study aimed to evaluate the human health implication of the veterinary drug use by livestock farmers in Cameroon.

Methods

A survey was conducted to describes the use of medications (plant and veterinary drug) by herders. Because the use of drug can result to their residues in food, the human health risk of dietary intake of antibiotic residues was evaluated after a nutrition survey and antibiotic residues determination in beef samples collected from 202 cattle slaughtered. Plant samples used by herders were also tested against bacteria that already showed resistance to antibiotic in the study area.

Results or Focus

The results showed that, the most commonly used drugs (penicillin G and oxytetracycline) were used in a manner inconsistent with the recommended dosage, and withdrawal period by 98% of herders. The estimated daily intakes per capita of oxytetracycline and penicillin G residues from beef consumption were 22.81 and 2.37 µg, respectively. Based on the mean value, it can be concluded that the estimated risk of antibiotic residues daily intake through beef is high (5.9% of acceptable daily intake). A sensitive inhibitory effect of plant extract was observed against S. aureus.

Conclusion or Scope

This extensive antibiotic misuse, and intake will certainly contribute to antimicrobial resistance development, which is a serious public health concern. It would therefore be important to advice the use of plants for managing animal diseases and therefore assuring food safety and consumer health, and reducing antimicrobial resistance.

Acknowledgement

Authors are grateful to the study participants.

Keywords: Antibiotic; Antimicrobial resistance; Human health; One Health; Cameroon

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14743

A NATIONAL ONE HEALTH COORDINATING CENTRE FOR ANTIMICROBIAL STEWARDSHIP

Ron Cheah[*1 2] ; Courtney Ierano[1 2] ; Rod James[1 2] ; Arjun Rajkhowa[1] ; Kirsty Buising[1 2] ; Karin Thursky[1 2 3] ; Glenn Browning[1] ; James Gilkerson[1]
[1]National Centre for Antimicrobial Stewardship/ The Peter Doherty Institute for Infection and Immunity/ Australia, [2]Guidance / Royal Melbourne Hospital/ Australia, [3]Infectious Diseases / Peter MacCallum Cancer Centre/ Australia

Introduction and Objectives or Purpose

The National Centre for Antimicrobial Stewardship (NCAS) was developed with a purpose to optimise antimicrobial use in human and animal health using a ‘One Health’ approach. The centre develops and implements platforms for antimicrobial use surveillance, interventions to support antimicrobial stewardship (AMS), and delivers educational resources and training to the healthcare workforce.

Methods

NCAS was established in 2015 through a National Health and Medical Research Council grant, evolving from more than 15 years of previous work in AMS by a team of hospital doctors, general practitioners, pharmacists, veterinarians, and microbiologists. The NCAS team was purposefully formed to upskill clinicians and support the curation and translation of research with the supervision of research fellows in human and animal health settings.

Results or Focus

The centre’s focus is to lead AMS research and build workforce capacity by providing education and tools required to manage AMS programs. Activities include providing educational seminars and resources for clinicians in human and animal health; delivering a national program which monitors and reports on the quality of antimicrobial use; implementing decision support software in hospitals to monitor and improve prescribing; and developing veterinary antimicrobial prescribing guidelines, policies, tools and program templates to support AMS in companion animal, bovine and equine veterinary practice settings.

Conclusion or Scope

NCAS has played a crucial role in the successful implementation of Australia’s first National Antimicrobial Resistance Strategy, collaborated with the World Health Organisation on AMS capacity assessment activities in the Asia-Pacific, and contributes to national reporting programs to influence and shape national policy with the data gathered from its programs. The centre is continuing to expand into other domains of practice such as specialised acute care interventions (e.g., sepsis and invasive fungal infections), general practice and indigenous health; and is assisting with the implementation of AMS programs internationally (Bhutan, Canada, Fiji, Malaysia, New Zealand, Timor Leste and Vietnam).

Keywords: Antimicrobial Stewardship; One Health; Antimicrobial Resistance; Antimicrobials; Public Health

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14803

Local genomic capacity in LMICs facilitates holistic understanding of antimicrobial resistance and pathogen evolution

Senjuti Saha*[1] ; Yogesh Hooda[1] ; Md Tanmoy[1] ; Samir Saha[1]
[1]Genomics / Child Health Research Foundation/ Bangladesh (□□□□□□□□)

Introduction and Objectives or Purpose

Many low- and middle-income countries still bear an unacceptably high burden of infectious diseases. Large gaps remain regarding infection etiologies, the burden of antimicrobial resistance (AMR), and transmission patterns, impeding evidence-based interventions. A hospital surveillance network linked to laboratory and environmental genomic surveillance has the potential to fill such gaps. When connected to local capacity building, such efforts can yield sustainable research output and public health benefits.

Methods

In Bangladesh, in the 1990s, we built a robust hospital surveillance system, linked to laboratory data on pathogens, and their phenotypic AMR patterns. In the 2000s, PCR was added to track AMR of culture-negative bacterial pathogens. Next, we started building computational capacity for bioinformatics, and in 2018, we established a genomics facility. In 2021, we added environmental surveillance to gain insights into the emergence, spread, and transmission of high-burden pathogens.

Results or Focus

The data from the surveillance system facilitated the introduction of Hib and pneumococcal vaccines in Bangladesh in 2009 and 2015, respectively. The genomics facility led to unraveling of the molecular mechanism behind macrolide resistance in typhoidal Salmonella, the discovery of chikungunya virus as an etiology of meningitis, sequencing of SARS-CoV-2, and the development of low-cost diagnostics. We have sequenced 1000s of drug-resistant gram-negative bacteria and developed a genotyping scheme, Paratype, for tracking Salmonella Paratyphi A globally. The addition of environmental surveillance of bacteriophages has been instrumental in understanding the roles of bacteriophages in driving the spread of multi-drug-resistant Salmonella Typhi.

Conclusion or Scope

Despite being in a resource-constrained setting, we have been able to set up a state-of-the-art research laboratory and generate both phenotypic and genotypic AMR data and link this data to clinical outcomes and facilitate policy interventions. This has all been possible to scale up and sustain due to a persistent focus on engaging, educating, and empowering local scientists and continuously incorporating newer technologies.

Keywords: capacity, genomics, amr, bangladesh, lmic

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14812

ANTIMICROBIAL RESISTANCE AND RATIONAL USE OF MEDICINE: KNOWLEDGE, PERCEPTIONS, AND TRAINING OF CLINICAL HEALTH PROFESSIONS STUDENTS IN UGANDA

Andrew Marvin Kanyike*[1] ; Felix Bongomin[5] ; Ronald Olum[1] ; Jonathan Kajjimu[2] ; Kennedy Kiyimba[3]
[1]Internal medicine/ Mengo Hospital/ Uganda, [5]Faculty of Medicine/ Gulu University/ Uganda, [1]Internal Medicine/ St Francis Hospital/ Uganda [2]Faculty of Medicine / Mbarara University of Science and Technology/ Uganda [3]Pharmacology and therapeutics/ Busitema University/ Uganda

Introduction and Objectives or Purpose

Antimicrobial resistance (AMR) is a dire global health concern, contributing to significant mortality, especially in developing countries. This study determined the knowledge, perceptions of clinical health professions students towards antimicrobial resistance and rational use of medicine, and their confidence level to prescribe antimicrobials.

Methods

An online descriptive cross-sectional survey was conducted among clinical health professions students across 9 medical schools in Uganda. A semi-structured questionnaire using Kobo Toolbox form was shared among participants via WhatsApp Messenger (Meta, California, USA). Knowledge was categorized using modified Bloom's cut-off. One-way ANOVA, Chi-square or Fisher's exact test and multivariate logistic regression were used to assess the association between dependent and independent variables. A $p<0.05$ was considered statistically significant.

Results or Focus

We surveyed 681 participants, the majority pursuing a Bachelor of Medicine and Surgery degree (n=433, 63.6%), with a mean age of 24 (standard deviation: 3.6) years. Most participants (n=596, 87.5%) had sufficient knowledge about antimicrobial resistance with a mean score of 85 ± 14.2%. There was a significant difference in mean knowledge scores of year 4 (86.6%) compared to year 3 (82.4%) ($p=0.002$) and year 5 (88.0%) compared to year 3 (82.4%) ($p<0.001$). For most participants (n=456, 66.9%), we're confident in making an accurate diagnosis of infection, and choosing the correct antimicrobial agent to use (n=484, 71.1%). However, a majority (97.5%) as well agreed they need more training and independent course unit on antimicrobial selection and rational use of medicine.

Conclusion or Scope

Health profession students exhibited good knowledge of antimicrobial resistance and high self-perceived confidence in antimicrobial prescriptions however they still agreed that a separate course unit on AMR is necessary. This can be leveraged to cultivate and maintain proper antimicrobial use among these future health professionals.

Keywords: Antimicrobial resistance, Health professions students, rational use of medicine.

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14815

Antimicrobial resistance at the human–animal interface in the Pastoralist Communities of Kasese District, South Western Uganda

Jacob Stanley Iramiot*[1] ; Henry Kajumbula[2] ; Joel Bazira[3] ; Catherine Kansiime[2] ; Benon Asiimwe[2]
[1]Microbiology and Immunology/ Busitema University/ Uganda, [2]Medical Microbiology/ Makerere University/ Uganda, [3]Microbi0ology/ Mbarara Ubiversity of Science and Technology/ Uganda

Introduction and Objectives or Purpose
intensive usage of antimicrobials in the management of animal diseases leads to selection for resistance among microorganisms. this study aimed to assess antimicrobial use and describe factors associated with the transmission of antimicrobial resistance between humans and animals in pastoralist communities of Kasese district.

Methods
A mixed-methods approach was employed in this study. Rectal swabs were collected from the participants and cattle and transported in carry–Blaire transport medium to the laboratory within 24 h of collection for culture and sensitivity to confirm carriage of multi-drug resistant bacteria. In-depth interviews were conducted among veterinary officers, veterinary drug vendors, human health facility in-charges in both public and private health facilities, and operators of human pharmacies and drug shops.

Results or Focus
carriage of multi-drug resistant bacteria among humans was 88 (93%) and 76(80%) among cattle. Consumption of lakeshore water and carriage of multi-drug resistant bacteria in cattle were associated with carriage of multi-drug resistant bacteria in the human population.

Conclusion or Scope
the prevalence of multi-drug resistance among organisms isolated from both humans and animals was high. There is a high likelihood of transmission of multi-drug resistance between humans and animals.

Acknowledgement
We gratefully acknowledge our respondents for making this study possible. Heartfelt thanks to Maxima Tibwita and Stallone Kisembo for the great work they did as research assistants. This work was supported by the DELTAS Africa Initiative [Grant# 107743/Z/15/Z]. The DELTAS Africa Initiative is an independent funding scheme of the African Academy of Sciences (AAS)'s Alliance for Accelerating Excellence in Science in Africa (AESA) and supported by the New Partnership for Africa's Development Planning and Coordinating Agency (NEPAD Agency) with funding from the Wellcome Trust [Grant #107743/Z/15/Z] and the UK government. The views expressed in this manuscript are those of the author(s) and not necessarily those of AAS, NEPAD Agency, Wellcome Trust, or the UK government.

Keywords: Anti-microbial resistance, the human-animal interface, Pastoralist Communities, South Western Uganda.

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14858

ANTIMICROBIAL USE IN HUMAN, COMMERCIAL CHICKEN AND AQUACULTURE USING ONE HEALTH APPROACH IN BANGLADESH

Nitish Debnath*[1] ; Md. Mahbubur Rashid[2] ; Zubair Akhtar[2] ; Sukanta Chowdhury[2] ; Md. Ariful Islam[2] ; Shahana Parveen[2] ; Probir Kumar Ghosh[2] ; Md. Ahasanul Hoque[3] ; Paritosh Kumar Biswas[3] ; Aninda Rahman[4]
[1]Fleming Fund Country Grant to Bangladesh/ DAI/ Bangladesh (□□□□□□□□□), [2]Infectious Diseases Division/ International Centre for Diarrhoeal Disease Research/ Bangladesh (□□□□□□□□□), [3]Veterinary Medicine/ Chattogram Veterinary and Animal Sciences University / Bangladesh (□□□□□□□□□), [4]Communicable Disease Control / Directorate General of Health Services/ Bangladesh (□□□□□□□□□)

Introduction and Objectives or Purpose

The incremental spread of AMR in Bangladesh is caused by inadequate knowledge on rational AMU by both practitioners and users. There is overuse, underuse, empirical use, and high levels of access to antimicrobials caused by over-the-counter sales and lack of monitoring and control of AMU. This study presents a One Health study design to better understand how and why antimicrobials are used in Bangladesh.

Methods

Point prevalence surveys were conducted on AMU in acute care hospitals (2 tertiary,2 district hospitals) and in private pharmacies using a questionnaire adopted from WHO and Global PPS protocol. Qualitative data was collected on hospital capacity, ward capacity, patient demographic, clinical, microbiological, and antimicrobials data. Mobile phone surveys were used to ask individuals about their illness, health-seeking behavior, medicines, and antimicrobials prescribed.

Results or Focus

As a part of the Bangladesh National Action Plan for AMR, a National AMR surveillance program was initiated for AMR and AMU in humans, animals, and aquaculture. Bangladesh has well-structured functioning One Health platform to generate systematic data on AMU. This study contributed to the platform by providing qualitative data on AMU in human health, commercial chicken, and aquaculture.

Conclusion or Scope

The PPS in hospitals, and the AMU study in hospitals, pharmacies, community, commercial chickens and in fish farms found that antimicrobials were frequently used. This may indicate irrational and inappropriate use of antimicrobials. The lack of adequate diagnostic capabilities in the human health sector and absence of appropriate biosecurity measures in farms cause animal and human health practitioners to prescribe more antimicrobials to create a false sense of security. Bangladesh urgently needs national policy on AMU, AMR social awareness, appropriate regulations with enforcement to address the over-the-counter access to antibiotics without prescriptions, which is an important contributor to emergence of AMR.

Acknowledgement
Authors: Guillaume Fournie, Damer Blake, Md.Zobaidul Haque Khan, Khaleda Islam, Mahmudur Rahman, Fahmida Chowdhury

Keywords: Antimicrobial use; Bangladesh; social awareness; human health; animal health

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14859

MULTICENTER BASELINE SURVEY TO OUTLINE ANTIMICROBIAL PRESCRIBING PRACTICES AT SIX SENTINEL SITES IN PAKISTAN

Nicole DeCastro*[8] ; Dr. Nazia Khursheed[1] ; Dr. Saba Jamal[1] ; Dr. Ayesha Rasheed[2] ; Makkiya Jawed[2]
[8]Global Health/ DAI/ United States, [1]Pathology/ Indus Hospital and Health Network/ Pakistan (پاکستان) [2]Fleming Fund Country Grant to Pakistan/ DAI/ Pakistan (پاکستان)

Introduction and Objectives or Purpose

AMR is an emerging global public health challenge. Monitoring of antimicrobial use is crucial in minimizing the irrational use of antibiotics and implementation of good clinical practices. An antimicrobial stewardship program was created to encourage rational use of antimicrobials by (a) improving the understanding of AMR of health professionals (b) enhancing communication and collaboration between lab staff and clinicians.

Methods

A multi-centered cross-sectional survey was conducted from February 2021 to March 2021 at six sentinel sites to assess the baseline using WHO Point Prevalence Survey Methodology. Inpatients from designated wards from six public sector hospitals, meeting the inclusion criteria were included. Standardized questionnaire and web-based data entry using an open-source Kobo Collect application was adopted. Data was pooled and analyzed using SPSS (version 22.0). Results were used to develop a tailored programme for clinicians and lab staff. Teaching sessions were conducted to enhance prescription-based treatment and to create awareness about appropriate antibiotic use.

Results or Focus

Medical records of 837 in-patients were surveyed, of which prevalence of antibiotics was 78.5%. The most prescribed class of antimicrobial was Ceftriaxone (21.7%) followed by Cefoperazone/Sulbactam (8.4%) and Piperacillin/Tazobactam (5.9%) (categorized in WHO AWaRe Classification – Watch Group). Other commonly prescribed medicines included Metronidazole (17.3%), and Co-Amoxiclav (6.3%). The antibiotics were prescribed largely for surgical prophylaxis (36.7%) followed by community acquired infections (24.7%). Single antibiotic was prescribed to 46.7%, two to 39.9% and three or more to 12.5 % of the assessed patients. Two of the six (30%) hospitals had functional drug and therapeutic committees, three (50%) had infection prevention and control committees and one had an antibiotic formulary.

Conclusion or Scope

The findings demonstrate high consumption of broad-spectrum antibiotics, specially third generation Cephalosporins. Stewardship programs can play a significant role in driving diagnostic based treatment, leading to rational use of antibiotics.

Keywords: Antimicrobial use; Pakistan; stewardship; point prevalence survey

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14873

STANDARDISED ANTIMICROBIAL SENSITIVITY TESTING METHODS FOR USE IN AMR SURVEILLANCE IN AQUACULTURE

David Verner-Jeffreys*[1 2] ; Sandrine Baron[3] ; Edel Light[1 2] ; Elliot Stanton[1] ; Andy Powell[1 2] ; Andrew Joseph[1 2] ; Craig Baker-Austin[1] ; Peter Smith[4] ; Roderick Card[2 5]
[1]Weymouth laboratory/ Cefas, Centre for Environment Fisheries and Aquaculture Research/ United Kingdom, [2]Veterinary Medicines Directorate / UK FAO Reference Centre for Antimicrobial Resistance/ United Kingdom, [3]Ploufragan-Plouzané-Niort Laboratory, Mycoplasmology, Bacteriology and Antimicrobial Resistance Unit / ANSES/ France, [4]Microbiology/ University of Galway/ Ireland, [5]Bacteriology/ Animal Pant Health Agency/ United Kingdom

Introduction and Objectives or Purpose

Aquaculture is the fastest growing food production sector globally. As with terrestrial livestock farming, antibiotics are used in intensive aquaculture production to control bacterial disease problems. Many practical issues need to be addressed to develop effective aquaculture AMR surveillance programmes, able to reliably detect emergence and spread of resistance.

Methods

We illustrate practicalities of implementing surveillance systems for AMR emergence in aquaculture pathogens, through description of a collaborative effort to establish EUCAST ECOFF and CLSI ECV interpretative criteria for disc diffusion and broth microdilution-based testing of a range of key aquaculture pathogens. We also present results of using appropriate standardized CLSI guidelines and Normalized Resistance Interpretation to analyze a historical collection of Aeromonas salmonicida ssp. salmonicida (causative agent of furunculosis) and Yersina ruckeri (causative agent of enteric redmouth disease- ERM) isolates gathered from UK rainbow trout farms over more than 30 years.

Results or Focus

The rationale and process behind establishing a custom broth microdilution testing panel for establishing ECOFF values for Vibrio anguillarum to eight antibiotics, and results of testing by partner labs are presented. Screening of Y. ruckeri isolates revealed low levels of resistance to antibiotics important to aquaculture. This matches previous findings that suggest, at least in the UK, that ERM is still largely susceptible to antibiotic chemotherapy. The A. salmonicida isolates tested showed markedly higher prevalence of non-wild type sensitivity than Y. ruckeri to antibiotics routinely used in aquaculture, including oxytetracycline, ampicillin, oxalinic acid, and trimethoprim/sulfamethoxazole.

Conclusion or Scope

The difference in susceptibilities between Y. ruckeri and A. salmonicida could be related to the widespread use of vaccination to control ERM in farmed rainbow trout. More generally, these examples illustrate the importance of developing and using of standardised approaches to characterise aquatic pathogens for AMR in surveillance programmes, and thus help inform action by industry and policy makers.

Keywords: Aquaculture; surveillance; AST; Standardized; AMR

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14884

ANTIBIOTIC USE PROFILE IN REFERRAL HOSPITALS ACROSS INDONESIA: A POINT-PREVALENCE SURVEY

Nani Hidayanti*[1] ; Nelly Puspandari[2] ; Dodi Safari[3] ; Mariyatul Qibtiyah[4] [5] ; Muchlis Ahsan Udji Sofro[6] [5] ; I Made Ananda Krisna[3] [7] ; Korrie Salsabila[3] ; Rahmadania Marita Yusuf[3] ; I.B. Anom[1] ; Desrina Sitompul*[8]
[1]Directorate of Referral Health Services, Directorate General of Health Services/ Indonesia Ministry of Health/ Indonesia, [2]Centre for Health Resilience and Health Resource Policy/ Health Policy Agency, Indonesia Ministry of Health / Indonesia, [3]National Research and Innovation Agency / Eijkman Research Centre/ Indonesia, [4]Department of Pharmacy/ Dr.Soetomo General Academic Hospital/ Indonesia, [5]Antimicrobial Resistance Control Committee/ Indonesia Ministry of Health/ Indonesia, [6]Department of Internal Medicine - Faculty of Medicine/ Diponegoro University/Dr Kariadi Hospital Semarang Indonesia/ Indonesia, [7]Nuffield Department of Clinical Medicine and Department of Biology/ University of Oxford/ United Kingdom, [8]Fleming Fund Country Grant to Indonesia/ DAI/ Indonesia

Introduction and Objectives or Purpose

Antimicrobial use and associated laboratory test results were surveyed in Indonesian hospitals. The study was designed to provide baseline data and enable national, hospital, ward, and patient comparisons to inform policymaking and hospital stewardship efforts. The study was designed in coordination with AMU surveying in commercial broiler and aquaculture farming.; it will contribute to Indonesian One Health AMU surveillance and stewardship and future integrated AMR, AMU and AMC surveillance and governance.

Methods

An adapted point prevalence survey (PPS) methodology drawing from WHO-PPS and Global-PPS 2019 guidelines was designed and implemented in seven public hospitals across Indonesia in 2021. Data on prescribing patterns were collected and analysed.

Results or Focus

In total 1237 patients were surveyed; 671 were prescribed antibiotics (54.24%). Most antibiotics were prescribed empirically (77.58%), fewer definitively (17.17%), and some prophylactically (5.25%). Third generation cephalosporins (33.43%), antituberculosis drugs (12.42%), fluoroquinolones (10.81%), and aminoglycosides (9.19%) were most commonly prescribed. Indications included community acquired infection (49.49%), hospital acquired infection (15.25%), surgical prophylaxis (3.43%), medical prophylaxis (2.02%), other (29,80%; post-surgical most common). All definitively prescribed drugs were accompanied with specific diagnoses, only 471 out of 768 (61.33%) of empirically prescriptions were subsequently diagnosed with bacterial infection. Pneumonia (34,48%), clinical sepsis (18,05%), and gastrointestinal infection (10,29%) were the most frequent diagnoses. In most cases reason for antibiotic prescription (56.77%) and plan for review/cessation (61.92%) was not in the patient's care plan.

Conclusion or Scope

The findings indicate high-levels of culture-guided antibiotic prescription, indicating more comprehensive antimicrobial stewardship programs are needed. Review of antibiotic use and guidelines is essential to prevent AMR emergence and spread. This surveying was conducted in coordination with other sector surveys and will contribute to Indonesian efforts to establish integrated One Health AMR, AMU, and AMC surveillance systems.

Keywords: Antimicrobial Use; Indonesia; Hospitals; PPS; Coordination

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14886

Building Laboratory Capacity for Antimicrobial Resistance (AR) Surveillance through PulseNet International: Asia Pacific Case Study

Kristy Kubota[1] ; Molly Freeman[2] ; Tuyet Hoang[3] ; Benjamin Howden[3] ; Heather Carleton[*2]
[1]Food Safety/ Association of Public Health Laboratories / United States, [2]Division of Foodborne, Waterborne and Environmental Diseases, Enteric Diseases Laboratory Branch/ U.S. Centers for Disease Control and Prevention (CDC)/ United States, [3]Microbiological Diagnostic Unit Public Health Laboratory, Department of Microbiology and Immunology/ The University of Melbourne at The Peter Doherty Institute for Infection and Immunity/ Australia

Introduction and Objectives or Purpose

Antimicrobial resistance (AR) is a growing concern in developed and low- and middle-income countries. As a result, global initiatives have been developed to support surveillance and identify emerging drug-resistant strains. PulseNet International was established in the early 2000s as a worldwide network for detecting foodborne disease clusters and outbreaks using molecular subtyping methods such as whole genome sequencing. In 2021, PulseNet International joined a larger CDC initiative, Global Antimicrobial Resistance Laboratory & Response Network, to build laboratory capacity for AR surveillance within PulseNet International. In 2022, PulseNet Asia Pacific launched a feasibility study to demonstrate the impact of the PulseNet surveillance system for monitoring AR trends in foodborne bacteria. A goal of this study is to determine the feasibility of developing genomics capacity for AR surveillance.

Methods

An application and needs assessment to determine sequencing and analysis capacity were sent to prospective participants in May 2022. By 30 July 2022, three sites will be selected based on ability to implement PulseNet protocols, access to cloud computing, and perform analysis of enteric bacteria. Trainings in sequencing and analysis tools will be offered to participants by January 2023. Participating laboratory sites will sequence and analyze up to 100 isolates within a 12-month period. A report will be developed to communicate study findings.

Results or Focus

As of early July, a total of 8 institutions applied for the feasibility study and submitted need assessments representing hospital and public health laboratories.

Conclusion or Scope

Laboratory-based surveillance networks such as PulseNet are critical to detect and monitor AR trends. This feasibility study will demonstrate the impact of public health genomics on the surveillance of AR trends and enteric within the Asia Pacific region. Future funding to expand to laboratories from different sectors will bring a One Health approach, which is critical for determining sources of drug resistant pathogens and identifying mitigation measures.

Keywords: Antimicrobial Resistance; Whole genome Sequencing (WGS); surveillance; enteric bacteria

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14895

ANTIMICROBIAL RESISTANCE IN ADULT PATIENTS WITH INVASIVE PNEUMOCOCCAL DISEASE IN HONG KONG – EPIDEMIOLOGICAL ANALYSIS OF MEDICAL RECORDS 2012-2019

Jack Chi Him Lau[*1] ; Natalie Tsz Ying Tsie[1] ; Qiuyan Yu[2] ; Kim Shijian Lao[3] ; Celine Sze Ling Chui[1 3]
[1]School of Nursing/ The University of Hong Kong/ Hong Kong (□□), [2]Centre for Safe Medication Practice and Research, Department of Pharmacology and Pharmacy/ The University of Hong Kong/ Hong Kong (□□), [3]Global Medical and Scientific Affairs/ MSD Hong Kong/ Hong Kong (□□)

Introduction and Objectives or Purpose

Streptococcus pneumoniae(Sp) is one of the most common pathogens causing pneumonia in Hong Kong. The pathogen can also cause invasive pneumococcal disease(IPD) and subsequent complications such as sepsis, meningitis, and bacteraemia. This study aims to identify the characteristics of antimicrobial non-susceptibility and serotypes for the Sp isolated.

Methods

Data were retrieved from the population-wide Clinical Data Analysis and Reporting System(CDARS), for all adult IPD hospitalization episodes from 2012–2019. Hospitalized patients aged ≥18 with IPD diagnosis defined by International Classification of Diseases, 9th Revision, Clinical Modification(ICD-9-CM) were included. Collected data include patient demographics, diagnoses, and microbiological culture and laboratory test results – antimicrobial sensitivity and serotyping. Laboratory results were captured within ±28 days from the date of admission. Hospital admissions within 56 days of the index hospitalization was considered as the same episode. Descriptive statistics were tabulated by each hospitalisation episode for (1)antimicrobial susceptibility (Sensitive/Intermediate/Resistance); and (2)serotype of the isolate.

Results or Focus

Of all 432 episodes identified from 425 patients with IPD, the majority(81%) had bacteraemic pneumonia. Other manifestations include bacteraemia(23%) and meningitis(8%). Sp isolates from 361 episodes were tested for antimicrobial susceptibility. Among the tested isolates, 31% had no evidence of antimicrobial resistance, 29% were resistant to 2 classes of antibiotics. Of the antibiotics tested, some notable antibiotics with non-susceptibility include Doxycycline(86%), Erythromycin(74%), Clindamycin(72%), Azithromycin(69%), Cotrimoxazole(55%), Penicillin(14%). For isolates from 159 IPD episodes, serotype information was available. Serotype 3 was the most prevalent serotype, accounting for 43% of all tested isolates.

Conclusion or Scope

Antimicrobial resistance narrows the treatment options and may cause extended hazards if it is being spread in the community. Despite coverage by pneumococcal vaccines currently widely available for local adult population, serotype 3 remains the predominant serotype. Therefore, there is an important public health need to new vaccines with superior protection against predominant serotypes and improve pneumococcal vaccine uptake among elderly.

Acknowledgement

This study is supported by Merck Sharp & Dohme LLC, a subsidiary of Merck & Co., Inc., Rahway, NJ, USA

Keywords: antimicrobial resistance, Invasive Pneumococcal Disease, pneumococcal conjugate vaccine, antibiotic treatment, laboratory surveillance

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14909

A GLIMPSE INTO ANTIMICROBIAL CONSUMPTION IN PAPUA NEW GUINEA

Marjorie Elijah*[1] ; Ron Cheah; Susan Luu; Jeannine Loh
[1]Medical Supplies Procurement & Distribution Branch/ National Department of Health/ Papua New Guinea

Introduction and Objectives or Purpose

Antimicrobial resistance (AMR) is driven by overuse and misuse of antimicrobials. To understand a country's AMR situation, systems for oversight of antimicrobial consumption (AMC) must be implemented. A country situation analysis on AMR was conducted in 2016, revealed limited information on the prevalence and burden of AMR in the country. As a result, AMR has been placed as a high priority of the country's Department of Health, Agriculture and Environment and efforts have been made to establish a baseline of the AMR situation.

Methods

Antimicrobial consumption data, obtained from mSupply, a Logistics Management information System used to manage procurement, supply and distribution of medical supplies throughout the country. Data was sourced for public hospitals and health centers, via five area medical stores from 2016 to 2019. Data excluded anti-tuberculosis, anti-malarial, anti-retroviral medications and medicines from private hospitals, community pharmacies and the informal market.

Results or Focus

The overall consumption of antimicrobials in PNG increased every year from 2016 to 2019 (Defined Daily Doses per 1000 inhabitants per day (DID); 2016 = 10.1; 2019 = 28.3). Beta-lactam penicillin were the highest consumed class of antimicrobials, followed by tetracycline and then trimethoprim and sulfamethoxazole over this time frame. Of the beta-lactam penicillin class, amoxicillin had the highest consumption rate (average DID from 2016 to 2019 = 6.43)

Conclusion or Scope

These data provide an insight into the situation of AMC in PNG. The overall steady increase in consumption of antimicrobials from the public health facilities is of concern. Establishing antimicrobial stewardship strategies and applying a systems approach to antimicrobial surveillance is necessary to ensure oversight of AMR.

Keywords: AMR;AMC

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14974

ESTABLISHING A ONE HEALTH AMR COMMUNITY OF PRACTICE IN NIGERIA

Roderick Card[1] ; Victoria Adetunji[2] ; Idowu Fagbamila[3] ; Ini Adebiyi[4] ; Eme Ekeng[5] ; Suliat Adeleke[6] ; Mwapu Ndahi[*7] ; Catherine Ryan[8] ; Hemanti Patel[9] ; Rene Hendriksen[10]
[1]Department of Bacteriology/ Animal and Plant Health Agency/ United Kingdom, [2]Department of Veterinary Public Health and Preventive Medicine/ University of Ibadan/ Nigeria, [3]Bacterial Research Division/ National Veterinary Research Institute/ Nigeria, [4]Department of Medical Microbiology/ University College Hospital Ibadan/ Nigeria, [5]National Reference Laboratory/ Nigeria Centre for Disease Control/ Nigeria, [6]Department of Veterinary and Pest Control Services/ Federal Ministry of Agriculture and Rural Development/ Nigeria, [7]Department of Veterinary and Pest Control Services/ Federal Ministry of Agriculture and Rural Development/ Nigeria, [8]Antimicrobial Resistance and Healthcare Associated Infections Reference Unit/ UK Health Security Agency/ United Kingdom, [9]Reference Services Division/ UK Health Security Agency/ United Kingdom, [10]Division of Global Surveillance/ Technical University of Denmark/ Denmark (Danmark)

Introduction and Objectives or Purpose

The One Health approach is an effective way to take coordinated action to tackle the threat of AMR. To help support the ambitions set out in Nigeria's national action plan for AMR, we established a One Health AMR Community of Practice comprised of Fleming Fund fellows and their mentors. This community is a multi-disciplinary team dedicated to addressing AMR in human and animal health sectors, with members from Nigeria, Denmark, and the United Kingdom.

Methods

We undertook gap analyses of systems in Fleming fellows' laboratories and institutions to identify areas for support. Tailor-made capacity support programmes were developed for each fellow. Fellows visited their mentors' institutes in Europe for in-person coaching in a variety of areas, including microbiology, epidemiology, and laboratory quality management systems. To demonstrate the establishment of strengthened systems in Nigerian institutes, the community has completed One Health collaborative projects investigating AMR at poultry and pig farms, the farm environment, and in-contact humans and hospital submissions.

Results or Focus

One area of focus was the AMR training of 132 Nigeria scientists from government, academic, and private laboratories. We ran four courses, each comprising a thoughtful balance of classroom teaching and hands-on sessions in the laboratory. This gave participants practical experience handling and testing bacterial cultures, as well as background and wider context for their AMR work.

Conclusion or Scope

The establishment of this community has helped to strengthen personal and institutional capacities in Nigeria, Denmark, and the United Kingdom. Routine and ad hoc networking strengthens ongoing activity, and the community has grown to include additional Fleming fellows and mentors. The up-skilling of Nigerian laboratory staff, through the 'train-the-trainer' approach, has enhanced capacity to produce high-quality microbiological data. This community has contributed to One Health AMR surveillance systems and supported implementation of Nigeria's national action plan for AMR

Acknowledgement

Fleming Fund Fellowship

Keywords: Community of Practice; AMR; Nigeria; Capacity Building

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14978

TRENDS OF ANTIMICROBIAL CONSUMPTION USING DISTRIBUTION DATA IN TIMOR-LESTE

Suzana Henriques Soares*[1] ; Agata Do Espirito Santo Soares*[2] ; Ron Cheah[3 4] ; Rodney James[3 4]
[1]Pharmacovigilance and Controls / National Directorate for Pharmaceutical and Medicines/ Timor-Leste, [2]Pharmacy / National Hospital Guido Valadares/ Timor-Leste, [3]National Centre for Antimicrobial Stewardship / The Peter Doherty Institute for infection and Immunity / Australia, [4]Guidance/ Royal Melbourne Hospital / Australia

Introduction and Objectives or Purpose

Antimicrobial resistance (AMR) is a growing global health threat that is associated with volume of antimicrobial use. Timor-Leste is a Southeast Asian country that shares a border with Indonesia with a population of 1,368,639. Despite recent research that indicates increasing resistance rates among human pathogens in this country, a knowledge gap on antimicrobial usage volume exists. This study intends to describe antimicrobial consumption trends in the 13 municipalities in Timor-Leste; and the only tertiary hospital in Timor-Leste (National Hospital Guido Valadares (NHGV).

Methods

Distribution data were obtained from 13 municipalities from 2016 to 2019; and from hospital distribution data 2016 to 2021. Antimicrobials were classified by class and by World Health Organization Access, Watch, Reserve categories. Estimated consumption was calculated by Daily Defined Doses per 1000 inhabitants per day (DID) of oral and parenteral routes for municipality data, and by Daily Defined Doses (DDD) per 1000 occupied bed days (OBD) for hospital data.

Results or Focus

Overall antimicrobial consumption in the 13 municipalities increased gradually over 2016 to 2019 (DID; 2016=6.18, 2019=8.04). Similar trends of consumption were observed at NHGV (DDD/1000 OBD; 2016=4153.9, 2019=6839.8). Amoxicillin was the highest consumed antimicrobial in both datasets over the timeframes (average DID=2.8; average DDD/1000 OBD=1793.7); followed by erythromycin (average DID=0.57) and sulfamethoxazole-trimethoprim (average DID=1.16) in the 13 municipality dataset; and ceftriaxone (average DDD/1000 OBD=328.4) and cloxacillin (average DDD/1000 OBD=367.16) for the NHGV dataset. Most antimicrobials were from the Access category (13 municipality average=83%, HNGV average=72%), with the remaining in the Watch category.

Conclusion or Scope

These data are useful in describing a baseline and trend of the consumption in Timor-Leste. Further efforts are required to better understand the rationale for these trends. Antimicrobial usage audits may provide additional clarity to the situation and improve antimicrobial surveillance for adequate AMR oversight in this country.

Keywords: AMR; AMC; antimicrobial resistance; antimicrobial consumption; antimicrobial stewardship;

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 14985

INVESTIGATING ANTIMICROBIAL RESISTANCE TRENDS OVER A THREE-YEAR PERIOD (2019-2021) AT THE PORT MORESBY GENERAL HOSPITAL (PMGH) IN PAPUA NEW GUINEA (PNG)

Gabriella Ak*[1] ; Gabriella Ak*[1] ; Sarah Baines; Rod James; Candice Domingos De Sa Lisboa; Benjamin P Howden; Samson Kangapu[1] ; Jamblyne Pamu[1]
[1]Pathology/ Port Moresby General Hospital/ Papua New Guinea

Introduction and Objectives or Purpose

In PNG, antimicrobial resistance (AMR) has long been recognized as a potential threat, receiving increased attention with the development of a National Action Plan (2019-2023). Little data on the extent of AMR and trends in the country and no systematic national AMR surveillance program exists. Data from the microbiology laboratory, PMGH represents the only baseline information available locally to identify AMR risks and priorities. Our objective was to expand knowledge on human health AMR patterns in PNG by systematically investigating data from PMGH, 2019 to 2021.

Methods

Standard laboratory data on all sample referred from 2019-2021 was collected, including sample demographics, organism isolated, and antimicrobial susceptibilities, performed using disk diffusion and interpreted with clinical breakpoints from the EUCAST (v9). Data analysis and presentation was performed in R using the AMR for R package.

Results or Focus

A total of 32,610 samples were processed; 28% (n=9197/32,610) had significant growth. The most common microbial species, compromising 70% of isolations, were Klebsiella pneumoniae 22% (2027/9197), Escherichia coli 18% (1647/9197), Staphylococcus aureus 18% (1647/9197) and Pseudomonas aeruginosa 12% (1124/9197). Extended-spectrum beta-lactamase (ESBL) production, based on ceftriaxone non-susceptibility, was 59% in K. pneumoniae and 34% in E. coli. Meropenem resistance was 2% and 4% for E. coli and K. pneumoniae, respectively. Methicillin resistance S. aureus (MRSA) rates were between 30% - 40% among all specimen types. Vancomycin resistant Enterococcus (VRE) was identified in 11% (22/196) of all enterococci recovered. Comparison of the AMR trends observed over the three years have shown an increase of ~3-7% in rates for MRSA, ESBL, CPE and VRE for all specimens.

Conclusion or Scope

The results show high rates of AMR in clinical specimens from PMGH, highlighting the need for action to address AMR in PNG. This data will be used to guide the first antibiotic guideline policy for PNG.

Acknowledgement

Fleming Fellowship Grant

Doherty Institute, Melbourne University.

Keywords: Antimicrobial resistance; Port Moresby General Hospital; Antibiogram; Extended spectrum Beta-lactamase, Methicillin resistance staphylococcus aureus.

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 15006

Global antimicrobial resistance: a system-wide comprehensive investigation using the new global One Health index

Min Li[*1] ; Nan Zhou[*1] ; Zile Cheng[*1]
[1]Department of Animal Health and Food Safety/ School of Global Health, Chinese Center for Tropical Diseases Research, Shanghai Jiao Tong University School of Medicine/ China (□□)

Introduction and Objectives or Purpose

Antimicrobial resistance (AMR) is one of the top ten global public health challenges. However, given the lack of a comprehensive assessment of worldwide AMR status, the objective of this study is to develop a One Health-based system-wide evaluation tool on global AMR.

Methods

We developed the three-hierarchical global One Health index (GOHI)-AMR indicator scheme, consisting five key indicators, 17 indicators, and 49 sub-indicators, by incorporating 146 countries' data from diverse authoritative databases. We investigated the overall- or sub-rankings and differences of GOHI-AMR scores at the international, regional, and national levels utilizing the GOHI methodology. Additionally, a correlation analysis was conducted between the GOHI-AMR scores and specified socioeconomic factors.

Results or Focus

As expected, high-income countries (HICs) outperform the other three income groups on overall rankings and all five key indicators of GOHI-AMR, whereas LICs unexpectedly outperform UMICs and LMICs on the antibiotics-resistant key indicator (ARR) and ARR-subordinate indicators. Surprisingly, there were no significant differences among the four groups on the environmental-monitoring indicator. GOHI-AMR was positively correlated with GDP, life expectancy, and AMR-related publications, but negatively with natural growth rate and chronic respiratory disease. In contrast to Cyprus, the remarkably lower prevalence of “ESKAPE pathogens” in high-scoring Sweden and Denmark highlights Europe’s huge gaps in addressing AMR. China and Russia outperformed the other three BRICS countries on all key indicators, particularly India’s ARR and Brazil’s AMR LNC. Furthermore, significant internal disparities in CRKP and MRSA prevalence were observed between China and the USA.

Conclusion or Scope

GOHI-AMR is the most comprehensive tool currently available for the assessment of AMR status worldwide. We discovered unique features impacting AMR in each country and offered precise recommendations to improve the capacity to tackle AMR in low-ranking countries.

Acknowledgement

Thanks for all participants for participating in this study.

Keywords: Global Antimicrobial resistance; Global One Health Index (GOHI); AMR surveillance networks; ESKAPE

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 15044

Antimicrobial consumption by livestock sector in Bhutan in comparison to European nations

Ratna Gurung*[1]
[1]Department of Livestock/ National Centre for Animal Health/ Bhutan (□□□□□)

Introduction and Objectives or Purpose

Antimicrobials are finite resource. Resistance development in pathogens is being reported in an unprecedented rate from both human and animal health care systems especially from Asia and Africa. This study looked at the volume and per animal unit availability of antimicrobials in Bhutan for last five years - 2017 to 2021.

Methods

Livestock population for each calendar years were collected from the published national statistics report. The total number of livestock for each calendar were converted into population correction unit (PCU). National level data on purchase and supply of antimicrobials were collected. Active constituents were calculated for each antimicrobial. The mg/PCU of antimicrobials for Bhutan was calculated and compared with that European nations.

Results or Focus

Predominantly used class of antimicrobials were penicillin, sulphonamides and trimethoprim. The mg/PCU of livestock in Bhutan was found at the range of 3.22 – 6.63. The average antimicrobial consumption of 31 European nations was 89 mg/PCU (2.30 – 393.9). The mg/PCU of Bhutan consumption was close to Norway (2.30 mg/PCU) and Iceland (3.8 mg/PCU).

Conclusion or Scope

The study looked at the overall consumption rate on the calculated PCU of livestock in Bhutan. The antimicrobial consumption rate by livestock in Bhutan in comparison to European nations was found low. This is perhaps due to strong regulation in place for the use of antimicrobials in Bhutan. However, use of antimicrobials in Bhutan needs to be continuously monitored to maintain this rate or further reduce in an effort to prevent resistance development. Strong antimicrobial stewardship, good farm biosecurity and vaccination program should support in reduction of antimicrobials in livestock in Bhutan.

Acknowledgement

The author is thankful to Fleming Fund country grant and Policy Fellowship prgram in supporting this study.

Keywords: Antimicrobials; PCU; Resistance; Farm biosecurity;

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 15108

Monitoring the use of antimicrobials in animals - an essential step in addressing AMR

Kinzang Dukpa[*1]
[1]Regional Representation for Asia and the Pacific/ World Organisation for Animal Health/ Japan (□□)

Introduction and Objectives or Purpose

With increasing demand for animal proteins, there is an increasing demand for antimicrobial use in animal production as more intensive livestock farms replace the traditional farms in the Asia Pacific (AP) Region. In its 6th annual report, the World Organisation for Animal Health (WOAH) reports that the AP Region uses almost double the amount of antimicrobials used globally. Although important to monitor and report the data on antimicrobials imported, produced, distributed, sold, and used in animals, this activity is not currently in the priority list for most countries. The WOAH thus supported countries in the AP Region to enhance AMU monitoring since 2018. The main objectives were to understand the prevailing legislations related to AMU, the state of play of AMU supply chain, the roles of different regulatory agencies and their coordination status related to AMU monitoring.

Methods

In-country multisectoral workshops were organised in countries in which relevant stakeholders from the government, private sector, research institutes, academia discussed the current legislations, the state of play of AMU supply chain, the roles of different stakeholders for collection and sharing of AMU data and ways of strengthening AMU monitoring in animal sector.

Results or Focus

Since 2018, WOAH organised thirteen national AMU monitoring workshops in the AP Region. Countries are at varying stages of implementing monitoring of antimicrobials usage in animals and are facing challenges such as weak legislations, weak intersectoral coordination, lack of capacity to collect AMU data from stakeholders including end users, and lack of awareness especially amongst the policy makers, producers and consumers. The priorities include a need to update legislations, enhance coordination amongst the key stakeholders, develop simple AMU database at national level, and set up national AMU monitoring system.

Conclusion or Scope

AMU monitoring activities in animals in countries need support in terms of capacity building, enhanced intersectoral coordination, sustainable governing mechanisms.

Acknowledgement

WOAH Members

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 15136

“Surveillance of Anti-microbial Resistance (AMR) of Escherichia coli from the dogs in Paklihawa, Nepal”

Keshav Lamsal[*1] ; Anil Gautam[2] ; Krishna Kaphle[3] ; Shambhu Shah[3] ; Sirjan Bastola[4]
[1]Veterinary Theriogenology/ Agriculture and Forestry University(AFU)/ Nepal (□□□□□), [2]Bachelor of Veterinary Science and Animal Husbandry (BVSc & AH/ Institute of Agriculture and Animal Science (IAAS), Tribhuvan University/ Nepal (□□□□□), [3]Department of Theriogenology and Physiology/ Institute of Agriculture and Animal Science (IAAS), Tribhuvan University/ Nepal (□□□□□), [4]Department of Veterinary Microbiology and Parasitology / Institute of Agriculture and Animal Science (IAAS), Tribhuvan University/ Nepal (□□□□□)

Introduction and Objectives or Purpose

The studies on the antimicrobial resistance (AMR) of enteric pathogens from food animals are commonly conducted in Nepal. There are limited data on the AMR of pathogens isolated from the companion animals. So, this study was conducted to monitor the status of AMR in dogs of Paklihawa, Nepal using E. coli as a model enteric pathogen. The study would help to compare the resistance pattern with previous findings from livestock and poultry.

Methods

A cross-sectional study was conducted in Paklihawa, Nepal from July to September of 2021. The faecal samples were collected from 103 dogs and transported in an ice cool box to the microbiology laboratory of the Paklihawa campus. E. coli was isolated on EMB agar and confirmed biochemically by IMViC tests. E. coli isolates were tested against eight different antibiotics by the disc diffusion method.

Results or Focus

The prevalence of E. coli in faecal samples of dogs was found to be 30.0 % (31/103). The occurrence of E. coli was statistically associated with animal factor (age, weight) and deworming status ($P \leq 0.05$). Out of eight antibiotics tested, the maximum resistance to an antibiotic was observed with Ceftazidime (100.0 %), followed by Amikacin (96.8 %), Ceftriaxone and Doxycycline (93.5 %), Ciprofloxacin (83.9 %), Chloramphenicol (83.9 %), Enrofloxacin (61.3 %), and Gentamycin (35.5 %). All 31 isolates were found to be multi-drug resistant (MDR) and had a Multiple Antimicrobial Resistance (MAR) index value greater than 0.2 which represents high risk source of contamination.

Conclusion or Scope

The presence of MDR isolates of E. coli from dogs indicates the possible circulation of resistant isolates from humans or food animals to dogs. Periodic surveillance with one health approach is necessary to understand the transmission of AMR among different species. The precautions should be taken while sharing the environment with the companion animals.

Keywords: E. Coli, Antimicrobial Resistance(AMR),Dogs, Paklihawa

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 15137

Health Professionals' and Pastoralists' Knowledge, Attitude, and Practice about Antimicrobial Resistance and Climate Change, Somali Region, Eastern Ethiopia: Qualitative Study.

Abdifatah Muktar Muhummed*[1 2] ; Andrea Kaiser-Grolimund [1] ; Yahya Maidane Osman[1 2] ; Jakob Zinsstag[1] ; Gueladio Cisse[1]
[1]Epidemiology and Public Health / Swiss Tropical and Public Health/ Switzerland (Schweiz), [2]Medicine and Health Science / Jigjiga University/ Ethiopia

Introduction and Objectives or Purpose

Despite the fact that AMR and climate change are among the most serious threats to the global health system and economy, many people around the world are unaware of their significant negative impact. Human behavior is the central plan to address AMR and climate change. This qualitative study aims to understand the knowledge, attitude, and practices on AMR and climate change of both pastoralists and health professionals in the Somali region, Ethiopia.

Methods

This qualitative research was carried out in three separate locations in the Somali region (Jigjiga, Gode, and Adadle). 44 in-depth interviews were conducted with health professionals in different health facilities in urban, semi-urban, and rural settings. Additionally, 12 focus group discussions with rural populations were conducted to understand their KAP towards antibiotics. A combination of content and thematic analysis was used to analyze the qualitative data.

Results or Focus

Except for doctors and pharmacists, the majority of other health professionals and communities had poor awareness of AMR and climate change. Conversely, after simple explanations of the term “climate change” the communities understood it better than health professionals. Furthermore, both the health professionals and communities poorly understood the source and transmission path of AMR. Educating health professionals and communities, imposing legislative constraints on antibiotic purchases, and improving diagnostics in health facilities, could mitigate at least part of the problem. Most participants had never heard of climate change, A few participants mentioned the relationship between climate change and antimicrobial resistance, despite different views of the participants.

Conclusion or Scope

The knowledge gap in AMR varied by profession rather than setting, while for climate change, the understanding differed by setting rather than profession. Thus, a transdisciplinary One Health research approach for further understanding of AMR and climate change in different stakeholders, as well as strategies to raise awareness of AMR and climate change to initiate behavioral change.

Keywords: Antimicrobial resistance; Climate change; Health profesionals,

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 15149

MINIMIZING AMR RISK IN THE UNITED STATES AGENCY FOR INTERNATIONAL DEVELOPMENT BUREAU FOR HUMANITARIAN ASSISTANCE's (USAID/BHA) LIVESTOCK PROGRAMMING

Christine Jost[*1 2] ; Mark Sellers[1] ; Daniel Forrister[1 2] ; Kathleen Downs[1] ; Joseph Tritschler[1] ; Leslie Brooks[1 3] ; Shaina Craige[1 3]
[1]Bureau for Humanitarian Assistance (BHA)/ United States Agency for International Development (USAID)/ United States, [2]Social Solutions International / Global Health Support Initiative III/ United States, [3]Science and Technology Fellows/ American Association for the Advancement of Science/ United States

Introduction and Objectives or Purpose

Purpose: Antimicrobial use in livestock is associated with resistance in systems with close human/livestock association like pastoral areas where access to animal health providers (AHPs) is difficult while access to unregulated veterinary pharmaceuticals is easy. USAID/BHA is working to protect human, animal, and ecosystem health by reducing AMR risk associated with humanitarian livestock programming.

Methods

Methods: In this case study we use internal USAID/BHA databases to review all veterinary pharmaceutical procurement since adoption of a Veterinary Essential Medicines List (VetEML). We assess the geographic distribution of use, types of disasters, vendors, drugs procured, quantities, and reason for use.

Results or Focus

Focus: USAID/BHA has developed its VetEML based on analysis of partners' frequently requested pharmaceuticals, review of reference manuals, and accepted global standards. Experts reviewed several drafts. Antimicrobials on the list treat most non-viral livestock pathogens while posing the least AMR risk. All USAID/BHA partners must restrict procurement to the VetEML or provide a strong justification for a non-VetEML product.

USAID/BHA partners must procure veterinary pharmaceuticals from USAID/BHA vetted and approved vendors; distribute pharmaceuticals only to AHPs; build capacity of AHPs and private veterinary pharmacies in good storage, distribution, disposal, and documentation practices, withdrawal periods, and issues related to AMR; adhere to strict policies on the procurement and use of topical pest control products; and implement a monitoring system to ensure that only approved pharmaceuticals are used in programs.

Conclusion or Scope

Scope: The USAID/BHA VetEML is the first of its kind for humanitarian programming. Together with associated requirements, it ensures that only safe and effective pharmaceuticals are used in USAID/BHA programs and reduces AMR risks while facilitating rapid humanitarian responses. Development and adoption of global standards for veterinary pharmaceuticals like the WHO Prequalification of Medicines Program (PQP) would further advance the safety and efficacy of pharmaceuticals used in humanitarian livestock programming and reduce associated AMR risk.

Acknowledgement

The opinions expressed in this paper are those of the author(s) and do not necessarily reflect the views of the U.S. Agency for International Development or the US Government.

Keywords: antimicrobial resistance; humanitarian assistance; One Health; veterinary essential medicines list

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 15189

Urgent Slaughtering Of Poor Prognosis Dairy Cows In Khartoum Outsikrt; A One Health Risk and Proposed solution

Hala Hashim*[1]
[1]Veterinary medicine / HALA HASHIM FATHALRAHMAN ABDALLHA/ Sudan

Introduction and Objectives or Purpose

Khartoum, the capital of Sudan. The City hosts most of the dairy farming projects and beef consumption particularly in Eastern Nile locality. slaughtering under-treatment poor prognosis and very sick dairy cattle in Khartoum State is practiced without considerations of drugs withdrawal periods. Dairy cattle always get continuous health care with several anti-arthropod chemicals, antimicrobial drugs and hormones. The majority of these chemicals and drugs have long withdrawal period. This make urgent slaughtering of dairy cows in the City outskirt for meat production, a serious threat for people health particularly through drug residues and antimicrobial resistance (AMR).

Methods

The study followed the qualitative research strategy using observation and interview techniques followed by focus group discussion (FGD).Data was analyzed, presented and discussed qualitatively based on the related hazard analysis and critical control points (HACCP) of antimicrobial residues and AMR challenges.

Results or Focus

The study revealed that urgent slaughtering of dairy cows after an uncountable number of treatment cycles or failure using long acting (20-30%) antimicrobial drugs of choice and their alternatives as well as hormones is a classic concept in the study area. Very sick animals could be slaughtered at any time with or without veterinary consultation, in or out of slaughter houses. Urgent slaughtered meat sometimes distributed for consumption without any kind of meat inspection. Even if slaughtered in abattoirs, the meat inspection never includes drug residue detection.

Conclusion or Scope

in addition to other health problem, urgent dairy cows slaughtering contribute in people AMR.

Acknowledgement

Farmers know some zoonosis, however, they don’t know the one health risk of drug residues and AMR.

The FGD agreed with government help as the best solution if the step of reporting the expensive cow death could be as easy for small producers. However, the intensive system farmers should be included in insurance companies programmes.

Keywords: One health, Urgent slaughtering, Dairy cows, Drug residues, AMR, Khartoum.

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 15274

ANTIMICROBIAL RESISTANCE PATTERNS OF COMMENSAL ESCHERICHIA COLI FROM THE GUT OF POULTRY: A CROSS-SECTIONAL STUDY FROM NEPAL

Rajesh Kumar Shah[1] ; Suraj Subedi[*1 2] ; Roshan Paudel[3] ; Rakesh Kumar Yadav[4] ; Sanjay Kumar Yadav[5] ; Mauricio JC Coppo[6] ; Glenn F Browning[6] ; Sulochana Shrestha[2]
[1]Masters in Veterinary Science (Veterinary Physiology), Faculty of Animal Sciences, Veterinary Sciences and Fisheries/ Agriculture and Forestry University/ Nepal (□□□□□), [1]Central Veterinary Laboratory/ Department of Livestock Services/ Nepal (□□□□□), [2]Antimicrobial Use Fellowship - Animal Health/ Fleming Fund Fellowship Program/ Nepal (□□□□□), [3]Masters in Veterinary Science (Veterinary Medicine), Faculty of Animal Sciences, Veterinary Sciences and Fisheries/ Agriculture and Forestry University/ Nepal (□□□□□), [4]Department of Pharmacology, Institute of Agriculture and Animal Sciences/ Tribhuvan University/ Nepal (□□□□□), [5]Veterinary Laboratory/ Department of Livestock Services/ Nepal (□□□□□) [6]Asia-Pacific Centre for Animal Health, Faculty of Veterinary and Agricultural Sciences/ The University of Melbourne/ Australia [2]Department of Livestock Services/ Ministry of Agriculture and Livestock Development/ Nepal (□□□□□)

Introduction and Objectives or Purpose

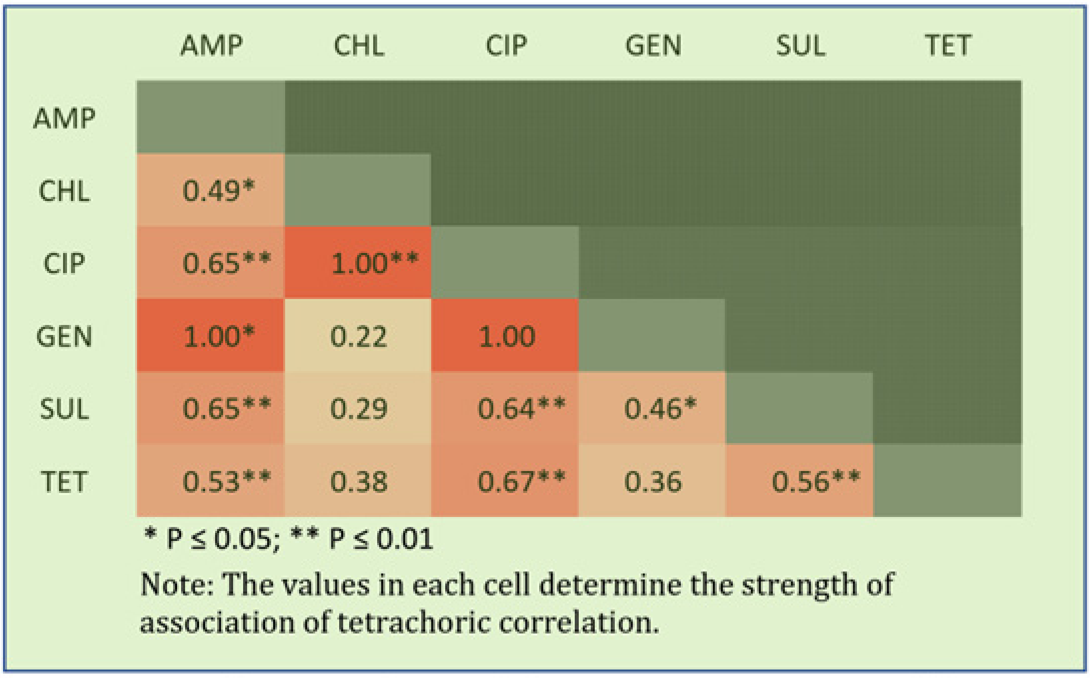
Antimicrobials are commonly used in the poultry industry in Nepal. E. coli are commensal bacteria in the gut of poultry and are potentially exposed to oral antimicrobials; therefore, their patterns may reflect antimicrobial usage. The objective of the current study was to better understand the antimicrobial resistance (AMR) patterns of commensal E. coli in the gut of healthy poultry.

Methods

A cross-sectional study was conducted in Province-1 of Nepal. Faecal and/or caecal samples (n=170) were collected from broiler, layer or local-breed poultry in farms or markets. E. coli were isolated, identified using biochemical tests and their resistance phenotype determined using disk-diffusion tests and interpreted using CLSI cut-offs for ciprofloxacin (CIP), tetracycline (TET), ampicillin (AMP), co-trimoxazole (SUL), chloramphenicol (CHL) and gentamicin (GEN). These antimicrobials represent the antimicrobial classes commonly used in poultry in Nepal.

Results or Focus

A total of 89 E. coli were isolated. Phenotypic resistance was observed against all classes of antibiotics, including CIP (84%), TET (81%), AMP (75%), SUL (63%), CHL (28%) and GEN (17%). Tetrachoric correlation analysis revealed a high correlation between resistance to different antimicrobials (Figure-1). No significant differences were seen in logistic regression analysis of phenotypic resistance in broilers, layers and local poultry for each antimicrobial (data not shown). Multi-drug resistance (≥3 antimicrobial classes) was seen in 78% of the isolates.



	AMP	CHL	CIP	GEN	SUL	TET
AMP						
CHL	0.49*					
CIP	0.65**	1.00**				
GEN	1.00*	0.22	1.00			
SUL	0.65**	0.29	0.64**	0.46*		
TET	0.53**	0.38	0.67**	0.36	0.56**	

* P ≤ 0.05; ** P ≤ 0.01

Note: The values in each cell determine the strength of association of tetrachoric correlation.

Figure 1. Tetrachoric correlation of phenotypic resistance to six different antimicrobials in avian E. coli isolates from healthy poultry.

Conclusion or Scope

As recent antimicrobial usage can have a greater influence on detection of phenotypic resistance, the data in this study should be interpreted with caution and might not necessarily reflect the resistance profiles of avian pathogenic E. coli involved in disease. The high correlation between resistance to different antimicrobials could be due to either high use of these antimicrobials or co-selection of resistance mechanisms. Further studies are thus warranted to better understand the genetic determinants of resistance in E. coli from Nepalese poultry.

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1. Institute of Agriculture and Animal Sciences, TU, Nepal

2. Veterinary Laboratory Biratnagar

3. Fleming Fund Country Grant Nepal

Keywords: Poultry; AMR; Correlation; Multi-drug resistance; Nepal

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 15275

AMR surveillance dashboard technology review to standardize One health capacity building

Varaidzo Mukwekwe*[1] ; Krupali Patel[1]
[1]Public Health, Faculty of Medicine / Parul University/ India

Introduction and Objectives or Purpose

Regardless of WHO declaring that AMR is one of the top 10 global public health and development threats facing humanity, implementation of global response action plans is lagging. Although national guidelines exist, the sources of data which form the basis of these guidelines are limited due to slackened One health implementation, poor quality epidemiological data collection and reporting of AMR at local community level.

Study Purpose: To generate evidence of architectural, technical and epidemiological data paucity inorder to streamline capacity building efforts for standardisation of Community AMR Surveillance in the context of One health

Methods

Dashboard design input data was assessed for quality using the OECD and WHO SCORE assessment tools. Literature scoping review followed the 2020 JBI guideline predesigned by Arksey and O'Malley (2005) and a few moderations were made. It included information sources that reveal information on AMR, AMU, AMC digital monitoring, dashboards, electronic records, reports and press statements aligning with the AMR Quadripartite guidelines. Excluded articles written in any other language apart from English. Relevant AMR dashboard publications made 10 years before the 2015 GAP AMR and after to date were incorporated.

Results or Focus

36 AMR Surveillance dashboards and systems were found to be of potential interest, 12 were desirable but only 10 were prominent for this review. Only 20% have the capacity to collect and report in the context of one health. There are no new community dashboards developed after 2015. National and regional ones available are very heterogeneous and require standardisation even though they are reporting AST results of common priority pathogens. Data registry, visualisation, scalability, extraction, representativeness, reproducibility and decision support was directly linked to the design set by the developer instead of being informed by the available AMR guidelines.

Conclusion or Scope

Incorporation of more epidemiological indicators in AMR surveillance dashboard design is an urgent need for standardisation.

Acknowledgement

PIPH

Keywords: AMR surveillance, epidemiological reporting, data visualisation, evidence

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 15312

EPIDEMIOLOGY OF VANCOMYCIN-RESISTANT ENTEROCOCCI (VRE) ISOLATED FROM THE FECES OF HEALTHY CHICKEN IN KATHMANDU, NEPAL

Tulsi Ram Gompo [*1] ; Trilok Mandal[2] ; Suraj Subedi[1] ; Binta Tamang[1] ; Sharmila Kafle[1]
[1]Department of Livestock Services/ Central Veterinary Laboratory/ Nepal (□□□□□), [2]Veterinary Sciences/ Nepal Polytechnic Institute (NPI)/ Nepal (□□□□□)

Introduction and Objectives or Purpose

Enterococci are the group of commensal bacteria that are found in the gut of animals and humans. Enterococci spp. causes severe infections in immunocompromised and hospitalized patients. The increase in resistance of Enterococcus spp., against Vancomycin, the last line of defense against these gram-positive bacterial infections is a major public health concern. A cross-sectional survey was conducted to estimate the burden of vancomycin-resistant enterococci (VRE) in the market-age chicken in Kathmandu valley from August 2021 to June 2022.

Methods

The pooled fecal samples were collected from 130 poultry holdings viz., slaughterhouses, live markets, and poultry farms. Out of 130 poultry holdings, 110 produced enterococci in culture. The identification of Enterococci spp. was confirmed by an automated identification system (MALDI-TOF MS). The antibiotic susceptibility testing of vancomycin against enterococci spp. was performed in the VITEK 2 system.

Results or Focus

The species wise of distribution of enterococci were; Enterococci hirae 44.5% (95%CI:35.6,53.9, $p>0.05$), Enterococcus faecalis 35.5% (95%CI:27,1,44.7, $p<0.05$), Enterococcus faecium 13.6% (95%CI:8.4,21.3,$p<0.001$), and Enterococcus durans 6.4% (95%CI:3.1,12.6, $p<0.001$).On average, 36.4% (95%CI:27.9,21.3,$p<0.001$) of the Enterococci spp. were resistant to vancomycin.The species wise resistance to vancomycin were; Enterococci hirae 20.4% (95%CI:10.86,33.37,$p<0.05$), Enterococcus fecalis 66.7% (95%CI:50.9,80.1,$P<0.05$), Enterococcus faecium 20%(95%CI:5.4,45.4,$p<0.05$)and Enterococcus durans 14.28% (95%CI:0.72,53.02,$p>005$).

Conclusion or Scope

The detection of VRE in the marketable age chicken's feces might be a public health risk. The higher counts of resistance among Enterococcus fecalis and Enterococcus faecium, the pathogenic strains of enterococci, is a serious issue. Yet, the vancomycin use data in the chicken population was not available which is a limitation of this study. Further information on the usage of vancomycin and the identification of possible risk factors by one health approach would provide more insight into the epidemiology of VRE.

Acknowledgement

The Central Veterinary Laboratory

The Fleming Fund Country Grant Nepal

Keywords: Enterococci, Vancomycin, VRE, poultry holdings, public health.

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 15347

Antimicrobial resistance profiles of Escherichia coli from foods and livestock in informal settlements, Nairobi Kenya.

Salome Kithiia*[1] [2] ; Gabriel Aboge
[1]Veterinary/ Ministry of Agriculture, Livestock & Fisheries/ Kenya, [2]Veterinary/ Ministry of Agriculture, Livestock & Fisheries/ Kenya

Introduction and Objectives or Purpose
Colibacillosis is one of the challenging diarrhoeal diseases which results in economic losses. Escherichia coli, especially enterotoxigenic E.coli (ETEC) has been incriminated as the most significant bacterial cause of colibacillosis.

This study was aimed at determining the pathotypes present in E.coli which were isolated from foods and water in informalsettlements of Nairobi, their phenotypic antimicrobial sensitivity and genotypic antimicrobial resistance.

Methods
Previously isolated and biochemically confirmed E.coli isolates were streaked on MacConkey agar plates and Tryptone Soy Agar (TSA.) The Kirby-Bauer disk diffusion method was employed to determine the phenotypic antimicrobial sensitivity according to Clinical and Laboratory Standards Institute(CLSI) guidelines (CLSI 2014). Each isolate was screened for antimicrobial sensitivity with twelve different antimicrobial agents

Results or Focus
Antibiotic resistance was detected for Amoxycillin- clavulanic acid (12.6%) ampicillin (45.4%),ceftazidime (1.7%), ceftriaxone (0%), nalidixic acid (10.4%), tetracycline (29.3%), ciprofloxacin (1.8%), trimethoprim-sulfamethoxazole (41.2%) gentamicin (0.6%), streptomycin (22.5%) and chloramphenicol(6.9%). Antibiotic resistance genes detected included blaTEM(91%), blaCMY (51%),tetA31%,tetB(29%), aac(3)V (17%), sul1(10%), sul2 (18%),aadA1 (8%), cml (14%) and cat1(18%).

Conclusion or Scope
E. coli present in foods from Nairobi per-urban areas is resistant to multiple antibiotics and contains antimicrobial resistance genes. The presence of β-lactam resistance genes bla TEM, bla CMY and bla SHV in food-producing animals is an indicator of the potential public health risk from the direct transfer of these strains to man through the food chain, close contact between man and animals and through the transfer of plasmids

Acknowledgement
The University of Nairobi, Public Health, Pharmacology and Toxicolody department.

Keywords: Antimicrobial resistance. aresistance genes. Escherichia coli

Topic: Antimicrobial Resistance (AMR): One Health approach to integrated AMR surveillance: Standardised integrated One Health AMR and Antimicrobial use (AMU)/ Antimicrobial consumption (AMC) surveillance
Abstract No: 15425

Benchmarking the key antibiotic prescribing indicators and appropriateness in 4 major hospitals in Bhutan using the Australian National Antimicrobial Prescribing Survey tool.

Pem Chuki [*1] ; Rodney James [2] ; Kirsty Buising [2] ; Karin Thursky [2] ; Sonam Wangda[1]
[1]Antimicrobial Stewardship Unit/ Jigme Dorji Wangchuck National Referral hospital / Bhutan (□□□□□), [2]Department of Infectious Diseases / The Royal Melbourne Hospital / Australia

Introduction and Objectives or Purpose

The promotion of the rational use of antibiotics is one the objectives of the National Action Plan to combat AMR in Bhutan. To plan and initiate an antimicrobial stewardship program as part of this plan, baseline data on the current use of antibiotics is required.

Objective: To benchmark the quality indicators associated with the prescription and use of antibiotics in four hospitals in Bhutan.

Methods

A hospital wide point prevalence survey was conducted in Dec 2021 and repeated again in June 2022, using the Australian Hospital National Antimicrobial Prescribing Survey (Hospital NAPS) tool.

Results or Focus

The overall rate antibiotic prescribing was 41.5% of hospitalized patients, with majority (42.2%) of the patients on a single antibiotic. 79.1% of the prescriptions had a documented indication, with only 26.9% having a planned review or stop date. For indications requiring surgical prophylaxis, 71.1% were administered beyond 24 hours. The commonest antibiotic prescribed was ceftriaxone (21.7%) followed by cefazolin (13.3%). The commonest indication was for surgical prophylaxis (14.2%), followed by sepsis (9.1%) and empiric treatment for community acquired pneumonia (8%). The overall compliance to the national antibiotic guidelines was 27.8% with 37.6% of all prescriptions being assessed as appropriate.

Conclusion or Scope

This study shows that there is a poor compliance to the national antibiotic guidelines in the inpatient setting within the four major hospitals in Bhutan, with ceftriaxone being used inappropriately as the first line antibiotic choice for common infections such as community acquired pneumonia.

Keywords: Antimicrobial use; Point prevalence survey; Antimicrobial stewardship; Guideline compliance; Bhutan

Topic: Impact on and Innovations in Clinical Practice (IICP): Management of Non-Communicable Diseases (NCD) - pivoting during a pandemic and beyond: Chronic NCD management in outbreaks: Leveraging mobile technology to improve patient care
Abstract No: 14666

DEVELOPMENT AND EXPLORATION OF THE EFFECTIVENESS AND FEASBILITY OF A DIGITAL INTERVENTION FOR TYPE 2 DIABETES MELLITUS (DESIRED)

Candy Hiu Nam Chan*[1] ; Hong Shen Lim[1] ; Yuan Wei[1] ; Alice Moi Ling Yong[2] ; Si Yee Chan[1] ; SuE Yu[1] ; Lina Pui Lin Chong[2] ; Dayang Hjh Musjarena bte Hj Awang Abd Mulok [2] ; Chee Kwang Yung [2]
[1]N/a/ EVYD Research Pte Ltd. (a subsidiary of EVYD Technology Limited)/ Singapore, [2]Endocrinology Unit/ Raja Isteri Pengiran Anak Saleha Hospital (RIPAS) Hospital/ Brunei

Introduction and Objectives or Purpose

The prevalence of type 2 diabetes mellitus (T2DM) is increasing worldwide, and the estimated prevalence is 12.4% amongst the 20-75 years old group in Brunei Darussalam. Digital intervention (DI) has been shown to be cost-effective in the management of T2DM and provide a better accessibility of lifestyle intervention. A combination of DI with support by professional management can enhance users with better self-efficacy than DI alone. This single-arm, non-randomised clinical study aims to evaluate the effectiveness of proposed DI programme with online and offline support by health coach (HC) as a pilot project before Brunei Ministry of Health rolls out a national-wide value-based care programme.

Acknowledgement

Methods

The 16 weeks structured DI programme is designed by healthcare professionals, which consists of weekly education materials of animations, videos, and infographics, dietitian group sessions, and individual online consultations with HCs. A personalised diet and exercise recommendations based on the health measurement of blood glucose levels, weight and heart rate via glucometer and smart devices together with meals and exercise log will be given by HCs via individual video consultations.

The study aims to recruit 180 T2DM individuals via online recruitment leveraging on eligibility screening based on electronic medical records (EMR), push notifications for study invitation via a national healthcare APP (BruHealth), official social media platforms for outreach and offline recruitment via healthcare centers. The primary outcome is proportion of participants with decrease in HbA1c by 0.6%. Secondary outcomes include changes in HbA1c, body mass index, lipid profile and EQ-5D-5L.

Results or Focus

The study has received ethics approval and is actively recruiting. The preliminary results will be available by September 2022.

Conclusion or Scope

The results will provide evidence to evaluate clinical effectiveness of this programme and serve as a pilot project to roll out national-wide value-based care programme via a Mobile Application as a digital solution in Brunei Darussalam

Keywords: EMR; Type 2 Diabetes Mellitus, Digital Intervention; Value-based Care; Chronic Disease Management

Topic: Impact on and Innovations in Clinical Practice (IICP): Management of Non-Communicable Diseases (NCD) - pivoting during a pandemic and beyond: Chronic NCD management in outbreaks: Leveraging mobile technology to improve patient care
Abstract No: 14826

ORAL CARE FOR VULNERABLE SENIORS THROUGH MEDICAL-DENTAL TELE-COLLABORATION

Christina Sim[*1] ; Patricia Lee[2] ; Alethea Foong[1] ; Milawaty Nurjono[3] ; Yen-Tung Lieu[1] ; Shi-Xuan Tang[4] ; Xin-Yi Lim[4] ; Priscilla Chan[4] ; HuiHua Li[4]
[1]Restorative Dentistry/ National Dental Centre Singapore/ Singapore, [2]Home Medical Services/ St Andrew's Community Hospital / Singapore, [3]Health Services Research/ Changi General Hospital/ Singapore, [4]ACP Research Office/ National Dental Centre Singapore/ Singapore

Introduction and Objectives or Purpose

Vulnerable seniors have difficulty in accessing oral health assessment and care, exacerbated by the COVID-19 pandemic. The TDOCS programme, a 2-year pilot oral care programme, seeks to trial the use of tele-dentistry to provide easier access to oral care services through remote detection and monitoring of oral conditions.

Objective: To assess baseline oral health status and dental treatment needs of participating vulnerable seniors; and their response to the tele-dental process.

Methods

Participants were recruited from residential care homes and a home care programme. Trained nurses performed intraoral imaging and upload images and clinical information for remote assessment by the dentist. A report of the remote assessment findings, diagnosis, suggested treatment plan and urgency of treatment was sent to the nurses for follow-up with the dentist if required.
The tele-dental assessment was carried out 6-monthly. Baseline clinical examination was also carried out. Descriptive analysis of baseline data was performed to examine participants' oral health status, dental treatment needs and response to the tele-dental assessment.

Results or Focus

130 participants (46 homebound seniors, 84 from residental care homes) were recruited and completed baseline clinical examination. 88.6% of intraoral imaging scans were completed. Based on clinical findings, 36.9% were completely edentulous. Mean number of natural teeth and DFT (decayed, filled teeth) score for partially dentate was 13.1 and 3.2 respectively. 44.4% and 40.0% presented with moderate-severe plaque accumulation and gingival inflammation respectively. 75.0% had no functional occlusal contacts. 77.7% of participants was identified to have unmet oral health needs, which was similarly identified during remote assessment. 81.0% of participants responded positively to the imaging procedure.

Conclusion or Scope

High unmet oral health needs in vulnerable seniors suggests a need to improve access to dental care for this growing population. The tele-dentistry model has potential to meet this need.

Acknowledgement

This study is funded by Temasek Foundation and Singhealth RHS PHDP grant.

Keywords: tele-dentistry, tele-collaboration, oral health needs, elderly, oral disease

Topic: Impact on and Innovations in Clinical Practice (IICP): Management of Non-Communicable Diseases (NCD) - pivoting during a pandemic and beyond: Chronic NCD management in outbreaks: Leveraging mobile technology to improve patient care
Abstract No: 15187

Educational program on insulin injection techniques in patients with diabetes mellitus at the Universitas Sumatera Utara Hospital

Afrinayanti. W Siregar[1] ; Dudut Tanjung[2] ; Nafi Yannis[1] ; Muhammad Rizki Yaznil[*1]
[1]Hospital/ Universitas Sumatera Utara Hospital/ Indonesia, [2]Faculty of Nursing/ Universitas Sumatera Utara/ Indonesia

Introduction and Objectives or Purpose

Management of type 2 DM aims to restore blood glucose concentrations to close to normal values. Providing education about the management of type 2 DM based on insulin therapy practices is a challenge for patients with type 2 diabetes. Hospitals must be able to develop educational strategies that are continuously implemented and sustainable. The purpose of this study was to analyze the effect of an evidence-based insulin injection technique education program on insulin injection technique practice and HbA1c values.

Methods

The research method used is Quasy Experimental Non-Equivalent Control Group Pretest-Postest Design. Respondents in this study were 60 type 2 DM patients who were selected by purposive sampling technique. The practice of insulin injection technique was measured using the Worldwide Injection Techniques Questionnaire. Data analysis was carried out univariate and bivariate. To determine the effect of the educational program on insulin injection techniques, a significance test was used, namely the paired sample t-test and t-test for independent groups.

Results or Focus

The results showed that the evidence-based insulin injection technique education program had an effect on the practice of insulin injection technique ($p=0.004$) and had an effect on the HbA1c value ($p=0.000$).

Conclusion or Scope

The education program for providing evidence-based practice-based insulin injection techniques has an effect on the HbA1c value of type 2 DM patients, so it is recommended for the hospital to hold an education program for providing evidence-based practice-based insulin injection techniques so that the glycemic levels of type 2 DM patients can be controlled.

Acknowledgement

Researchers are grateful to the USU Research Institute for funding research through the TALENTA program in 2021. Thanks also to PT. Becton Dickinson Indonesia for assistance in the form of insulin pen needles, alcohol swabs, and safety boxes distributed to respondents.

Keywords: diabetes mellitus type 2; Educational Programs; Insulin Injection Technique

Topic: Impact on and Innovations in Clinical Practice (IICP): Management of Non-Communicable Diseases (NCD) - pivoting during a pandemic and beyond: Chronic NCD management in outbreaks: Leveraging mobile technology to improve patient care
Abstract No: 15235

Effectiveness of behaviour strategies in addressing obesity among low-income adults in high-income countries: A systematic review and meta-analysis of randomised controlled trials.

Priscilla Li*[1] ; Tuba Mazhari[1]
[1]School of Population Health & Environmental Sciences/ King’s College London/ United Kingdom

Introduction and Objectives or Purpose

In high-income countries, obesity disproportionately affects the poor and perpetuates health inequalities. Adult obesity is linked to chronic diseases and imposes health and socioeconomic burden. This systematic review and meta-analysis examines the effectiveness of behavioural strategies for weight reduction among low-income adults in high-income countries.

Methods

Randomised-controlled trials that investigated the use of behavioural strategies in obesity management were identified by systematically reviewing the literature within Web of Science, PubMed and CENTRAL, published between 1 November 2011 and 1 May 2022. Meta-analyses and subgroup analyses were undertaken to analyse the pooled and individual effects of behavioural strategies. Risk of bias (RoB 2.0) and Grades of Recommendation, Assessment, Development and Evaluation (GRADE) criteria were used to assess evidence quality and certainty.

Results or Focus

Three out of 14 trials were omitted from meta-analyses due to high RoB. Results favoured interventions, demonstrating significant reductions in body weight (MD: -1.56kg, [95% CI –2.09, -1.03]) and HbA1c (MD: -0.05%, [95% CI -0.10, -0.001]). There were no improvements in waist circumference, blood pressure or serum lipids. Nine unique strategies were identified but only financial incentives and interactive feedback produced weight losses of ³2kg, with moderate certainty of evidence.

Conclusion or Scope

Behavioural strategies are effective in helping low-income persons in high-income countries lose modest, but significant weight. However, the impact of these interventions on CVD risk factors remains unclear. Future research should reflect population diversity and conduct cost-effectiveness studies.

Acknowledgement

Disclosures:
There are no competing interests or funding to be declared.

Keywords: Obesity, Behavioural Strategies, High Income Countries, Low Income Adults

Topic: Impact on and Innovations in Clinical Practice (IICP): Management of Non-Communicable Diseases (NCD) - pivoting during a pandemic and beyond: Chronic NCD management in outbreaks: Leveraging mobile technology to improve patient care
Abstract No: 15281

EXPLORATION OF A MOBILE APPLICATION AND CONTENT MANAGEMENT SYSTEM TO DETERMINE RESPONSE PATTERN OF COVID-19 NUTRITIONAL SURVEY IN BRUNEI DARUSSALAM

Si Yee Chan[2] ; Sattha Engpornsin[*2] ; Sharleen Othman[2] ; Norhayati Kassim[1] ; Lubna Razak[1] ; Wei Jin[4] ; Yijing Zhong[2] ; Yan Wang[2] ; Yuan Wei[4] ; Hong Shen Lim[4]
[2]Research/ EVYD Technology Ptd Ltd/ Brunei, [1]Health Promotion Centre/ Ministry of Health Brunei/ Brunei [4]Research/ EVYD Research Pte Ltd/ Singapore [2]Research/ EVYD Technology Co. Ltd/ China (□□)

Introduction and Objectives or Purpose

Digital platforms ensure rapid and accurate data collection. In Brunei, a mobile health application (BruHealth) and its Content Management System (CMS) with behavior sciences libraries were utilized to provide remote nutritional surveys during the COVID-19 pandemic. This study aims to validate the use of BruHealth and CMS for national surveys and to investigate the most efficient push notification schedules.

Methods

Using electronic medical records, eligible individuals were sampled accordingly: Parents of <1 - 5.9 months old (Group CU2A), 6-23 months old, (CU2B), and 2 - 14 years old children (CU19A), 15 – 18 years old individuals (CU19B), pregnant (MQA) and early post-natal women (MQB). 5 different times, days, and nudge content (N1, N2, N3, N4, N5) with sub-groups were configured to an initial ‘assigned’ schedule, followed by a ‘micro-randomization’ schedule for eligible groups. Randomization was performed for each day and time to push or not push notification, alongside another randomization layer of nudge content. Targeted surveys were then disseminated through BruHealth.

Results or Focus

During the assigned phase, CU2A and CU2B responded best on Thursday 8AM (N1.1) and Tuesday 8PM (N2.1) respectively, while CU19A and CU19B responded best on Thursday 2PM (N3.1) and Tuesday 11AM (N2.1) respectively. MQA and MQB responded most on Monday 8PM (N5.1) and Thursday 8AM (N1.2) respectively. During micro-randomisation, CU2B responded best on Monday 8PM (N3.1), while CU19A and CU19B responded best on Monday 11AM, but with N2.2 and N4.1 respectively. CU19B also had an equal number of responses at 8PM.

Conclusion or Scope

Parents with younger children tended to respond earlier in the morning or evenings, compared to those with older children. The best response days were Mondays, followed by Thursdays, while the best response nudge was N2. BruHealth and CMS have been instrumental tools in this study, and such digital platforms may be utilized for future national surveys.

Acknowledgement

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Topic: Impact on and Innovations in Clinical Practice (IICP): Management of Non-Communicable Diseases (NCD) - pivoting during a pandemic and beyond: Impact of the COVID-19 pandemic on NCD care
Abstract No: 14918

Impact of the COVID-19 pandemic on Non-Communicable Diseases care in Nigeria

Onyekachi Nwitte-Eze*[1] ; Morenike Alex-Okoh[1]
[1]Department of Public Health/ Federal Ministry of Health/ Nigeria

Introduction and Objectives or Purpose

Non-Communicable Diseases (NCDs) suffered setbacks since the start of the COVID-19 pandemic. One of such was the lack of access to healthcare facilities, especially during the lockdown period for people with non-communicable diseases. The country was also compelled to reprioritize resources at the start of the COVID-19 pandemic. The Nigeria STEPwise survey for NCDs has been in the works since 2016. We looked at how the COVID-19 pandemic impacted the survey.

Methods

An in-depth interview with key stakeholders from the Non-communicable Diseases division in the Department of Public Health, Federal Ministry of Health was carried out. The questions revolved around what benefits and losses COVID-19 had caused on the STEPs survey

Results or Focus

The STEPs survey experienced a 2-year delay as resources were channeled by the Ministry and funding partners to COVID-19 response. Activities for the STEPwise survey only resumed in October, 2021. Interestingly, the Non-Communicable Diseases division, leveraged funds for COVID-19. It was observed that patients with comorbidities (non-communicable diseases) were the most affected by COVID-19.

Conclusion or Scope

COVID-19 slowed down research, surveys, and treatment for people with non-communicable. However, it also opened opportunities for new partnerships and resource mobilization.

Keywords: Non-communicable diseases, COVID-19, Impact

Topic: Impact on and Innovations in Clinical Practice (IICP): Management of Non-Communicable Diseases (NCD) - pivoting during a pandemic and beyond: Impact of the COVID-19 pandemic on NCD care
Abstract No: 15175

SLEEP DEPRIVATION AND SELF-REPORTED ANXIETY AMONG WORK FROM HOME ADULTS IN THE NATIONAL CAPITAL REGION DURING THE COVID-19 PANDEMIC

Maria Leah Joyce Santos[1] ; Heavenlee Grace Afurong[1] ; Kristeen Kyle Geronimo[1] ; Francene Bea Libunao[*1] ; Emil Lim[1] ; Aubrey Pineda[1]
[1]Medical Technology/ University Of Santo Tomas/ Philippines

Introduction and Objectives or Purpose

Sleep is an essential factor for one's health, and sleep deprivation may negatively affect cognition. With the Coronavirus Disease 2019, people have been compelled to stay at home, and such isolation and fear of acquiring the virus may affect the mental status of a person. With these, the study primarily aims to determine the relationship between sleep deprivation and self-reported anxiety among work-from-home adults in the National Capital Region (NCR) of the Philippines during the COVID-19 pandemic.

Methods

The study utilizes a quantitative correlational research design, survey questionnaires were utilized to collect data. The questionnaire included the socio-demographic profile, the Penn State Worry Questionnaire (PSWQ), and the Pittsburgh Sleep Quality Index (PSQI). The PSWQ determined the general anxiety of the participants, while the PSQI assessed their quality of sleep. The scores of both tests were computed using a system provided by the authors. Spearman's rho correlation test was used to determine the relationship between sleep deprivation and self-reported anxiety, while Kruskal-Wallis test was used for the sociodemographic profile, as the Kolmogorov-Smirnov Test suggested non-normal distribution.

Results or Focus

Older age groups were more likely to have higher self-reported anxiety ($r = -0.284$; $p < 0.001$), and a poorer sleep quality ($r = -0.248$; $p = 0.002$). Furthermore, female adults were found to be more susceptible to having higher self-reported anxiety ($r = 0.197$; $p = 0.015$). As for the occupational groups, there were significant differences found in self-reported anxiety ($p = 0.033$), but none in terms of sleep quality ($p = 0.342$). Finally, the study could not confirm if income or occupational status have associations with sleep quality ($p = 0.601$) or anxiety ($p = 0.930$).

Conclusion or Scope

A positive minor correlation ($r = 0.372$) between sleep deprivation and self-reported general anxiety was detected among the work from home adults during the COVID-19 pandemic.

Keywords: Sleep Deprivation; Generalized Anxiety Disorders; Work-from-Home; Sleep Quality; COVID-19 Pandemic

Topic: Impact on and Innovations in Clinical Practice (IICP): Multidrug Resistant Organisms (MDRO) - roles, responsibilities and interests of the non-ID physicians: Applying One Health concepts in hospitals to counter MDRO
Abstract No: 15424

CHALLENGES IN PREANALYTICAL PHASE OF LABORATORY MEDICINE: SPECIMEN REJECTION IN CLINICAL MICROBIOLOGY LABORATORY IN PORT MORESBY GENERAL HOSPITAL.

Temas Ikanofi*[1] ; Samson Kangapu [1] ; Gabriella Ak [1] ; Russell Cole [1] ; John Ferguson [1] ; Colleen Allen [1] ; Sarah Baines ; Candice Lisboa
[1]Department of Health / Central Public Health Laboratory / Papua New Guinea

Introduction and Objectives or Purpose

Specimen rejection is a pre-analytical error in laboratory testing. Of the three phases of laboratory workflow processes, 50 -70% of errors occur in the pre-analytical phase. Quality in medical diagnostics is essential to providing safe health care to patients. Port Moresby General Hospital (PMGH) is a teaching and referral hospital (1200 bed-spaces) in Papua New Guinea (PNG). This study aimed to analyze the specimen rejection registry logbook and develop interventional measures to help reduce specimen rejection rates in the clinical microbiology laboratory.

Methods

The specimen rejection registry logbook was analysed for 2021, using MS-Excel. Patients with full name, ward, specimen type and reason for rejection clearly recorded in the rejection logbook were included in this study.

Results or Focus

A total of 9,539 specimens were received in the clinical microbiology laboratory in 2021. 395 were registered in the logbook as being rejected; 351 met the inclusion criteria of this study. Urine (n=131, 37%), blood culture (n=75, 21 %) and pus (n=61, 17%) specimens were commonly rejected due to labelling discrepancies and/or sent in an unsuitable specimen container. A high rate of blood culture rejections was from children's emergency department (n=28/75, 37%), followed by special care nursery (n=6/75, 8%).

Conclusion or Scope

Specimen rejection delays laboratory testing that may be critical for patient care and management. Low-cost interventions can help reduce specimen rejection rates at PMGH. This study has indicated that specimens have been rejected due to errors that can potentially be reduced through awareness campaigns to all health personnel and phlebotomy staff. Awareness will also be communicated through the PMGH quarterly newsletter. Afterwards, we will re-audit rejections to look for improvement. This campaign to help reduce the specimen rejection rate will also be implemented across other hospitals in PNG and help raise the quality service provided by our laboratories.

Acknowledgement

I would like to acknowledge the Fleming Fund Fellowships program, Mott MacDonald, Burnet Institute, Pacific Region Infectious Disease Association (PRIDA), Pacific Pathology Training Centre (PPTC), The Doherty Insitute, Port Moresby General Hospital, National Department of Health, and the Central Public Health Laboratory.

Keywords: specimen collection; specimen rejection; laboratory specimen; blood culture; microbiology; pre-analytical

Topic: Impact on and Innovations in Clinical Practice (IICP): Multidrug Resistant Organisms (MDRO) - roles, responsibilities and interests of the non-ID physicians: MDRO in patients with non-communicable diseases
Abstract No: 14944

CHARACTERISTIC OF PRE-EXTENSIVELY AND EXTENSIVELY DRUG-RESISTANT TUBERCULOSIS PATIENTS AT ADAM MALIK HOSPITAL, MEDAN, INDONESIA

Bintang Yinke Magdalena Sinaga*[1] ; Parluhutan Siagian[1]
[1]Department of Pulmonology and Respiratory Medicine/ Bintang Yinke Magdalena Sinaga/ Indonesia

Introduction and Objectives or Purpose

Emergence of Multi-Drug Resistant Tuberculosis (MDR-TB) become a serious challenge for TB prevention and care program in Indonesia. Among MDR-TB, pre-XDR and XDR-TB cases are also getting more common. It is important to know the characteristic of pre-XDR-TB and XDR-TB patients. The aim of this study is to find the characteristics of Pre-XDR and XDR-TB patients.

Methods

This is a cross-sectional study, data were obtained from the medical records of MDR-TB patients who were treated at the MDR-TB polyclinic, Adam Malik Hospital, Medan, Indonesia, from July 2019 to June 2022. The characteristic observed were age, gender, comorbidities, anti-tuberculosis treatment history, and outcome of treatment

Results or Focus

Of the 170 MDR-TB patients, 24 patients were pre-XDR-TB (14.1%) and 3 patients were XDR-TB (1.8%). The most age group was 40-59 years old in 13 patients (48.2%) and aged 20-39 years were 9 patients (33.3%). Male was found in 18 patients (66.7%). Diabetes Mellitus was the highest comorbid found in 15 patients (55.6%), 11 patients (40.7%) had no comorbid, and 1 patient (3.7%) had Diabetes Mellitus with Chronic Kidney Disease. No history of previous TB treatment was found in 3 pre-XDR-TB patients (11.1%). The highest treatment history was having received drug-sensitive TB treatment for 1 time in 16 patients (59.3%), while 5 patients (18.5%) had a history of drug-sensitive TB treatment more than1 time and 3 patients (11.1%) had received drug-sensitive TB and MDR-TB treatment previously. Treatment outcome was cured 14.8%, complete treatment 3.8%, died 25.9%, dropped out 11.1%, moved 14.8%, on treatment 29.6%.

Conclusion or Scope

Productive age, Diabetes Mellitus comorbid, male patients, history of anti-tuberculosis treatment and low success rate outcome are the characteristics found most frequently. More efforts and strategies are needed in the prevention and treatment programs of drug-sensitive and drug-resistant tuberculosis.

Acknowledgement

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Keywords: Characteristic; MDR-TB; Pre-XDR-TB; XDR-TB

Topic: Impact on and Innovations in Clinical Practice (IICP): Multidrug Resistant Organisms (MDRO) - roles, responsibilities and interests of the non-ID physicians: MDRO in patients with non-communicable diseases
Abstract No: 15007

MULTIDRUG RESISTANT BACTERIA IN HOSPITAL ACQUIRRED PNEUMONIA AT UMC VIETNAM

Tran Luu*[1] ; Khanh Phan[2] ; Van Ly Khanh[1]
[1]Medicine/ University of Medicine and Pharmacy at Ho Chi Minh/ Vietnam (Việt Nam), [2]Emerging Infection/ Oxford University Clinical Research Unit/ Vietnam (Việt Nam)

Introduction and Objectives or Purpose

Multidrug resistant (MDR) organisms have become more prevalent over the past decades, threatening safe and effective treatment for hospitalized patients. Hospital-acquired pneumonia is the most common form of hospital infection with a high prevalence of multidrug-resistant bacteria. There is a strong need for frequent surveillance with unified standards and systematic reports.

Methods

We conducted a retrospective study at the University Medical Center – a tertiary general hospital located in Ho Chi Minh City, Vietnam. Electronic health records were used to screen for pneumonia patients with at least one positive culture, diagnosis were reviewed by the investigators. To ensure a referencable and meet international standards for classifying MDR pathogens, we used The standardized international terminology from the Joint initiative by European Centre for Disease Prevention and Control (ECDC) and the Centers for Disease Control and Prevention (CDC) [1]. The study was approved by the local ethic committee, informed consent was waived.

Results or Focus

From January to December 2020, we have identified 177 records that met our criteria, resulting in 297 positive cultures with a full antimicrobial resistance profile. Klebsiella pneumoniae is the leading pathogen, accounting for 37.4% of the total positive culture, followed by Acinetobacter baumannii, Staphylococcus aureus, Pseudomonas aeruginosa, and Escherichia coli. These pathogens occur in more than 85% of the isolates and are highly resistant to antibiotics (>60% isolates classified as Multi Drug Resistance).

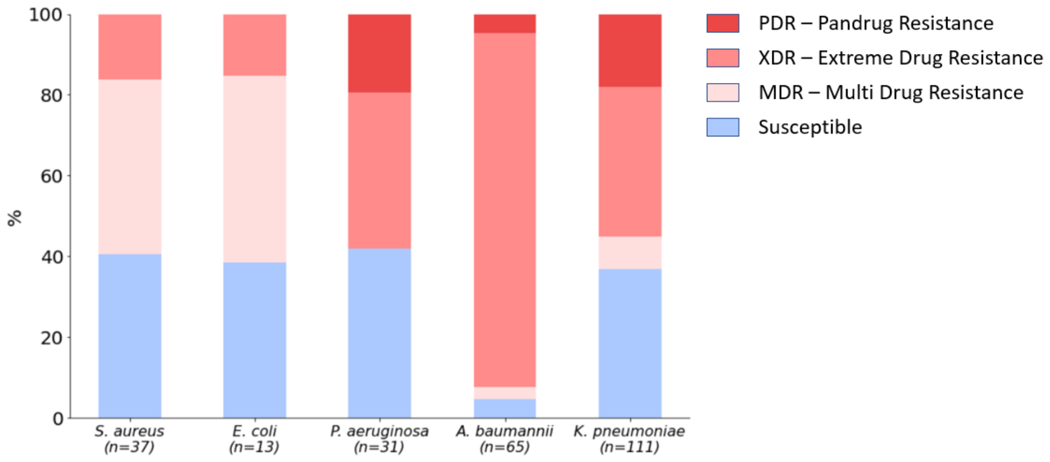

Figure 1: Multidrug resistant classification of top 5 bacterial pathogens

Conclusion or Scope

Our study contributes to the growing evidence of the alarming increasing resistance of bacteria. Standardized, systematic antimicrobial surveillance and stewardship should become routine practices to inform safe and effective treatment.

Acknowledgement

We would like to send our sincerest thanks to the healthcare workers at University Medical Center for their warm support. Keywords: AMR; antimicrobial surveillance; Hospital-acquired pneumonia

Topic: Impact on and Innovations in Clinical Practice (IICP): Multidrug Resistant Organisms (MDRO) - roles, responsibilities and interests of the non-ID physicians: The interdependence of animal and human health - MDRO in pet animals and livestock
Abstract No: 14806

Effect of awareness training to frontline health workers and e-based technology on brucellosis reporting in pastoral communities in Tanzania

Belinda Mligo*[1] ; Calvin Sindato; Richard Yapi; Mpoki Mwabukusi; Coletha Mathew; Ernatus Mkupasi; Esron Karimuribo; Rudovick Kazwala
[1]Veterinary medicine and public health/ Sokoine University of Agriculture/ Tanzania, United Republic of

Introduction and Objectives or Purpose
Brucellosis is an endemic bacterial disease reported in many sub-Saharan Africa countries. Awareness of frontline healthcare workers (FHWs) influences diagnosis, reporting and management of the disease. The study aimed at assessing the effect of training on FHWs knowledge, attitude and practices (KAP) as well as the use of digital technology on reporting of brucellosis in pastoral communities

Methods
A quasi-experimental study was utilized. Structured questionnaires were used to assess KAP of FHWs in two districts of eastern Tanzania which agropastoralism is endemic, following training enhanced by electronic application called AfyaData app to promote early detection and reporting of brucellosis. A pre- and post-intervention survey was conducted. Blood sera samples were collected from 141 patients with febrile illnesses attending selected health facilities in treatment community. The blood samples were screened for brucellosis using RBPT and positive samples confirmed by c-ELISA test and reported using AfyaData app back to the facility. KAP was assessed by 5-point Likert scale. Descriptive analysis was performed. Chi-square/fisher exact test were used to compare KAP and categorical variables while analysis of continuous variables was done by t-test and ANOVA

Results or Focus

Results showed knowledge and practice of FHWs on brucellosis in pretest were not satisfactory, although they had good attitude towards brucellosis prevention while after training participant’s awareness, practice and attitude increased significantly (p=0.003, p=0.001, p=0.032). Prevalence was diagnosed among febrile patients but in low prevalence (2.8%). AfyaData app was proven to be a quick tool in providing reports on the diseases.

Conclusion or Scope

It can be concluded that before training FHWs had a deficit knowledge and practices although they showed good attitude. Meanwhile, after intervention FHWs’ performance was significantly improved that reflects the importance of continuous education for FHWs working at hospital.

Acknowledgement

Refresh seminars and training programs on the use of digital technologies to improve FHWs awareness and detection on brucellosis.

Keywords: Knowledge, attitude, practices, brucellosis, frontline health workers, reporting

Topic: Impact on and Innovations in Clinical Practice (IICP): Multidrug Resistant Organisms (MDRO) - roles, responsibilities and interests of the non-ID physicians: The interdependence of animal and human health - MDRO in pet animals and livestock
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A quasi-experimental study was utilized. Structured questionnaires were used to assess KAP of FHWs in two districts of eastern Tanzania which agropastoralism is endemic, following training enhanced by electronic application called AfyaData app to promote early detection and reporting of brucellosis. A pre- and post-intervention survey was conducted. Blood sera samples were collected from 141 patients with febrile illnesses attending selected health facilities in treatment community. The blood samples were screened for brucellosis using RBPT and positive samples confirmed by c-ELISA test and reported using AfyaData app back to the facility. KAP was assessed by 5-point Likert scale. Descriptive analysis was performed. Chi-square/fisher exact test were used to compare KAP and categorical variables while analysis of continuous variables was done by t-test and ANOVA

Results or Focus

Results showed knowledge and practice of FHWs on brucellosis in pretest were not satisfactory, although they had good attitude towards brucellosis prevention while after training participant’s awareness, practice and attitude increased significantly (p=0.003, p=0.001, p=0.032). Prevalence was diagnosed among febrile patients but in low prevalence (2.8%). AfyaData app was proven to be a quick tool in providing reports on the diseases.

Conclusion or Scope

It can be concluded that before training FHWs had a deficit knowledge and practices although they showed good attitude. Meanwhile, after intervention FHWs’ performance was significantly improved that reflects the importance of continuous education for FHWs working at hospital.

Acknowledgement

Refresh seminars and training programs on the use of digital technologies to improve FHWs awareness and detection on brucellosis.

Keywords: Knowledge, attitude, practices, brucellosis, frontline health workers, reporting

Topic: Impact on and Innovations in Clinical Practice (IICP): Multidrug Resistant Organisms (MDRO) - roles, responsibilities and interests of the non-ID physicians: The interdependence of animal and human health - MDRO in pet animals and livestock
Abstract No: 15061

Operationalization of One Health with the Blockchain technology to enhance rabies control in West Africa

Zakaria Keita[*1] ; Stephanie Mauti [3] ; Mathias Flierl[3] ; Hervé Bourhy[1] ; Seydou Doumbia [1] ; Isaac Tiembré[2] ; Kathrin Heitz-Tokpa [3] ; Bassirou Bonfoh[3] ; Abdallah Traoré[2] ; Jakob Zinsstag [3]
[1]University of Sciences, Technics and Technologies of Bamako (USTTB). Department of Education and Research in Public Health and Specialties. BP 1204./ University Clinical Research Centre of Point G (UCRC)/ Mali, [3]University of Basel, Basel, Switzerland. Department of Epidemiology and Public Health/ Swiss Tropical and Public Health Institute/ Switzerland (Schweiz), [1]WHO Collaborating Centre for Reference and Research on Rabies/ Institut Pasteur, Université Paris Cité, Unit Lyssavirus Epidemiology and Neuropathology / France [2]Centre antirabique/ Institut National d'Hygiène Publique/ Ivory Coast [3]Centre Suisse de Recherches Scientifiques en Côte d'Ivoire/ Centre Suisse de Recherches Scientifiques en Côte d'Ivoire/ Ivory Coast [2]Département recherche et diagnostique/ Laboratoire Central Vétérinaire/ Mali

Introduction and Objectives or Purpose

Deaths due to human rabies are estimated at 59,000 per year and are particularly common in Asia and Africa. Despite the existing prevention measures through post-exposure prophylaxis (PEP), its burden remains high in West Africa, especially in Côte d'Ivoire and Mali. Evidence showed that there are insufficient resources for Rabies Control Program through mass dogs vaccination, and access to PEP is limited due to stock shortage, but also to lack of public awareness and communication between public and veterinary health sectors.

The implementation of the One Health approach with Blockchain technology has the potential for transparent and secure information sharing and management between different sectors, in combination with a social dynamic of rabies control.

The project aims to assess the effectiveness of the innovation to achieve the goal of zero human rabies by 2030.

Methods

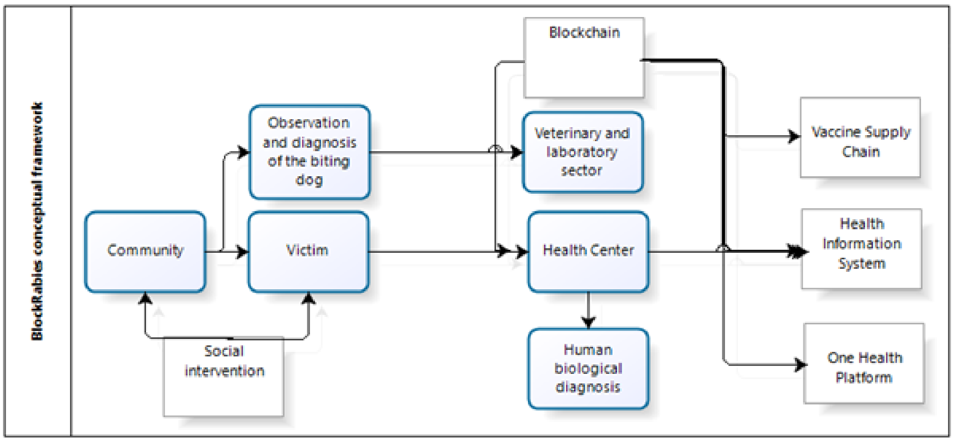
The project adopts a step wedge design with a conceptual framework of Blockchain technology, a shared, immutable ledger. It allows the establishment of threshold stocks of vaccines at each level to avoid shortage and thus improve transparency and efficient use of the rabies vaccine. Here, social intervention implies both interventions for humans and animals with the environment such as children's education and waste management (figure 1). Four areas are covered:

i. Train staff on the integrated management of dog bites with the Blockchain.

ii. Shortened intradermal ID PEP coverage.

iii. Develop human rabies diagnostic and strengthen animal rabies diagnostic in rural areas.

iv. Increase social awareness about rabies by a transdisciplinary social process.



Topic: Impact on and Innovations in Clinical Practice (IICP): Multidrug Resistant Organisms (MDRO) - roles, responsibilities and interests of the non-ID physicians: Use of bioinformatics for the control and containment of infectious diseases
Abstract No: 15022

Revealing the pretentious implications of Thymus Serpyllum for enhancing the immunity of native cows

Asif Nadeem[*1]
[1]Department of Biotechnology/ Virtual University of Pakistan/ Pakistan (پاکستان)

Introduction and Objectives or Purpose

Due to the heavy use of antibiotics in livestock sector, there is rising concern about the antimicrobial resistance. Due to AMR, recurrent infections and new strains of pathogens are developing compromising the herd health at mass level. There is a dire need for therapeutic approaches to manage this stress in the transition cows. Recently, the use of phytochemicals as feed additives in cows' nutrition has gained a lot of interest in managing various disease conditions.

Methods

In the current study, potential effects of phytochemicals derived from methanolic extract of Thymus serpyllum was evaluated (in-silico) for autoimmunity via inhibition of bovine nuclear factor kappa B (NF-κB). Seeds of the plats were processed for the analysis via GC-MS and important constituents were identified. The free radicals scavenging activity of Thymus serpyllum seed and leaf extracts at 100 µg/mL was 71.8% and 75.6%, respectively. Similarly, both extracts displayed maximum radicals reducing power and inhibition of lipid-peroxidation at 100 µg/mL. Then in-silico analysis was performed to evaluate the fnctional importance of each constituent in various cellular pathways.

Results or Focus

The GC-MS analysis identified 52 methanolic extracts compounds, and five (Thymol, Luteolin 7-o-glucuronide, Rosmarinic acid, Apigenin 6,8-di-c-glucoside, Kaempferol) had binding free energy values of -11.6433, -10.002, -8.2615, -7.1714, -6.4870, respectively, in complexes with bovine NF-κB. The Arg160 was the common residue formed non-bonded interactions with the screened compounds. Predictable with these impacts, the screened compounds showed good pharmacokinetic parameters, including non-toxicity, non-carcinogenic, high gastrointestinal absorption and thus can serve as potential drug candidates.

Conclusion or Scope

The combined biochemical and in silico study revealed that Thymus serpyllum would potentially manage a load of oxidative stress and autoimmune reactions in transition dairy cows. However, further in vivo studies are required for the validation of these findings and to reveal the actual potential of identified phytochemicals.

Keywords: Thymus serpyllum; Phytochemicals; Oxidative stress; Autoimmunity; Transition dairy cows

Topic: Impact on and Innovations in Clinical Practice (IICP): Multidrug Resistant Organisms (MDRO) - roles, responsibilities and interests of the non-ID physicians: Use of bioinformatics for the control and containment of infectious diseases
Abstract No: 15091

Epidemiology of Staphylococcus aureus in Timor-Leste

Virginia De Lourdes Da Conceicao [*1 2] ; Nevio Sarmento [1 2] ; Edson Matoso[3] ; Narcisio Soares[3] ; Tessa Oakley[1 2] ; Ian Marr[1 2 4] ; Lucsendar Alves[1] ; Jennifer Yan [1] ; Joshua Francis [1] ; Tereza Wozniak[5]
[1]Microbiology/ Menzies School of Health Research,Dili, Timor-Leste / Timor-Leste, [2]Microbiologia/ Laboratorio Nacional da Saude, Dili, Timor-Leste / Timor-Leste, [3]Pediatria/ Hospital Nacional Guido Valadares, Dili, Timor-Leste / Timor-Leste, [4]Infectious Diseases / The Canberra Hospital, Canberra, Australia / Australia, [5]Health Research/ Australian e-Health Research Centre CSIRO, Brisbane, Queensland, Australia / Australia

Introduction and Objectives or Purpose

Timor-Leste has a significant burden of infectious diseases but previously limited diagnostic capacity and availability of microbiology data on human health. Recent developments in both the diagnosis and reporting of key pathogens in Timor-Leste, including Staphylococcus aureus (S. aureus), have allowed better understanding of the burden of key infectious diseases and their impact on the population.

Methods

A prospective observational study on clinical isolates of S. aureus received at the Laboratorio Nacional da Saude (LNS) in Dili, Timor-Leste, between January 2020 and July 2020 was performed. Clinical samples representing 85% (11/13) of the municipalities in Timor-Leste were included in the analysis. Standard microbiology culture, identification, and antimicrobial susceptibility testing (AST) were performed, and clinical and demographic data collected on laboratory-confirmed S. aureus isolates.

Results or Focus

A total of 61 clinical samples were confirmed as S. aureus. Most patients in our study were found to have community-acquired S. aureus infection (75%), whilst the remaining 25% were hospital-associated infection (HAI). 26% of S. aureus isolates were found to be methicillin-resistant (MRSA).

Conclusion or Scope

This is the first comprehensive description of S. aureus infection in Timor-Leste. The high MRSA rates identified in this study can be used to better inform guidelines for empirical treatment of S. aureus infections. Continuous investment in detecting clinically important pathogens and understanding their susceptibility profiles is critical for the development of treatment guidelines and antibiotic stewardship activities.

Keywords: Staphylococcus aureus, MSSA, MRSA, antibiotic resistance, Timor-Leste

Topic: Impact on and Innovations in Clinical Practice (IICP): Multidrug Resistant Organisms (MDRO) - roles, responsibilities and interests of the non-ID physicians: Using Clinical Decision Support System (CDSS) to guide antibiotic prescriptions
Abstract No: 14875

Randomised Controlled Trial of Fosfomycin in Neonatal Sepsis

John Musembi*[1] ; Jay Berkley[1] ; Phoebe Williams; Christina Obiero[1]
[1]CLINICAL TRIALS/ KEMRI/ Kenya

Introduction and Objectives or Purpose

Antimicrobial resistance is a global health priority and neonates are a particularly vulnerable population. Fosfomycin has the potential to be re-purposed as part of a combination therapy to treat neonatal sepsis where resistance to current Standard Of Care (SOC) is common. Objectives: To assess the safety of fosfomycin among neonates with clinical sepsis

Methods

Design. A single-centre open-label randomised controlled trial. Setting. Kilifi County Hospital, Kenya. Patients. 120 neonates aged ≤28 days admitted being treated with standard-of-care (SOC) antibiotics for sepsis: ampicillin and gentamicin between March 2018 and February 2019.
Intervention. We randomly assigned half the participants to receive additional intravenous (IV) then oral fosfomycin at 100mg/kg twice daily for up to 7 days (SOC-F) and followed up for 28 days. Main outcome(s). Safety for 28 days.

Results or Focus

61 and 59 infants aged 0-23 days were assigned to SOC-F and SOC respectively. We observed 35 adverse events (AEs) among 25 SOC-F participants and 50 AEs among 34 SOC participants during 1,560 and 1,565 infant-days observation respectively (2.2 vs 3.2 events/100 infant-days; incidence rate difference -0.95 events/100 infant-days [95%CI -2.1 to 0.20]). Four SOC-F and 3 SOC participants died. There was no evidence of impact of fosfomycin on serum sodium or gastrointestinal side-effects.

Conclusion or Scope

Conclusion and relevance. Fosfomycin offers potential as a safe and affordable regimen with a simple dosing schedule for neonatal sepsis, so fosfomycin is recommended to be used in combination with another antimicrobial.

Acknowledgement

We thank the trial participants and their parents/guardians for their contribution to this trial. In addition, we acknowledge and thank KEMRI-Wellcome Trust Research Programme nurses and clinical staff.

Topic: One Health Science (OHS): Discovery and Surveillance: Digital-aided events based syndromic and genomics surveillance
Abstract No: 14865

A zoonotic henipavirus from febrile patients in China

Feng Zhu[*1] ; Xiao-Ai Zhang[2] ; Lin-Fa Wang[1] ; Wei Liu[2]
[1]Programme in Emerging Infectious Diseases/ Duke-NUS Medical School/ Singapore, [2]State Key Laboratory of Pathogen and Biosecurity/ Beijing Institute of Microbiology and Epidemiology/ China (□□)

Introduction and Objectives or Purpose

Hendra virus and Nipah virus, belonging to the genus Henipavirus in the family Paramyxoviridae, are the only two bat-borne henipaviruses known to infect humans with high fatality rate. Other henipaviruses have been isolated from bats and rodents with no known human infections.

Methods

We performed a hospital-based surveillance study on febrile patients who had recent history of animal exposure in Shandong and Henan Province, China, between 2018 and 2021. A henipavirus was identified through metagenomic analysis and subsequently isolated from a patient. The prevalence of the henipavirus in febrile patients, healthy individuals, domestic and small animals were further characterized by molecular and serological investigations.

Results or Focus

We identified and isolated a phylogenetically distinct henipavirus, named Langya virus (LayV), in patients with febrile illness in Langya, Qingdao, China. The genome of LayV is comprised of 18,402 nucleotides and shares 71.1% nucleotide identity with Mojiang henipavirus (MojV). Further investigation confirmed a total of 26 patients with acute LayV infection presenting with fever (100%), fatigue (54%), cough (50%), anorexia (50%), myalgia (46%), nausea (38%), headache (35%), vomiting (35%), accompanied by abnormalities of thrombocytopenia, leukopenia, and impaired liver and kidney functions. Surveillance studies in the affected areas revealed four individuals PCR positive (4/1027, 0.39%) without symptoms and twenty one who were IgG-positive (21/1027, 2%). All had a history of animal exposure. Serosurvey of domestic animals identified seropositivity in goats (3/168, 1.8%) and dogs (4/79, 5.1%). Among 25 species of wild small animals, LayV RNA was predominantly detected in shrews (71/262, 27.1%), suggesting shrews are a natural reservoir of LayV. The similarity of LayV to MojV G protein revealed by phylogeny and protein structure modeling by AlphaFold2 indicated the unlikelihood of Ephrin-B2 as an entry receptor to LayV.

Conclusion or Scope

A newly identified henipavirus of probable animal origin was found to be associated with febrile illness in China.

Keywords: Langya virus; Henipavirus; Shrew; Zoonosis; Emerging infectious diseases

Topic: One Health Science (OHS): Discovery and Surveillance: Digital-aided events based syndromic and genomics surveillance
Abstract No: 15050

Opportunities, challenges, and risks of integrating digital health technologies into preparedness and response for emerging zoonotic infectious diseases

Melanie Bannister-Tyrrell*[1] ; Juan Pablo Villanueva Cabezas[1 2] ; Clare Strachan[1] ; Angus Campbell[1]
[1]Nossal Institute for Global Health/ University of Melbourne/ Australia, [2]Global Health/ The Peter Doherty Institute for Infection and Immunity/ Australia

Introduction and Objectives or Purpose

The COVID-19 pandemic sparked a proliferation of digital health technologies to support the response throughout the Western Pacific region. In contrast, digital health technologies have had a more limited role as part of health programs to prevent and detect other emerging zoonotic infectious diseases with the potential to cause public health emergencies. The aim of this study was to review the development and implementation of digital health technologies for emerging infectious diseases other than COVID-19.

Methods

A systematic scoping review was conducted of peer-reviewed literature, technical reports and other information sources that described the design or implementation of digital health technologies for prevention, surveillance or response to priority emerging infectious diseases, as defined by the World Health Organization Research and Development Blueprint.

Results or Focus

A systematic search retrieved 58 records related to digital health technologies for emerging infectious diseases other than COVID-19, compared to 6183 records related to COVID-19. Apart from COVID-19, the number of participants, range of settings and digital health technology types included in studies for emerging infectious diseases is limited. Drawing on the lessons learned from the COVID-19 response, recommendations for addressing key One Health issues related to the governance, implementation challenges, effectiveness, and risks of digital health technologies for emerging infectious diseases were developed.

Conclusion or Scope

The paucity of research into digital health technologies and emerging infectious diseases other than COVID-19 demonstrates significant gaps and a continuing low level of preparedness for future health emergencies. There are clear opportunities, as well as important risks and challenges, to use digital technologies to strengthen early warning and early detection surveillance in human, domestic animal, and wildlife populations, particularly at critical interfaces for zoonosis (re-)emergence and spread.

Keywords: digital health; emerging infectious diseases; syndromic surveillance

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 14663

Implementing a One Health Approach to Rabies Surveillance: Lessons from Integrated Bite Case Management

Catherine Swedberg*[1] ; Stella Mazeri[2 3] ; Richard J. Mellanby[2 3] ; Katie Hampson[1] ; Nai Rui Chng[4]
[1] Institute of Biodiversity, Animal Health & Comparative Medicine/ University of Glasgow / United Kingdom, [2]Royal (Dick) School of Veterinary Studies/ University of Edinburgh/ United Kingdom, [3]Roslin Institute/ University of Edinburgh/ United Kingdom, [4]Institute of Health and Wellbeing/ University of Glasgow/ United Kingdom

Introduction and Objectives or Purpose

As part of the 'Zero by 30' strategy to end human deaths from dog-mediated rabies by 2030, international organizations recommend a One Health framework that includes Integrated Bite Case Management (IBCM). However, little is understood about the implementation of IBCM in practice. This study aims to understand how IBCM is conceptualized, exploring how IBCM has been operationalized in different contexts, as well as barriers and facilitators to implementation.

Methods

Semi-structured interviews were conducted with seventeen practitioners and researchers with international, national, and local expertise across Africa, Asia, and the Americas. Thematic analysis was undertaken using both inductive and deductive approaches.

Results or Focus

Four main themes were identified: 1) stakeholders' and practitioners' conceptualization of IBCM and its role in rabies elimination; 2) variation in how IBCM operates across different contexts; 3) barriers and facilitators of IBCM implementation in relation to risk assessment, PEP provisioning, animal investigation, One Health collaboration, and data reporting; and 4) the impact of the COVID-19 pandemic on IBCM programs.

Conclusion or Scope

This study highlights the diversity within experts' conceptualization of IBCM, and its operationalization. The range of perspectives revealed that there are different ways of organizing IBCM within health systems and it is not a one-size-fits-all approach. The issue of sustainability remains the greatest challenge to implementation. Contextual features of each location influenced the delivery and potential impact of IBCM. Programs spanned from highly endemic settings with PEP charged to patients, to low endemicity settings with large patient loads associated with free PEP policies and sensitization. In practice, IBCM was tailored to meet the demands of the local context and level of rabies control. Thus, experts' experiences did not necessarily translate across contexts, affecting perceptions about the function, motivation for, and implementation of IBCM. These findings provide insights to how IBCM can support programs aiming to reach the Zero by 30 goal.

Keywords: implementation research; One Health; rabies elimination; surveillance; zoonosis

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 14676

Tracking the elimination of dog-mediated rabies from Pemba Island, Tanzania: an observational study

Kennedy Lushasi*[1 2 3] ; Kirstyn Brunker[2] ; Malavika Rajeev[4] ; Emmanuel Mpolya[3] ; Ally Z Mohamed[5] ; Msanif Masoud[2 6] ; Chanasa Ngeleja[7] ; Joel Changalucha[1 2] ; Sarah Cleaveland[2] ; Katie Hampson[2]
[1]Environmental Health and Ecological Sciences/ Ifakara Health Institute/ Tanzania, United Republic of, [2]Boyd Orr Centre for Population and Ecosystem Health, Institute of Biodiversity, Animal Health & Comparative Medicine, College of Medical, Veterinary & Life Sciences/ University of Glasgow/ United Kingdom, [3]Department of Global Health and Biomedical Sciences, School of Life Sciences and Bioengineering/ Nelson Mandela African Institution of Science and Technology,/ Tanzania, United Republic of, [4]Department of Ecology and Evolutionary Biology, / Princeton University/ United States, [5]Department of Livestock Development/ Ministry of Livestock Development and Fisheries, Zanzibar/ Tanzania, United Republic of, [6]Biology/ Bates College/ United States, [7]Tanzania Veterinary Laboratory Agency/ Tanzania Veterinary Laboratory Agency/ Tanzania, United Republic of

Introduction and Objectives or Purpose

Dog-mediated rabies is endemic across Africa causing thousands of deaths annually. We investigated the contributions of a One Health approach, comprising human post-exposure vaccination and mass dog vaccination, in reducing the public health burden and eliminating rabies from Pemba, Tanzania

Methods

From 2010 to 2020 we conducted island-wide contact tracing to map animal rabies cases, resultant human exposures, and deaths and undertook whole-genome sequencing of confirmed cases. With the resulting data, we statistically inferred transmission chains, estimated case detection, and quantified the public health burden, evaluating the impact and cost-effectiveness of a One Health approach.

Results or Focus

We resolved five transmission chains circulating on Pemba from 2010 that were all eliminated by May 2014. During this period, rabid dogs, human rabies exposures and deaths all progressively declined following the introduction and improved implementation of four annual dog vaccination campaigns. In late 2016 we identified two introductions to the island that seeded re-emergence. The ensuing large outbreak was eliminated in October 2018 through reinstated island-wide dog vaccination. Over the 10 years, post-exposure vaccines were highly cost-effective ($211/death averted), but only dog vaccination interrupted transmission ($738/death averted). Together, public health and veterinary interventions eliminated rabies and saved 20-120 families from being bitten by rabid dogs annually.

Conclusion or Scope

A One Health approach underpinned by dog vaccination is a highly cost-effective, equitable and feasible approach to rabies elimination, but needs scaling up across connected populations to sustain the benefits of elimination, as seen on Pemba, and for similar progress to be achieved elsewhere

Acknowledgement

We are grateful for the support of staff from Pemba's Animal and Health Departments, and local community members. The Tanzania Ministries of Health and Social Welfare, Livestock Development and Fisheries, the WHO Country Office-Tanzania, the National Institute for Medical Research, the Zanzibar Ministry of Health and Research Council, Afrique One-ASPIRE all provided permissions and support

Keywords: vaccination, One Health, surveillance, Zero by Thirty, zoonoses

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 14693

Direct Detection of Brucella Species in Livestock Blood Clots from Northern Tanzania

AbdulHamid Lukambagire*[1] [2] ; JAMES AKOKO[1] ; COLETHA MATHEW[1] ; RICHARD YAPI[5] ; BASSIROU BONFOH[2] ; GABRIEL SHIRIMA[3] ; BLANDINA MMBAGA[2] ; CHRISTOPHER KASANGA[1] ; JO HALLIDAY[6] ; RUDOVICK KAZWALA[1] ; Mr Ahmed Lugelo*
[1]VETERINARY MEDICINE AND PUBLIC HEALTH/ SOKOINE UNIVERSITY OF AGRICULTURE/ Tanzania, United Republic of, [2]KILIMANJARO CLINICAL RESEARCH INSTITUTE/ KILIMANJARO CHRISTIAN MEDICAL CENTRE/ Tanzania, United Republic of [1]DEPARTMENT OF BIOMEDICAL SCIENCES AND TECHNOLOGY/ MASENO UNIVERSITY/ Kenya [5]CENTRÉ D'ENTOMOLOGIE MÉDICALE ET VÉTÉRINAIRE/ UNIVERSITÉ ALASSANE OUATARRA/ Ivory Coast [2]AFRIQUE ONE-ASPIRE/ CENTRE SUISSE DE RESERCHES SCIENTIFIQUES EN CÔTE D'IVOIRE/ Ivory Coast [3]LIFE SCIENCES AND BIOENGINEERING/ THE NELSON MANDELA AFRICAN INSTITUTION FOR SCIENCE AND TECHNOLOGY/ Tanzania, United Republic of [6]INSTITUTE OF BIODIVERSITY, ANIMAL HEALTH AND COMPARATIVE MEDICINE/ UNIVERSITY OF GLASGOW/ United Kingdom

Introduction and Objectives or Purpose

Brucellosis is an endemic zoonotic disease of public health priority in many low-and middle-income countries. Control strategies requiring information on Brucella species are hampered by the lack of robust surveillance tools. This study aimed to detect and characterise Brucella DNA in livestock on a ranch in northern Tanzania using real-time, molecular assays.

Methods

Blood was randomly collected from 481 cattle, 20 sheep and 30 goats that were suspected to have brucellosis. DNA was extracted from blood clots and tested for IS711 and bcsp31 targets to determine Brucella spp. All positive samples were then characterized using qPCR assays specific for detection of B. abortus and B. melitensis. Serum from all animals was also tested using the Rose Bengal test (RBT). Mixed-effects regression models were run to determine association of Brucella spp. positivity and B. abortus or B. melitensis positivity with animal level variables observed. The performance of RBT and qPCR assays was compared by cross tabulation.

Results or Focus

Fifty-eight (13.1%) extracts were positive for Brucella spp. while Brucella melitensis was identified in 38.0% of samples and B. abortus in 31.0% of samples positive for Brucella spp. A seroprevalence of 14.5% was found, with poor agreement (K = 0.102) between the RBT and qPCR assay results. No associations were observed between Brucella spp. or species-specific positivity and animal level determinants observed in this herd.

Conclusion or Scope

Brucella spp. DNA was detected in this livestock population from northern Tanzania; Brucella abortus was detected in cattle and goat samples while B. melitensis was detected in all three livestock species. The study findings support the detection of brucellosis using molecular approaches, which have potential to significantly improve surveillance programs in resource-limited settings in sub-Saharan Africa.

Acknowledgement

Additional co-authors acknowledged: Rosamystica M. Sambu, Raphael R. Mwampashi, Nelson B. Amani, Judith S. Njau, Robab Katani, Roland T. Ashford

Keywords: Brucella; Zoonosis; Livestock; Blood clots; qPCR assays; Tanzania

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 14775

Modelling modifiable factors associated with the probability of human rabies deaths in Nigeria

Philip Mshelbwala*[1] [2] ; Ricardo J. Soares Magalhães[1] ; J. Scott Weese[3] ; Nasir Ahmed[4] ; Charles E. Rupprecht[5] ; Nicholas Clark[1]
[1]Veterinary Science / The University of Queensland/ Australia, [2]Veterinary Science / University of Abuja/ Nigeria, [3]Veterinary Science / University of Guelph / Canada, [4]One Health / Nigeria Centre for Disease Control, Abuja, Nigeria / Nigeria, [5]Rabies / LYSSA LLC/ United States

Introduction and Objectives or Purpose

Rabies is a vaccine-preventable zoonotic disease with a substantial global burden. In Abuja, Nigeria there have been multiple rabies outbreaks, with associated human deaths. However, the lack of quality data on human rabies hinders advocacy and resource allocation for effective prevention and control.

Methods

We used a novel Bayesian approach with expert-solicited prior information to guide multiple imputations for missing data to model the additive effects of the covariates on the predictive probability of death after rabies virus exposure (RABV) exposure.

Results or Focus

Of 1,155 dog bite victims reported, 4.2% (n=49/1155) died of rabies. The odds for risk of death were predicted to decrease among individuals who were bitten by owned dogs (OR= 0.230,95% CrI: 0.075- 0.683) compared to those bitten by free-roaming dogs. Similarly, there was a predicted decrease in the probability of death among victims bitten by owned vaccinated dogs (OR= 0.111 (95% CrI: 0.021-0.447) compared to those bitten by unvaccinated dogs. The odds for the risk of death after bitten individuals received at least one human rabies vaccine were predicted to decrease (OR=0.001, 95% CrI: 0.0001-0.008) compared to zero doses.

Conclusion or Scope

Our analytic pipeline demonstrated the practical application of regularized Bayesian approaches to model sparse dog bite surveillance data to uncover risk factors for human rabies with broader applications in other endemic rabies settings.

Acknowledgement

We are grateful to the DSNOs and student volunteers who assisted in the data collection. We thank Mrs Sanny Adeniyi and Dr Irene Esu for their immense support while seeking ethical clearance and Dr Humphrey N. Okoroukwu, for engaging the DSNO and hospital heads throughout the study. We dedicate this work to the memory of the late Miss Constance Idalla, a student of the first author who made several extended trips to support data collection.

Keywords: Bayesian; Epidemiology; Lyssavirus; Nigeria; One Health; Rabies, Zoonosis

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 14914

PRIORITIZATION OF ZOONOTIC DISEASES FOR CONDUCTING SURVEILLANCE IN THEIR LIVESTOCK HOSTS TO PROTECT PUBLIC HEALTH

Yu Qiu*[1] ; Javier Guitian[2] ; Joanne Webster[2] ; Najmul Haider[2] ; Junxia Song[1]
[1]Joint collaboration centre on Zoonoses and AMR/ FAO/ Italy (Italia), [2]Royal Veterinary College/ University of London/ United Kingdom

Introduction and Objectives or Purpose

Zoonoses maintained in livestock pose a continuous threat to animal health and production and public health and livelihood. Effective surveillance of zoonoses in their livestock hosts is critical for understanding disease burden, for the timely detection and control of disease before its further spread, and for providing sentinel warning to humans. The objective of this study was to prioritize zoonoses according to the extent to which disease surveillance in livestock is important for disease prevention in humans.

Methods

An initial list of diseases was compiled by merging diseases from 1) WOAH Lists A and B of notifiable diseases (before 2004), 2) WOAH Terrestrial Animal Health Code, 3) WHO Neglected Tropical Diseases 2021-2030 Roadmap, and 4) authoritative sources of animal/public health data. Subsequently, diseases were selected if 1) recognised as a zoonosis, 2) zoonotic transmission is an important contributor to human infection, 3) livestock play an important role in the disease life cycle or serve as sentinels for disease presence, and 4) human cases are not rare.

Results or Focus

The initial list included 148 diseases, and 31 remained after applying the above criteria such as brucellosis, echinococcosis, avian and swine influenza, Rift Valley fever or porcine cysticercosis, etc. Most diseases are present in more than one continent or have complicated life cycles involving multiple animal species. Despite their importance, significant data gaps in health and economic burden exist, and many are considered neglected zoonoses. This, in turn, further highlights the need for improved surveillance.

Conclusion or Scope

Surveillance of zoonoses in livestock is frequently challenged by the lack of typical symptoms, resource limitations and other competing priorities. A systematic approach for the surveillance of livestock diseases with common epidemiological features or causing similar syndromes, and integrated surveillance across animal, human, and environment sectors may improve the sensitivity, timeliness and cost-effectiveness of surveillance and be the future direction.

Acknowledgement

We acknowledge colleagues of FAO CJWZ/NSAH and RVC for their contributions to this study

Keywords: Zoonoses; endemic and neglected; livestock hosts; surveillance

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 14938

Assessment of Knowledge on Rabies and Bite Management among Health Care Workers in Kitui West Sub-county-Kenya

Augusta Kivunzya*[1] ; Grace Rabuti[2] ; Alice Ngesa[3] ; Peris Kungu[4] ; Royford Mwombobia[5] ; Daniel Mutinda[6] ; Ngina Kisangau[1]
[1]Ministry of Livestock, Apiculture and Fisheries/ County government of Kitui/ Kenya [2]Ministry of Health/ County government of Kitui/ Kenya [3]Ministry of Health/ County government of Kitui/ Kenya [4]One Health/ Global Implementation solutions/ Kenya [5]Ministry of Livestock, Apiculture and Fisheries/ County government of Kitui/ Kenya [6]Ministry of Health/ County government of Kitui, / Kenya [1]Ministry of Health/ County government of Kitui/ Kenya

Introduction and Objectives or Purpose

Rabies is a fatal disease transmitted to human via saliva, scratches or bites by infected animals. Timely bite-wound care, post exposure prophylaxis (PEP) and rabies immunoglobulins (RIG) administration is important in prevention of human rabies. This survey was triggered by a patient who succumbed to suspected rabies despite completing PEP, in August 2021, in Kitui West Sub-county. We aimed to assess healthcare workers (HCW) knowledge on bite-wound and human rabies management

Methods

We conducted a cross-sectional survey among HCW in all facilities (private and public) health in Kitui West sub-county. Semi-structured questionnaires were administered. Data collected included demographics, knowledge on bite classification, PEP schedule, use of RIG, human rabies identification, PEP and RIG availability. We calculated descriptive statistics

Results or Focus

A total of 34 HCW were interviewed, 27 (79%) from public facilities. The median age was 35 years (range 23-68), and females were majority 23 (68%). Fifteen (44%) HCWs encountered a dog-bite patient in the last month. Only 5 (15%) were aware of the three World Health Organization bite (WHO) wound categories, 5(15%) would clean a scratch and multiple bites with water and soap for 15 minutes. Nineteen (56%) would give PEP for a scratch while 22 (65%) would give PEP for multiple bite-wound. Twenty (59%) were aware of PEP's five dose anti-rabies vaccine schedule. Eight (24%) were aware of when to stop PEP. Although RIG was available in the sub-county facility, no HCW was aware of RIG indication. Eighteen (53%) knew the signs and symptoms of human rabies. PEP was available in the private facilities at an average cost of $80 while there were stock-outs in the public facilities for the past year

Conclusion or Scope

Inadequate knowledge on bite-wound management, PEP stock-outs in public facilities and high costs in private facilities increase the risk of human rabies

Acknowledgement

Global Implementation solutions

County government of Kitui,Kenya

Keywords: Rabies;Health care workers;PEP;Kitui

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 14948

Reducing the burden of zoonotic diseases in Kenya: One Health Strategic Plan for the Prevention and Control of Zoonotic Diseases in Kenya (2021-2025)

Athman Mwatondo*[1] ; Augusta Kivunzya[2] ; Mathew Muturi[3]
[1]Kenya Zoonotic Disease Unit/ Ministry of Health/ Kenya, [2]County Department of Health/ County Government of Kitui/ Kenya, [3]Kenya Zoonotic Disease Unit/ Ministry of Agriculture, Livestock and Fisheries/ Kenya

Introduction and Objectives or Purpose

About 60% of all infectious diseases in humans and over 75% of emerging and re-emerging infectious diseases are zoonotic. Kenya is at high risk of zoonotic diseases, as evidenced by recurrent zoonotic outbreaks and the country's recognition as a global hotspot for (re)emerging diseases. Since 2012, the Zoonotic Disease Unit (ZDU) has implemented zoonotic disease control activities guided by a 5-year strategic plan (2012-2017). A revised 5- year strategy (2021-2025) has been developed to strengthen One Health collaboration in Kenya

Methods

The previous strategy was evaluated in 2018 through key informant interviews and a review of performance indicators during the implementation period. This guided the revision of objectives, targets and activities for the new strategic plan, gaps and challenges in zoonotic disease prevention and control to inform the development of the revised strategy. A comprehensive situational analysis was conducted to guide the development of strategic activities in the revised plan by identifying strengths, weaknesses that need improvement, and existing opportunities. The strategy drafts were reviewed exhaustively in three stakeholder meetings to ensure alignment with global and national sectoral strategies, policies and new zoonotic disease threats.

Results or Focus

The situation analysis identified strengths in prioritising zoonotic diseases and improved response to zoonotic disease outbreaks. Limited domestic funding and weak collaboration at the subnational levels were key weaknesses. Three strategic objectives are outlined; to strengthen the implementation of the One Health approach at national and sub-national levels through enhancing multi-sectoral coordinating mechanisms, to strengthen surveillance and response of priority zoonoses and to promote applied research for endemic and emerging diseases. The strategic objectives have detailed activities to be implemented based on a strategic framework.

Conclusion or Scope

The successful implementation of this strategic plan shall significantly reduce the burden posed by zoonotic diseases in Kenya through the One Health approach.

Keywords: One Health; Surveillance; Collaboration

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15002

Characteristics of human leptospirosis in three different geographical and climatic zones of Vietnam: a hospital-based study

Mai Le*[1] ; Dung Luu[1]
[1]Dept. of Public Health/ National Institute of Hygiene and Epidemiology/ Vietnam (Việt Nam)

Introduction and Objectives or Purpose

Background: The purpose of the present study was to determine the seroprevalence of human leptospirosis and describe its epidemiological profile in 3 different geographical and climatic zones of Vietnam.

Methods

Methodology: A hospital-based surveillance in 11 public hospitals in 3 provinces in Vietnam enrolled 3,815 patients with suspected leptospirosis. Two consecutive enzyme-linked immunosorbent assay IgM and a single microscopic aggregation test were applied at a 1:100 to 1:800 dilution for probable or confirmed cases.

Results or Focus

Results: The findings showed that of the 3,815 suspected cases, 68 (1.8%) were Leptospira-confirmed and 248 (6.5%) probable cases, whereas more than a third were positive for acute ELISA-IgM sera. Furthermore, 20 different serovars were found, of which Wolffi (14.2%), Hebdomadis (13.8%), and Icterohaemorrhagiae (12.6%) were the most predominant. The ratio of probable and confirmed cases of leptospirosis between females and males was 1.4:1, and their clinical manifestation was not specific. Cases were more likely to be detected in groups that are farmers, pet raising or livestock farming, of working age, practicing either wading in mud or walking barefoot, or exposed to heavy rainfall.

Conclusion or Scope

Conclusions: Analysis of human leptospirosis has indicated fairly high seroprevalence and diversity of Leptospira serovars circulating in all studied geographical zones in Vietnam. The findings suggest an imperative need for effective measures of disease prevention, especially in high-risk groups.

Acknowledgement

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Keywords: characteristics of leptospirosis, hospital surveillance, human leptospirosis, seroprevalence, Vietnam

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15019

ZOONOTIC AND ANIMAL DISEASES SURVEILLANCE AT SLAUGHTER HOUSES IN CAMEROON: PREVALENCE AND ECONOMIC IMPACT OF CATTLE CARCASS AND OFFAL SEIZURE

Müller FOTSAC DZOUSSE[*1 2] ; Berto KENNE KEAMBOU[1] ; Arouna NJAYOU NGAPAGNA[1 3] ; Florence FONTEH [2 4]
[1]Agroveterinary Department/ Université des Montagnes/ Cameroon (Cameroun), [2]Physiology and Animal Health/ University of Dschang/ Cameroon (Cameroun), [3]School of Veterinary Sciences and Medicine/ University of Ngaoundere/ Cameroon (Cameroun), [4]Food Sciences and Technology/ University of Bamenda/ Cameroon (Cameroun)

Introduction and Objectives or Purpose

The study of seizures at slaughterhouses constitute a rich source of information for the surveillance of animal diseases and various zoonosis. It enables the implementation of preventive and corrective measures to preserve animal health, reinforce food safety and better protect public health. In this study, we hypothesize that slaughterhouses may block the spread of zoonotic agents to human population.

Methods

To test this hypothesis, we conducted a descriptive study from March to May 2021 at the SODEPA slaughterhouse in Douala-Cameroon. We carried out a convenience sampling to determine the prevalence and incidence of seizures of cattle carcasses and offal. Chi-square test was used for qualitative analysis and the student and fisher tests for quantitative analysis. Values of $P<0.05$ were considered to be statistically significant.

Results or Focus

A total of 7645 cattle were inspected, of which 501 showed seizure cases. The prevalence of seizures was 6.5% (0.79% for carcasses and 5.75% for offal). The results showed a high frequency (86.8%) of seizures in animals from the northern part of Cameroon. The White-fulani(59.7%) and Red-fulani(38.5%) breeds, as well as animals aged between 5-8 years, were the subject of most seizures. Total seizures reasons were dominated by tuberculosis (56.6%) and cadaverism (44.4%). Regarding partial seizures, seized carcasses were dominated by trauma (86.5%) and offal seizures dominated by tuberculosis (50.3%), distomatosis (60.6%), pericarditis (53.9%), which were diagnosed in the lungs, liver and heart respectively. During our study period, the economic losses due to different seizures were estimated to 8.338.950Fcfa.

Conclusion or Scope

Taking together the above results, this study demonstrate that the SODEPA slaughterhouse was capable to prevent the release of contaminated meat and prevent the spread of zoonotic agents (tuberculosis-distomatosis) to the human population in Douala. Nevertheless, there is yet the need for active surveillance of seizures at slaghterhouses taking into account the multi-sectorial and collaborative one-health approach.

Keywords: Cattle carcass ; Offal ; Zoonosis ; Slaughterhouse ; Inspection

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15028

Tracking Tenia solium cysticercosis in the pork entering the food chain, lessons from Rwanda

Anselme Shyaka*[1]
[1]Center for One Health/ University of Global Health Equity/ Rwanda

Introduction and Objectives or Purpose

Tenia solium cysticercosis is a major neglected disease with the highest burden in sub-Saharan Africa, Asia, and south America. In Africa, the disease is characterized by a high prevalence of both human and porcine cysticercosis, and the resulting burden of epilepsy is exacerbated by low treatment availability and severe stigma. In Rwanda pig slaughtering is carried out in formal and informal settings; the former, through slaughter slabs and the later characterized by backyard slaughter at farm level or in bar/restaurant settings that lack regular veterinary inspection to ensure pork safety. In the framework of the global commitment to end NTDs, it is important to map and characterize cysticercosis risk to develop a robust strategy for control. Therefore, this study aimed at determining the prevalence of porcine cysticercosis in pigs entering food chain to assess the exposure of pork consumers to porcine cysticercosis.

Methods

The selection of slaughter slabs was guided and informed by our previous study on pig production value chains in Rwanda. Blood samples were collected from a total of 763 pigs. In addition, 77 pigs were randomly selected and bought for full dissection to confirm Taenia species. Slices of maximum 0.5 cm thickness were made and cysticerci were searched and enumerated in the carcass. Blood was processed to collect serum and were analysed using a commercial ELISA Kit to detect circulating Antigen.

Results or Focus

Seroprevalence of infection varied from 10 – 40%, and carcass dissection showed high cyst burdens in many pigs. Dissection results confirmed that cysts were T. solium, which represent a public health risk to pork consumers. The results presented here show that pigs have a variable cyst burden and may reach the consumer even if veterinary inspection is done correctly

Conclusion or Scope

These results suggest that measures to improve the safety of pork production should be considered.

Keywords: pig, Rwanda, carcass dissection, cysticercosis

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15032

Setbacks to achieving zero rabies cases by 2030: A case scenario for Kenya

Nassoro Mwanyalu*[1 2] ; Kimani Maina; Veronica Chuchu; Mathew Mutiiria; Daniel Chepkwony; Mathew Muturi; Maurice Owiny; Athman Mwatondo
[1]Ministry of Health/ Field Epidemiology and Laboratory Training Program/ Kenya, [2]Ministry of Health/ Zoonotic Disease Unit/ Kenya

Introduction and Objectives or Purpose

Rabies is a neglected zoonotic disease though 100% vaccine-preventable. Kenya launched Rabies Elimination Strategy in 2014, aiming to end human rabies deaths by 2030. In March 2022, Lamu County reported three suspected rabies deaths. We aimed to establish the extent of rabies outbreaks in humans and animals in Lamu and identify the setbacks to achieving zero rabies cases by 2030

Methods

We performed a retrospective investigation and retrieved dog bite reports from Kenya Health Information System(KHIS), 2017 to April 2022. Medical records for suspected human rabies deaths and files for rabid animals were retrieved, 2019-2022. A verbal autopsy was conducted on the families of the suspected human rabies death to understand the circumstance surrounding the bite and patient management. Descriptive analysis was conducted.

Results or Focus

A total of 1,616 dog bite cases were reported on KHIS. County Crude Attack Rates(CAR) was 540/100,000 population. Six cases were investigated with a Case Fatality Rate(CFR) of 100%, age 4-27 years(median 10 years). Lamu East sub-county had highest Death Rate at 7.4/100,000 population in 2021. All the deaths were due to dog bites; bite sites were arms at 50%(3/6) and multiple sites 17%(1/6). Four cases washed the bite wounds with water within 24 hours before seeking medical care, and none was washed at the health facility. Three cases received Rabies Immunoglobulin(RIG) in the deltoid region. All the fatal dog bites were unprovoked. No rabies sample was collected from these biting dogs.

Lamu county conducted targeted dog vaccination since 2017, and brain samples collected were five; cats were 40%(2/5) and dogs 40%(2/5). All tested positive for rabies on Sellar's staining.

Conclusion or Scope

There was poor surveillance, use of targeted dog vaccination, and lack of awareness on bite wound management by the community and health workers. We recommend routine Mass Dog Vaccination with 70% coverage and improvement of One Health collaboration.

Keywords: Rabies; One Health; Zoonotic; Kenya

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15062

Dog demography and incidence of dog bites for rabies control in Sikasso (Mali)

Brahima Sylla[1] ; Zakaria Keita[*1] ; Fatou Diawwara[1] ; Seydou Doumbia[1] ; Abdallah Traoré[2] ; Stephanie Mauti[3] ; Jan Hattendorf[3] ; Felix Gerber[3] ; Cheick Abou Coulibaly[1] ; Jakob Zinsstag[3]
[1]University of Sciences, Technics and Technologies of Bamako (USTTB). Department of Education and Research in Public Health and Specialties. BP 1204./ University Clinical Research Centre of Point G (UCRC)/ Mali, [2]Département recherche et diagnostique/ Laboratoire Central Vétérinaire/ Mali, [3]University of Basel, Basel, Switzerland. Department of Epidemiology and Public Health/ Swiss Tropical and Public Health Institute/ Switzerland (Schweiz)

Introduction and Objectives or Purpose

Dog bites are considered dangerous because of the deadly zoonotic infection that rabies can cause.

It remains endemic in Mali, with a delay in notification to district health authorities. In addition, access to post-exposure prophylaxis (PEP) remains limited.

This study aimed to determine the incidence of dog bites and dog demography in the Sikasso region in the south of Mali.

Methods

This study describes potential exposure to dog bites, associated factors, and the dog-to-human ratio in households surveyed in the Sikasso region from 2016 to 2017.

A series of simulations were conducted to identify an appropriate sample size proportional to the cluster size of 4593 households surveyed.

•Cluster sampling is stratified by rural and urban communities.

•Other data used for triangulation from the literature review

•Decision tree simulations to estimate PEP, and deaths.

Results or Focus

The sample size was 4593 households with 16 victims. The dog-human ratio in Sikasso was 1/33 [95% CI: 1/34 to 1/31] with a dog bite incidence rate of 84 [95% CI: 49 to 135] per 100,000 people. The victims were children (62.5%), male (62.5%) and from rural areas (68.8%).

No significant association was found between sociodemographic and economic factors to the number of dog bites and the demand for care.

Conclusion or Scope

This study showed a high incidence of dog bites and less than half of these victims received PEP.

Provision of PEP and preventive strategies are needed, with specific programs for children under 15 years.

Acknowledgement

We acknowledge GAVI, the vaccine alliance for funding this research in West and Central Africa countries (Mali, Côte d'Ivoire, Tchad and Liberia).

Keywords: Canine population; bites incidence; West Africa; Rabies; Vaccine

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15081

RABIES DETECTION IN STRAY DOGS THROUGH PASSIVE SURVEILLANCE IN NEPAL

Suraj Subedi *1 ; Sulochana Shrestha[2] ; Manju Maharjan[1] ; Nabaraj Shrestha[1] ; Ram Chandra Sapkota[1] ; Tulsi Ram Gompo[1] ; Pragya Koirala[1] ; Surendra Karki[3] ; Sharmila Chapagain[1]
[1]Central Veterinary Laboratory/ Department of Livestock Services/ Nepal (□□□□□), [2]Department of Livestock Services/ Ministry of Agriculture and Livestock Development/ Nepal (□□□□□), [3]Emergency Center for Transboundary Animal Disease/ Food and Agriculture Organization of the UN (FAO-UN)/ Nepal (□□□□□)

Introduction and Objectives or Purpose

Rabies is a priority zoonosis in Nepal and a notifiable disease in animal health. It is estimated that around 100 human rabies cases occur annually. Nepal aims to eliminate dog-mediated rabies in humans by 2030.

Methods

The Central Veterinary Laboratory screens for rabies with rapid antigen test and confirms the diagnosis with the direct fluorescent antibody test.

Results or Focus

Between July 2021 and June 2022, a total of 72 cases were submitted for rabies confirmatory diagnosis. The majority of samples (52/72) came from the Kathmandu valley. In total, 40 submissions (31/51 dogs, 1/2 horses, 5/8 buffaloes and 3/4 cattle) were positive for rabies. Most of the cattle and buffalo that tested positive had a history of a dog bite. Clinical disease was most frequently observed in ruminants. More free-roaming dogs (23/30) tested positive than pet dogs (8/20). Three pet dogs that were positive had been vaccinated against rabies within the last year. The dogs diagnosed with rabies did not always show signs of aggression or salivation, and some of the household dogs were still responding to their owner up till the time of their death.

Conclusion or Scope

The involvement of multiple organisations in spay/neuter activity, animal welfare and management of free-roaming dogs could have led to the greater number of submissions from these dogs. Most of these dogs are often rescued from Kathmandu valley (22) and Kavre district (7) after reports of community problem and/or health issues. The geographical coverage of testing is limited. The continuing diagnosis of rabies in free-roaming dogs suggests that a widespread vaccination campaign needs to target this population. Given the difficulty of administering injectable rabies vaccines, oral bait vaccination could be an effective alternative to reduce the incidence of rabies in free-roaming dogs and achieve the goal of zero dog-mediated rabies in humans by 2030.

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Keywords: Rabies; Nepal; Free-roaming dogs; Central Veterinary Laboratory

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15102

Rabies in Viet Nam

Pawin Padungtod*[1] ; Long Pham Thanh[2] ; Thuy Nguyen Thu[2] ; Huong Nguyen Thi[3] ; Huong Nguyen Thi Thanh[4] ; Phuc Nguyen Thi[5]
[1]Emergency Center for Transboundary Animal Diseases/ FAO Country Office for Viet Nam/ Vietnam (Việt Nam), [2]Department of Animal Health/ Ministry of Agriculture and Rural Development/ Vietnam (Việt Nam), [3]General Department of Preventive Medicine/ Ministry of Health/ Vietnam (Việt Nam), [4]National Institute of Hygiene and Epidemiology/ Ministry of Health / Vietnam (Việt Nam), [5]Viet Nam Country Office/ World Health Organization/ Vietnam (Việt Nam)

Introduction and Objectives or Purpose

Rabies remains one of the deadliest infectious diseases in the world. Up to 99% of human rabies cases are acquired through dog bites. Despite being recognized as one of the five priority zoonoses, rabies continues to kill people including children in Viet Nam. The Government of Viet Nam is committed to achieve the 2030 goal of eliminating human deaths from dog-mediated rabies by renewing the new National Programme on the Control and Elimination of Rabies 2022–2030.

Methods

From 2017 to 2021, 35 provinces and cities in Viet Nam actively monitor and test for rabies in suspected dogs.

Results or Focus

A total of 1,989 samples were tested of which 218 (11%) were positive for rabies virus. In 2021, there were 53 deaths from rabies in 28 provinces with 531,204 people bitten by dogs requiring preventive treatment while 78 out of 222 samples, collected from rabies suspected dogs, were positive (35.13%). Despite the significantly decreased number of rabies deaths in some provinces, the total number of human rabies deaths from 2017 to 2021 increased in 20 provinces compared to the period from 2011 to 2016. Rabies has also been reported from provinces where no cases were reported previously.

Conclusion or Scope

There is a need to strengthen actions, especially at provincial level, to prioritize and increase resources for the management of dog populations, the vaccination of dogs, and provision of post-exposure prophylaxis for those bitten by dogs.

Keywords: Rabies; Zoonoses; Post-Exposure Prophylaxis; Humans; Animals

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15111

Way forward for rabies control and elimination in South Asia

Kinzang Dukpa*[1]
[1]Regional Representation for Asia and the Pacific/ World Organisation for Animal Health/ Japan (□□)

Introduction and Objectives or Purpose

Rabies is endemic in both humans and animals in seven of the eight South Asian Association for Regional Cooperation (SAARC) countries, contributing to about 45% of the global burden of human rabies. Although a priority disease, it is a neglected disease in most SAARC countries. There are no lead agencies in most countries and there is lack of ground-level surveillance due to lack of resources and investments. The World Organisation for Animal Health (WOAH) along with its partners implemented activities to support SAARC countries in building capacity and networking to catalyse actions in preparations for the global target of zero-by-30. The objectives of this poster are to share progress made and challenges faced by countries and the interventions made by WOAH and partners.

Methods

The information collected from workshops, trainings, and webinars organised for SAARC countries by WOAH and its partners was used to prepare the contents. Additionally, information collected via surveys and direct contacts have also been included.

Results or Focus

Rabies is still endemic in South Asia with dog-mediated rabies being the primary concern. It is still a neglected disease with only four countries having a national action plan and only three countries having an ongoing nationally coordinated dog rabies vaccination program funded by the government. Five countries have the capacity to diagnose rabies at both national and sub-national level. India recently approved the use of oral rabies vaccines in dogs in pilot basis in Goa State which is a big step for South Asia. Except Maldives (rabies-free), Bhutan may be able to reach the global target even before 2030.

Conclusion or Scope

There is a need for tripartite, donors, and NGOs to coordinate and consolidate our efforts to ensure optimal impacts. Key priority areas to focus would be sustained high-level advocacy, enhancing intersectoral coordination, and focusing on mass dog vaccination programs.

Acknowledgement

FAO WHO partners

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15152

Systematic map of ruminant disease prevalence in Ethiopia

Isla MacVicar*[1] ; Theodora Tsouloufi[1] ; Louise Donnison[1] ; Karen Smyth[1] ; Andrew Peters[1]
[1]SEBI-Livestock/ University of Edinburgh/ United Kingdom

Introduction and Objectives or Purpose

Approximately 1 billion people in lower-income countries depend on the health of their livestock for their livelihoods, family nutrition and health. One objective of SEBI-Livestock is to improve the availability of livestock health and productivity data to enable better policy decision-making in animal and human health. This project aims to increase the availability of such data by systematic analysis of existing literature sources and to accelerate the process using machine learning (ML). This presentation describes one step in that process, that of systematically mapping publications on ruminant disease in Ethiopia.

Methods

Searches on bibliographic and organisational databases were conducted for the period 2010-2019. After screening, 716 articles were identified as relevant to the research question. Data extracted from the papers included the prevalence of disease, location, agro-ecological zone, years studied, species, breed and age of animals, and methodologies used.

Results or Focus

The systematic map revealed an increased publication output from 2012-2017, compared to 2010-2011 and 2018-2019. Most studies were conducted in Oromia (44.8%) and Amhara (21.4%). A substantial body of evidence was found for trypanosomiasis (17.7%), ectoparasite infestation (14.9%), fasciolosis, nematodiarasis, echinococcosis and brucellosis. Of the 57 search queries, no evidence was found relating to 13 specific ruminant diseases.

Conclusion or Scope

We suggest that despite the high output of epidemiological publications, further understanding of a significant number of diseases is required and where evidence is abundant, detailed reviews should be carried out to better inform decisions on disease control priorities. A parallel mapping process is underway using the same search terms and ML to automate the process. Validation of this automation tool is almost complete and it will then be used to accelerate the mapping of similar data for multiple countries and other applications with a One Health focus.

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Keywords: Cattle; disease frequency; small ruminants; sub-Saharan Africa; systematic mapping;

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15181

A COMPARATIVE DESCRIPTIVE EPIDEMIOLOGY OF HUMAN AND ANIMAL RABIES IN NIGERIA 2017- 2021

Nasir Ahmed*[1] ; Abubakar Jafiya[1] ; Elsie Ilori[1] ; Ifedayo Adetifa[1]
[1]Surveillance and Epidemiology/ Nigeria Centre for Disease Control/ Nigeria

Introduction and Objectives or Purpose

Rabies is a fatal zoonotic viral disease of the nervous system of all mammals caused by Genus Lyssavirus family Rhabdoviridae with a case fatality rate of almost 100%. The disease is endemic in domestic dogs in Nigeria. This study discusses trends to compare the descriptive epidemiology of human and animal rabies in Nigeria between 2017-2021

Methods

Secondary data for both human and animal rabies were obtained via the integrated disease surveillance and response (IDSR) and national disease information system (NADIS) respectively. Data were analyzed using Epi info was used for the spatial distribution of cases across the country

Results or Focus

A total of 998 suspected human cases were reported from 2017-2021 of which 273 (27.3%) in 2017, 113 (11.3%) in 2018, 365 (36.6%) in 2019, 159 (15.9%) in 2020 and 88 (8.8%) in 2021. A total of 291confirmed animal rabies were reported. Among these, 51 (18%) in 2017, 79 (27%) in 2018, 71 (24%) in 2019 and 90 (31%) in 2020. In the year 2017, 15 (68%) states reported suspected human rabies while only 6 (16) reported animal rabies. In 2018, 23 (62%) reported suspected human cases as opposed to 9 (24%) animal cases. In 2019, 23 (62%) states reported human cases while 12 (62%) reported animal cases. In 2020, 16 (43%) states reported suspected human cases and 14 (38%) reported animal rabies. Five (13%) states reported suspected human rabies while only 4 (10%) reported animal rabies.

Conclusion or Scope

Despite the endemicity of rabies, Human and Animal surveillance systems fail to pick up sufficient cases of rabies in the country. However, it can be argued that some states battling the insurgency make rabies reporting difficult. While most states underreport the disease partly because it occurs in rural communities and among young children. Also, most states lack the One Health approach in terms of rabies reporting

Keywords: Rabies; IDSR; NADIS; States;

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15229

Serologic evidence of human exposure to known and unknown henipaviruses, Cambodia

Spencer L. Sterling[*1 2] ; Phireak Hip[3] ; Piseth Ly[3] ; Pidor Ouch[3] ; Menghou Mao[3] ; Dolyce H.W. Low[4 5] ; Christopher C. Broder[1] ; Jeffrey C. Hertz[6] ; Ian H. Mendenhall[5] ; Eric D. Laing[1]
[1]Microbiology and Immunology/ Uniformed Services University/ United States, [2]Microbiology and Immunology/ Henry M. Jackson Foundation for the Advancement of Military Medicine/ United States, [3]Virology/ Navy Research Unit No. 2 Phnom Penh Detachments/ Cambodia (□□□□□□□), [4]Graduate School for Integrative Sciences and Engineering/ National University of Singapore/ Singapore, [5]Programme in Emerging Infectious Disease/ Duke-NUS Graduate Medical School/ Singapore, [6]Virology/ Navy Research Unit No. 2/ Singapore

Introduction and Objectives or Purpose

Emerging zoonotic viruses in the genus Henipavirus (family Paramyxoviridae) can cause severe and often fatal disease in livestock and humans and are listed in the WHO priority pathogen blueprint. Nipah virus (NiV), the prototypical henipavirus, has been isolated from flying foxes (genus Pteropus) in the Battambang province of western Cambodia, and surveys suggest bat foraging behaviors occur near human settlements. Despite this, there have been no documented human cases of NiV infection in Cambodia.

Methods

Convalescent serum samples from patients with undiagnosed febrile illness from 10 provinces in Cambodia were screened for antibodies reactive with the receptor binding proteins (RBP) of four henipaviruses and paired acute samples from the convalescent positives were screened for IgG reactivity.

Results or Focus

Cedar virus (CedV) specific antibodies were detected in three convalescent samples and further were screened for neutralizing antibodies. Of which, one serum sample was able to neutralize recombinant CedV. Additionally, forty convalescent serum samples reacted with Ghana virus RBP, and twenty-three paired acute samples demonstrated similar reactivity. We did not find an association between provinces with flying fox roosts and serological prevalence

Conclusion or Scope

Here, we have demonstrated evidence of cryptic henipavirus infections in humans in Cambodia, with a majority of the samples demonstrating reactivity with Ghana virus, suggesting infection with a yet-described ancestral henipavirus that shares antigenic-similarity with Ghana virus. Lastly, we observed exposure to a CedV-like virus that can use human ephrin-B2 as an entry mechanism.

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Keywords: Henipavirus, bat-borne virus, serology, multiplex

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15245

Assessment of cross-border surveillance system for control transborder zoonotic diseases through transhumance in West Africa

Wilfried Délé Oyetola*[1] ; Rianatou Bada Alambedji[1] ; Bassirou Bonfoh[2]
[1]Service de Microbiologie, Immunologie, Pathologie Infectieuse/ Ecole Inter-Etats des Sciences et Médecine Vétérinaires / Senegal (Sénégal), [2]CSRS/Afrique One ASPIRE/ Centre Suisse de Recherche Scientifique en Côte d'Ivoire/ Ivory Coast

Introduction and Objectives or Purpose

The mechanisms of controlling transboundary diseases at the borders of the Economic Community of West African States (ECOWAS) are based on the International Certificate of Transhumance (ICT) used during seasonal pastoral mobility. However, most priority zoonotic diseases and especially brucellosis listed in 78% of ECOWAS countries are not considered in the ICT. This study aimed to assess the cross-border surveillance systems using brucellosis model during seasonal transhumance between Mali and Côte d'Ivoire to improve control tools at the human and livestock interface.

Methods

Two sets of interviews with questionnaires were conducted at the Côte d'Ivoire-Mali border. The first was conducted with 6 agents of border control posts and 6 heads of veterinary or public health services overseeing border surveillance. The second was addressed to 241 mobile pastoralists. 111 herds and 4 pastoralists were screened for brucellosis. The issuance ICT process and the crossing borders procedures have been observed.

Results or Focus

Transhumance between Mali and Côte d'Ivoire mainly involved cattle and fewer sheep, with a ratio of 1.8 herdsmen and average of 83 animals per herd. In three of four situations of crossing borders observed, the herds received a health certificate ("Laissez-passer") to enter the host country, although, in two situations animals were not inspected. The transborder control process varied among the veterinary services of each country, and the public health service was not involved in the control of pastoralists' health. Only 4.2% of pastoralists held the ICT and border control agents did not request it for control. 24.1% of herders suspected brucellosis in their herds while the brucellosis seroprevalence was 11.7% that undergone undetected with the ICT and Laissez-passer tools.

Conclusion or Scope

Communication between border teams of human and animal health sectors and random rapid tests would improve the border surveillance system. The ICT should include some zoonotic diseases of regional spread risk for humans and animals.

Acknowledgement

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Keywords: transboundary zoonotic diseases, transhumance, border surveillance, brucellosis

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15310

PARATYPE: A GENOMIC SURVEILLANCE FRAMEWORK AND AN OPEN-SOURCE TOOL FOR SALMONELLA PARATYPHI A

Arif Mohammad Tanmoy[*1] ; Yogesh Hooda[1] ; Mohammad Saiful Islam Sajib[1] ; Farah N. Qamar[2] ; Stephen Baker[3] ; Zoe A. Dyson[3] ; Denise Garrett[4] ; Jason R. Andrews[5] ; Samir K. Saha[1] ; Senjuti Saha[1]
[1]Genomics/ Child Health Research Foundation/ Bangladesh (□□□□□□□□), [2]Paediatrics and Child Health/ Aga Khan University/ Pakistan (پاکستان), [3]Cambridge Institute of Therapeutic Immunology and Infectious Disease, Department of Medicine/ University of Cambridge/ United Kingdom, [4]./ Sabin Vaccine Institute/ United States, [5]Division of Infectious Diseases and Geographic Medicine/ Stanford University School of Medicine/ United States

Introduction and Objectives or Purpose

Salmonella enterica serovar Paratyphi A, a causative agent of paratyphoid fever, is responsible for 3.4 million cases globally per year. With rising antimicrobial resistance (AMR) and no licensed vaccines, genomic surveillance is of utmost importance to track the evolution of this pathogen and monitor transmission. However, little is known about its genomic and AMR characteristics, and there is no robust genotyping system to assist genomic-epidemiological studies. Therefore, we developed Paratype, an open-access genotyping tool for Salmonella Paratyphi A.

Methods

To develop Paratype we sequenced 819 Salmonella Paratyphi A strains from Bangladesh, Nepal, and Pakistan, and combined them with existing 560 genomes to generate a database of 1,379 genomes isolated during 1917- 2019 from 37 countries. Using BEAST, fastbaps, and RAxML, we developed a genotyping scheme that segregated the Paratyphi A population into three primary, seven secondary, and 18 subclades/genotypes (Figure 1). Each clade was assigned a unique allele definition. We developed a python script for rapid genotyping and detecting mutations in gyrA, parC, and acrB genes reported to cause ciprofloxacin and azithromycin resistance.

Results or Focus

Using Paratype, we identified genomic variation between different sampling locations. Genotype 2.4.4 was dominant in Bangladesh, 2.4.3 in Nepal, and 2.4 and 2.3.3 in Pakistan. We also identified specific AMR genes, mutations, and plasmids, and correlated them with resistance phenotype. For Bangladesh, the presence of these AMR elements; is low; ciprofloxacin resistance is the most common.

Conclusion or Scope

We report the first large-scale analysis of Salmonella Paratyphi A genomes and propose the first genotyping tool. We released Paratype (https://github.com/CHRF-Genomics/Paratype) as an open-access tool that can use sequences from Illumina and Nanopore platforms. It is an easy-to-use, command-line tool, which is already being adopted by researchers for genomic analysis. This tool will assist future genomic surveillance studies and will help inform intervention strategies for this neglected pathogen.

Keywords: Paratyphi A; Paratype; Genomics; Genotyping; Surveillance

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15320

IMPLEMENTING ONE HEALTH: A CASE STUDY OF RABIES IN THE PHILIPPINES

Mary Elizabeth Miranda*[1] ; Nai Rui Chng[2] ; Katie Hampson[2] ; Jobin Maestro[1] ; Daria Manalo[1] ; Duane Manzanilla[1] ; Beatrice Quiambao[3] ; Catherine Swedberg[2] ; Sally Wyke[2] ; Mirava Yuson[1]
[1]FETPAFI/ Field Epidemiology Training Programme Alumni Foundation Inc/ Philippines, [2]MVLS/ University of Glasgow/ United Kingdom, [3]Research Institute for Tropical Medicine/ Department of Health/ Philippines

Introduction and Objectives or Purpose

Elimination of rabies requires a One Health approach with human healthcare and animal health workers coordinating effective prevention and control measures. However, operationalizing One Health remains challenging.

Methods

We conducted implementation research (SPEEDIER: Surveillance integrating Phylogenetics and Epidemiology for Elimination of DIsease: Evaluation of Rabies control in the Philippines) in the provinces of Romblon and Oriental Mindoro, Philippines. We adapted WHO guidelines on Integrated Bite Case Management (IBCM) to increase rabies detection, with risk assessment of bite patients triggering animal investigations. SPEEDIER involved joint training of healthcare and animal health workers with technical and peer support to build proficiency and confidence in risk assessments and investigations.

Results or Focus

High incidence of bite patients presenting to animal bite treatment centres (>900/100,000 persons/year) lead to excessive workload, strain budgets and interrupt supplies of post-exposure prophylaxis (PEP). Only a small proportion of patients were assessed as high-risk for rabies (<2.5%, <30/100,000 persons/year) making PEP cost-effectiveness low at $14,000-33,000/ death averted (16-35 deaths prevented/ year). Paradoxically, deaths continue (5-9/ year) indicating that lifesaving PEP remains inaccessible to those in need. Routine surveillance detects <5% of animal cases which is inadequate for outbreak response and informing control. Sub-optimal rabies surveillance, prevention and control is due to poor collaboration and communication between sectors. Poor PEP provisioning is exacerbated by clinical assessment using outdated guidance, while animal investigations are rarely undertaken or done too late to support patient care and inform surveillance. Despite pandemic challenges, implementation of IBCM led to a sevenfold increase in case detection through improved intersectoral One Health working and identified localities needing improved control.

Conclusion or Scope

IBCM offers an example of how One Health can be operationalised to overcome dysfunctional and siloed ways of working, and improve our ability to deal with both endemic and emerging zoonoses.

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Keywords: Implementation research, surveillance, sustainability, elimination, One Health

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15343

Improvement of Rabies surveillance in Madagascar from 2013 to 2021

Dany Bakoly RANOARITIANA *[1] ; Nivohanitra Perle RAZAFINDRAIBE[2] ; Bodonarivo Olivia ANDRIAMBAHINY[1] ; Soa Fy ANDRIAMANDIMBY[3] ; Yassa Daniel NDJAKANI[4] ; A Harena RASAMOELINA[4]
[1]Direction de la Veille Sanitaire, Surveillance Epidémiologique et Riposte » (Disease Surveillance and Response Department), Ministry of Health, Madagascar/ Ministry of Public Health (Madagascar)/ Madagascar (Madagasikara), [2]Direction des Services Vétérinaires » (National veterinary services)/ Ministtry of Agriculture and livestock/ Madagascar (Madagasikara), [3]Virology Department/ Institut Pasteur de Madagascar/ Madagascar (Madagasikara), [4]RSEI/ Unité de Veille Sanitaire » (Health Unité), Indian Ocean Commission/ Mauritius (Moris)

Introduction and Objectives or Purpose

Rabies is a zoonotic disease that is 100% fatal once clinical symptoms appear. It is endemic in many poor countries like Madagascar, and is underestimated due to the weakness of surveillance. As from 2016, the surveillance of rabies in Madagascar was strengthened (use of NTIC in data collection, One Health approach, training of frontliners). This study assessed the impact of these reinforcements on the surveillance results.

Methods

Data came from surveillance and investigation databases from the Ministries of livestock and health for the period of 2013 to 2021. Surveillance results before and after June 2016 were compared. The number of notifications, the timeliness of the alert and the proportion of information shared between two sectors (human and animal health) were calculated.

Results or Focus

From 2013 to 2021, 64 human cases were recorded, including 50 suspected cases (SC) and 14 confirmed cases (CC). For animals, 841 cases including 497 SC, 162 probable cases (PC) and 182 CC were recorded.

Before June 2016, we counted 34 cases (30 SC, 5 CC) in humans and 37 cases (27 SC, 11 CC) in animals. After June 2016, there were 29 human cases (20 SC, 9 CC) and 803 animal cases (470 SC, 162 PC, 171 CC).

The alert timeliness was 45 days (average) before 2016, versus 4 days after.

Before June 2016, the information sharing between two sectors was informal and not recorded systematically. Since June 2016, all CC for both sectors and 60% of PC animals have been shared.

All of the CC and PC animal cases were investigated after 2016, compared to 18% of them before.

Conclusion or Scope

The effort in rabies surveillance in Madagascar since 2016 was effective. However, biological surveillance needs actions to improve the proportion of confirmed cases. The next challenges are the preventive and response measures.

Acknowledgement

Strengthen rabies ONE HEALTH surveillance in Madagascar

Keywords: rabies, surveillance, improvement, One Health, Madagascar

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15343

Improvement of Rabies surveillance in Madagascar from 2013 to 2021

Dany Bakoly RANOARITIANA *[1] ; Nivohanitra Perle RAZAFINDRAIBE[2] ; Bodonarivo Olivia ANDRIAMBAHINY[1] ; Soa Fy ANDRIAMANDIMBY[3] ; Yassa Daniel NDJAKANI[4] ; A Harena RASAMOELINA[4]
[1]Direction de la Veille Sanitaire, Surveillance Epidémiologique et Riposte » (Disease Surveillance and Response Department), Ministry of Health, Madagascar/ Ministry of Public Health (Madagascar)/ Madagascar (Madagasikara), [2]Direction des Services Vétérinaires » (National veterinary services)/ Ministtry of Agriculture and livestock/ Madagascar (Madagasikara), [3]Virology Department/ Institut Pasteur de Madagascar/ Madagascar (Madagasikara), [4]RSEI/ Unité de Veille Sanitaire » (Health Unité), Indian Ocean Commission/ Mauritius (Moris)

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Acknowledgement

Strengthen rabies ONE HEALTH surveillance in Madagascar

Keywords: rabies, surveillance, improvement, One Health, Madagascar

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15383

Strengthening One Health Approach Rabies Control Program to Reduce Rabies Deaths in Bangladesh

SADIA AFRIN[*1] ; M SALIM UZZAMAN[2] ; S. M. GOLAM KAISAR[3] ; TAHMINA SHIRIN[4] ; QUAZI ZAKI[5]
[1]Field Epidemiology Training Program, Bangladesh/ Institute of Epidemiology Disease Control And Research / Bangladesh (□□□□□□□□□), [2]EIDs & One Health/ Institute of Epidemiology Disease Control And Research/ Bangladesh (□□□□□□□□□), [3]Zoonotic Disease Control Program/ Communicable Disease Control, Directorate General of Health Services/ Bangladesh (□□□□□□□□□), [4]Director/ Institute of Epidemiology Disease Control And Research/ Bangladesh (□□□□□□□□□), [5]Technical Advisor/ Global Health Development (GHD)/ Bangladesh (□□□□□□□□□)

Introduction and Objectives or Purpose

Rabies is a major public health concern in Bangladesh. Rabies Prevention & Control program (RPCP) is implemented by Communicable Disease Control, Directorate general of Hospital Services (CDC, DGHS) under ‘One-Health Approach’. Mass Dog Vaccination (MDV) program followed by Post Exposure Prophylaxis (PEP) in Human are the major components of rabies control program, followed by community awareness and dog population control. We assessed RPCP data to identify the areas need strengthen for timely vaccination in human to prevent mortality and contain rabies sources in animals.

Methods

We accessed RPCP rabies case-data from 2019-2021 at Infectious Disease Hospital, Mohakhali, Dhaka (National Rabies Prevention and Control Centre). Descriptive analysis of the rabies exposures, interventions and outcome in urban and rural setting from all 67 Rabies Prevention and Control Centre was done.

Results or Focus

A total of 118 cases of clinically confirmed rabies cases were identified between 2019 and 2021 with 100% mortality. Most of the victims were male (69.5%), resided in the rural area (73.7%), and middle age 31-45 years (32.2%). Among the deaths 68.6% was bitten by dogs, 11.9% by jackals/foxes, 5.9% by cats and 3.4% by mongoose. Upper and Lower Limbs were the most common (72.8%) exposure sites. Only 50.9% had severe bite. The shortest incubation period was identified in bites to face (18.11±6.69 days; $p<0.001$) and neck (26.67±11.93 days; $p<0.05$). Among deaths 30.5% received PEP.

Conclusion or Scope

Rabies death is preventable if timely PEP could be ensured in human. Successful Rabies prevention and control program can only be achieved if the approach is “One Health Approach” which includes community awareness to seek early healthcare for PEP, mass dog vaccination and control of dog population.

Acknowledgement

The authors are grateful to the respective Officer, In-charge and staffs of CDC, DGHS and IDH, Mohakhali, Dhaka for their support for the collection of baseline data for this study.

Keywords: Rabies; Bangladesh; One-health approach; Post exposure prophylaxis

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15396

SPATIAL AND TEMPORAL DISTRIBUTION OF TAENIA SOLIUM AND ITS RISK FACTORS IN UGANDA

Nicholas Ngwili*[1] ; Derrick Sentamu [1] ; Moses Adriko[2] ; Prudence Beinamaryo [2] ; Michel Dione [3] ; Joyce Moriku Kaducu [4] ; Alfred Mubangizi[2] ; Pauline Mwinzi [5] ; Lian Thomas [1 6] ; Matthew Dixon [7 8 9]
[1]Animal and Human Health / International Livestock Research Institute (ILRI)/ Kenya, [2]Vector Borne and Neglected Tropical Disease Control Division/ Ministry of Health, Uganda/ Uganda, [3]Animal and Human Health/ International Livestock Research Institute (ILRI)/ Senegal (Sénégal), [4]Primary healthcare/ Ministry of Health/ Uganda, [5]Regional Office for Africa/ World Health Organization/ Congo, Democ. Republic of the, [6]Institute of Infection, Veterinary & Ecological Sciences/ University of Liverpool/ United Kingdom, [7]Department of Infectious Disease Epidemiology and London Centre for Neglected Tropical Disease Research (LCNTDR)/ School of Public Health, Imperial College / United Kingdom, [8]Edinburgh House, 170 Kennington Lane/ SCI Foundation/ United Kingdom, [9]MRC Centre for Global Infectious Disease Analysis/ Imperial College London/ United Kingdom

Introduction and Objectives or Purpose

Lack of sub-national mapping of Taenia solium infections in endemic countries presents a major challenge to achieving intensified T. solium control milestones. The aim of this study was to map all available T. solium prevalence data and PCC risk factors (including assessing the temporal change in risk factors) within Uganda, to understand the T. solium landscape and sub-national variation of indicators.

Methods

We combined a systematic literature review (SLR) of T. solium infection data and geospatial mapping of porcine cysticercosis (PCC) risk factors in Uganda. T. solium prevalence data identified through the SLR was adjusted for diagnostic sensitivity and specificity in a Bayesian Framework. Spatial autocorrelation and interpolation techniques were used to transform and map Demographic and Health Survey cluster-level sanitation and poverty indicators. These were overlaid onto a pig density map for Uganda to model combined PCC risk.

Results or Focus

Sixteen articles (n = 11 PCC and n = 5 human cysticercosis (HCC) and/or human taeniasis) were included in the final analysis. HCC observed prevalence ranged from 0.01%–6.0 % (confidence interval range: 0.004–11.4%), while adjusted PCC ranged from 0.3 – 93.9% (uncertainty interval range: 0–99.8%). There was substantial variation in the modelled PCC risk factors and prevalence across Uganda and over time.

Conclusion or Scope

There was marked variation in T. solium prevalence across Uganda, and in combination with the PCC risk maps, highlights geographic areas of potentially high risk, especially in Northern areas. The high PCC prevalence and moderate HCC exposure estimates indicate the need for urgent implementation of T. solium control efforts in Uganda.

Acknowledgement

Max Korir ; m.korir@cgiar.org ; ILRI

Keywords: Taenia solium, risk factor mapping, Spatial statistics, One Health, zoonotic diseases

Topic: One Health Science (OHS): Discovery and Surveillance: Neglected tropical diseases
Abstract No: 15392

One Health in The Americas: A Veterinary Public Health Approach

Natalia Margarita *[1] ; Marco Vigilato[2] ; Baldomero Molina[3] ; Alvaro Faccini[4] ; Alexander Biondo[5] ; Wagner Chiba[6]
[1]Facultad de Ciencias Agropecuarias/ Universidad de La Salle / Colombia, [2]Coordination Zoonoses Area / PANAFTOSA-PAHO/ WHO/ Brazil (Brasil), [3]Zoonoses area/ PANAFTOSA-PAHO/WHO/ Brazil (Brasil), [4]Instituto de Investigaciones/ Fundación Universitaria de Ciencias de la Salud – FUCS/ Colombia, [5]Graduate Program of Cellular and Molecular Biology/ Federal University of Paraná/ Brazil (Brasil), [6]ILACVN/ Instituto Latino-Americano de Ciências da Vida e da Natureza/ Brazil (Brasil)

Introduction and Objectives or Purpose

In September 2021, during the 59th Directing Council of the Pan American Health Organization (PAHO) and the 73rd Session of the Regional Committee of WHO for the Americas, it was adopted the policy One Health: A Comprehensive Approach for Addressing Health Threats at the Human-Animal-Environment Interface. The objective of this policy is to foster coordination and collaboration between the different governance frameworks of human, animal, vegetal and environmental health programs aiming the improvement of prevention and preparation for current and future health challenges and threats.

Methods

In July 12-13th, 2022, Brazil (PANAFTOSA/VPH-PAHO/WHO) – PANAFTOSA/PAHO held a meeting bringing together recognized public health and agricultural defense authorities from countries in the Americas with the objective of developing a baseline for the region regarding the use of the One Health approach in intersectoral actions for the achievement of better operationalization to manage public health problems associated with the human-animal-environment interface, in accordance with PAHO's One Health Policy. The meeting was attended by 17 authorities from Ministries of Health and Agriculture from 10 different countries of the region, including representatives of the Americas in the World Health Organization's Panel of One Health Experts (OHHLEP-WHO).

Results or Focus

During the working days, the professionals were able to present initiatives carried out in their countries and exchange successful experiences with examples of actions applied at local levels and restructure and formation of national agencies encompassing the One Health approach in their mission, as well as discussing perspectives and the main challenges they envision for policy implementation. Topics such as governance and legal frameworks, the identification of priorities and actors involved, and the sustainability of actions were some of the most discussed topics.

Conclusion or Scope

It was established a strategy for the implementation of One Health policies for the Americas and the consolidation of shared experiences.

Acknowledgement

We thank to the authorities from Ministries of Health and Agriculture from the different countries of the region who participated in the Meeting (Argentina, Brazil, Belize, Bolivia, Colombia, Cuba, Chile, Honduras, Mexico, Uruguay).

Keywords: One Health; Policy; Implementation; Veterinary Public Health; The Americas

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 14730

The feasibility of SARS-CoV-2 surveillance using wastewater and environmental sampling in Indonesia

Indah Kartika Murni*[1 2] ; Vicka Oktaria[1 3] ; Amanda Handley[4 5] ; David T McCarthy[6] ; Celeste M Donato[4 7] ; Titik Nuryastuti[8] ; Endah Supriyati[9] ; Ida Safitri Laksono[1 2] ; Jarir At Thobari[1] ; Julie E Bines[4 10 7]

[1]Center for Child Health – Pediatric Research Office / Faculty of Medicine, Public Health and Nursing, Universitas Gadjah Mada/ Indonesia, [2]Child Health Department / Faculty of Medicine, Public Health and Nursing, Universitas Gadjah Mada/ Indonesia, [3]Department of Biostatistics, Epidemiology and Population Health/ Faculty of Medicine, Public Health and Nursing, Universitas Gadjah Mada/ Indonesia, [4]Enteric Diseases Group / Murdoch Children's Research Institute/ Australia, [5]Medicine Development for Global Health/ Medicines Development for Global Health/ Australia, [6]Environmental and Public Health Microbiology Lab (EPHM Lab), Department of Civil Engineering/ Monash University/ Australia, [7]Department of Paediatrics/ The University of Melbourne/ Australia, [8]Department of Microbiology/ Faculty of Medicine, Public Health and Nursing, Universitas Gadjah Mada/ Indonesia, [9]Center for Tropical Medicine/ Faculty of Medicine, Public Health, and Nursing, Universitas Gadjah Mada/ Indonesia, [10]Department of Gastroenterology and Clinical Nutrition/ Royal Children's Hospital Melbourne/ Australia

Introduction and Objectives or Purpose

There is a need to explore the feasibility of wastewater-based epidemiology (WBE) surveillance for monitoring community transmission of SARS-CoV-2 in the setting where sewer and non-sewer sewage systems are implemented.

Methods

A routine WBE surveillance in 3 districts in Yogyakarta province, Indonesia, for 6-month (Phase 1, during Delta wave surge) and 3-month (Phase 2, during Omicron wave surge) periods, was conducted. Samples were collected on a weekly or fortnightly basis with grab and/or passive sampling methods, as well as to conduct qualitative and quantitative identification of SARS-CoV-2 Ribonucleic acid using the real-time RT-PCR in the environmental samples were explored. Water samples were collected from central and community wastewater treatment plants (WWTPs), including manholes flowing to central WWTP, and additional soil samples were collected for the near-source tracking locations (i.e., public spaces where people congregate).

Results or Focus

We collected 1,233 samples (Phase 1, 27 July 2021 to 7 January 2022) and 214 samples (Phase 2, 18 January to 7 April 2022). The positivity rate of wastewater detection decreased as the COVID-19 cases in the community reduced over time. During the Delta waves, the highest and the lowest positivity rates were 83.7%, and 1.8% whereas when the Omicron wave hit, the highest and lowest positivity rates were 94.4% and 12.5%, respectively. Challenges included providing real-time results during peak COVID-19 outbreaks due to overburdened staff and limited access to equipment, the availability of imported reagents have delayed laboratory analysis during periods of high output, and data interpretation to link environmental and community data.

Conclusion or Scope

A WBE surveillance system for SARS-CoV-2 in Indonesia is feasible to conduct for monitoring community burden of infections. In order to successfully implement a real-time WBE surveillance for SARS-CoV-2, the challenges will need to be addressed.

Acknowledgement

We thank PATH, WWTP team, research assistants, and laboratory team for their support during the study conduct.

Keywords: wastewater-based epidemiology surveillance; environmental sampling; SARS-CoV-2; COVID-19; Indonesia

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 14784

Hand, foot and mouth disease in southern Vietnam during 2015 – 2021

Hong Nguyen Thi Thu*[1] ; Nhan Le Nguyen Thanh[2] ; Khanh Truong Huu[2] ; Van Hoang Minh Tu[1] ; Ny Nguyen Thi Han[1] ; Nhu Le Nguyen Truc[1] ; Nguyet Lam Anh[1] ; Thanh Tran Tan[1] ; Qui Phan Tu[3] ; Tan Le Van[1]
[1]Emerging Infection group/ Oxford University Clinical Research Unit/ Vietnam (Việt Nam), [2]Department of Infection – Neurology/ Children’s Hospital 1/ Vietnam (Việt Nam), [3]Ward D/ Hospital for Tropical Diseases/ Vietnam (Việt Nam)

Introduction and Objectives or Purpose

Hand, foot and mouth disease (HFMD) continues to challenge Asia with pandemic potential. In Vietnam, there have been two major outbreaks occurring during 2011–2012 (>200,000 hospitalizations and >200 deaths) and more recently in 2018 (>130,000 hospitalizations and 17 deaths). Given the high burden and the complex epidemic dynamics of HFMD, synthesizing its clinical and epidemiological data remains essential to develop appropriate interventions and apply public health measures.

Methods

From 2015-2021, clinical samples were collected from patients enrolled in a HFMD study conducted at three referral hospitals in Ho Chi Minh City, Vietnam. Enterovirus diagnosis and serotypes determination was carried out using a combination of PCR and sequencing approaches. All EV-A71 positive cases were then subtyped by Sanger sequencing and/or whole-genome sequenced using next-generation based approach

Results or Focus

A total of 19 enterovirus serotypes were detected in 1660 HFMD patients enrolled in the study during 2015–2021. EV-A71 (26.2%, n=435) remains the leading cause of HFMD in Vietnam, followed by coxsackievirus A6 (CV-A6, 17.8%, n=296), CV-A16 (11%, n=184) and CV-A10 (7.1%, n=118). There are two main EV-A71 subgenogroups, C4 and B5, and their prevalence interchanges over the years. EV-A71 C4 displayed low activity during 2015 – early 2018 and then emerged in late 2018, early 2019 and late 2020. Compared with B5, C4 was more likely to be associated with severe HFMD. During the study period, the proportion of CV-A6 and CV-A16 increased in 2017 followed by a drop in 2018, and then went up again between 2019 and 2021

Conclusion or Scope

Our data have provided significant insights into important aspects of HFMD over seven years (2015–2021) in Vietnam, and emphasize active surveillance for pathogen circulation remains essential to inform the local public health authorities in the development of appropriate intervention strategies to reduce the burden of this disease. Multivalent vaccines are urgently needed to control HFMD

Keywords: Hand, foot and mouth disease; EV-A71; Coxsackievirus;

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 14786

DIVERSITY OF SARS-COV-2-RELATED CORONAVIRUS IN THE LEAST HORSESHOE BAT (RHINOLOPHUS PUSILLUS) IN THAILAND

Ananporn Supataragul*[1] ; Sininat Petcharat[1] ; Khwankamon Rattanatumhi[1] ; Sasiprapa Ninwattana[1] ; Opass Putcharoen[1] ; Supaporn Wacharapluesadee[1]
[1]Thai Red Cross Emerging Infectious Diseases Clinical Center/ King Chulalongkorn Memorial Hospital/ Thailand (□□□)

Introduction and Objectives or Purpose

SARS-CoV-2-related coronaviruses have been reported in several Rhinolophus bats. At least 23 horseshoe bat species are roosting in Thailand, however, only one complete genome sequence of SARS-CoV-2-related coronavirus is available. Therefore, this study aims to identify novel genomes in Rhinolophus pusillus, a host for SARS-CoV-2-related coronaviruses in Laos.

Methods

Novel bat coronavirus genomes were sequenced from rectal swabs of R. pusillus using Illumina MiSeq with library enrichment. Genome sequences were assembled by performing reference mapping and de novo assembly. Phylogenetic analyses were performed on nucleotide sequence alignment of the whole genome, spike gene and receptor-binding domain (RBD).

Results or Focus

Three complete SARS-CoV-2-related coronavirus genomes were identified from a single population of R. pusillus in Thailand, labelled as Rp65, Rp105 and Rp146. The three genomes create a new clade close to SARS-CoV-2 in the whole-genome phylogenetic tree. Rp65 shared the highest nucleotide identities of 92% with SARS-CoV-2 and other closely related bat coronaviruses, RaTG13 and BANAL-52. While the other two genomes shared 90% and 88%, respectively. In contrast, the spike phylogenetic tree split the three genomes into different clades with 91%, 81% and 78% similarity to SARS-CoV-2, respectively. Moreover, the RBD phylogenetic tree separates the genomes to a greater extent with sequence similarity to SARS-CoV-2 of 86%, 71% and 70%, respectively. Prediction of angiotensin-converting enzyme 2 (ACE2) receptor utilization from the RBD indicates that only one genome appeared to be non-ACE usage coronavirus.

Conclusion or Scope

Three distinct SARS-CoV-2 related coronaviruses were identified from a single population of R. pusillus in Thailand. Despite a relatively similar overall genomic sequence, their spike and RBD are considerably different. This implies that several SARS-CoV-2 related coronaviruses are circulating in the same population of R. pusillus bat, thus increasing the possibility of recombination between multiple variants.

Acknowledgement

This study was supported by the National Institute of Allergy and Infectious Diseases (NIAID-CREID:U01AI151797,EID-SEARCH)

Keywords: SARS-CoV-2-related coronaviruses; Rhinolophus bats

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 14787

COEXISTENCE OF MULTIPLE CORONAVIRUS IN CHAEREPHON PLICATUS IN RATCHABURI PROVINCE, THAILAND

Khwankamon Rattanatumhi[*1] ; Nattakarn Thippamon[1] ; Sininat Petcharat[1] ; Sasiprapa Ninwattana[1] ; Opass Putcharoen[1] ; Supaporn Wacharapluesadee[1]
[1]King Chulalongkorn Memorial Hospital/ Thai Red Cross Emerging Infectious Diseases Clinical Center/ Thailand (□□□)

Introduction and Objectives or Purpose

Bats are presumed as natural reservoirs of many emerging zoonotic viruses, including coronaviruses (CoVs). The genome of severe acute respiratory syndrome coronavirus (SARS-CoV), Middle East respiratory syndrome coronavirus (MERS-CoV), and SARS-CoV-2 are associated with bat coronaviruses. This study determined the diversity of coronaviruses circulating in one bat species, Chaerephon plicatus, collected from the same cave.

Methods

We performed a cross-sectional survey twice in Ratchaburi province in September 2020 and October 2021. A total of 122 bats were sampled; oral and rectal swabs of individual bats were collected. Two pan-coronavirus PCR protocols were performed using consensus primers amplified at the RdRp gene region.

Results or Focus

We found 4.10% CoVs positive from rectal and oral swab specimens, with 3.28% (4/122) Alphacoronavirus and 0.82% (1/122) Betacoronavirus. Analysis of the coronavirus RdRp sequences (~300-400 bp) revealed a high genetic diversity of coronaviruses found in one bat species. Three different subgenera in the Alphacoronavirus were identified, including; Rhinacovirus (n=1), Pedacovirus (n=1), and unclassified Alphacoronavirus (n=2). Furthermore, MERS like coronavirus (genus Betacoronavirus, subgenus Merbecovirus; n=1) was found in the rectal swab of one bat.

Conclusion or Scope

At least five coronavirus species were identified from C. plicatus bats roosting in the same cave. Interestingly two zoonotic-related viruses were found from bat rectal swab specimens; Porcine epidemic diarrhea-like virus and MERS-like coronavirus, with 90.91% and 82.35% similarity, respectively. The whole-genome sequence needs to be further characterized to better understand the similarity and risk of these viruses to humans and other livestock animals.

Acknowledgement

This study was supported by the National Institute of Allergy and Infectious Diseases of the National Institute of Health (NIAID-CREID U01AI151797 EID-SEARCH).

Keywords: Coronaviruses; Chaerephon plicatus; Thailand

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 14796

UNIQUE ANTIGENIC PROFILES OF SARS-COV-2 OMICRON SUBVARIANTS DEFINE DISTINCTIVE SEROTYPES OF HUMAN-INFECTING SARS-RELATED CORONAVIRUSES

Chee Wah Tan*[1] ; Feng Zhu[1] ; Wan Ni Chia[1] ; Beng Lee Lim[1] ; Aileen Ying-Yan Yeoh[1] ; Wee Chee Yap[1] ; Jinyan Zhang[1] ; Yun Yan Mah[1] ; Shiwei Chen[1] ; Lin-Fa Wang[1]
[1]Progromme in Emerging Infectious Diseases/ Duke-NUS Medical School/ Singapore

Introduction and Objectives or Purpose

Multiple Omicron sub-lineages have emerged, with Omicron BA.2.12.1 and BA.4/BA.5 already taking over BA.2 in some nations.

Methods

Using a pseudovirus virus neutralization system, we compared the different profiles of NAb evasion by BA.1, BA.2, BA.2 L452R, BA.2 F486V, and BA.4/BA.5 using 149 plasma samples representing nine different immune statuses.

Results or Focus

Here, we provide data showing that BA.4/BA.5 is the most potent in evading neutralizing antibody (NAb) activities and that Omicron BA.2 with point mutation L452R or F486V was sufficient to cause significant loss of NAb activities. Infection of naïve population by either Omicron BA.1 or BA.2 produced an overall low level of NAbs. Close examination of cross-neutralization activities using convalescent sera from naïve individuals who had recovered from SARS-CoV-2, Omicron BA.1/BA.2, or SARS-CoV-1 infection, respectively, revealed no significant cross-neutralization in any of the three-way analyses. This new finding would argue for an assignment of distinct serotypes for SARS-CoV-1, SARS-CoV-2, and Omicron BA.1/BA.2. Finally, it is noted that while infection in the naïve population showed no significant cross-neutralization activities, booster vaccination and/or Omicron-breakthrough infection can still lead to the production of cross-NAbs against Omicron BA.4/BA.5.

Conclusion or Scope

Our current data hence indicate that distinctive serotypes exist for the different SARS-related CoVs which are capable of infecting and causing diseases in humans.

Acknowledgement

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Keywords: SARS-CoV-2, Omicron subvariants, serotyping

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 14926

CHARACTERIZING HOW ONE HEALTH IS USED AND DEFINED WITHIN PRIMARY RESEARCH: A SCOPING REVIEW

Sydney Pearce*[1] ; David Kelton[1] ; Charlotte Winder[1] ; Jan Sargeant[1] ; Jamie Goltz[1] ; Jane Parmley[1]
[1]Department of Population Medicine/ University of Guelph/ Canada

Introduction and Objectives or Purpose

One Health (OH) can be used to tackle a variety of complex problems, making its wide-ranging research applications and definitions difficult to summarize. To improve our ability to describe and track OH's evolution, our objectives were to characterize (1) the who, what, where, when, why, and how (5W&H) of primary research articles that include a statement about using One Health, and (2) the One Health definitions used.

Methods

A scoping review was conducted using nine discipline-diverse databases and the search term 'One Health' in June 2021. Articles were screened by two reviewers using pre-specified eligibility criteria. The search collected 11,441 results and screening identified 252 primary research articles indicating use of OH. 5W&H data and definitions were extracted from these studies.

Results or Focus

Articles began in 2010 and of the total (n=252), approximately half were published in 2020-June 2021 (n=130). First authors most often had European (n=101) and North American (n=70) affiliations, but data collection location was more evenly distributed. Common disciplines represented in affiliations were human health/biology (n=198), animal health/biology (n=157), food/agriculture (n=81), and environment/geography (n=80). Infectious disease was the only research topic addressed until 2014 and continues to be the most published (n=171) with antimicrobial resistance second (n=47) and diversity increasing over time. Study designs similarly became more diverse and included both quantitative and qualitative methods. Studies' objectives indicated that they were conducted for the benefit of humans (n=187), animals (n=130), physical-environment (n=55), social-environments (n=33), and plants (n=4). Among definitions, many consider OH an 'approach' (n=79) that is 'multi/cross/inter/trans-disciplinary' (n=77), 'collaborative' (n=54), 'interconnected' (n=35), applied 'locally/regionally/nationally/globally' (n=84), and includes health pillars ('human'=124, 'animal'=122, 'environmental/ecosystem'=118).

Conclusion or Scope

Characterizing the 5W&H of primary OH research showed a rapidly growing and diversifying body of work, illuminating how OH has evolved and tackled global issues. It also revealed potential gaps and inconsistencies for future actors to address.

Keywords: One Health applications; primary research; One Health evolution; infectious disease; antimicrobial resistance

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 14956

The growing issue of influenza infections in pigs and the related zoonotic risk

Annika Graaf*[1] ; Christin Hennig[1] ; Kathrin Schmies[2] ; Kathrin Lillie-Jaschniski[3] ; Monika Koechling[3] ; Martin Beer[1] ; Elisabeth Grosse Beilage[2] ; Timm Harder[1]

[1]Institute of Diagnostic Virology/ Friedrich-Loeffler-Institute/ Germany (Deutschland), [2]Field Station for Epidemiology/ University of Veterinary Medicine, Foundation/ Germany (Deutschland), [3]Veterinary Services/ Ceva Animal Health/ Germany (Deutschland)

Introduction and Objectives or Purpose

Self-sustaining (enzootic) forms of swine influenza A infections (swIAV) in pig holdings are gaining ground. Covert respiratory disease adversely affects animal wellbeing and economics. Moreover, global pig populations must be considered as a broad and deep reservoir of IAV with building blocks of zoonotic and even (pre-)pandemic potential. Endemic virus circulation in pigs and reverse zoonotic transmission events from human to pig constantly feed the pool of potentially zoonotic influenza viruses. The focus of our study lies on defining the epidemiological and economic factors that drive the prevalence and dynamics of swIAV in large pig herds.

Methods

The conditions sustaining enzootic swIAV infections may depend on several factors, many of them being poorly understood (herd size, production systems, biosecurity level, housing conditions, co-infections, vaccination protocols and pre-existing herd immunity, local pig density). Therefore, longitudinal studies are implemented in selected herds that face continuous swIAV infections in Germany.

Results or Focus

A diagnostic algorithm for the simultaneous detection and characterization by reverse transcription real-time PCR (RT-qPCR) of swIAV and the recently described porcine Respiro- (PReV-1) and swine Orthopneumoviruses (SOV) was established. Samples from 101 piglet producing herds were analyzed, of which 89 were RTq-PCR positive for swIAV, 71 for PReV-1 and three for SOV until today. Looking on co-infections, in 45 herds double and two triple infections were detected. Two of the herds with continuous swIAV circulation were selected for a longitudinal, several months lasting study including regular samplings and further antigenic determination.

Conclusion or Scope

The most recent human influenza pandemic demonstrated the potential impact of swIAV in terms of sparking pandemics, underscoring the necessity for continuous swIAV surveillance. An increase in knowledge of within-herd virus dynamics and evolution is needed in order to optimize intervention and prevention measures which counteract continuous production losses and emergence of new swIAV with zoonotic or even (pre)pandemic potential.

Keywords: swine Influenza A Virus; zoonosis; diagnosis; surveillance

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 14967

Detection of SARS-CoV-1/2 Antibodies in Domestic and Wild Animals in Nigeria

Ebere Agusi[*1] ; Clement Meseko[2] ; Olayinka Asala[3] ; Ismaila Shittu[2] ; Emmanuel Eze[4] ; Valerie Allendorf[5] ; Anja Globig[5] ; Jacob Schon[6] ; Donata Hoffmann[6] ; Anne Balkema-Buschmann[6]
[1]Biotechnology Centre/ National Veterinary Research Institute,Vom,Nigeria/ Nigeria, [2]Avian Influenza and other Transboundary animal diseases/ National Veterinary Research Institute,Vom,Nigeria/ Nigeria, [3]Viral Vaccine Production/ National Veterinary Research Institute,Vom,Nigeria/ Nigeria, [4]Microbiology/ University of Nigeria Nsukka/ Nigeria, [5]Institute for International Animal Health/ One Health/ Friedrich-Loeffler-Institut/ Germany (Deutschland), [6]Institute for Viral Diagnostics/ Friedrich-Loeffler-Institut/ Germany (Deutschland)

Introduction and Objectives or Purpose

Introduction: As at June 2022, the COVID-19 pandemic, caused by SARS-CoV-2 (subgenus Sarbecovirus), has killed more than six million people among 536 million recorded cases worldwide. Though animals are the natural reservoir of most known Coronaviridae, reverse zoonotic transmission from humans to animals and further propagation within different host populations could diversify SARS-CoV-2 evolution and complicate epidemiology. Transmission events of SARS-CoV-2 to animals have been documented worldwide, but limited information exists in Africa. In addition, it cannot be excluded that other, undiscovered, but potentially zoonotic Sarbecoviruses are circulating in African animals.

Objectives: To allow a better understanding of the role of domestic animals and wildlife in the ecology of Sarbecoviruses in Nigeria.

Methods

Methods: We tested 504 sera samples from dogs, rabbits, bats and pangolins using an indirect multi-species Enzyme Linked Immunosorbent Assay (ELISA) based on the receptor binding domain (RBD) of SARS-CoV-1 and SARS-CoV-2. ELISA reactive sera were analyzed by Virus Neutralization Test (VNT) in Vero E6 cells.

Results or Focus

Results: In this study, we found presence of SARS-CoV-1 and SARS-CoV-2 specific antibodies in some animals in Nigeria.

Conclusion or Scope

Conclusion: Anthropogenic exposure of domestic animals as well as close interactions with wildlife can result in bi-directional zoonotic transmissions of known and unknown Sarbecoviruses and reservoir status of animals. This requires further One Health-oriented surveillance including a particular emphasis on the potential reservoir role different species might play.

Acknowledgement

The project is funded by the German Global Health Protection Program (GHPP) and implemented jointly by: National Veterinary Research Institute (NVRI) and Friedrich-Loeffler-Institut (FLI).

Keywords: One Health, SARS-CoV, ELISA, Virus Neutralization, Animals, Wildlife, Nigeria

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 14987

Serological evidence of Sarbecovirus exposure in trafficked Sunda pangolins points to complex origins of infection

Brian M. WORTHINGTON[*1 2 3] ; Portia Y.-H. WONG[4] ; Kishoree K. KUMAREE[1 2 3] ; Tracey-Leigh PRIGGE[4] ; Kar Hon NG[1] ; Paolo MARTELLI[5] ; Yi GUAN[1 2 3 6] ; Hua Chen ZHU[1 2 3 6] ; Timothy C. BONEBRAKE[4] ; Tommy T.-Y. LAM[1 2 3 7 6]
[1]State Key Laboratory of Emerging Infectious Diseases, School of Public Health/ The University of Hong Kong, Li Ka Shing Faculty of Medicine/ Hong Kong (□□), [2]Guangdong-Hongkong Joint Laboratory of Emerging Infectious Diseases/ Joint Institute of Virology (Shantou University/The University of Hong Kong)/ China (□□), [3]Pathogen Research Institute/ EKIH (Gewuzhikang)/ China (□□), [4]Division of Ecology and Biodiversity, School of Biological Sciences/ The University of Hong Kong/ Hong Kong (□□), [5]Veterinary Department/ Ocean Park Corporation/ Hong Kong (□□), [6]Laboratory of Data Discovery for Health Limited/ (The University of Hong Kong)/ Hong Kong (□□), [7]Centre for Immunology & Infection Limited/ (Institut Pasteur/The University of Hong Kong)/ Hong Kong (□□)

Introduction and Objectives or Purpose

Pangolins are exceptional as the second group of mammals (after bats) from which diverse Severe Acute Respiratory Syndrome coronavirus 2 (SARSCoV2) related coronaviruses had been isolated prior to the COVID-19 pandemic. In this study, we conducted retrospective examination of archived Sunda pangolin specimens to identify any potential SARS-CoV-2 progenitors or other coronaviruses in this animal species, as well as to approximate the origins of these animals from wild populations throughout Southeast Asia.

Methods

We performed molecular screening of SARS-CoV-2 and a broader spectrum of coronaviruses in 815 specimens from 89 pangolins confiscated by Hong Kong authorities in 2013 (n=1) and 2018 (n=88). Methods for molecular detection of SARS-CoV-2 and coronavirus RNA were employed, as well as a serological survey for detection of antibodies cross-reactive with SARS-CoV-2.

Results or Focus

Six individuals were found to be seropositive using a double-antigen bridging assay to detect anti-SARS-CoV-2 spike antibodies. Coronavirus RNA was not detected through targeted polymerase chain reaction (PCR) detection. Putative seropositive individuals were determined to have originated from populations in Borneo, Java, and Sumatra, indicating that natural exposure to SARS-related coronaviruses (SARSr-CoVs) may be common due to the shared ecology of pangolins, bats, and potentially other host species, or this may indicate infection acquired during the illegal trafficking of these animals.

Conclusion or Scope

Although our study did not identify substantial evidence of SARS-CoV-2 related coronavirus in pangolins, the infection history of coronaviruses in pangolins should not be neglected. This work may better inform intervention and surveillance targets for implementation wildlife conservation and biosecurity measures.

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Extended list of coauthors: (University of Hong Kong) Y. Liao, M.P. Pierce, M.H.-H. Shum, E.F. Miot, W.Y.-M. Cheung, S. McIlroy, D.M. Baker, C. Dingle, G.M. Leung; (National University of Singapore) H.C. Nash; (Indonesian Institute of Sciences) Wirdateti, G. Semiadi; (Oxford University; Royal Veterinary College) O.G. Pybus; (University of Syndney) E.C. Holmes.

Keywords: pangolins, Sarbecovirus, SARS-related coronavirus, conservation forensics, serology

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15009

Informing biosurveillance: Contribution of pteropodid fruit bats to virus spillover in the Philippines

Sophie Borthwick*[1] ; Fedelino Malbas[2] ; Catalino Demetria[2] ; Phillip Alviola[3] ; Mary Grace Dacuma[3] ; Eric Laing[4] ; David Hayman[5] ; Gavin Smith[1 6 7 8]

[1]Program in Emerging Infectious Diseases/ Duke-NUS Medical School/ Singapore, [2]EID/ Research Institute for Tropical Medicine/ Philippines, [3]EID/ University of the Philippines Los Banos/ Philippines, [4]School of Medicine/ Uniformed Services University of the Health Sciences/ United States, [5]School of Veterinary Science/ Massey University/ New Zealand, [6]Centre for Outbreak Preparedness/ Centre for Outbreak Preparedness, Duke-NUS Medical School/ Singapore, [7]SingHealth Duke-NUS Global Health Institute/ SingHealth Duke-NUS Global Health Institute, SingHealth Duke-NUS Academic Medical Centre/ Singapore, [8]Duke Global Health Institute/ Duke University/ United States

Introduction and Objectives or Purpose

Bats are reservoirs for a multitude of zoonotic viruses. Cross-species transmission of bat-borne viruses to naïve hosts can result in mortality. However, predicting transmission risk is challenging. Environmental and biological factors contribute to population level virus shedding, but little is known about the mechanistic drivers of shedding episodes.

Methods

Efficacious biosurveillance can improve understanding of virus shedding pulses. Thus we propose to identify temporal trends in viral shedding and seroprevalence of high priority pathogens in fruit bats and determine the exposure of incidental hosts, such as humans and wild and domestic animals in the Philippines. We will also obtain serological samples from humans and livestock near sampling sites to establish evidence of previous spill-over.

Results or Focus

Our findings will identify risk factors that promote virus transmission.

We will build surveillance and advance diagnostic capabilities at the Research Institute of Tropical Medicine (RITM) in the Philippines, train numerous students, scientists, researchers and technicians, and initiate standardization of data collection to facilitate genomic analyses.

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15018

One Health community-based wildlife mortality surveillance for Ebola

Alain Ondzie[1] ; Sarah Olson[*2]
[1]Republic of Congo/ Wildlife Conservation Society/ Republic of the Congo, [2]Health Program/ Wildlife Conservation Society/ United States

Introduction and Objectives or Purpose

Central Africa remains a high-risk Ebolavirus (EBOV) region, but the Republic of Congo (RoC), home to the largest remaining populations of great apes, has not had an epidemic since 2005. EBOV ecology is not fully understood but infected wildlife and consumption of animal carcasses have been linked to human outbreaks, especially in the Congo Basin.

Methods

Since 2005, our One Health community-based wildlife mortality surveillance for EBOV has partnered with the Congolese Ministry of Health to reach communities and protected areas in northern RoC where people and great apes have died from past Ebola virus disease outbreaks. The outreach and surveillance is designed as an intervention to prevent contact between humans and infected animals and as an early warning system to locate carcasses or diseased animals and enable rapid detection of EBOV epizootics.

Results or Focus

Between April 2008 and September 2022, we conducted a total of 641 visits to 328 villages spread over 34 separate missions in four departments in the North of the RoC. We delivered the educational message to a total of 8,503 hunters, and to thousands of women and children who frequently visit the forest to gather food. Many villages were revisited each year. We achieved specimen collection by training project staff on a safe sampling protocol and equipping geographically distributed bases with sampling kits. We established in-country diagnostics, including recent deployment of mobile field-based platforms for EBOV testing, reducing diagnostic turnaround time to hours and days and demonstrated the absence of EBOV in 80 carcasses.

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Keywords: surveillance; community-based; ebola; One Health; Africa

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15035

Prevalence, Diversity and habitat association of Bartonella in Bat Communities Across Cambodia

Sophie Borthwick[*1] ; Alan Hitch[1] ; Dolyce Low[1] ; Lena Chng[1] ; Sothyra Tum[2] ; Sorn San[2] ; Dany Chheang[3] ; Ian Mendenhall[1] ; Gavin Smith[1 6 7 8]

[1]Program in Emerging Infectious Diseases/ Duke-NUS Medical School/ Singapore, [1]Department of Wildlife, Fish and Conservation Biology/ University of California, Davis/ United States, [2]National Animal Health Production and Research Institute/ General Directorate of Animal Health and Production/ Cambodia (□□□□□□□) [3]Department of Agriculture, forestry and fisheries/ Forestry Administration/ Cambodia (□□□□□□□) [6]Centre for Outbreak Preparedness/ Centre for Outbreak Preparedness, Duke-NUS Medical School/ Singapore [7]SingHealth Duke-NUS Global Health Institute/ SingHealth Duke-NUS Global Health Institute, SingHealth Duke-NUS Academic Medical Centre/ Singapore [8]Duke Global Health Institute/ Duke University/ United States

Introduction and Objectives or Purpose

Bartonella species are Gram-negative, facultative intracellular bacteria that represent the only genus in the family Bartonellaceae. Bats are natural reservoirs of many Bartonella species.

Methods

We investigated Bartonella presence and diversity in bats across 227 probabilistic locations in 23 provinces and 22 opportunistic locations in Cambodia from 2016 to 2020.

Results or Focus

A total of 1,744 bat blood and lung spleen kidney (LSK) samples were screened with pan-bartonella PCR primers targeting the beta subunit of bacterial RNA polymerase (rpoB) gene. Bartonella DNA was detected in 18.99% (331/ 1,744) of the bats collected during this project in Cambodia, from 61 species. Highest prevalence was detected Rhinolophus acuminatus from evergreen forest (38.89%). Phylogenetic analyses of 145 rpoB gene sequences showing the Bartonella genotypes circulating in the bat populations across Cambodia are presented.

Acknowledgement

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Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15101

OMICRON BA.1 AND BA.2 DISPLACEMENT DYNAMICS AT COMMUNITY AND UNIVERSITY CAMPUS LEVEL IN SINGAPORE

Desmond Chua*[1] ; Germaine Kwok[1] ; Wei Jie Ng[1] ; Se Yeon Kim[1] ; Wei Lin Lee[2 3] ; Xiaoqiong Gu[2 3] ; Martin Tay[4] ; Judith Chui Ching Wong[4] ; Stefan Wuertz[1 5] ; Janelle Thompson[1 6 3]
[1]Singapore Centre for Environmental Life Sciences Engineering / Nanyang Technological University/ Singapore, [2]Antimicrobial Resistance Interdisciplinary Research Group/ Singapore MIT Alliance for Research and Technology / Singapore, [3]Campus for Research Excellence and Technological Enterprise/ CREATE/ Singapore, [4]Microbiology & Molecular Epidemiology Division/ National Environmental Agency/ Singapore, [5]School of Civil and Environmental Engineering / Nanyang Technological University / Singapore, [6]Asian School of the Environment / Nanyang Technological University / Singapore

Introduction and Objectives or Purpose

Wastewater-based surveillance has demonstrated to be a useful complement for clinical community-based tracking of SARS-CoV-2 variants of concern (VOCs). We developed a method involving allele-specific (AS)-RT-qPCR to examine the dynamics of VOCs in wastewater. Using these assays, we were able to track the incidence and dynamics of the Omicron sublineages BA.1 and BA.2 in Singapore's wastewater.

Methods

Using design principles of our previous assays that detect SARS-CoV-2 variants (Alpha and Delta), we developed two additional AS-RT-qPCR assays which simultaneously target the stretch of mutations from Q493R to Q498R and L24- to A27S for quantitative detection of spike protein mutations associated with prevailing Omicron variant sublineages in wastewater.

Results or Focus

A retrospective analysis was carried out on water reclamation plant (WRP) influent and four University hostel sites in Singapore, from September 2021 to May 2022. We report co-arrival of mutations associated with Omicron BA.1 and BA.2 VOCs at two WRP streams in January 2022. Quantitation suggests that by January 2022 the two Omicron linages comprised nearly all of the SARS-CoV-2 signal, in alignment with the incidence of clinical cases. Co-arrival of the two lineages is an interesting result as many countries such as the USA, Denmark, South Africa and Italy reported initial BA.1 arrival before being displaced by BA.2. By mid-March BA.1 was completely displaced by BA.2 at the community level. At the University hostels, we report mixed results where two out of four sites showed initial BA.1 arrival before being outpaced by BA.2.

Conclusion or Scope

This work demonstrates that wastewater surveillance can be used to track the incidence of SARS-CoV-2 and its VOCs using samples collected in aggregate. We show here that SARS-CoV-2 variant concentrations, as determined using our allele-based qPCR-based assays, can be used to closely and quantitatively trace the displacement dynamics of VOCs in a catchment without biases associated with clinical case reporting.

Acknowledgement

SCELSE,SMART,NEA

Keywords: Covid-19; SARS-CoV-2; Variants of Concern; Wastewater Surveillance; Omicron

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15115

Phylodynamics of SARS-CoV-2 causing a large national-wide outbreak in Vietnam, 2021

Anh Nguyen*[1] ; Tung Trinh Son [2] ; Tam Nguyen Thi [2] ; Trang Dinh Van [3] ; Mai Le Thi Quynh [4] ; Thomas Kesteman[2] ; Dung Nguyen Thanh[5] ; Chau Nguyen Van Vinh[6] ; H. Rogier van Doorn[2] ; Tan Le Van[1]
[1]Emerging Infection/ Oxford University Clinical Research Unit/ Vietnam (Việt Nam), [2] Oxford University Clinical Research Unit/ Oxford University Clinical Research Unit/ Vietnam (Việt Nam), [3]National Hospital of Tropical Diseases/ National Hospital of Tropical Diseases/ Vietnam (Việt Nam), [4]NATIONAL INSTITUTE OF HYGIENE AND EPIDEMIOLOGY/ NATIONAL INSTITUTE OF HYGIENE AND EPIDEMIOLOGY/ Vietnam (Việt Nam), [5]Hospital of Tropical Diseases/ Hospital of Tropical Diseases/ Vietnam (Việt Nam), [6]Department of Health / Department of Health of Ho Chi Minh City/ Vietnam (Việt Nam)

Introduction and Objectives or Purpose

In 2021, Vietnam experienced a large national-wide outbreak of the severe acute respiratory syndrome coronavirus 2 (SARS-COV-2), with 1,896,723 cases and 34,082 deaths recorded. Here, we applied whole-genome sequence based phylogeographic analysis to unravel the patterns of SARS-CoV-2 dispersal and evolution in Vietnam.

Methods

1365 nasopharyngeal swabs, representing of community cases across Vietnam, were selected for whole-genome sequencing using ARTIC or University of Sydney's protocol. The evolutionary history of SARS-CoV-2 were assessed using maximum-likelihood and time-scaled Bayesian phylogenetic analyses.

Results or Focus

A total of 1303 SARS-CoV-2 genome sequences were generated. Various variants were documented with >99.5% of the sequences belonging to either Alpha or Delta variant. Between January and May, Alpha variant caused sporadic outbreaks in Red River Delta and Central Coast areas. Phylogenetic analysis indicated different introductions of the virus into Vietnam, attributed to the relaxing control measures applied at the time. From June onward, Delta replaced Alpha to become the dominant variant. The main lineage was AY.57, accounting for 99.2% of the Delta sequences obtained. Phylodynamic interference indicated that AY.57 was first introduced into the Northern Vietnam through a single event, explained by the strict control measures applied after the sporadic Alpha outbreaks between January and May. The dispersal of AY.57 to Southern Vietnam resulted in a major outbreak in Ho Chi Minh City. Subsequently, Ho Chi Minh City acted as a source seeding the virus back to the North and other regions. The estimated time to the most recent common ancestor was March 14, 2021 (February 22, 2021 to April 8, 2021), and the estimated evolutionary rate was 5.29×10^{-4} (4.966×10^{-4} to 5.639×10^{-4}) substitutions per site per year.

Conclusion or Scope

We demonstrated that genomic surveillance is critical to inform pandemic response. Our analysis illustrated the influence of public health measures on the patterns of SARS-CoV-2 importation into and dispersal within a local setting.

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OUCRU COVID-19 research group

Keywords: SARS-COV-2; whole genome sequence; phylodynamics; Vietnam; 2021

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15125

INVESTIGATING SPILLOVER OF SARS-COV-2 INTO NORWAY RATS (RATTUS NORVEGICUS) IN ONTARIO, CANADA

Sarah J. Robinson*[1] ; Jonathon D. Kotwa*[2] ; L. Robbin Lindsay[3] ; Antonia Dibernardo[3] ; Nikki Toledo[3] ; Bradley S. Pickering[4 5 6] ; Melissa Goolia[4] ; Samira Mubareka[2 7] ; Claire M. Jardine[1 8]
[1]Pathobiology/ Ontario Veterinary College, University of Guelph/ Canada, [2]Biological Sciences/ Sunnybrook Research Institute/ Canada, [3]National Microbiology Laboratory/ Public Health Agency of Canada/ Canada, [4]National Centre for Foreign Animal Disease/ Canadian Food Inspection Agency/ Canada, [5]Medical Microbiology and Infectious Diseases/ University of Manitoba/ Canada, [6]Veterinary Microbiology and Preventative Medicine/ College of Veterinary Medicine, Iowa State University/ United States, [7]Faculty of Medicine/ University of Toronto/ Canada, [8]Canadian Wildlife Health Cooperative/ Ontario Veterinary College, University of Guelph/ Canada

Introduction and Objectives or Purpose

Host plasticity of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has become apparent over the course of the pandemic and raised concerns about the establishment of novel wildlife reservoirs. Norway rats (Rattus norvegicus) live in close proximity to humans, providing opportunity for spillover of SARS-CoV-2. New animal species have been identified as competent hosts with emergence of novel variants, as demonstrated by the susceptibility of rats to the SARS-CoV-2 Alpha variant of concern (VOC) despite not being susceptible to ancestral SARS-CoV-2. We investigated SARS-CoV-2 infection and exposure in Norway rats from Ontario, Canada.

Methods

From October 2019 to June 2021, 224 rats were submitted by collaborating pest control companies. Nasal turbinate (n=164) and small intestinal (n=213) tissue samples were analyzed for SARS-CoV-2 RNA by RT-PCR. Thoracic cavity fluid samples (n=213) were tested for neutralizing antibodies using a surrogate virus neutralization test (sVNT); confirmatory plaque reduction neutralization test (PRNT) testing was conducted on presumptive positive samples.

Results or Focus

The majority of samples were collected in Windsor (79.9%; n=179), Hamilton (13.8%; n=31), and the Greater Toronto Area (5.8%; n=13). Overall, 50.0% (n=112) were female and 55.8% were sexually mature (n=125). Notably, 202 samples, including the two seropositives, were collected prior to the emergence of VOCs, and 22 were collected while the Alpha variant was the predominant circulating VOC in humans. We did not detect SARS-CoV-2 RNA in any rats. Two of eleven samples positive by sVNT had neutralizing antibodies by plaque reduction and neutralization (1:40 and 1:320 PRNT70).

Conclusion or Scope

We report evidence of past exposure to SARS-CoV-2 in Norway rats in North America. Monitoring SARS-CoV-2 in wildlife within a One Health framework is paramount to detection of spillover events and establishment of novel wildlife reservoirs.

Acknowledgement

Chelsea G. Himsworth, David L. Pearl, J. Scott Weese, Simon Jeeves, Hsien-Yao Chee, Juliette Blais-Savoie, Emily Chien, Winfield Yim, Lily Yip

Keywords: rats; SARS-CoV-2; surveillance; wildlife; zoonoses

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15148

DETECTING SARS-COV-2 IN DOGS AND CATS USING RAPID ANTIBODY AND ANTIGEN TEST KITS INTENDED FOR USE IN HUMANS

Lauren Cybulska*[1] ; Jean Grassman[1] ; Sarah Hamer[2]
[1]Environmental, Occupational, and Geospatial Health Sciences/ City University of New York Graduate School of Public Health and Health Policy/ United States, [2]School of Veterinary Medicine and Biological Sciences/ Texas A&M University/ United States

Introduction and Objectives or Purpose
SARS-CoV-2 is the virus that causes the disease Coronavirus-2019 (COVID-19) in humans. SARS-CoV-2 can also be found in animals such as dogs, cats, and non-human primates among others. The transmission cycle between humans and animals is not well understood. The purpose of this study was to develop an economical and practical method for disease surveillance that could be used by veterinarians and public health professionals in real-time for the detection of SARS-CoV-2 in domesticated canines and felines.

Methods
Commercially available human rapid COVID-19 lateral flow immunochromatographic assays used to detect virus antibodies and antigen have been used with canine and feline serum and molecular samples in a laboratory setting. SARS-CoV-2 virus was detected in the serum samples using viral neutralization methods. The virus was detected in molecular samples, derived from nasal and oral swabs, using RT-PCR and were stored in viral transport media (VTM) solution.

Results or Focus
The tests were more sensitive to canine samples compared when compared with feline samples. The rapid antibody tests resulted in 70% sensitivity and 60% specificity for dogs, and 50.0% sensitivity and 100% specificity for cats when compared with the gold standard method of viral neutralization. The rapid antigen tests resulted in 75.0% sensitivity and 79.2% specificity for dogs, and 57.1% sensitivity and 95.2% specificity for cats when compared with the gold standard method of RT-PCR.

Conclusion or Scope
These tests will be used in an upcoming field study in which pets will be tested in veterinary practices across New York City, and the rapid lateral flow immunoassays will be compared side-by-side with these gold standard techniques. The goal is to measure the prevalence of SARS-CoV-2 in domesticated dogs and cats across NYC using a cross-sectional study design and to determine the sensitivity and specificity of these commercially available tests in the detection of SARS-CoV-2 in a clinical setting.

Keywords: SARS-CoV-2; COVID-19; Animals; Veterinary; Surveillance

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15158

A SURVEY OF EXPOSURE TO SARS-COV-2 IN HUMANS WHO WORK WITH WILDLIFE IN THAILAND

Suthida Hearn*[1] ; Pawinee Doung-gnern[1] ; Sahaphap Poonkesorn[1] ; Kirana Noradechanon[2] ; Somying Thunhikorn[2] ; Teerasak Chuxnam[1]
[1]Division of Epidemiology/ Department of Disease Control/ Thailand (□□□), [2]Wildlife Conservation Office/ Department of National Parks, Wildlife and Conservation Office/ Thailand (□□□)

Introduction and Objectives or Purpose

This study aims to explore the risk exposure to SARS-CoV-2 in people who work with wildlife and persons residing in the surrounding community.

Methods

106 workers directly exposed to wildlife and a control group made up of 209 additional participants who live in areas nearby were included in the study during the period of late August 2021 to January 2022. The Wildlife exposure group had been in contact to bats and/ or other wild mammals because of their occupation in 7 high-risk provinces (Chachoengsao, Narathiwat, Ratchaburi, Nakhon Sawan, Sukhothai, Phang-gna and Surat Thani), that meet the following criteria: i.) evidence of the previous detection of MERS-CoV and/or SARS-CoV in bats in the area; and/or ii) report of sightings of intermediate horseshoe bats. Serum samples were collected to detect antibodies against nucleocapsid and spike protein of SARS-CoV-2 by using ELISA. Nasopharyngeal swabs were taken for molecular testing of SARS-CoV-2 in symptomatic participants afflicted with COVID-19 within the past two weeks.

Results or Focus

All nasopharyngeal swabs from wildlife workers and control group showed negative results (except one with invalid result). Almost 70% of the participants were seropositive. Most of the participants were vaccinated (246, 77.8%). Nine percent (2/22) of the unvaccinated wildlife exposure group were seropositive, whereas seroprevalence in the unvaccinated control group was 14.9% (7/47). When considering nucleocapsid protein antibodies in participants vaccinated with spike protein-based vaccines to identify pre-exposure to SARS-CoV-2, seropositivity due to exposure to SARS-CoV-2 in wildlife workers was less than with the control group, 3.8% (4/106) versus 5.3% (11/209) suggesting the main route of transmission is between humans.

Conclusion or Scope

Infection within the wildlife workers could indicate the circulation of this virus among human and wildlife population. This provides background information in monitoring viral transmission between human and wildlife for future prompt response.

Acknowledgement

Acknowledgement to Soawapak Hinjoy, Pasakorn Akarasewi and US CDC for their technical assistance to the project.

Keywords: SAR-CoV-2; wildlife worker; seropositive

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15178

Measuring Health Protocol Compliance during Regional Election Using Integrated Monitoring System in Indonesia

Dewi Nur Aisyah*[1 2 3] ; Thifal Kiasatina[2 3] ; Agus Heri Setiawan[2 3] ; Indira Rezki Wahyuni[2 3] ; Alfiano Fawwaz Lokopessy[2 3] ; Wiku Adisasmito[2 4 3] ; Logan Manikam[1 5] ; Zisis Kozlakidis[6]
[1]Department of Epidemiology and Public Health/ Institute of Epidemiology and Health Care, University College London/ United Kingdom, [2]Data and Information Technology/ COVID-19 National Task Force/ Indonesia, [3]INDOHUN/ Indonesia One Health University Network/ Indonesia, [4]Faculty of Public Health/ Universitas Indonesia/ Indonesia, [5]ACESO/ Aceso Global Health Consultants Limited/ United Kingdom, [6]International Agency for Research on Cancer/ World Health Organization/ France

Introduction and Objectives or Purpose

During COVID-19 pandemic, Indonesia held simultaneous 270 regionals elections including provincial, regency, and city election on December 9, 2020. The aim of this study is to describe the health protocol compliance during simultaneous regional elections in Indonesia using an integrated monitoring system.

Methods

The data has been collected from the Indonesia National Task Force for the Acceleration of COVID-19 Mitigation by using the Bersatu Lawan COVID-19 (BLC) digital monitoring app. The monitoring system was reported in real-time by Indonesian front-line public order forces (such as police and military) at regional election places. Individual and polling stations compliance were monitored to minimize COVID-19 transmission during the election process.

Results or Focus

A total of 309,236 voters' behaviours were monitored in 272 districts/cities across 32 provinces in Indonesia. The overall figures show 95.96% compliance of wearing masks and 90.77% of people kept a social distance during the election day. However, the compliance might vary between districts and cities. A total of 4,065 polling stations were observed with 92.82% had high compliance to the implementation of health protocol with details as follow: 91.55% provided hand washing facilities; 90.71% provided hand sanitizers; 89.52% had temperature check; 87.29% had health protocol compliance supervisors; 75.23% performed disinfection; 91.66% provided plastic gloves for voters; 92.91% election committee wore face shield; 88.98% provided ink drops; and 77.80% provided special chamber for voters with 37.3°C.

Conclusion or Scope

In conclusion, using the application of digital health, Indonesia as the 4th most populous country in the world enable to monitor the compliance rate of health protocol implementation during simultaneous regional elections in 2020. This represents the first time in which an app implemented nationally can produce data to be analysed on real-time basis and using an integrated approach to inform policy makers.

Keywords: COVID-19 pandemic, integrated system, election

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15250

WASTEWATER SURVEILLANCE REVEALS DYNAMICS OF SARS-COV-2 VARIANT DISPLACEMENT

Wei Lin Lee[*1] ; Federica Armas[*1] ; Flavia Guarneri[2] ; Xiaoqiong Gu[1] ; Nicoletta Formenti[2] ; Feng Jun Desmond Chua[3] ; Hongjie Chen[1] ; Franciscus Chandra[1] ; Giovanni Loris Alborali[2] ; Eric Alm[1] ; Janelle Thompson[3]
[1]AntiMicrobial Resistance/ Singapore-MIT Alliance for Research and Technology/ Singapore, [2]Sede Territoriale di Brescia/ Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna Italy/ Italy (Italia), [3]SCELSE/ Nanyang Technological University/ Singapore

Introduction and Objectives or Purpose

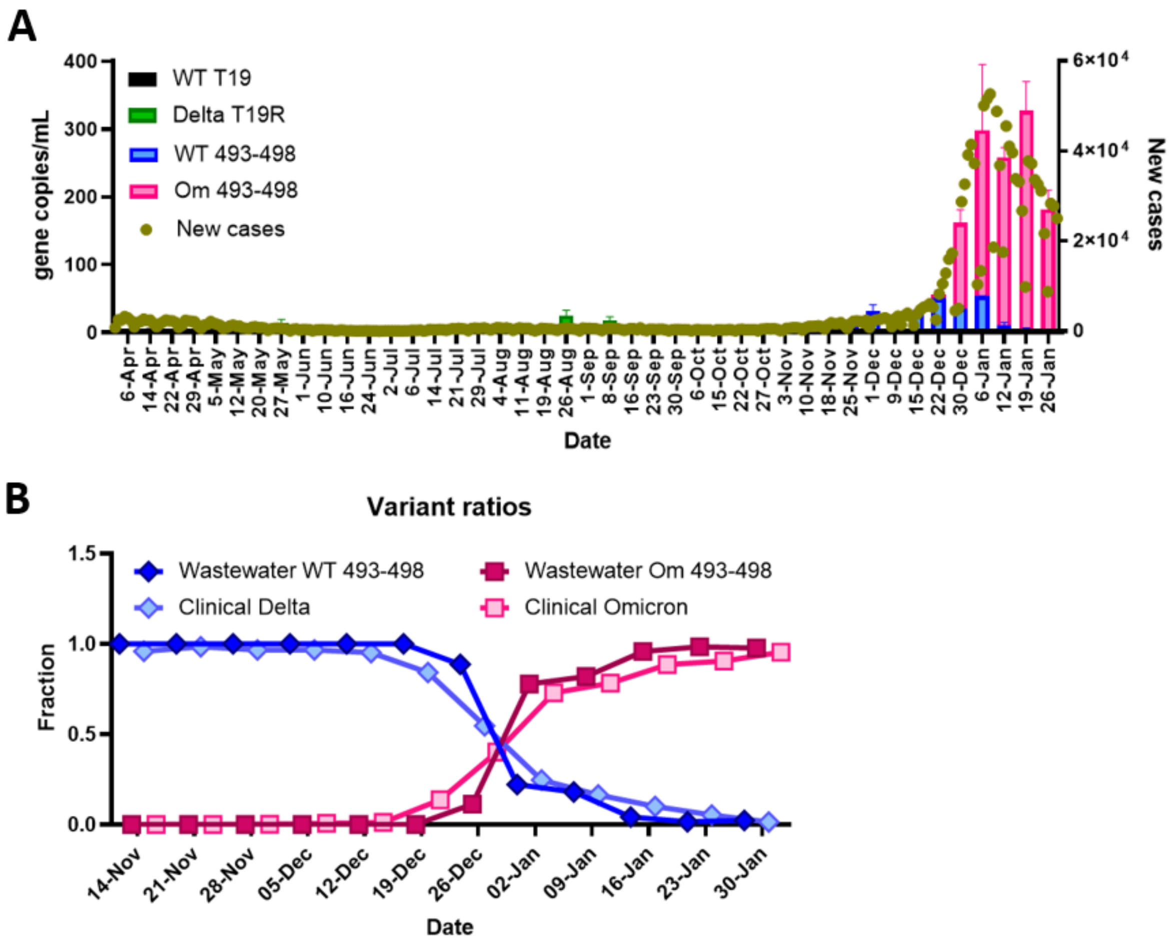
Wastewater surveillance has been shown to provide a low-cost, real-time, and unbiased snapshot of infection prevalence within its catchment, independent of clinical diagnostic capacities. In this work we develop qPCR methods for measuring levels of SARS-CoV-2 variants of concern (VOCs) in wastewater, and using a 10 month longitudinal wastewater samples, determine how well wastewater variant surveillance reflects clinical variant frequencies.

Methods

Using principles of allele-specific qPCR, we developed assays targeting variant-specific genomic loci for quantitative detection and discrimination of VOCs (Delta and Omicron) in wastewater, for wastewater-based determination of variant circulation trends.

Results or Focus

SARS-CoV-2 RNA concentrations and variant frequencies in wastewater determined using these variant assays agree with clinical cases, revealing rapid displacement of the Delta variant by the Omicron variant within three weeks. These variant trends, when mapped against vaccination rates, support clinical studies that found the rapid emergence of SARS-CoV-2 Omicron variant being associated with an infection advantage over Delta in vaccinated persons.



A) Wastewater concentrations determined using allele-specific RT-qPCR assays agree with daily positive clinical cases. Wastewater samples were influent samples from a wastewater treatment plant in Lombardy, Italy. B) Comparison between clinically derived variant ratios against variant ratios derived from wastewater testing.

Conclusion or Scope

This work has demonstrated that wastewater variant concentrations, as determined using our allele-based qPCR based assays, can be used to closely and quantitatively trace the displacement dynamics of one variant by another in a community. As SARS-CoV-2 becomes an endemic disease, the transition of clinical testing towards decentralised antigen rapid tests and the reduction of clinical sequencing, strongly suggests that variant tracking through wastewater would play an essential role in guiding public health response in the future.

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Keywords: Covid-19; SARS-CoV-2; Variants of Concern; Wastewater Surveillance; Omicron

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15256

TARGETED WASTEWATER SURVEILLANCE IN HIGH-DENISTY LIVING ENVIRONMENTS: FROM PANDEMIC TO ENDEMIC

Wei Jie Ng*[1] ; Germaine Kwok[1] ; Mats Leifels[1] ; Desmond Chua[1] ; Martin Tay[2] ; Dzulkhairul Maliki[2] ; Judith Chui Ching Wong[2] ; Lee Ching Ng[2] ; Stefan Wuertz[1 3] ; Janelle Thompson[1 4 5]
[1]Singapore Centre for Environmental Life Sciences Engineering/ Nanyang Technological University/ Singapore, [2]Environmental Health Institute/ National Environmental Agency/ Singapore, [3]School of Civil and Environmental Engineering/ Nanyang Technological University/ Singapore, [4]Asian School of the Environment/ Nanyang Technological University/ Singapore, [5]Campus for Research Excellence And Technological Enterprise (CREATE)/ Campus for Research Excellence And Technological Enterprise (CREATE)/ Singapore

Introduction and Objectives or Purpose

The COVID-19 pandemic has highlighted the importance of targeted environmental (wastewater) surveillance (WWS) for zoonotic viruses – such as its etiological agent SARS-CoV-2, which is shed by symptomatic and asymptomatic individuals alike. Due to its relatively low cost and ability to complement clinical surveillance, WWS has been widely adopted by governments and institutions worldwide. Here, we highlight the results and challenges from a yearlong longitudinal wastewater surveillance campaign deployed on a university campus.

Methods

Composite wastewater samples were collected twice a week by autosamplers located downstream of forty-five student dormitories throughout the campus. Samples were concentrated by PEG precipitation or using centrifugal columns. Total nucleic acids were then extracted, and SARS-CoV-2 gene copies were quantified using widely-used qPCR assays targeting the N and orf1 gene.

Results or Focus

During the monitoring campaign, two distinct waves of SARS-CoV-2 variants of concern were observed in September to November 2021 (Delta) and January 2022 onwards (Omicron). The prevalence of campus sites with positive detection of SARS-CoV-2 showed close correspondence to island-wide trends in SARS-CoV-2 wastewater levels at the water reclamation plants and to COVID-19 cases. Furthermore, analyses of the percentage of positive sampling sites and SARS-CoV-2 gene copies/L were carried out to understand virus transmission trends.

Conclusion or Scope

Data collected from the university campus WWS was communicated to relevant health authorities and university administrators, allowing for timely implementation of evidence-based responses and policies. This helped reduce the spread of COVID-19 on campus and maintained in-person learning.

The robust and highly flexible campus surveillance network has supported the management of COVID-19 through several transmission waves. As we learn to live with COVID-19 and prepare for future epidemics, it is important to develop advanced assays for SARS-CoV-2 (e.g., those targeting novel SARS-CoV-2 variants of concern) and other relevant human pathogens.

Keywords: Campus Surveillance; Wastewater Surveillance; SARS-COV-2

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15264

TITLE: ASSESSING THE EFFECTIVENESS OF COVID-19 VACCINES IN PAKISTAN: A TEST-NEGATIVE CASE-CONTROL STUDY.

Nadia Ansari*[1] ; Kiran Lalani[1] ; Ayesha Younus[1] ; Maaheen Chandna[1] ; Amyn Malik; Muhammad Qazi[1] ; Zahra Hasan[1] ; Saad Omer; Fyezah Jehan[1] ; Muhammad Nisar[1]
[1]Pediatrics and Child Health/ The Aga Khan University/ Pakistan (پاکستان)

Introduction and Objectives or Purpose

There is a dearth of data on effectiveness of COVID-19 vaccines from developing countries. In Pakistan, inactivated vaccines were used from the onset of the national vaccination program in February 2021. Later, viral vector vaccines and mRNA vaccines were added. We used a test-negative case-control design to describe the effectiveness of the vaccines used in Pakistan.

Methods

Adult residents of Karachi tested for COVID-19 using RT-PCR between June-September 2021 at the testing facility of a tertiary care hospital, were contacted via phone calls. Symptomatic individuals, with onset within a week prior to the test who provided verbal consent, were enrolled. Those who had received a single dose regimen, or second shot of a two-dose regimen 14 days before the test, were categorized as fully vaccinated. Those who received the second dose less than 14 days before the test or had received only one dose of a two-dose regimen were considered partially vaccinated. People who had not received the vaccine or less than 14 days had elapsed since receiving the first shot of any vaccine were considered unvaccinated.

Effectiveness of different vaccines was calculated by comparing vaccination rates between cases and controls, after adjusting for known confounders.

Results or Focus

A total of 1597 people who tested positive on PCR (cases) and 1590 people who tested negative on PCR (controls) were enrolled. Overall, 38.1% of cases and 53.3% of controls were fully vaccinated. For the inactivated vaccines, Sinopharm and Sinovac, the adjusted vaccine effectiveness (VE) was 33.8% (95% CI:18.6% - 46.1%) and 49.3% (95% CI: 34.8% - 60.6%), respectively. The VE was highest for mRNA vaccines at 67.4% (95% CI: 1.8-89.2%).

Conclusion or Scope

A wide variety of vaccines against SARS-CoV-2 have been used in Pakistan. We report that the inactivated vaccines are moderately effective against symptomatic COVID-19, while mRNA vaccines have greater effectiveness, concurrent with global evidence.

Keywords: SARS-CoV-2, Pakistan, Vaccine effectiveness, inactivated vaccines, delta variant

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15268

SEROLOGIC EVIDENCE OF MARBURGVIRUSES AND BUNDIBUGYO-LIKE EBOLAVIRUS IN MADAGASCAN ROUSETTES

Marana Tso*[1] ; Spencer Sterling[1 2] ; Hafaliana Ranaivoson[3 4] ; Gwenddolen Kettenburg[5] ; Angelo Andrianiaina[3] ; Santino Andry[6] ; Ny Ravelomanantsoa[3] ; Jean-Michel Héraud[4 7] ; Eric Laing[1] ; Cara Brook[5]
[1]Microbiology & Immunology/ Uniformed Services University of Health Sciences/ United States, [2]N/A/ The Henry M. Jackson Foundation for the Advancement of Military Medicine, Inc./ United States, [3]Department of Zoology and Animal Biodiversity/ University of Antananarivo/ Madagascar (Madagasikara), [4]Virology Unit/ Institut Pasteur de Madagascar/ Madagascar (Madagasikara), [5]Department of Ecology and Evolution/ University of Chicago/ United States, [6]Department of Entomology/ University of Antananarivo/ Madagascar (Madagasikara), [7]Virology Department/ Institut Pasteur de Dakar/ Senegal (Sénégal)

Introduction and Objectives or Purpose

Ebolaviruses and Marburgviruses are causative agents of viral hemorrhagic fever diseases with a high case fatality in humans. Marburg (MARV) and Ravn virus (RAVV) are distinct lineages within the Marburg marburgvirus species, both isolated from Egyptian rousette bats (ERBs;Rousettus aegyptiacus). Historically, outbreaks have occurred in Central and South Africa, associated with mining or cave-tourism where cave bats like ERBs roost. Recently, MARV was isolated from ERBs in Sierra Leone and fatal human cases have occurred in Guinea and Ghana, highlighting gaps in our current knowledge of Marburgvirus distribution and at-risk areas for spillover. On Madagascar, a single species of rousette bat, Madagascan rousette (Rousettus madagascariensis), resides. We conducted serology-based biosurevillance to assess whether ebolaviruses and marburgviruses circulate enzootically in Madagascan rousettes

Methods

Serum samples from 579 Madagascan rousettes were tested by a multiplex microsphere-based immunoassay for immunoglobulin (Ig) G reactivity against soluble envelope glycoprotein (GP) ectodomain trimers of RAVV, Ebola, Bundibugyo (BDBV), Bombali, Sudan, Reston, Mengla, and Lloviu virus. Antigen-antibody complexes were detected via Luminex xMAP-based technologies, with IgG levels reported as a median fluorescence intensity. To determine IgG-positivity cutoffs, we applied a three-sigma-rule (99.7%) probability distribution of naïve ERB sera and latent cluster analysis of field-collected Madagascan rousette sera.

Results or Focus

We detected RAVV and BDBV IgG binding antibodies in 16.1% (93/579) and 5.4% (31/579) of serum samples, respectively. Additionally, 2.6% (15/579) were double positive for RAVV and BDBV IgG binding antibodies.

Conclusion or Scope

This serological profile of Madagascan rousettes suggests co-circulation and maintenance of ebolaviruses and marburgviurses in Madagascar. More broadly, specific serological footprints of RAVV in Rousettus species native to Madagascar supports the current understanding of rousette bats as natural reservoirs for marburgviruses. Future research is necessary to determine possible evidence of viral chatter between bats and other wildlife or domestic animals, and spillover risk to humans.

Keywords: Marburgviruses; Ebolaviruses; Rousette bats; Madagascar

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15273

SARS-CoV-2 WASTEWATER-BASED SURVEILLANCE IN THE COVID-19 VACCINATION ERA

Federica Armas*[1] ; Fraciscus Chandra*[1] ; Wei Lin Lee[1] ; Xiaoqiong Gu; Flavia Guarneri[2] ; Nicoletta Formenti[2] ; Hongjie Chen[1] ; Feng Jun Desmond Chua[1] ; Eric Alm[1] ; Janelle Thompson [3]
[1]AMR/ Singapore MIT Alliance for Research and Technology/ Singapore, [2]Sede Territoriale di Brescia/ Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna "Bruno Ubertini" (IZSLER), Italy/ Italy (Italia), [3]Singapore Centre for Environmental Life Sciences Engineering, Nanyang Technological University, Singapore/ Nanyang Technological University, Singapore/ Singapore

Introduction and Objectives or Purpose

Wastewater-based surveillance (WBS) has been critical in managing the COVID-19 pandemic. However, the high vaccination coverage has changed the population's immune status substantially. We asked whether COVID-19 vaccinations might 1) give rise to vaccine shedding, 2) affect the viral load to wastewater of infected people, influencing epidemiological interpretations for the WBS of SARS-CoV-2.

Methods

We analyzed publicly available data of SARS-CoV-2 wastewater concentrations before and after vaccination programs in the Netherlands. We quantified the virus concentration in a wastewater treatment plant in Italy during the vaccination program. Further, we analysed available vaccine types to understand their ability to influence viral shedding.

Results or Focus

Relationship between clinical cases against wastewater variant concentrations agrees with clinical data despite the vaccination coverage increase. The analysis of the vaccination rate and ICU against wastewater concentrations shows the importance of vaccination in pandemic management.

Our analysis suggested first, that all WHO-authorized COVID-19 vaccines do not lead to viral shedding and do not give false-positive signals. Second, the utility of SARS-CoV-2 WBS is preserved, with strong correlation between new clinical cases and SARS-CoV-2 in wastewater and that SARS-CoV-2 viral load to wastewater is not impacted.

Conclusion or Scope

Our analysis showed that the global vaccination marked a turning point in the fight against the pandemic, decreasing the intensive unit care occupancies despite the spike in infections and high SARS-CoV-2 RNA concentrations in wastewater. WBS remains a useful tool to monitor vaccination efficacy. If other vaccines, will be adopted, changes in the wastewater virus tracking methodology might be needed. However, the pandemic's dynamic nature, marked by new variants and disease-fighting tactics, necessitates re-evaluation of the strategies used to monitor virus signals in wastewater.

Acknowledgement

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Keywords: COVID-19; SARS-CoV-2; Wastewater Surveillance; COVID-19 vaccine

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15299

Singapore’s National Wastewater Surveillance Programme

Judith Chui Ching Wong*[1] ; Martin Tay[1] ; Jue Tao Lim[1] ; Jane Griffiths[1] ; Benjamin Wee Meng Lee[1] ; Dzulkhairul Maliki[1] ; Marc Ho[2] ; Yee Leong Teoh[2] ; Alex Richard Cook[3] ; Lee Ching Ng[1]
[1]Environmental Health Institute/ National Environment Agency/ Singapore, [2]Communicable Disease Division/ Ministry of Health/ Singapore, [3]Saw Swee Hock School of Public Health/ National University of Singapore/ Singapore

Introduction and Objectives or Purpose

As an early adopter of wastewater surveillance, Singapore has progressively expanded wastewater testing (WWT) across high density living premises types, residential hubs, and at larger geographical areas to provide sensitive and timely monitoring of COVID-19. As a non-intrusive method that is also independent of health-seeking behaviours, wastewater signals complement clinical surveillance to provide situational assessment for timely risk mitigation. In this study, we present the use-cases of wastewater testing (WWT) in Singapore and its role in facilitating case detection and situational awareness.

Methods

Wastewater samples were concentrated using ultrafiltration and tested for SARS-CoV-2 using qRT-PCR. Temporal WWT virus load data from about 400 autosamplers deployed in the community and in worker’s dormitories were analyzed and corroborated with reported case data from the respective populations.

Results or Focus

We demonstrate the utility of WWT to facilitate case detection, where the surveillance approach has facilitated the dormitory clearance programme and averted swab operations at more than 200 residential blocks. As Singapore transited to COVID-19 endemicity, surveillance objectives shifted towards situational assessment, where WWT of community and workers’ dormitory sites correlate well with respective case data (0.90 and 0.78, respectively), providing a good indication of the trajectory of infections. Interestingly, WWT signals at the water reclamation plants do not correlate as well, suggesting unaccounted infections.

Conclusion or Scope

These findings highlight the usefulness of WWT for COVID-19 monitoring, where it has supported COVID-19 responses through several waves of resurgences. This also underscores the potential of WWT for monitoring other infectious diseases of One-Health concern.

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PUB, Singapore’s National Water Agency
Ministry of Manpower, Assurance, Care and Engagement (ACE) Group

Keywords: Wastewater surveillance, COVID-19, SARS-CoV-2, Wastewater-based epidemiology

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15304

ANTIGENIC DISTANCES BETWEEN EMERGING SARS-COV-2 VARIANTS OF CONCERN

Mariana Gonzalez Hernandez*[1] ; Derek J. Smith[2] ; Geert Van Amerongen[3] ; Guus Rimmelzwaan[1] ; Stefan Pöhlmann[4] ; Albert D.M.E. Osterhaus[1] ; Imke Steffen[5]
[1]Research Center for Emerging Infections and Zoonoses (RIZ)/ University of Veterinary Medicine Hannover, Foundation/ Germany (Deutschland), [2]Center for Pathogen Evolution, Department of Zoology/ University of Cambridge/ United Kingdom, [3]Xplore / Viroclinics / Netherlands, [4]Infection Biology/ Deutsches Primatenzentrum GmbH / Germany (Deutschland), [5]Department of Biochemistry / Research Center for Emerging Infections and Zoonoses/ University of Veterinary Medicine Hannover, Foundation/ Germany (Deutschland)

Introduction and Objectives or Purpose

Since the appearance of SARS-CoV-2, variants of concern (VOCs) have emerged, largely due to selective pressure exerted by mounting immunity in the human population. WHO has defined VOCs as variants associated with major changes in epidemiology, virulence, transmissibility and/or effectiveness of vaccines and therapeutics. Five major VOCs have been identified: Alpha, Beta, Gamma, Delta, and Omicron; Omicron lineage BA.5 being the current dominant variant in most affected countries. The continuing evolution of SARS-CoV-2 will be a major issue in the future selection of SARS-CoV-2 candidate vaccines and therapeutic human monoclonal antibodies. We used antigenic cartography to monitor and visualize the evolution of antigenic distances between VOCs, using pseudoviruses harboring the spike protein of the major VOCs, to determine VOC neutralizing antibody titers.

Methods

Syrian golden hamsters were infected with VOCs Wuhan, Gamma, Delta, Omicron BA.1 and Omicron BA.5, respectively, and serum samples were collected three weeks after infection.

Results or Focus

These sera effectively neutralized the corresponding variants. Serum derived from hamsters infected with VOC Wuhan neutralized VOC Delta but not VOCs Omicron BA.1 and BA.5. Similar results were obtained with sera derived from hamsters infected with VOC Delta. However, hamsters infected with either VOCs Omicron BA.1 or BA.5 developed more specific antibodies: these did not cross-neutralize the respective VOCs, not even the related VOC Omicron lineages.

Conclusion or Scope

Therefore, VOC Omicron is antigenically more distant to previous VOCs and within variant lineages exhibits major antigenic differences, confirming previously published data. Cartography data obtained with the hamster sera will be presented, together with those obtained with a panel of 459 human sera collected in Germany, Italy, Ethiopia, the US Southwest, the US Northeast, and Mexico, soon after the emergence of the respective VOCs in these countries. Data generated indicate that antigenic cartography will help guide future selection of SARS-CoV-2 candidate vaccines and therapeutic human monoclonal antibodies.

Keywords: SARS-CoV-2; Variants of concern; antigenic cartography

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15317

Serial Population-Based Serosurveys For COVID-19 In District East of Karachi, Pakistan

Mashal Amin*[1] ; Nadia Ansari[1] ; Farah Khalid[1] ; Imran Nisar[1] ; Fyezah Jehan[1] ; Junaid Iqbal; Daniel B Larremore ; Bailey Fosdick Fosdick ; Sierra Pugh; Aneeta Hotwani
[1]Pediatrics and Child Health / Aga Khan University / Pakistan (پاکستان)

Introduction and Objectives or Purpose

Objective

To determine the prevalence and trend of SARS-CoV-2 in a densely populated community of Karachi.

Methods

Methods

Six serial cross-sectional surveys were conducted in April, June, August, and November 2020 and then in February, and December 2021 in Karachi's District East. Households were selected to provide serum samples for the detection of SARS-CoV-2 antibodies using Elecsys® immunoassay. Bayesian regression was used to adjust for assay performance and estimate seroprevalence. Conditional Risk of Infection (CRI) with a 95% confidence interval was calculated using a non-parametric bootstrap of households.

Results or Focus

Results

We enrolled 3038` participants in total including all age groups and genders. The adjusted seroprevalence was estimated to be 0.4% (95% CI 0 - 1.3), 15.1% (95% CI 9.4 -21.7), 21.5% (95% CI 15.6-28), 24.0% (95% CI 18.0-31.0), 53.9% (95% CI 45.5–63.2), 84.9% (95% CI 78.5 – 92.3) in the 1st , 2nd , 3rd , 4th , 5th , and 6th surveys, respectively. CRI was calculated as 41% (95% CI 27.7-51.5) in survey 2, 38.8 (95% CI 26.7-51.7) in survey 3, 41% (95% CI 29.9-51.6) in survey 4, 56.7% (95% CI 50.4–62.6) in survey 5 and 77.8% (95% CI 73.0-81.7) in survey 6. Only 13% of participants overall reported symptoms related to COVID-19.

Conclusion or Scope

Conclusion

There was a progressive increase in seroprevalence in Karachi's District East during the first 18 months of the SARS-CoV-2 pandemic. At the end of 2021, a vast majority of the population had evidence of past infection, as indicated through detectable anti-SARS-CoV-2 antibodies, although few reported symptoms. This study highlights the role of seroprevalence survey in estimating the true proportion of the population that has been infected. These estimates can enable policymakers make informed public health decisions and predict the future spread of the disease in similar settings.

Keywords: Population-Based, COVID-19, seroprevalence, Pakistan

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15329

PREVALENCE AND RISK FACTORS OF SARS-COV-2 INFECTION IN WOMEN AND CHILDREN IN PERI-URBAN COMMUNITIES IN PAKISTAN: A PROSPECTIVE COHORT STUDY

Usma Mehmood*[1] ; Imran Nisar[1] ; Nadia Ansari[1] ; Farah Khalid[1] ; Asra Usmani[1] ; Sachiyo Yoshida; Sunil Sajawal; Abdullah Baqi; Rajiv Bahl; Fyezah Jehan[1]
[1]Paediatrics and Child Health/ Aga Khan University/ Pakistan (پاکستان)

Introduction and Objectives or Purpose

Severity of COVID-19 increases with age, but the young are just as vulnerable to getting infected. We compare prevalence estimates and factors associated with COVID-19 among women and children from two serial serological surveys in a peri-urban area of Karachi, Pakistan.

Methods

First survey was conducted between March-June 2021 and second was done between September-December 2021 among consenting participants of the AMANHI-COVID-19 study. Participants were followed weekly for symptoms of COVID-19. We report the proportion of cohort who had anti-SARS-CoV-2 antibodies and symptoms of the disease. Stepwise logistic regression analysis was used to determine risk factors of COVID-19.

Results or Focus

Adjusted seroprevalence among women in first and follow-up surveys was 45.3% (95% CI: 42.6, 47.9), and 82.3% (95% CI: 79.9,84.4), respectively. Among children, it was 18.4% (95% CI: 16.1, 20.7) and 57.4% (95% CI: 54.3, 60.3) respectively. A high proportion of participants (82.7% and 80.9%) were asymptomatic.

At follow-up, 404 (74.4%) previously seronegative women tested positive and 365 (50.4%) of previously seronegative children tested positive.

Low socioeconomic status (Women: RR= 0.6; 95% CI: 0.7, 0.9; Children: RR=0.7; 95% CI: 0.5, 1.0), and poor access to safe drinking water (Women: RR= 1.2; 95% CI: 1.1, 1.4; Children: RR= 1.4; 95% CI: 1.0, 1.8) were associated with COVID-19 in first survey. At follow-up, risk was lower for underweight women and children, (RR=0.4;95% CI: 03, 0.7 and RR= 0.7; 95% CI: 0.5, 0.8, respectively), 30–39-year-old women (RR=0.6 ;95% CI: 0.3, 0.7) and 24–36-month-old children (RR= 0.7; 95% CI: 0.5, 0.9).

Of paternal risk-factors, lack of education (RR= 1.3 (95% CI: 1.0, 1.6) and employment were important (RR 0.7; 95% CI: 0.6, 0.9, and RR: 0.8; 95% CI: 0.7, 1.0).

Conclusion or Scope

High seroconversion rates reflect rapid spread of SARS-CoV-2. Illness was mild. Parental awareness is an important determinant of infection among children.

Acknowledgement

Word Health Organization

Aga Khan University

Keywords: PREVALENCE, RISK FACTORS, SARS-COV-2 INFECTION, WOMEN, CHILDREN

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15339

Validating the COVIDSeq and SINAI protocols for wastewater-based sequencing of SARS-CoV-2

Said Rachida*[1] ; Mukhlid Yousif[1] ; Setshaba Taukobong; Nkosenhle Ndlovu[1] ; Chinwe Iwu-Jaja; Wayne Howard[1] ; Shelina Moonsamy[1] ; Jay Bhagwan; Melinda Suchard; Kerrigan McCarthy[1]
[1]Centre for Vaccines and Immunology/ National Institute for Communicable Diseases/ South Africa

Introduction and Objectives or Purpose

SARS-CoV-2 can be shed from asymptomatic and symptomatic infected individuals, thus rendering wastewater-based sequencing an unbiased epidemiological tool that can identify clusters of mutations reported or not by clinical surveillance. Wastewater-based sequencing of SARS-CoV-2 is challenged by the potential viral genome degradation and the complexity of the wastewater matrix, which requires validating sequencing protocols before implementation. We compared two amplicon-based sequencing protocols (the ARTIC-based SINAI and COVIDSeq v3 protocols) using the number and quality of reads produced and genome coverage from each wastewater sample.

Methods

Raw wastewater samples (n=21) were collected from treatment plants within South African urban areas. Nucleic acids extracted from virus concentrates were tested by RT-qPCR using the Seegene 2019-nCoV Assay kit. Nucleic acids were re-extracted from positive virus concentrates and subjected to whole-genome amplification using SINAI and COVIDSeq v3 protocols on an Illumina platform. The Exatype Next Generation Sequencing SARS-CoV-2 pipeline v1.7.12 was used to assess the quality and identity of raw reads, and, the genome coverage.

Results or Focus

Through the SINAI and COVIDSeq v3 protocol one million reads were produced from 90% (19/21) samples. The percentage of mapped reads was 82% and 23% for the SINAI and COVIDSeq v3, respectively. More than 50% of the SARS-CoV-2 genome was recovered from 76% (16/21) and 38% (8/21) samples using the SINAI and COVIDSeq v3, respectively.

Conclusion or Scope

The SINAI protocol outperformed the COVIDSeq v3 protocol in successfully recovering SARS-CoV-2 genomes from wastewater. As SINAI amplifies the SARS-CoV-2 genome in 84 overlapping 1500 and 2000 nucleotide tiled amplicons, whilst COVID-Seq v3 uses 98 overlapping 400 nucleotide tiled amplicons, the production of long size amplicons from wastewater was unexpectedly favoured. Latest versions of the COVIDSeq protocol may provide different results. Our findings pave the way for production of high quality sequencing results of SARS-CoV-2 from wastewater, and will thus facilitate epidemiological monitoring of variants.

Keywords: SARS-CoV-2; Wastewater-based sequencing; ARTIC-based protocol

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15346

Broad antibody reactivity against bat SARS-related coronaviruses found in SARS-CoV-2 vaccinees with a high risk of viral spillover from bats

Sasiprapa Ninwattana[*1 2] ; Khwankamon Rattanatumhi [1] ; Sininat Petcharat[1] ; Luddawul Somjit[3] ; Spencer Sterling[4 5] ; Eric D. Laing[4] ; Supaporn Wacharapluesadee[1] ; Opass Putcharoen[1 2]
[1]Thai Red Cross Emerging Infectious Diseases Clinical Center/ King Chulalongkorn Memorial Hospital/ Thailand (□□□), [2]Faculty of Medicine/ Chulalongkorn University/ Thailand (□□□), [3]-/ Taopoon Health Promoting Hospital/ Thailand (□□□), [4]-/ Uniformed Services University/ United States, [5]-/ Henry M. Jackson Foundation/ United States

Introduction and Objectives or Purpose

Coronaviruses originating from bats have caused multiple outbreak events, including severe acute respiratory syndrome coronavirus (SARS-CoV) and SARS-CoV-2, resulting in a significant disease burden at the global level. This study aims to determine seroprevalence among villagers at high risk of viral spillover from bats.

Methods

173 human sera collected in 2017 (n=65), 2018 (n=52), and 2021 (n=56) in Thailand were included in this study. 127 participants reported exposures to bat or bat excretions during the past 12 months (bat contact group), and 46 reported no exposure. A multiplex microsphere immunoassay (MMIA) containing a customized panel of beads targeting SARS-CoV-2, SARS-CoV, and three bat SARSr-CoVs including Rs4874 (WIV16), RaTG13, and ZXC21, was performed to determine the anti-spike IgG levels in the sera.

Results or Focus

For sera collected in 2017 and 2018 (n=117), all participants with and without bat contact history showed seronegativity for all bat SARSr-CoVs, SARS-CoV-2, and SARS-CoV, while 22 of 41 (53.7%) sera of bat contact participants who received SARS-CoV-2 vaccination in 2021 were antibody positive for bat SARS-CoVs (at least one antigen), compared with 3 of 9 (33%) sera collected from non-exposed participants. We found that 10 participants from the bat contact group were seropositive for both SARS-CoV and SARS-CoV-2 compared to 1 non-contact participant.

Conclusion or Scope

These findings show a broader cross-reactive antibody against bat SARSr-CoV and SARS-CoV after SARS-CoV-2 vaccination observed in participants with a high level of bat contact. The elevated antibodies against bat SARS-CoVs in the bat contact group may be caused by cross-activation from SARS-CoV-2 vaccine from previous bat viruses exposure. A greater number of non-exposed participants with vaccination are needed to better understand cross-reactivity against bat SARSr-CoV in populations with high levels of bat contact.

Acknowledgement

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Keywords: Bat SARSr-CoV; Antibody

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15351

GENOMIC EPIDEMIOLOGY OF PSEUDOMONAS AERUGINOSA TO GUIDE THE DESIGN OF NOVEL PHAGE-BASED THERAPEUTICS

Nazifa Tabassum*[1] ; Yogesh Hooda[1] ; Rajan Saha[1] ; Himadree Sarkar[1] ; Hafizur Rahman[1] ; Dipu Das[1] ; Arif Tanmoy[1] ; Samir Saha[1] ; Senjuti Saha[1]
[1]Microbiology/ Child Health Research Foundation (CHRF)/ Bangladesh (□□□□□□□□)

Introduction and Objectives or Purpose

Pseudomonas aeruginosa, an opportunistic pathogen, causes multi-drug resistant infections in immunocompromised individuals and young infants. Some multi locus sequence types (MLST) are associated with poor clinical outcomes. The most frequently reported globally emerging, and extensively-drug resistant clone is ST235, highlighting the need for novel therapeutics. One novel alternative are stable phage-tail-like-bacteriocins, called tailocins, which are bacteriocins naturally produced by P. aeruginosa to kill other related strains. However, insufficient data on genomic analysis and pyocin activity of P. aeruginosa in South Asia hamper development of such potential novel therapeutics.

Methods

We conducted a prospective hospital surveillance in urban and rural pediatric hospitals in Bangladesh from 2009-2021. P. aeruginosa was detected by blood culture followed by PCR, and antimicrobial susceptibility testing (AST) by disc diffusion was conducted. Whole genome sequencing was performed for selected 54 strains. Bioinformatic analysis was done to determine MLST; pyocin gene clusters were detected and annotated. Tailocins were induced with mitomycin C and spotting assays were performed to experimentally assess killing activity.

Results or Focus

Out of the 96 P. aeruginosa detected, most infections (n=46) were seen in neonates. Bioinformatic analysis of 54 sequenced strains found a diverse range of known and novel STs. ST235 (n=6) was the most commonly occurring ST. All six ST235 strains were extensively resistant to the antibiotics tested. Tailocin gene clusters were identified through genomics in all 54 strains, and they belonged to different known and novel groups. All unique tailocins were tested against all different STs. The only tailocin to kill ST235 was a novel tailocin produced by a Bangladeshi strain.

Conclusion or Scope

We found a novel tailocin which effectively kills ST235, a global multidrug resistant P. aeruginosa clone. This can be developed as a novel therapeutic with narrow specificity, high stability, and potential to be engineered.

Keywords: neonatal sepsis, amr, nosocomial, pseudomonas, tailocins

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15356

CHARACTERIZATION AND IDENTIFICATION OF VARIANTS OF CONCERNS OF SARS-COV-2 AT WASTEWATER TREATMENT PLANTS IN SOUTH AFRICAN URBAN AREAS

Mukhlid Yousif*[1 2] ; Said Rachida[1] ; Setshaba Taukobong[1] ; Nkosenhle Ndlovu[1] ; Chinwe Iwu-Jaja[1] ; Wayne Howard[1] ; Shelina Moonsamy[1] ; Jay Bhagwan[3] ; Melinda Suchard[4] ; Kerrigan McCarthy[1 5]
[1]Centre for Vaccines and Immunology/ National Institute for Communicable Diseases/ South Africa, [2]Department of Virology, School of Pathology, Faculty of Health Sciences/ University of the Witwatersrand/ South Africa, [3]Water Research Commission/ Water Research Commission/ South Africa, [4]Department of Chemical Pathology, School of Pathology/ University of the Witwatersrand/ South Africa, [5]School of Public Health/ University of the Witwatersrand/ South Africa

Introduction and Objectives or Purpose

Several reports have confirmed that SARS-CoV-2 is shed into stools and is detectable in wastewater. The use of wastewater for SARS-CoV-2 surveillance has proven to be a useful complementary tool to clinical surveillance during the pandemic. The aims of this study were to characterize SARS-CoV-2 from wastewater samples, and to identify variants of concerns present in samples collected at sentinel wastewater treatment plants in South African urban metros from April 2021 to the end of the fourth wave in January 2022.

Methods

A total of 325 samples were collected from 15 wastewater treatment plants in metropolitan areas in South Africa. Nucleic acids were extracted from concentrated samples, and subjected to amplicon-based whole genome sequencing. Sequence reads were trimmed, filtered, and mapped to the reference genome (NC_045512.2) using ARTIC bioinformatics pipeline (https://artic.network/ncov-2019). To identify variants at each geographic location, we used the Freyja tool (https://github.com/andersen-lab/Freyja), which assigns each sample with the prevalence of each variant present.

Results or Focus

A total of 229 samples generated more than one million reads. A 50% genome coverage was recovered from 183 samples (50.3%). We identified 78 mutations, of which 59 were previously reported and 19 were not commonly detected. Using the Freyja tool, the overall proportion of the beta variant was 7%, the delta variant was 47%, and the Omicron variant was 16%, while 27% could not be assigned to any variant.

Conclusion or Scope

Sequencing of wastewater has limitations. The ability to identify variants in wastewater relies on the identification of mutations known in clinical strains and which are uniquely associated with these variants, therefore it is not possible to identify new variants. Our data showed concordant results of SARS-CoV-2 variants prevalence in clinical isolates.

Keywords: Variant; enviroment

Topic: One Health Science (OHS): Discovery and Surveillance: SARS-CoV-2 and other emerging pathogens
Abstract No: 15362

GENOMIC SURVEILLANCE FOR MONITORING THE PREVALENCE OF OMICRON SUBVARIANTS—SINGAPORE, MAY – JULY 2022

Xie Cheng Alvin Goh*[1] ; Calvin Chiew[2] ; Cui Lin[3] ; Abigail Wong[4] ; Celine Tan[4] ; Sae-Rom Chae[1] ; Jayne Lim[1] ; Yi Ding Lim[1] ; Marc Ho[1] ; Vernon Lee[4]
[1]Contact Tracing and Epidemiology Centre/ Ministry of Health, Singapore/ Singapore, [2]National Public Health and Epidemiology Unit/ National Centre for Infectious Disease/ Singapore, [3]National Public Health Laboratory/ National Centre for Infectious Disease/ Singapore, [4]Communicable Disease Division/ Ministry of Health, Singapore/ Singapore

Introduction and Objectives or Purpose

The Singapore Ministry of Health enhanced its genomic surveillance programme to monitor the prevalence and distribution of circulating SARS-CoV-2 (sub)variants among 3 major groups: general community, severe, and imported cases.

Methods

Nasopharyngeal samples polymerase chain reaction (PCR)-positive for SARS-CoV-2 were selectively screened for S-gene Target Failure (SGTF) by TaqPath™ Combo kit before selection for whole genomic sequencing at the National Public Health Laboratory (NPHL) based on viral load and source. Community swabs collected under the Acute Respiratory Infection surveillance programme at sentinel public clinic sites were tested for common respiratory pathogens including SARS-CoV-2 by PCR (FilmArray Respiratory Panel 2.1). Samples positive for SARS-CoV-2 by PCR from severe cases (oxygen requirement, intensive care unit care, or death) were submitted by hospital labs while mobile swab teams collected swabs from Antigen Rapid Test-positive imported cases.

Results or Focus

A total of 4936 samples were sequenced: 3052 (62%) general community cases, 1458 (30%) imported cases, and 426 (8%) severe cases. Subvariant BA.5 increased from 3%, 3%, and 1% in community, imported, and severe cases in May; to 43%, 38%, and 14% in June, respectively. By July, BA.5 comprised 72%, 70%, and 68%. Subvariant BA.2.75 was first detected on 12 July and had a prevalence of 2% among community cases and <1% for imported and severe cases during the month of July.

Conclusion or Scope

Genomic surveillance allowed monitoring of the shift in predominance of Omicron BA.2 to BA.5 from May to July in different community groups. Subvariant trends were clear and our programme underscores the importance of this critical tool in tracking the importation and circulation of emerging SARS-CoV-2 variants in the community for situation awareness, risk assessment, and policy decision-making.

Acknowledgement

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Keywords: Genomic Surveillance

Topic: One Health Science (OHS): Discovery and Surveillance: Vector borne diseases
Abstract No: 14814

RANGE EXPANSION OF DERMACENTOR VARIABILIS IN BRITISH COLUMBIA, CANADA

Grace Nichol*[1] ; Shaun Dergousoff[2] ; J. Scott Weese[3] ; Amy Greer[1] ; Katie Clow[1]
[1]Population Medicine, Ontario Veterinary College/ University of Guelph/ Canada, [2]Lethbridge Research and Development Centre/ Agriculture and Agri-Food Canada/ Canada, [3]Pathobiology, Ontario Veterinary College/ University of Guelph/ Canada

Introduction and Objectives or Purpose

Tick range expansion is a One Health issue. Biotic and abiotic factors influence tick distribution, and ticks can transmit pathogens to humans and animals. Dermacentor variabilis, a tick species native to North America, can transmit pathogens including Rickettsia species bacteria. The historical range of D. variabilis in Canada extended from eastern Saskatchewan to the Atlantic provinces. However, a recent passive surveillance study revealed the current range of D. variabilis may include British Columbia (BC), a west coast province far from other Canadian D. variabilis populations. It›s unknown if this population of ticks represents westward range expansion from established areas in central Canada or northward range expansion from the western USA coast.

Western USA D. variabilis populations are believed to be genetically distinct from east coast populations, which led to the proposal of a new species, D. similis. This suggests populations on Canada’s west coast could be genetically distinct too, but this has not been investigated.

This study aims to identify the species and geographic distribution of Dermacentor genus ticks in BC.

Methods

Sites across southern BC were sampled via tick dragging (pulling a cloth along the ground for 2000 m^2) in spring 2022. Environmental factors believed to affect tick habitat and activity such as soil temperature and moisture, canopy cover, and weather conditions were recorded. Collected ticks will undergo 16S next-generation sequencing (NGS) for species identification.

Results or Focus

Tick dragging was conducted at 33 sites, with a total of 149 ticks collected from 14 sites. DNA extraction is ongoing in preparation for NGS, which will be completed by September.

Conclusion or Scope

This study will assist in understanding the current distribution of Dermacentor tick species in BC. The collected data will be incorporated into models, which may identify important environmental factors and areas of increased risk for encountering pathogens.

Acknowledgement

Funding: NSERC, OVC, OVC Pet Trust, OMNI/RÉUNIS

Keywords: Dermacentor variabilis; range expansion; western Canada; climate; environment

Topic: One Health Science (OHS): Discovery and Surveillance: Vector borne diseases
Abstract No: 14834

The composition and distribution of mosquito population in Hanoi city, Vietnam: its association with urban livestock keeping and flavivirus detection

Thang Nguyen-Tien*[1 2] ; Anh Bui Ngoc[3] ; Jiaxin Ling[1] ; Son Tran Hai[4] ; Long Pham-Thanh[1 2 5] ; Vuong Bui Nghia[3] ; Åke Lundkvist[1] ; Hung Nguyen-Viet[2] ; Ulf Magnusson[6] ; Johanna Lindahl[1 2 6]
[1]Medical Biochemistry and Microbiology/ Zoonosis Science Center/ Sweden (Sverige), [2]Bioscience/ International Livestock Research Institute/ Vietnam (Việt Nam), [3]Virology/ National Institute of Veterinary Research/ Vietnam (Việt Nam), [4]Zoology/ National Institute of Hygiene and Epidemiology/ Vietnam (Việt Nam), [5]Department of Animal Health/ Ministry of Agriculture and Rural Development/ Vietnam (Việt Nam), [6]Department of Clinical Sciences/ Swedish University of Agricultural Sciences/ Sweden (Sverige)

Introduction and Objectives or Purpose

Dengue virus and Japanese encephalitis virus are two common flaviviruses that are spread widely by Aedes and Culex mosquitoes. Livestock keeping is vital for cities; however, it can pose the risk of increasing the mosquito population. Our study explored how livestock keeping in and around a large city is associated with the presence of mosquitoes and the risk of them spreading flaviviruses.

Methods

An entomological study was conducted in 6 districts with 233 households with livestock, and 280 households without livestock, in Hanoi city. BG-Sentinel traps and CDC light traps were used to collect mosquitoes close to animal farms and human habitats. Adult mosquitoes were counted, identified to species level, and grouped into 385 pools, which were screened for flaviviruses using a pan-flavivirus qPCR protocol and sequencing.

Ethics: This study was conducted in accordance with the guidelines of the Declaration of Helsinki and approved by the Ethical Committee of Hanoi University of Public Health (No 406/2018/YTCC-HD3, 06/08/2018).

Results or Focus

A total of 12,861 adult mosquitoes were collected at the 513 households, with 5 different genera collected, of which the Culex genus was the most abundant. Our study found that there was a positive association between livestock keeping and the size of the mosquito population - most predominantly between pig rearing and Culex species ($p < 0.001$). One pool of Culex Tritaeniorhynchus collected in a peri-urban district, was found to be positive for Japanese encephalitis virus.

Conclusion or Scope

The risk of flavivirus transmission in urban areas of Hanoi city due to the spread of Culex and Aedes mosquitoes could be facilitated by livestock keeping.

Acknowledgement

We want to give thanks to the data collection team from NIVR and Ms. Nguyen Thanh and Ms. Le Hanh of ILRI in Hanoi for their help in the project administration and financing. We also thank all households participating in this study.

Keywords: vector abundance; urban livestock keeping; mosquito-borne flavivirus; Japanese Encephalitis virus; Hanoi city.

Topic: One Health Science (OHS): Discovery and Surveillance: Vector borne diseases
Abstract No: 14851

Application of One Health Approaches to Surveillance and Control of Tick-Borne Zoonotic Pathogens at the Vector/Livestock Interface

Nicholas Johnson*[1] ; Harriet McFadzean[1] ; Arran Folly[1] ; Sara Gandy[2] ; Kayleigh Hansford[2] ; Jolyon Medlock[2] ; Suzanna Bell[1] ; Sharon Brookes[1]
[1]Virology/ Animal and Plant Health Agency/ United Kingdom, [2]Medical Entomology and Zoonoses Ecology/ UK Health Security Agency/ United Kingdom

Introduction and Objectives or Purpose

Tick-borne diseases present an increasing threat to human and animal health throughout the world. Pathogen transmission is driven by a range of human, environmental and biological factors that can lead to the emergence of severe zoonotic diseases including babesiosis, anaplasmosis, borreliosis and tick-borne encephalitis. The diversity of pathogens and the range of control measures needed indicate that control of tick-borne disease requires a One Health approach.

Methods

In this study we report the findings of tick-borne pathogen surveillance at the interface between ticks, livestock and wildlife within the United Kingdom between 2020 and 2022 with a focus on zoonotic pathogens (Babesia species, Anaplasma phagocytophilum, Borrelia burgdorferi s.l. and tick-borne flaviviruses). The flagging techniques was used extensively to sample tick populations. Pathogen-specific PCR assays were used to screen samples.

Results or Focus

A number of pathogens including Babesia motasi were detected in populations of the red sheep tick, Haemaphysalis punctata, in southern England, and were associated with disease outbreaks in sheep. Borrelia miyamotoi was also detected in this species. A. phagocytophilum was detected extensively within Ixodes ricinus populations throughout the UK, with levels exceeding 20% in some areas. This is reflected in sporadic outbreaks of febrile illness in cattle and sheep. In cattle, infection with Babesia divergens was often responsible for severe disease, in some cases linked to co-infection with A. phagocytophilum. However, Babesia divergens and louping ill virus, a cause of meningoencephalitis in livestock were rarely detected in ticks. A single human case of babesiosis due to infection with Babesia divergens was confirmed during this study.

Conclusion or Scope

Raising awareness of tick-borne disease within the general public, veterinarians and livestock keepers remains key to preventing transmission of tick-borne diseases. This must be underpinned by surveillance of both ticks and tick-borne pathogens.

Acknowledgement

This study was funded by Defra and the Scottish and Welsh Governments (project SV3045).

Keywords: Tick, Babesia, Borrelia, Anaplasma, Virus

Topic: One Health Science (OHS): Discovery and Surveillance: Vector borne diseases
Abstract No: 14929

One Health surveillance of Lyme disease risk in Canada, 2021: Results from a pilot project of the Canadian Lyme Sentinel Network (CaLSeN) in Ontario, Canada

Cyril Akwo*[1] ; Olaf Berke[1] ; Mark Nelder[2] ; Scott Weese[3] ; Claire Jardine[3] ; Katie Clow[1]
[1]Population Medicine/ University of Guelph/ Canada, [2]Enteric, Zoonotic, and Vector-Borne Diseases/ Public Health Ontario/ Canada, [3]Pathobiology/ University of Guelph/ Canada

Introduction and Objectives or Purpose

Lyme disease (LD) is rapidly emerging in Canada due to the range expansion of the tick vector, Ixodes scapularis. In 2019, the Canadian Lyme Disease Research Network (CLyDRN) launched a pan-Canadian sentinel surveillance program, the Canadian Lyme Sentinel Network (CaLSeN). As part of CaLSeN, in 2021, a pilot study was launched in four sentinel regions in Ontario to determine the feasibility and utility of veterinary sentinel surveillance in a One Health surveillance system.

Methods

Sentinel regions were selected using multi-criteria decision analyses. In each region, field sampling was performed at selected sites while participating veterinary clinics submitted ticks collected from dogs and cats, and canine tick-borne pathogen serology results. Ticks were identified to species, and I. scapularis were tested via PCR for Borrelia burgdorferi and Anaplasma phaogocytophilum.

Results or Focus

272 I. scapularis were identified, and the serology results of 134 dogs were obtained from 16 veterinary clinics. 216 I. scapularis were collected via field sampling at 43 sites. The B. burgdorferi infection prevalence in pet-collected ticks, field-collected ticks, and the canine seroprevalence were 36.7%, 20.8%, and 10% in Kingston, 23.3%, 19.6%, and 6.1% in Ottawa-Gatineau, and 16.7%, 0.0%, and 6.2% in Hamilton-Guelph respectively. Borrelia burgdorferi was not detected in I. scapularis from the Muskoka Lakes region. A. phagocytophilum (5.2%) was detected in canine serum but not from any I. scapularis tested

Conclusion or Scope

The 23% overall B. burgdorferi infection prevalence is like the 20.0% reported in I. scapularis from the CaLSeN’s national field sampling initiative. We also found I. cookei and I. muris, which were not collected from field sampling. Therefore, veterinary sentinel surveillance would complement active surveillance and generate early signals of tick and tick-borne pathogen invasion in new regions. Our findings suggest that a One Health surveillance approach is feasible and would enhance tick and tick-borne disease monitoring.

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CLyDRN

OVC

Keywords: Lyme disease; Borrelia burgdorferi ; Ixodes scapularis; surveillance

Topic: One Health Science (OHS): Discovery and Surveillance: Vector borne diseases
Abstract No: 14931

Sickness Positioning System (SiPoS): Mapping transmission hotspots of infectious diseases using GPS data from mobile phones of infected patients

Jeevan Giddaluru[*1 2] ; Lucas Cardozo[1] ; Bernardo Silva[3] ; Felipe Martins[3] ; Alinne Antolini[3 4] ; Daniel Bargieri[5] ; Marcus Lacerda[6 7] ; Wuelton Monteiro[8 6] ; Vanderson Sampaio[3 8 9 6] ; Helder Nakaya[1 2 10]
[1]Department of Clinical and Toxicological Analyses, School of Pharmaceutical Sciences/ University of São Paulo/ Brazil (Brasil), [2]Integrative Biology/ Scientific Platform Pasteur USP/ Brazil (Brasil), [3]Programa de Pós-Graduação em Medicina Tropical/ Universidade do Estado do Amazonas/ Brazil (Brasil), [4]Gerência Ambiental/ Secretaria Municipal de Saúde de Manaus/ Brazil (Brasil), [5]Department of Parasitology, Institute of Biomedical Sciences/ University of São Paulo/ Brazil (Brasil), [6]-/ Fundação de Medicina Tropical Dr. Heitor Vieira Dourado/ Brazil (Brasil), [7]Instituto de Pesquisa Leônidas e Maria Deane/ Fiocruz Amazonas/ Brazil (Brasil), [8]Programa de Pós-graduação em Ciências da Saúde/ Universidade Federal do Amazonas/ Brazil (Brasil), [9]-/ Fundação de Vigilância em Saúde do Amazonas/ Brazil (Brasil), [10]-/ Hospital Israelita Albert Einstein/ Brazil (Brasil)

Introduction and Objectives or Purpose

Most infectious diseases are either transmitted through vectors or direct person-to-person contact. A critical way to reduce the spread of infectious diseases is by identifying the transmission hotspots. At hospitals, infected patients are often obligated to inform where they work and live and the places they visited during the past several days. Health agencies receive this information from hospitals for infection surveillance and containment. However, this data relies on patients' memory, which is often inaccurate, vague, and imprecise.

Methods

We developed an online platform called Sickness Positioning System (SiPoS) that anonymously retrieves Global Positioning System (GPS) data from mobile phones. The platform automatically downloads, processes, and analyzes the location history of infected patients to identify potential transmission hotspots. Simultaneously, our SiPoS-Explorer dashboard facilitates real-time visualization and interpretation of these findings for public health officers to implement necessary intervention activities.

Results or Focus

We collaborated with Municipal health authorities, hospitals, and researchers in Manaus, Amazonas region of Brazil, to use our platform for pinpointing Malaria hotspots. Up on receiving location data of Malaria-positive patients, our platform identified multiple clusters of transmission sites, including the locations previously not defined by the Municipal authorities as 'likely transmission zones'. We sent a team of health agents and entomologists to these locations and could locate putative mosquito breeding sites near these places.

Conclusion or Scope

Our low-cost innovative approach enables public health authorities to examine and implement intervention strategies quickly and decide where to spend their limited budget and human resources, thus controlling a disease outbreak. Finally, we recognize that the applicability of our platform extends to other vector-borne and contagious diseases such as Leishmaniasis and Tuberculosis, respectively.

Acknowledgement

We thank FVS-RCP/AM and SEMSA/GA for the support with entomological validation of putative hotspots. This work is supported by São Paulo Research Foundation (FAPESP: 2018/14933-2 and 2019/16419-7) and Bill & Melinda Gates Foundation.

Keywords: Malaria; Vector-borne diseases; Outbreak; Global positioning system; Disease surveillance

Topic: One Health Science (OHS): Discovery and Surveillance: Vector borne diseases
Abstract No: 15064

RISK OF DENGUE TRANSMISSION IN URBAN AREAS OF MALANG, INDONESIA

Alidha Nur Rakhmani*[1] ; Lilik Zuhriyah[1]
[1]Family Medicine/ Faculty of Medicine, Universitas Brawijaya/ Indonesia

Introduction and Objectives or Purpose

Background. Larvae monitoring through community participation is one of dengue prevention programs to control mosquito larvae. Entomology index could be an indicator of the existence of mosquito larvae in an area.

Objectives. This study aimed to determine the entomology index in the urban areas in Malang city and key container which could be the breeding ground of mosquito.

Methods

Method. This study was a cross-sectional study conducted in five subdistricts in Malang city from November 2017 to April 2018. A semi-structured questionnaire delivered using interviews to 400 respondents was used to explore the practice of Dengue prevention behavior. Observations were performed to examine the mosquito larva existence among the houses of health volunteers.

Results or Focus

Results. Density figure in Malang was indicated as moderate density that had range 2-5 . Blimbing subdistrict had the highest House Index (HI) value, which was 30.3% with Container Index (CI) value of 10.6% and Breteau Index (BI) value of 36,3 %. The most common positive Controllable Containers were bathroom tub/container (8.5%) and the water reservoir of a refrigerator (3%).

Conclusion or Scope

Conclusion. Bathroom container and the water reservoir of a refrigerator are the most type of positive container found. Urban area in Malang has a moderate risk of transmitting dengue fever whose highest risk area was Blimbing subdistrict.

Acknowledgement

Public Health office Of Malang

Primary health care provider in Malang

Keywords: dengue, entomology, Indonesia, prevention, urban, Malang

Topic: One Health Science (OHS): Discovery and Surveillance: Vector borne diseases
Abstract No: 15078

A review on the insecticide resistance of ticks in Asia and Australia

Nora Cleary*[1] ; Joanna Pacori[1] ; Michael Von Fricken[1] ; David Pecor[2 3 4] ; Alexander Potter[2 3 4] ; Yvonne-Marie Linton[2 3 4] ; Cynthia Tucker[5]
[1]Global and Community Health/ George Mason University/ United States, [2]Smithsonian Institution Museum Support Center/ Walter Reed Biosystematics Unit/ United States, [3]National Museum of Natural History/ Smithsonian Institution/ United States, [4]Entomology/ Walter Reed Army Institute of Research/ United States, [5]One Health Branch/ Walter Reed Army Institute of Research/ United States

Introduction and Objectives or Purpose

One Health is a transdisciplinary approach to improve health by studying the interactions of people, animals, and the environment. Tick-borne diseases (TBD) are a threat to Deployed War Fighters in the INDOPACOM (Australia, Bhutan, Guam, Korea, Palau, and Philippines) region. The primary mode of defense for DWFs against TBDs are their pyrethroid treated uniforms. This review is part of a larger effort supported by Walter Reed Army Institute of Research (WRAIR) – One Health Branch to provide data on insecticide resistance of ticks in these regions for surveillance and future control measures.

Methods

A systematic literature review on insecticide resistance, ticks, and tick-borne diseases in each country was performed using PubMed, Web of Science, and Scopus. Data was extracted to a standardized form in Microsoft Excel and uploaded to VectorMap.

Results or Focus

There was a total of 7688 articles from the initial search from Australia (4730), Bhutan (17), Guam (48), Korea (2479), Palau (7), and Philippines (463). Inclusion criteria was met for Australia (54), Korea (4), and Philippines (4). No articles met the criteria for full review in Bhutan, Guam, and Palau. There is limited data about insecticide resistance in the INDOPACOM region aside from Australia.

Conclusion or Scope

This poster serves to provide georeferenced locations to reports of acaracide resistance in ticks and what potential risk that might pose to DWFs. Specifically, highlighting the importance of insecticide resistance surveillance in areas where this is used a first line of defense against TBDs. Further studies are needed about the distribution and prevalence of ticks and TBDs to understand the scope of insecticide resistance in Asia and other regions. This knowledge will enable decision makers to create products or implement strategies to protect those at high risk of tick bites.

Keywords: One Health; insecticide resistance, tick-borne disease, surveillance

Topic: One Health Science (OHS): Discovery and Surveillance: Vector borne diseases
Abstract No: 15118

Utilizing the TREMoR stationary robot to assist in tick collections for disease surveillance in Kenya

Michael Von Fricken*[1] ; Carson Stewart[1] ; Shahan Salam[1]
[1]Department of Global & Community Health/ George Mason University, / United States

Introduction and Objectives or Purpose

Ecological research on tick distribution and the diseases they carry is highly relevant to global health. As the climate continues to change, the range and burden of tick-borne diseases that afflict humans, wildlife, and livestock will continue to expand. Tick density studies are usually performed by dragging a 1sqm cloth behind an individual actively walking through tick habitat, who then checks every 10-15m to calculate estimate ticks per sqm. Common issues with this approach include the risk of tick bite to the individual(s) conducting field work and inconsistent pacing and capture of ticks while dragging through vegetation.

Methods

By creating an inexpensive “Tick-collecting Robot for Entomological Modeling Research” AKA “TREMoR”, that attracts ticks from the environment through vibration and CO2, we aimed to standardize quantitative surveillance data that could reliably be collected over set intervals of time. Our multidisciplinary team leveraged expertise in engineering, epidemiology, and medical entomology, during the creation of our prototype that was recently field tested at the Mpala Research Center, Kenya.

Results or Focus

After running TREMoR for only sixty minutes, 25% of marked ticks were recaptured adjacent to the bot, with testing stopped due to complaints that noise was disrupting wildlife. Vibrations from the device could be detected via ground sensors up to 150cm in each direction, which was lower from previous trials in softer soil, where vibrations were detected up to 400cm radius. CO2 sensors at 160cm detected increases of between 550 PPM and 720PPM over ambient CO2 levels to simulate the presence of small mammals but were subject to wind speed and direction.

Conclusion or Scope

Additional optimization of vibration force and rate of CO2 gas exchange, as well as further testing of TREMoR performance over time, are needed before multiple prototypes can be deployed in a swarm formation to test the feasibility of this method for passive tick collection.

Keywords: surveillance; tick-borne diseases; robotics; sample collection; Kenya

Topic: One Health Science (OHS): Discovery and Surveillance: Vector borne diseases
Abstract No: 15120

Applying a One Health approach to detect tick pathogens in Mongolia using Next-Generation Sequencing.

Graham Matulis[1] ; Bazartseren Boldbaatar[1] ; Nora Cleary[1] ; Ratree Takhampunya[2] ; B. Katherine Poole-Smith[2] ; Abigail Lilak[1] ; Doniddemberel Altantogtokh[3] ; Erica Lindroth[2] ; Jodi Fiorenzano[4] ; Michael Von Fricken[*1]
[1]Department of Global & Community Health/ George Mason University, / United States, [1]School of Veterinary Medicine/ Mongolian University of Life Sciences/ Mongolia (Монгол), [2]Department of Entomology/ US Army Medical Directorate of the Armed Forces Research Institute of Medical Sciences/ Thailand (□□□), [3]Department of Epidemiology/ National Center for Zoonotic Diseases/ Mongolia (Монгол) [4]Department of Entomology/ Naval Medical Research Unit Two/ Singapore

Introduction and Objectives or Purpose

Ticks and tick-borne diseases represent a major public health threat in Mongolia, where an estimated 26% of the population live a traditional nomadic pastoralist lifestyle that puts them at increased risk of tick-bite exposure.

Methods

Using Next-Generation Sequencing, with confirmatory PCR and DNA sequencing, we sought to characterize the microbial species present in pools of Dermacentor nuttalli (n=98), Hyalomma asiaticum (n=38), and Ixodes persulcatus (n=72) ticks collected from Khentii, Selenge, Tuv, and Umnugovi aimags (provinces) of Mongolia.

Results or Focus

Rickettsia spp. were detected in 90.4% of tick pools, with Khentii, Selenge, and Tuv all having 100% pool positivity. Coxiella spp. were detected at an overall pool positivity rate of 60%, while Francisella spp. were detected only in H. asiaticum ticks (92% pool positivity), while multiple Borrelia species were detected across all pooled samples. Confirmatory testing and sequencing allowed for species characterization of preliminary NGS analysis. Rickettsia raoultii was the primary Rickettsia spp., while Candidatus Rickettsia tarasevichiae was only detected in I. persulcatus (n=65), followed by two detections of R. slovaca/R. sibirica from the Gobi region. For the Coxiella spp. reads, most samples were identified as a Coxiella endosymbiont (n=117), although Coxiella burnetii was detected in eight pools collected in Umnugovi. Borrelia species that were identified include Borrelia burgdorferi (n=3), B. garinii (n=2), B. miyamotoi (n=16), and B. afzelii (n=3). All Francisella spp. reads were identified as Francisella endosymbiont species.

Conclusion or Scope

Continued monitoring and detection of current and emerging pathogens in Mongolia will contribute to the knowledge of tick-borne diseases for the greater region. Future studies should incorporate NGS technology to detect and analyze medically relevant tick pathogens endemic to Mongolia in human and livestock populations.

Acknowledgement

This work was supported by the Armed Forces Health Surveillance Division (AFHSD) Global Emerging Infections Surveillance (GEIS) Branch, ProMIS ID# PO133_19_AF_N2. Lab analysis was funded by AFHSD-GEIS under study#P0128_20_AF_14.

Keywords: Mongolia; Tick-borne disease surveillance; NGS; infectious disease epidemiology; bacteria

Topic: One Health Science (OHS): Discovery and Surveillance: Vector borne diseases
Abstract No: 15123

Surveillance of zoonotic tickborne haemoprotozoans in understudied non-human primates in Kenya.

Mercy Akinyi*[1] ; Stanislaus Kivai[1] ; Purity Oreng[1] ; Vincent Obanda[2] ; Edward Kingori[2] ; Isaac Lekolol[3] ; Atunga Nyachieo[1] ; Ismael Ng'ang'a[4] ; Isabella Ochola-Oyier[5] ; Lucy Ochola[1]
[1]Animal sciences/ Institute of Primate Research/ Kenya, [2]Research/ Wildlife Research and Training Insitute/ Kenya, [3]Veterinary Capture Unit/ Kenya Wildlife Service / Kenya, [4]SAJOREC/ Jomo Kenyatta University of Agriculture and Technology/ Kenya, [5]Biosciences/ KEMRI-Wellcome Trust Program, Kilifi/ Kenya

Introduction and Objectives or Purpose

Wildlife such as non-human primates (NHPs) are known to harbor zoonotic pathogens because they have close genetic, behavioural and physiological similarity to humans. Pathogens infecting NHPs are thus likely to cross the species barrier to humans. In Kenya, surveillance of potential tickborne zoonoses is rare and has focused only on the most commonly occurring NHP species. The main objective of this study was to identify and characterize a subset of circulating zoonotic tickborne haemoprotozoans in understudied wild NHP populations in Kenya.

Methods

We sampled Colobus sp. (n=27) and Cercopithecus sp. (n=31) from four main locations in Kenya between 2019-2021. Haemoprotozoal screening involved DNA extraction of blood samples and PCR detection using previously validated primers. The PCR amplicons generated will undergo further confirmatory testing after purification and sequencing, followed by phylogenetic analysis.

Results or Focus

We present preliminary results based on PCR detection using previously validated primers. We screened for five main zoonotic haemoparasites. Approximately 19.35% (6/31) of Cercopeithecus sp samples and 7.4% (2/27) tested positive for Babesia sp, None of the samples tested positive for Coxiella brunetti, 83% 25/30) Cercopeithecus sp samples and 5.9% (1/17) Colobus sp. samples for Rickettsia sp., 23.3% (7/30) Cercopeithecus sp samples for Borrelia sp., and 20% (6/30) Cercopeithecus sp samples tested positive for Anaplasma sp,

Conclusion or Scope

These preliminary results point to the presence of potential zoonotic hoemoprotozoans circulating in these wild NHP and underscores the need for continuous disease surveillance in wildlife. These data contribute information that can be helpful towards the 1) development of control strategies during disease emergence and 2) development of conservation strategies for endangered wild NHPs. The data can also give insight to the origins of human pathogens.

Acknowledgement

Co author: Griphin Ochieng

Keywords: Ticks, zoonoses, primates, surveillance, One Health

Topic: One Health Science (OHS): Discovery and Surveillance: Vector borne diseases
Abstract No: 15179

The Changing Incidence of Malaria in Indonesia: A 11 Year Analysis of Surveillance Data

Dewi Nur Aisyah[*1 3] ; Desrina Sitompul[3] ; Wiku Adisasmito[4 3] ; Logan Manikam[1 5] ; Zisis Kozlakidis[6]
[1]Department of Epidemiology and Public Health/ Institute of Epidemiology and Health Care, University College London/ United Kingdom [3]INDOHUN/ Indonesia One Health University Network/ Indonesia [4]Faculty of Public Health/ Universitas Indonesia/ Indonesia [5]ACESO/ Aceso Global Health Consultants Limited/ United Kingdom [6]International Agency for Research on Cancer/ World Health Organization/ France

Introduction and Objectives or Purpose
Globally, it was estimated that there were 241 million cases of malaria in 2021 and Indonesia was accounted for 21% of Southeast Asia malaria burden. To date, there was lacking studies describing malaria trends over time in Indonesia. This study conducted to fill the dearth of studies regarding the changing incidence of malaria over 11 years of span in Indonesia with nationwide malaria surveillance data.

Methods
We collected data on number of malaria cases and API from Sub directorate of malaria, Directorate of Vector borne disease and Zoonosis, Indonesian Ministry of Health between January 2010 and December 2020. We conducted a descriptive analysis of malaria incidence in 27 provinces to identify the trends of malaria in Indonesia.

Results or Focus
The annual incidence of malaria in Indonesia has declined significantly from 2010 (479,215 cases) to 2020 (251,561 cases) – almost a half from 11 years before. The highest number of malaria cases was contributed by Papua province (total of 1,982,819 cases within 10 years), followed by East Nusa Tenggara (621,507 cases) and West Papua (288,879 cases). In 2020, Papua showed the highest number of cases in Indonesia (215,396/251,561), accounting for 85.6% of the national cases, followed by East Nusa Tenggara (6.1%; 15,320/251,561) and West Papua (4.0%; 9,965/251,561). In general, geographical distribution of API in Indonesia had been decreased over 11 years period. Despite the number of provinces with high endemicity had declined, West Papua and Papua still had high endemicity of malaria between 2010 and 2020 with API>5 per 1000 population.

Conclusion or Scope
The incidence rate of malaria has substantially decreased over the past 11 years. However, the incidence rate and API of malaria remains high in Papua provinces. A preventive measure for malaria control should be enhanced in order to meet the target of malaria eradication especially in high endemicity area.

Keywords: malaria, incidence, surveillance

Topic: One Health Science (OHS): Discovery and Surveillance: Vector borne diseases
Abstract No: 15327

GENETIC CHARACTERIZATION OF DENGUE VIRUS SUBTYPE DIVERSITY IN BANGLADESH.

Josefina Abedin[1 2] ; Shusmita Dutta Choudhury[*1 2] ; Emily Hagan[2] ; Shahnaj Shano[1 2] ; Otun Shaha[1 1] ; Mohammed Ziaur Rahman[3] ; Jonathan H Epstein[2] ; Tahmina Shirin[4] ; Meerjady Sabrina Flora[5] ; Ariful Islam[1 2]
[1]EcoHealth Alliance Bangladesh Programs/ Institute of Epidemiology, Disease Control and Research (IEDCR)/ Bangladesh (□□□□□□□□□) [2]Emerging Infectious Disease Research/ EcoHealth Alliance/ United States [1]Department of Microbiology/ Noakhali Science and Technology University/ Bangladesh (□□□□□□□□□) [3]One Health Laboratory/ International Centre for Diarrhoeal Disease Research (icddr,b)/ Bangladesh (□□□□□□□□□) [4]Director and Professor, Department of Virology/ Institute of Epidemiology, Disease Control and Research (IEDCR)/ Bangladesh (□□□□□□□□□) [5]Directorate General of Health Services/ Ministry of Health and Family Welfare/ Bangladesh (□□□□□□□□□)

Introduction and Objectives or Purpose

Dengue is a mosquito-borne viral disease, one of the major causes of morbidity and mortality in tropical and subtropical regions, including Bangladesh, in last few decades. Understanding spread and virulence patterns of dengue virus (DENV) and identifying strains responsible for epidemic outbreaks requires accurate identification of genetic variations. DENV genotypes in Bangladesh were demonstrated in this study, focusing on molecular epidemiology.

Methods

We tested biological specimens from 862 individuals between 2017 and 2019 using consensus PCR targeting the NS5 gene for DENV. Positive PCR products were confirmed by sequencing. To understand genomic characteristics and diversity of DENV, 228 DENV sequences and their metadata from July 2000 to October 2019 in Bangladesh were extracted from NCBI Dengue Virus Database. Phylogenetic analysis has been employed using the maximum likelihood tree method to understand the genetic evolution and diversity of DENV subtypes.

Results or Focus

In DENV diversity, we found prevalence of serotype 1, 2, and 3 were 10.09%, 57.46%, 32.46% respectively. DENV serotype 1 occurrence was more common in summer (66.67%) and serotype 2 in monsoon (56.57%) and winter season (70.37%). The highest prevalence of DENV was found in Dhaka (94%). DENV 3 was commonly a circulating strain over time, although serotypes 1 and 2 have a high rise of prevalence in 2017-2019. Phylogenetic analysis suggests that Bangladeshi DENV type 2 have a close evolutionary relatedness with one another and a more distant genetic relationship with any of three clades of DENV2 circulating in other Asian countries. In the context of DENV3, strains from Bangladesh cluster with China, Singapore, and Sri Lanka, but not with DENV3 strains from the rest of South Asia.

Conclusion or Scope

Findings from this study provide fresh insights into the genetic evolution of DENV subtypes and emphasize the importance of continuous DENV case management and vector control surveillance to prevent DENV epidemics in Bangladesh.

Keywords: Epidemiology, Molecular characterization, Dengue virus, Diversity, Bangladesh.

Topic: One Health Science (OHS): Discovery and Surveillance: Vector borne diseases
Abstract No: 15387

Molecular and serological investigation of Shuni virus in South Africa

Matshepo Rakaki*[1] ; Miné van der Walt1[1] ; Marietjie Venter[1]
[1]Medical Virology / University of Pretoria / South Africa

Introduction and Objectives or Purpose

There are several neglected re-emerging zoonotic Orthobunyaviruses associated with Africa such as Shuni Virus (SHUV), Ngari virus (NRIV) and Bunyamwera virus (BUNV). The goal of this study was to investigate the incidence of Shunivirus in cases of acute fever of unknown cause (AFDUC) with or without neurological signs in sentinel hospitals in Gauteng and Mpumalanga, South Africa. In addition, incidence of Shunivirus in animal sample with neurological signs through a survallience program was also investigated.

Methods

Samples from animals with fever, neurological signs or unexplained deaths were submitted through a veterinary network from across the country as part of the arbovirus surveillance network and clinical samples from patients with AFDUC were collected from hospitals in Gauteng (Kalafong hospital) and Mapulaneng and Matikwane hospitals. These samples are from arbovirus season season (January-June) in 2019 and 2020 were screened using a using a Simbu serogroup orthobunyavirus RT-PCR specific to the M-segment. Viral neutralization assay was carried out to screen patients with AFDUC.

Results or Focus

Since 2020, 8/448 (1.8%) animals tested positive for Orthobunyavirus using an inhouse Orthobunyavirus realtime RT-PCR. Sanger sequencing was performed on the S gene confirmed 6 were identified as SHUV on the phylogenetic tree with a fatality rate of 71%. In total, 3/278 (1%) of human samples tested positive by Simbu, Orthobunyavirus RT-PCR during this time (January-June, 2019-2020). In total there are 9/65 (13.8%) human positive sera that showed to be neutralizing against SHUV (2019) and 80% were from Kalafong whereby 30% were pateints with Meningitis.

Conclusion or Scope

An IgG ELISA has been developed and validated using horse sera this ELISA will be adapted to develop a human IgG ELISA. Future work is to determine the seroprevalence of SHUV in humans in South Africa, the IgG assay will be used to screen sera from health donors in the region.

Acknowledgement

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Keywords: Shunivirus, Neutralization, Orthobunyavirus, RT-PCR, ELISA

Topic: One Health Science (OHS): Discovery and Surveillance: Vector borne diseases
Abstract No: 15389

Environment friendly vector control (Slash and clear) to accelerate onchocerciasis elimination in a high transmission area: a pilot study in the Mbam valley (Centre Region, Cameroon)

André Domche*[1] ; Hugues Clotaire Nana Djeunga[2] ; Guy Roger Njitchouang[2] ; Philippe Nwane[1 2] ; Michel Boussinesq[3] ; Sébastien Pion[3] ; Flobert Njiokou[1] ; Joseph Kamgno[2 4]
[1]Animal Biology and Physiology/ University of Yaoundé 1, Yaoundé, Cameroon/ Cameroon (Cameroun), [2]Molecular Parasitology/ Centre for Research on Filariasis and other Tropical Diseases (CRFilMT), Yaoundé, Cameroon/ Cameroon (Cameroun), [3]Tropical Diseases/ Institut de Recherche pour le Développement (IRD), UMI 233 INSERM U1175 Montpellier University, Montpellier, France/ France, [4]Department of Public Health/ Faculty of Medicine and Biomedical Sciences, University of Yaoundé 1/ Cameroon (Cameroun)

Introduction and Objectives or Purpose

Although “slash and clear” has already proven its effectiveness in reducing blackfly densities in low transmission foci, the feasibility and impact of this strategy in very high transmission foci with large rivers and important vector densities is yet to be demonstrated. We therefore initiated a pilot study in the Mbam valley (Centre Region, Cameroon) to evaluate the impact of “slash and clear” approach on blackfly densities and onchocerciasis transmission.

Methods

Two first-line villages (Bayomen used as control site and Biatsota used as intervention site) where targeted for the study. In each village, baseline data were collected for one year (October 2019 to December 2020), using human landing catching (HLC) method. Two days of ground and boat prospection was done, for the identification and characterization of blackflies breeding sites. The slashing and clearing trailing vegetation where blackflies breed was conducted from December 2020 to August 2021. Generalized estimating equations were used to evaluate the effect of intervention, adjusted on baseline data.

Results or Focus

Prior to intervention, a total of 56,870 and 51,240 blackflies were collected in Bayomen and Biatsota, respectively. No significant difference was found between the two villages (p= 0.7545). The main attachment points for the blackfly larvae were the plant namely Pandanus candelabrum (>90% of larvae/pupae). After the intervention (destruction of the blackfly habitat) period, blackfly densities declined from 51,240 to 25,520 in the intervention site (50.2% reduction) while in the control site, the densities declined from 56,870 to 49,471 (13% reduction); the observed reduction was significantly more important in the intervention site compared to the control site (p=0.0213).

Conclusion or Scope

This study revealed that the “slash and clear” approach has a significant impact on vector densities in a very high transmission setting. Additional studies are needed to investigate the long-term impact of the “slash and clear” strategy, and how it can be used to supplement mass drug administration in high transmission settings to accelerate the onchocerciasis elimination.

Acknowledgement

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Keywords: Onchocerciasis; blackfly; slash and clear; Mbam valley; Cameroon

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Biosafety and biosecurity for outbreak prevention
Abstract No: 14862

Setting the Standard for Field Biosafety at the Human-Animal Interface

Marc Valitutto*[1] ; Cadhla Firth[1] ; Peter Daszak[1]
[1]NA/ EcoHealth Alliance/ United States

Introduction and Objectives or Purpose

As local and international travel restrictions are lifted, scientists are returning to the field, but are they safe? The COVID-19 pandemic has highlighted the risk of zoonotic disease transmission at the human-animal interface and led to questions about how investigators working in various disciplines practice personal biosafety in the field. There are currently no standardized guidelines for what level of personal protection should be applied when field teams are working directly with animals and in their natural habitats. This lack of standardized "best safety practices" is largely due to the immense variation in risk factors associated with each field activity at each field setting. This includes the goals of the research, the species involved, and the pathogens that are targeted in the research, or that could also be found in the study system.

By leveraging the expertise of One Health researchers across the world, we have developed a set of peer-reviewed, risk-based, comprehensive field biosafety guidelines applicable across scientific disciplines. These guidelines were created to recognize the various risks that may be encountered, designed to maximize personal protection and comfort, to take into account the need for flexibility under different environmental or community settings, and to minimize negative environmental impact. Our goal is to create globally accepted standards and lay the foundation to develop widely accessible educational resources.

In this presentation, we introduce the concept of the "Field Biosafety Levels 1-4" analogous to and adapted from the United States' Center for Disease and Control's Laboratory Biosafety Levels 1-4. We also share the risk-based design for field biosafety and how these are applied for investigators conducting research activities at the human-animal interface. Our goal is to make these biosafety resources globally accessible for all interested parties, adaptable, and able to be refined and updated as new techniques and information become available.

Keywords: field, biosafety

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Biosafety and biosecurity for outbreak prevention
Abstract No: 15066

Filling the Governance Gap: A Convention on Animal Protection to Prevent Future Pandemics

Laurie Morgan*[1] ; Nigel Blackaby QC[1] ; Nicolas Cordoba[1] ; Rosario Galardi[1] ; David Favre[2] ; Daina Bray[3] ; Joan Schaffner[4] ; Rajesh Reddy[5] ; Marcia Condoy Truyenque[5] ; Vanessa Gischkow Garbini[5]
[1]Public International Law / Dispute Resolution/ Freshfields Bruckhaus Deringer/ United States, [2]Law / Michigan State University/ United States, [3]Law, Ethics, and Animals / Yale University/ United States, [4]Law School/ George Washington University/ United States, [5]Animal Law / Lewis and Clark School of Law/ United States

Introduction and Objectives or Purpose

The COVID-19 pandemic has drawn a renewed focus on an existing gap in international law: the lack of international standards for human interactions with animals and the environment. Our research addresses environmental law, animal well-being, and the causes of zoonotic spillover by promoting the adoption of a Convention on Animal Protection (CAP).

Methods

The CAP is based on case studies on the causes of spillover of zoonotic diseases. Nearly all spillovers have resulted from practices that lack strong international regulations, namely, the wildlife trade, unnecessary mixing of livestock and wild animals, treatment of animals in live animal markets or medical testing facilities, and destruction of natural habitats.

After better understanding the causes of pandemics, our team engaged in legal research to understand (1) which regulations, if accepted, would best mitigate the risk of spillover and (2) which regulations are most likely to gain traction globally.

Results or Focus

The result of our research is the Convention on Animal Protection. In particular, the CAP provides regulations on human interactions with animals in three broad categories: regulations on all animals, regulations on animals under human care, and regulations on wildlife.

The CAP contemplates the adoption of the first sets of international minimum standards of care for animals, including obligations that states integrate the protection of animal well-being in relevant programs across sectors.

Conclusion or Scope

While many aspects of the science behind pandemics remains under study, it is clear that there is a gap in international law on human interactions with animals. The CAP is a framework for further discussion on practical, binding ways to implement the One Health principle and fill this gap.

Our team has written a first draft of the treaty. Now, we are looking for state policymakers to pick up the pen.

Keywords: One Health; International Law

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Biosafety and biosecurity for outbreak prevention
Abstract No: 15098

A Pandemic Instrument under a One Health Approach

Katherine Ginsbach*1 ; Stefania Negri [4] ; David Sherman[3] ; Kelsey Galantich [3] ; Carmen Bullon[2] ; Alison Durran*
[1]Center for Transformational Health Law / O'Neill Institute for National and Global Health Law/ United States [4]International Law / UNISA School of Law / Italy (Italia) [3]Capacity Building Department / The World Organisation for Animal Health / France [2]FAO Development Law Service / Food and Agriculture Organization of the United Nations/ Italy (Italia)

Introduction and Objectives or Purpose

The COVID-19 pandemic revealed the fractured state of global health law infrastructure. Establishing a pandemic instrument under a One Health approach is necessary to address the multitude of interlinked global health and sustainability challenges, including the risk of emerging and re-emerging infectious diseases, climate change, antimicrobial resistance, and food insecurity.

Methods

Conducting a systematized review of how the new instrument can address: the limitation of the IHR and existing treaties for human, animal, and environmental health; challenges associated with the regulation of animal health, including wildlife trafficking and live animal markets; and barriers to effective legislation regarding antimicrobial resistance, food safety, land use, and biodiversity loss. This review will also address how the new instrument will interact with the IHR and illustrate the value of creating a new instrument instead of revising the existing frameworks, including the IHRs.

Results or Focus

The One Health approach is necessary to respond to new and emerging infectious diseases based on the prompt and efficient exchange of scientific information, pathogens, and associated data. For example, collaboration between authorities allows more timely access to high-quality pathogen specimens and genomic data, which remains a major barrier for the rapid development and fair and equitable deployment of safe and effective diagnostics and vaccines. Enhancing and expanding networks, mechanisms, and incentives for the sharing of data is vital to global pandemic preparedness.

Conclusion or Scope

A One Health approach incorporated into the proposed WHA/WHO pandemic treaty would not only strengthen countries abilities to respond to a multitude of biological threats, but also would enhance multilateral cooperation at the international level. propose incorporating into a new instrument the central role that One Health plays in pandemic prevention and preparedness, which we will demonstrate through concrete solutions that a One Health pandemic treaty would offer to legal preparedness.

Keywords: Pandemic Instrument; One Health; Legal Preparedness; Pandemic Prevention & Preparedness; WHO

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Biosafety and biosecurity for outbreak prevention
Abstract No: 15282

STRENGTHENING BIOSAFETY, BIOSECURITY AND QUALITY ASSURANCE AT COVID-19 TESTING LABORATORIES IN BANGLADESH: A UNIQUE ONE HEALTH APPROACH

Eric Brum[1] ; Md. Mohibul Hassan Afrad[*1] ; Mohammad Rafique Islam[1] ; Nawsher Alam Ahmed; Md. Tanbirul Islam; Mustafizur Rahman; Md. Abul Kalam; Samir K. Saha; Tahmina Shirin; Meerjady Sabrina Flora
[1]Emergency Centre for Transboundary Animal Disease (ECTAD) / FAO/ Bangladesh (□□□□□□□□)

Introduction and Objectives or Purpose

To promptly identify COVID-19 cases, the Government of Bangladesh (GoB) rapidly expanded the RT-PCR testing facilities across the countries. However, many laboratories assigned to COVID-19 testing had no prior experience of molecular detection of any highly transmissible pathogen, laboratory biosafety, biosecurity, and quality assurance (QA). Available laboratory experts in the public health sector were fully engaged in their own laboratories. However, a good number of laboratory scientists in the academia and research institutes with expertise in molecular diagnosis, laboratory biosafety and biosecurity are available at the animal health and other life science sectors. This programme was undertaken to take on board the expertise and experiences of animal health and other life science sectors for the improvement of biosafety, biosecurity and QA of newly established COVID-19 testing laboratories.

Methods

A pool of 18 expert volunteers with the background of animal health, animal genetics, general microbiology and biochemistry were identified mostly from the academia and research. They were trained intensively on laboratory biosafety, biosecurity, and QA. Assessment tools and scoring rubrics were developed. The experts routinely visited the laboratories, assessed their biosafety, biosecurity, and QA status, provided on-site training and mentoring supports and reported to the reference laboratory of the health department.

Results or Focus

Between July 2020 and March 2022, 128 expert missions were conducted in 71 laboratories. A total of 877 laboratory professionals received training and mentoring support. The overall laboratory biosafety and QA score (out of 100, based on 20 indicators) at the first visit was 30-90.9 (average 65.45) and that at the 4th visit was 51.8-97.4 (average 77.88).

Conclusion or Scope

A multisectoral cooperation significantly contributed to the improvement of biosafety, biosecurity and QA of COVID-19 testing laboratories, which further underlines the importance of one health approach in national technical capacity building to combat public health emergencies.

Keywords: Biosafety; Biosecurity; COVID-19; One Health

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Biosafety and biosecurity for outbreak prevention
Abstract No: 15325

OUTCOME MAPPING AS AN APPROACH FOR HIGH-RISK INTERFACE PRIORITIZATION AND INTERVENTION DESIGN TO REDUCE RISK OF ZOONOTIC SPILLOVER IN BANGLADESH

Nadia Rimi[*1] ; Julius Nyangaga[2] ; Rebeca Sultana[1] ; Md. Mustafizur Rahman[1] ; Md. Khaled Saifullah[1] ; Monjur Shahjada[3] ; Tahmina Shirin[4] ; Md. Jahidul Kabir[5] ; Nitish Debnath[6] ; Janetrix Amuguni[7]
[1]Infectious Diseases Division/ Icddr,b/ Bangladesh (□□□□□□□□), [2]Monitoring and Evaluation Department/ Right Track Africa/ Kenya, [3]Department of Livestock Services/ Ministry of Fisheries and Livestock/ Bangladesh (□□□□□□□□), [4]Institute of Epidemiology, Disease Control and Research/ Ministry of Health and Family Welfare/ Bangladesh (□□□□□□□□), [5]Forest Department/ Ministry of Environment, Forest and Climate Change/ Bangladesh (□□□□□□□□), [6]N/A/ One Health Bangladesh/ Bangladesh (□□□□□□□□), [7]Department of Infectious Disease and Global Health/ Tufts University/ United States

Introduction and Objectives or Purpose

Bangladesh is a 'hotspot' for emerging and re-emerging infectious disease epidemics. Although the basic features of some zoonotic pathogens are well-researched and key reservoir and bridging hosts identified, there remain challenges in designing and implementing effective interventions. USAID's Strategies to Prevent (STOP) Spillover used outcome mapping (OM), a participatory approach, to engage stakeholders and identify high-risk zoonotic viral spillover interfaces and risk reduction interventions.

Methods

A one-day consultation was held with 79 stakeholders from multiple disciplines. Participants identified the country's high-risk interfaces and relevant actors for a national-level OM workshop, where 124 stakeholders prioritized interfaces using a set of co-developed criteria. The workshop was followed by multiple workshops with participants from the selected interface. At both national and interface levels, participants mapped risk management barriers, critical partners, outcome targets and proposed interventions. Using the outcome targets and a set of co-developed criteria, specific research and development areas were selected.

Results or Focus

Participants identified 20 high-risk interfaces during the one-day meeting, and consolidated those into nine interfaces during the six-day workshop. Two interfaces were prioritized: poultry value chain and bat-human ecosystem. The former ranked highest with most participants choosing Dhaka's live bird markets (LBM) as the initial focus. Identified gaps and barriers at LBMs included inadequate infrastructure, sanitation, waste management, and lack of coordination and monitoring, integrated surveillance and early detection systems and context-appropriate guidelines/SOPs for market's functions. Thirteen consolidated "intervention/research areas" were proposed, from which the program selected three interventions and two research areas.

Conclusion or Scope

Outcome mapping enabled us to identify a broad range of traditional and non-traditional stakeholders and encouraged multi-stakeholder dialogue, which is critical for One Health platforms. While the process encouraged stakeholders' ownership of project outcomes, some steps were modified to fit the project's goal and country context. Lessons on what can be utilized in other similar project designs were learned.

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Biosafety and biosecurity for outbreak prevention
Abstract No: 15355

IDENTIFYING NON-TRADITIONAL LIVE BIRD MARKET ACTORS AND EXPLORING THEIR BARRIERS AS PART OF AVIAN INFLUENZA RISK REDUCTION INITIATIVES IN BANGLADESH

Md. Mustafizur Rahman*[1] ; Rebeca Sultana[1] ; Md. Imran Hossain Mithu[1] ; Elizabeth Gold[2] ; Esther Kihoro[3] ; TABM Muzaffar Goni Osmani[4] ; M. Salim Uzzaman[5] ; AFM Rakibul Hasan Bhuiyan[4 6] ; Md. Rashedul Kabir Bhuiyan[6 7] ; Nadia Rimi[1]
[1]Infectious Diseases Division/ Icddr,b/ Bangladesh (□□□□□□□□□), [2]N/A/ JSI Research & Training Institute, Inc./ United States, [3]Monitoring and Evaluation Department/ Right Track Africa/ Kenya, [4]Department of Livestock Services/ Ministry of Fisheries and Livestock/ Bangladesh (□□□□□□□□□), [5]Institute of Epidemiology, Disease Control and Research/ Ministry of Health and Family Welfare/ Bangladesh (□□□□□□□□□), [6]N/A/ One Health Secretariat/ Bangladesh (□□□□□□□□□), [7]Forest Department/ Ministry of Environment, Forest and Climate Change/ Bangladesh (□□□□□□□□□)

Introduction and Objectives or Purpose

The live bird market (LBM) is a critical interface for zoonotic spillover of avian influenza involving interrelationships among people, poultry/birds, and the environment. In Bangladesh, previous attempts to improve LBM biosecurity involved poultry shop owners and workers. However, understanding the role of different actors connected to the LBMs is essential for a holistic approach toward sustainable changes. We aimed to identify all potential LBM actors and explore their roles, connectedness, and barriers to improving LBM biosecurity as part of avian influenza risk reduction initiatives.

Methods

We used Outcome Mapping (OM), a stakeholder-driven approach to identify a broad range of traditional and non-traditional stakeholders for project outcomes in zoonosis risk management. We engaged 76 participants in three workshops and 21 group discussions at one retail and one wholesale LBM in Dhaka city and the Department of Livestock Services to describe the risk behavior, limitations, and possible actor-mitigation measures.

Results or Focus

Along with poultry shop owners, workers, and market authorities, we identified several non-traditional stakeholders: mobile poultry vendors, fishery owners and workers, poultry feather collectors, pet animal owners, three categories of cleaners, including sewer divers, and several regulatory authorities. Workers and cleaners mentioned insufficient capacity to improve practices and fear of job loss. Mobile vendors reported a lack of equipment and support to improve practices, were demoralized and aspired to own a shop in the market. Regulatory authorities mentioned the absence of guidelines, insufficient logistic support, and a shortage of skilled workforce for inspection and monitoring. We explored the interrelationships of LBM stakeholders and found that the connections were mostly business-oriented and not for biosecurity or hygiene measures.

Conclusion or Scope

We identified some critical groups of non-traditional LBM actors who can contribute significantly to risk reduction and prevention initiatives. These findings can help us to design sustainable avian influenza risk reduction interventions in LBMs of Bangladesh.

Keywords: avian infuenza; live bird market; zoonotic; risk reduction; intervention

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Biosafety and biosecurity for outbreak prevention
Abstract No: 15408

PERCEPTIONS OF HEALTH WORKERS IN TESTING, TRACING, TREATMENT STUDIES FOR THE PREVENTION OF THE SPREAD OF COVID-19 IN EAST JAVA PROVINCE, INDONESIA

Fedik Abdul Rantam*[1] [2] [3] ; Melyana [2] ; Firdausy Kurnia Maulana[2] ; Dhimas Toni Angger Prambudi[2] ; Briantono Willy Rendragraha[2] ; Annisa Vivianti[2] ; Siti Shofiya Novita Sari[2] [4] ; Wiku Adi Sasmito[5] ; Agus Suwandono[5] [6]
[1]Secretary/ Institute Tropical Disease/ Indonesia, [2]One Health Collaborating Center/ Airlangga Disease Prevention and Research Center/ Indonesia, [3]Microbiology/ Faculty of Veterinary Medicine, Universitas Airlangga/ Indonesia, [4]Epidemiology/ Faculty of Public Health, Universitas Airlangga/ Indonesia, [5]-/ Indonesia One Health University Network/ Indonesia, [6]Epidemiology/ Faculty of Public Health, Universitas Diponegoro/ Indonesia

Introduction and Objectives or Purpose

At the end of 2020, confirmed positive cases of COVID-19 in Indonesia were still increasing with a massive spike in positive cases occurred since September-October 2020 with a total of 440,569 confirmed cases as of November 9, 2020. Mortality rate due to COVID-19 had reached 14,689 deaths with a case fatality rate of 3.34%. East Java was one of 10 priority provinces for COVID-19 response in Indonesia. The government continues to carried out COVID-19 prevention and control efforts to reduce the burden on the state in all sectors. One of the efforts that have been made was to implement the Testing, Tracing, Treatment (3T) strategy.This study aimed to evaluate the characteristics of field officers, factors that influence the implementation of laboratory testing, tracing, and treatment, especially in East Java.

Methods

The study was survey with primary data collection and conducted on November to December 2020. We used online questionnaire that regarding description of the implementation of COVID-19 testing, tracing and treatment. The respondents were 743 health workers who were working on 3T. with various professions including doctors, midwives, nurses, pharmacists, public health experts, etc. Univariate analysis was used to analyze the data from the survey results.

Results or Focus

Most respondents were female (73.9%), diploma degree educational level (49.5%), >10 years length of work (61.3%). The most health workers were midwives (33.6%) and nurses (26.4%). The adequacy of 3T human resources was 41-80%. Most of the respondents' working hours were more than 8 working hours for testing staff (60.8%), tracing (54.65%). All health workers stated that they did not receive compensation for testing (76.5%), tracing (85.3%), treatment (82.8%) for working more than 8 hours. Most respondents were able to do testing 101-1000 people per week (42.4%), had traced <5 contacts per week (60.6%), had treated <5 patients per week (34.1%).

Conclusion or Scope

The implementation of 3T in East Java Province had been carried out well, but health workers feel burdened in carrying out their duties due to work overload and did not get compensation. We recommend adding health workers or volunteers to assist in the implementation of the 3T and providing compensation for health workers who work overtime.

Acknowledgement

- National Disaster Management Agency

Keywords: testing, tracing, treatment, COVID-19

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Diagnostic and discovery platforms
Abstract No: 14912

Diagnostic and Discovery platforms use at Points of Entry in Nigeria

Onyekachi Nwitte-Eze*[1] ; Morenike Alex-Okoh[1] ; Geoffrey Okatubo[1] ; Olutola Bamsa
[1]Department of Public Health/ Federal Ministry of Health/ Nigeria

Introduction and Objectives or Purpose

International Health Regulations stipulate traveler access to diagnostic laboratories as a core competency for Points of Entry (POE). However, diagnostics and discovery platforms are non-existent at POE in Nigeria however, during the COVID-19 pandemic, there was RDT testing at POE. The need to identify and triage ill travelers as ground crossings were re-opened to the mobile population in Nigeria, was accentuated by the COVID-19 pandemic. We decided to highlight the usefulness of establishing diagnostic and discovery platforms at POE; as the gateway for the importation and exportation of diseases and public health events.

Methods

In July – September 2021, the Port Health Services Division; Department of Public Health of the Federal Ministry of Health carried out rapid diagnostic COVID-19 testing on all travelers arriving at Seme and Idi-Iroko ground crossings.

Results or Focus

Of one thousand, nine hundred and eighty-nine (1989) travelers that crossed the borders at Seme and Idi-Roko, eighteen (18) cases of COVID-19 were detected through the rapid diagnostic test. Travelers who tested positive were linked up with the state surveillance structure for follow-up and management. These positive cases could lead to the infection of new cases. Diagnostic and discovery platforms at POE will mitigate the risks of importation and exportation of infectious diseases across borders. Similar platforms can be set up to intensify screening and commence surveillance for other aspects of health for humans, animals, and their shared environment.

Conclusion or Scope

Diagnostic and discovery platforms at POE will mitigate the risks of importation and exportation of infectious diseases across borders. Similar platforms can be set up to intensify screening and surveillance for other aspects of health for humans, animals, and their shared environment.

Acknowledgement

Appreciation goes to the Director; Department of Public Health and the Director; Port Health Services Division for their guidance and support.

Keywords: Diagnostics, Travelers, POE, Health

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Diagnostic and discovery platforms
Abstract No: 15160

DETERMINING THE ROLE OF PHAGE IMMUNOPRECIPITATION SEQUENCING FOR NOVEL PATHOGENS

Charles Kevin Dee Tiu*[1 2] ; You Jiang Tan[3 4] ; Kaavya Narasimhalu[3 4] ; Lin-Fa Wang[1 2]
[1]Programme in Emerging Infectious Diseases/ Duke-NUS Medical School/ Singapore, [2]Singhealth Duke-NUS Global Health Institute/ Duke-NUS Medical School/ Singapore, [3]Department of Neurology (SGH/SKH Campus)/ National Neuroscience Institute/ Singapore, [4]-/ Duke-NUS Medical School/ Singapore

Introduction and Objectives or Purpose

Phage ImmunoPrecipiation Sequencing (PhIP-Seq) is phage-based mega-plexable serological assay that allows users to determine the antibody repertoire using a minimal sample volume. The power of PhIP-Seq is in its ability to include protein sequences from various known viruses and pathogens, if the amino-acid sequence is known. While PhIP-Seq has great flexibility, a question is whether PhIP-Seq will be able to identify antibodies to novel pathogens not included in the original design.

Methods

Plasma and cerebrospinal fluid samples from a patient with new onset refractory status epilepticus (NORSE) following one dose of mRNA SARS-CoV-2 vaccination (0 days post immunization, dpi) was analyzed with the PhIP-Seq VirScan library. VirScan was initially published in 2015 and contains peptides representing human viruses. While it includes several Coronaviruses, it does not include SARS-CoV-2. We validated our findings with conventional serological techniques.

Results or Focus

We find that most of the top VirScan hits for the patient's CSF (14 dpi) are peptides from Coronaviridae family of viruses spike proteins. On the other hand, the top hits for the patient's plasma at two timepoints are from endemic human viruses such as Epstein-Barr Virus, Human Herpesvirus 1, Adenoviruses and Rhinoviruses. Neutralizing antibodies in the sera against SARS-CoV-2 were found to be borderline positive at 14 dpi and negative at 25 dpi.

Conclusion or Scope

While further work is needed, the data is supportive of the hypothesis that SARS-CoV-2 antibodies – a virus not included in the original library - can be detected by VirScan. This notion extends the versatility of VirScan to possibly include pathogens not included in the original library design. We hope this can potentially pave the way for PhIP-Seq to be used to surveil the epidemiology of novel or emerging pathogens.

Acknowledgement

We thank Prof Steve Elledge for providing the VirScan Library and the patients who consented to be part of the study.

Keywords: Serology; NORSE; PhIP-Seq; Phage Display; Emerging Pathogens

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Diagnostic and discovery platforms
Abstract No: 15212

Detection of Two Alphacoronaviruses in Bats in Eastern Ontario, Canada

Jonathon Kotwa*[1] ; Winfield Yim[1] ; Finlay Maguire[2 3 4] ; Arinjay Banerjee[5 6 7 8] ; Oliver Lung[9 10] ; Vikram Misra[7] ; Valerie Von Zuben[11] ; Lily Yip[1] ; Samira Mubareka[1 8] ; Christina Davy[11 12 13]
[1]Biological Sciences/ Sunnybrook Research Institute (Toronto, Ontario)/ Canada, [2]Faculty of Computer Science/ Dalhousie University/ Canada, [3]Institute for Comparative Genomics/ Dalhousie University/ Canada, [4]Department of Community Health and Epidemiology/ Dalhousie University/ Canada, [5]Vaccine and Infectious Disease Organization/ University of Saskatchewan/ Canada, [6]Department of Biology/ University of Waterloo/ Canada, [7]Department of Veterinary Microbiology/ University of Saskatchewan/ Canada, [8]Faculty of Medicine/ University of Toronto/ Canada, [9]National Centre for Foreign Animal Disease/ Canadian Food Inspection Agency/ Canada, [10]Department of Biological Sciences/ University of Manitoba/ Canada, [11]Wildlife Research and Monitoring Section/ Ontario Ministry of Natural Resources and Forestry/ Canada, [12]Department of Biology/ Trent University/ Canada, [13]Department of Biology/ Carleton University/ Canada

Introduction and Objectives or Purpose

Bats are key hosts for coronaviruses, some of which pose spillover risks to humans and other animals. Surveillance for bat coronaviruses in Canada remains limited, representing a critical blind spot for pandemic preparedness and bat conservation. Therefore, we began screening bats for endemic coronaviruses in Ontario, Canada.

Methods

Oral swabs were collected from 40 big brown bats (Eptesicus fuscus), 119 little brown myotis (Myotis lucifugus), 31 eastern small-footed myotis (Myotis leibii), and 35 tri-coloured bats (Perimyotis subflavus) in eastern Ontario, Canada from July to September in 2020 and 2021. RNA from sample pools of 2-4 individuals were extracted and analyzed using a nested pan-coronavirus RT-PCR targeting the highly conserved RNA-dependent RNA-polymerase (RDRP) of the coronavirus genome; samples from positive pools were re-analyzed individually for confirmation. Partial RDRP sequencing was conducted on positive samples and resultant consensus sequences were identified using BLASTn, limiting the search to North American coronavirus sequences. Phylogenetic analysis was performed including alphacoronavirus genomes, with SARS-CoV-2 as an outgroup representing betacoronaviruses.

Results or Focus

Overall, 2.5% (1/40) E. fuscus and 0.8% (1/119) M. lucifugus samples were RT-PCR-positive. Two coronaviruses from the alphacoronavirus genus were identified, with 70% similarity between the two. The sequence from the E. fuscus sample had 95% similarity to an Eptesicus bat coronavirus (EbCov) previously identified from E. fuscus in South Dakota, USA. The sequence from the M. lucifugus sample had 97% similarity to a Myotis lucifugus coronavirus (MylCov) previously identified in M. lucifugus in Manitoba, Canada. Notably, EbCov is related to swine acute diarrhea syndrome coronavirus, and both EbCov and MylCov are related to porcine epidemic diarrhea virus.

Conclusion or Scope

Our study provides preliminary insights into coronavirus diversity in bats in a previously under-sampled region. This work provides a baseline for more rigorous surveillance, and for exploring the potential relationship between bat and swine coronaviruses in our study area.

Acknowledgement

Many thanks to Juliette Blais-Savoie, Hsien-Yao Chee, Emily Chien, and Aaron Hou for assistance with sample analysis.

Keywords: bats; coronaviruses; one health; pandemic preparedness; conservation

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Diagnostic and discovery platforms
Abstract No: 15230

SARS-CoV-2 Surrogate virus neutralization test for next-generation vaccine development and immunity status monitoring

Chengxun Su[1] ; Yanfeng Li*[1]
[1]Diagnostics/ GenScript Biotech (Singapore) Pte. Ltd./ Singapore

Introduction and Objectives or Purpose

Neutralizing antibodies (NAb) are critical human immune defense mechanisms against viral infections as NAb can bind to sites on the virus and inhibit entry of that virus into the host. NAb are produced post COVID-19 infection or vaccination and has been shown as a good biomarker for adaptive immunity. High level and long-lasting NAb is one of the key objectives of vaccination. NAb titer post-vaccination is conventionally measured using cell-based neutralization assays which is laborious and time-consuming. Since the invention of surrogate virus neutralization test (sVNT) by Prof Wang Linfa, it has been widely used as the “Gold Standard” for neutralizing antibody detection due to the ease in assay set up, high throughput and fast turnaround time (less than 2 hours). This work aims to review the application of sVNT in vaccine development, serosurveillance projects, as well as its clinical use in assessing individual immunity status.

Methods

ELISA-based neutralizing antibody detection assay/surrogate virus neutralization test

Results or Focus

The application of sVNT technology in serosurveillance and vaccine development; the difference between NAb and total antibody, and impact of new variants. Clinical performance of cPass™ sVNT, individual differences in NAb longevity post infection/vaccination.

Conclusion or Scope

sVNT technology is a powerful tool for next-generation vaccine development, and can be used to inform the need for booster at individual level.

Acknowledgement

Prof Wang Linfa is the inventor of this technology

Keywords: SARS-CoV-2, immunity, serology, neutralizing antibody, detection

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Diagnostic and discovery platforms
Abstract No: 15242

EPIDEMIOLOGY AND GENETIC DIVERSITY NOVEL PARAMYXOVIRUSES RELATED TO JEILONGVIRUS AND LANGYA VIRUS IN RODENTS AND SHREWS, BANGLADESH.

Ariful Islam*[1 2] ; Mohammed Ziaur Rahman[3] ; Shariful Islam[1 2] ; Mohammad Enayet Hossain[3] ; Melinda K Rostal[2] ; Tahmina Shirin[4] ; Meerjady Sabrina Flora[5] ; Simon J Anthony[6] ; Peter Daszak[2] ; Jonathan H Epstein[7]
[1]EcoHealth Alliance Bangladesh Program/ Institute of Epidemiology, Disease Control and Research (IEDCR)/ Bangladesh (□□□□□□□□□), [2]Emerging Infectious Disease Research/ EcoHealth Alliance/ United States, [3]One health Laboratory/ International center for diarrheal disease research (icddr,b), / Bangladesh (□□□□□□□□□), [4] Department of Epidemiology/ Institute of Epidemiology, Disease Control and Research (IEDCR)/ Bangladesh (□□□□□□□□□), [5]Directorate General of Health Services/ Ministry of Health and Family Welfare/ Bangladesh (□□□□□□□□□), [6]Department of Pathology, Microbiology, and Immunology/ University of California-Davis,School of Veterinary Medicine, / United States, [7]Vice President, Science and Outreach Program/ EcoHealth Alliance/ United States

Introduction and Objectives or Purpose

Rodents and shrews live in close proximity to humans and have been identified as critical hosts of zoonotic pathogens. As part of a broad One Health surveillance effort, we conducted surveillance for novel zoonotic viruses in wildlife, domestic animals, and people. Paramyxoviruses (PMV) were among the priority groups of viruses targeted by surveillance. Here, we report PMV detected in Bangladesh wild rodents and house shrews.

Methods

We collected oral and rectal swab samples from rodents (n= 1019) and house shrews (n=186) twice a year, in the dry and wet seasons, from three districts in Bangladesh from 2016 to 2018. To detect known and novel paramyxovirus, we tested swab samples using consensus PCR assay targeting RDRP genes of paramyxovirid specific generate primers.

Results or Focus

Overall, 2.1% (25/1205; 95% CI: 1.3-3.0) animals was positive against PMV. The prevalence of PMV was similar in rodents (2.06%; 21/1019) and shrews (2.15%; 4/186). We detected 04 strains of PMV from 25 samples of 04 species of rodents and house shrew. The PMV was more prevalent in wet than dry seasons. We identified landscape, sex, and health conditions significantly associated with PMV shedding in multivariable logistic regression model. Phylogenetic analysis revealed that 03 PMV strains identified in rodents are genetically related to Jeilongvirus. One PMV strain was detected in shrews' resemblance to the novel zoonotic Langya virus, which warranted further investigation. However, the whole genome and molecular characterization are required to ascertain the virus pathogenicity and similarity with Langya or a novel strain of PMV.

Conclusion or Scope

This study's findings revealed that diverse strains of paramyxovirus, including that related to Langya virus, are present in shrews and rodents in Bangladesh. Future studies in Bangladesh should continue to characterize PMV viral diversity, and Langya virus should be included as possible etiologies for humans at high-risk human-animal interfaces that test negative for common pathogens.

Keywords: Surveillance, Novel, Diversity, interface, discovery

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Diagnostic and discovery platforms
Abstract No: 15262

Identification and characterization of emerging and re-emerging viruses in European wildlife and domestic animals

Franziska Kaiser*[1] ; Sonja Jesse[1] ; Monica Mirolo[1] ; Wendy K. Jo[1] ; Martin Peters[2] ; Madeleine De le Roi[3] ; Wolfgang Baumgärtner[3] ; Martin Ludlow[1] ; Albert Osterhaus[1]
[1]Research Center for Emerging Infections and Zoonoses/ University of Veterinary Medicine Hannover/ Germany (Deutschland), [2]CVUA/ Chemisches und Veterinäruntersuchungsamt Westfalen/ Germany (Deutschland), [3]Department of Pathology/ University of Veterinary Medicine Hannover/ Germany (Deutschland)

Introduction and Objectives or Purpose

Emerging pathogens have affected mankind for centuries. Many of these spilled-over from wildlife reservoirs. Important elements of epidemic and pandemic prevention and preparedness include pathogen surveillance, pathogen discovery and virus characterization in wild and domestic animals.

Methods

Guided by recent clinical, epidemiological, and pathological indications, we have identified and characterized several pathogens in zoo and wildlife animals in Germany. Therefore, we have used next generation sequencing technologies combined with virus family specific PCR assays. Phylogenetic analyses, in vitro susceptibility test, serological surveys and further molecular characterization were carried out to obtain further clues about their ability for interspecies transmission.

Results or Focus

In the past years we have detected several hitherto unidentified viruses in different mammalian species with and without disease symptoms. These include a previously unknown gammaherpesvirus causing a malignant catarrhal fever disease in an antelope species, a novel pestivirus (PhoPeV) of porpoises (Phocoena phocoena) and a kobuvirus in a porpoise (Phocoena phocoena) with encephalitis, as well as a paramyxovirus in a hedgehog (Erinaceus europaeus). Besides the discovery of not previously discovered viruses, we detected an Umatilla-like orbivirus in a penguin from a Lower Saxony zoo and bovine rota- and kobuviruses in the central nervous system of a calf with encephalitis. Furthermore, we characterized swinepox viruses from both deceased domestic pigs and wild boars (Sus scrofa), investigated an ancestral canine distemper virus strain causing an epizootic in Caspian seals (Phoca caspica) and a canine kobuvirus causing a systemic infection in a moribund fox (Vulpes vulpes).

Conclusion or Scope
Identification and characterization of previously unknown viruses that may have an impact on human or animal health, can serve as an early warning system for potential outbreak scenarios. Expanding our skills and knowledge about natural pathogen reservoirs, diagnostic tools, cell and host tropism and probability of interspecies transmission, are all key elements of outbreak prevention and preparedness strategies.

Keywords: virus discovery; next-generation sequencing; surveillance; European wildlife

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Diagnostic and discovery platforms
Abstract No: 15288

Rapid antigen testing by community health workers for detection of SARS-CoV-2 in Dhaka, Bangladesh: community-based diagnostic accuracy study

Eric Brum[*1] ; Motahara Tasneem[1] ; Joanna Andrecka[1] ; Tahmina Shirin; A. S. M. Alamgir; Mahbubur Rahman; Ahmed Nawsher Alam; Farzana Khan; Katie Hampson; Ayesha Sania
[1]Emergency Centre for Transboundary Animal Disease (ECTAD) / FAO/ Bangladesh (□□□□□□□□)

Introduction and Objectives or Purpose

Since the start of the COVID-19 pandemic, countries around the world have quickly developed accessible approaches to diagnostic testing, with Reverse Transcription Polymerase Chain Reaction (RT-PCR) as the gold standard. Despite efforts to improve laboratory capacity, access to RT-PCR in Bangladesh is still limited, even negligible, in the poorest communities, typically those worst hit by the pandemic. This study evaluated the performance and feasibility of rapid antigen testing by community health workers at the household level as an alternative SARS-CoV-2 diagnostic platform.

Methods

Community workers in this study were members of Community Support Teams (CST), a platform formed in response to COVID-19 pandemic crisis. During the study, the CST members performed rapid antigen tests on symptomatic individuals identified during routine community search.

Results or Focus

In total, 1240 nasal and saliva samples were collected from symptomatic individuals and 993 samples from additional household members. Test sensitivity, specificity, positive predictive values, negative predictive values and accuracy of rapid antigen tests with their 95% exact binomial CIs were estimated. The results were calibrated against RT-PCR.

The key findings were that (1) Rapid tests performed in communities have sensitivity, equivalent to expectations under controlled laboratory conditions when using nasal swabs (2) CSTs were able to collect samples and perform tests, achieving anticipated sensitivity of 68% (3) During the study period, testing in low-income communities increased fourfold through the mobilization of community health workers for sample collection.

Conclusion or Scope

Our study showed that deploying low cost rapid tests in the community could be far more effective and efficient than conventional PCR testing. Trained community workers under the supervision of specialists could increase capacity and address many challenges of access to testing in resource-poor communities. Finally, training and mentoring programs for community workers (such as CST) could increase testing and improve reporting when integrated into national surveillance systems.

Keywords: Rapid test; CST; Reporting; SARS-CoV-2; Sensitivity

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Focus on pandemic prone pathogens
Abstract No: 14682

One Health advocacy through education: An initiative by University of Pretoria Centre for Viral Zoonoses

Tedson Nkoana*[1 2] ; Wanda Markotter[1 2]
[1]Centre for Viral Zoonoses/ University of Pretoria/ South Africa, [2]Future Africa Institute/ University of Pretoria/ South Africa

Introduction and Objectives or Purpose

The University of Pretoria Centre for Viral Zoonoses (UP CVZ) leads and collaborates in biosurveilleince of zoonotic pathogens in bats, potential spillover hosts and drivers of spillover in rural and urban areas of South and Southern Africa. Research mostly takes place in communities where bats inhabit nearby caves. To promote participation from stakeholders outside the professional expertise, the UP CVZ engages in educational activities with youth, the next generation of professionals, to create awareness and understanding about infectious diseases including a One Health approach to prevention.

Methods

Education takes the form of interactive activities and presentations in schools and covers topics such as bat ecology and importance, disease transmission from humans to animals, safe interactions with bats and other wildlife, the history and importance of vaccines, and the One Health concept. Informal assessments held after each session instill further understanding and promote critical thinking. Material for activities is developed using UP CVZ expertise and collaborations with other departments. Furthermore, select material is translated into local languages to suit specific communities.

Results or Focus

We developed specific target material. Continued interactions with some of the schools show better knowledge base and understanding of bats and their importance to people and other wildlife, and knowledge on simple practices to live safely with bats and other wildlife. This understanding needs to be further quantified through surveys, to identify existing gaps.

Conclusion or Scope

A common and concerning trend is that youth generally have little knowledge about zoonotic risk and other concepts in science. The UP CVZ has therefore embarked on a school programme that will expand on the existing educational activities by adding activities that promote learner support and critical thinking, and provide career guidance.

Acknowledgement

University of Pretoria Centre for Viral Zoonoses, Biosurveillance and Ecology of Emerging Zoonoses research group.
Future Africa Institute
EcoHealth Alliance
Generation Unlimited
UNICEF

Keywords: Bats, Zoonoses, Education, One Health, Youth

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Focus on pandemic prone pathogens
Abstract No: 14907

National Strategy for Prevention and Control of Anthrax in Humans and Animals in Kenya, 2021-2036

Augusta Kivunzya[*1] ; Athman Mwatondo[2] ; Mathew Muturi[3] ; Harry Oyas[4] ; Mark Nanyingi[5] ; Mark Obonyo[6]
[1]Ministry of Livestock, Apiculture and Fisheries/ County government of Kitui/ Kenya, [2]Ministry of Health/ County government of Kitui/ Kenya, [3]Ministry of Health/ County government of Kitui/ Kenya, [4]One Health/ Global Implementation solutions/ Kenya, [5]Ministry of Livestock, Apiculture and Fisheries/ County government of Kitui/ Kenya, [6]Ministry of Health/ County government of Kitui, / Kenya

Introduction and Objectives or Purpose

Anthrax is a bacterial zoonotic disease of global security and public health importance. In Kenya, anthrax is ranked as the topmost zoonotic disease of public health importance, based on a systematic analysis of burden, social-economic impact, epidemic potential and disease severity. It is also outlined as a priority disease in Kenya's national action plan for health security (NAPHS), the Joint external evaluation (JEE) and the performance of veterinary service (PVS) reports. The main objective is to eliminate human anthrax and reduce the incidence of anthrax in animals to less than 1% of the 2020 baseline by 2036. We hereby describe the strategies key points.

Methods

The zoonotic disease unit (ZDU) coordinated a series of multi-sectorial subject matter expert meetings from various institutions with support from partners. A literature review and situational analysis on anthrax were conducted. In addition, preliminary versions of the document were subjected to stakeholder's review and validation process through workshops for the last two years.

Results or Focus

The strategy describes the strengths and opportunities to be harnessed and weaknesses and threats that must be addressed for effective implementation. Eight strategic pillars are outlined: coordination, collaboration and partnership, surveillance, reporting systems and outbreak response, prevention and control of anthrax in animals and humans, laboratory diagnostic capacity, risk communication, operational research, biosafety and biosecurity and resource mobilization. The strategies will be implemented in four phases that run from 2021 to 2036. Each phase has a set of activities and clear targets for the country to move from one phase to the next.

Conclusion or Scope

This strategy is designed to provide a systematic way to reduce the risk of the disease from a state of high burden through coordinated and sustained efforts using one health approach towards the elimination of human anthrax by 2036

Acknowledgement

Food and Agriculture Organization (FAO)

Global Health Security Agenda (GHSA) project

Keywords: Anthrax;strategy;elimination;Kenya

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Focus on pandemic prone pathogens
Abstract No: 15056

Influenza A virus in circulation in Cambodian swine, 2020-2021

Michael Zeller[*1] ; Sothrya Tum[2] ; Sorn San[2] ; Chou Monidarin[3] ; Arata Hidano[4] ; Hannah Holt[4] ; Jordan Ma[1] ; Foong Ying Wong[1] ; Geok Kee Ng[1] ; Gavin Smith[1 5 6 7] ; James Rudge[4] ; Yvonne Su[1]
[1]Programme in Emerging Infectious Diseases/ Duke-NUS Medical School/ Singapore, [2]General Directorate of Animal Health and Production/ Ministry of Agriculture, Forestry and Fisheries, General Directorate of Animal Health and Production/ Cambodia (□□□□□□□), [3]Head of Faculty/ University of Health Sciences/ Cambodia (□□□□□□□), [4]Communicable Diseases Policy Research Group/ London School of Hygiene & Tropical Medicine/ United Kingdom, [5]Centre for Outbreak Preparedness/ Duke-NUS Medical School/ Singapore, [6]SingHealth Duke-NUS Global Health Institute/ SingHealth Duke-NUS Academic Medical Centre/ Singapore, [7]Duke Global Health Institute/ Duke University/ United States

Introduction and Objectives or Purpose

The diversity of swine Influenza A Virus (IAV) within Cambodia is currently uncharacterized. Recent transitions to large scale swine production operations in Cambodia have unknown implications for the potential of IAV to spread between swine herds or zoonosis resulting from human-swine contact. The objective of this study is to understand the current diversity of IAV in circulation in Cambodia.

Methods

Nasal swabs were collected from slaughter houses serving four contiguous provinces in Cambodia. Samples were screened for IAV using real-time reverse transcription polymerase chain reaction. Next Generation Sequencing (NGS) was performed on positive samples using the illumina MiSeq sequencing platform. Resultant reads were mapped to reference genomes via Unipro UGENE and consensus sequences were extracted. Phylogenetic trees were inferred for each of the eight gene segments based on a subsample of global IAV diversity reference sets using RAxML.

Results or Focus

Of 2,220 swine nasal swab samples collected, 41 samples were RT-qPCR positive indicating a 1.8% IAV positivity rate. NGS resulted in sequences from 31 samples: 32 H1, 8 H3, 30 N1, and 8 N2 sequences. The hemagglutinin (HA) diversity of swine IAV in circulation within Cambodia includes H1N1-pdm09 (1A.3.3.2), classical swine (1A.1.2), and human seasonal-like H3 lineages. Neuraminidase diversity included N1-pdm09, N1 Eurasian avian-like, and N2 lineages. Internal genes were primarily derived from pandemic lineage, with one Eurasian avian-like matrix identified. Temporal reconstruction using BEAST v1.10 suggests the H1N1-pdm09 is derived from a recent human-to- swine transmission event, whereas the classical swine and H3 human seasonal-like have been in circulation in Southeast Asia for over a decade.

Conclusion or Scope

Phylogenetic analysis indicated the presence of genetic diversity that had not been prior observed from Cambodia. Cambodia, as well as South East Asia as a whole remains as a surveillance gap in Influenza monitoring, despite hosting broad IAV diversity.

Acknowledgement

n/a

Keywords: influenza A, evolution, swine, pandemic, zoonosis, surveillance

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Focus on pandemic prone pathogens
Abstract No: 15100

Dr

Long -Thanh Pham*[1] ; Tung Nguyen[2] ; Thuy - Thu Nguyen[3] ; Tho - Dang Nguyen[4] ; Dung - Thi Le[5] ; Pawin Padungtod[5]
[1]Epidemiology Division/ Department of Animal Health, Ministry of Agriculture and Rural Development/ Vietnam (Việt Nam), [2]Planning Division/ Department of Animal Health, Ministry of Agriculture and Rural Development/ Vietnam (Việt Nam), [3]Department of Animal Health/ Ministry of Agriculture and Rural Development/ Vietnam (Việt Nam), [4]National Center for Veterinary Diagnosis/ Department of Animal Health, Ministry of Agriculture and Rural Development/ Vietnam (Việt Nam), [5]Emergency Centre for Transboundary Animal Diseases (ECTAD), Country Office / Food and Agriculture Organisation of the United Nations (FAO)/ Vietnam (Việt Nam)

Introduction and Objectives or Purpose

Since the first outbreaks of highly pathogenic avian influenza (HPAI) H5N1 notified in 2003, three subtypes of HPAI, H5N1, H5N6 and H5N8, have been detected in Vietnam. HPAI outbreaks caused loss of several millions of poultry, and more seriously the H5N1 virus infected 127 humans with 64 deaths in the country up to 2014. Active surveillance for avian influenza viruses at live poultry markets (LPMs) supported by the Food and Agriculture Organization of the United Nations (FAO) through the Department of Animal Health of Vietnam was implemented in 14 provinces from May 2020 to June 2022. The surveillance aimed to monitor subtypes and genetic characterization of HPAI H5Nx viruses circulating across the country as well as to detect the incursion of H7N9.

Methods

A total of 15,030 oropharyngeal swabs from poultry and environmental swabs collected from 62 LPMs were screened for influenza A viruses, H5, H7, N1, N6, N8 by Real-time Reverse-transcriptase PCR and selected H5 genes were sequenced to determine virus clade.

Results or Focus

Detection rates for Influenza A, H5, N1, N6, and N8 subtypes were 47.6%, 8.4%, 3.6%, 2.9%, and 1.4%, respectively. While HPAI H5N1 (2.3.4.4b) and H5N6 (2.3.4.4h) viruses have been circulating in all seven regions, H5N8 (clade 2.3.4.4b) was first introduced in the North of Vietnam in June 2021. Our surveillance showed that H5N8 virus has quickly spread to central highland region in December 2021. In contrast, the H7 subtype was not identified in any samples.

Conclusion or Scope

A safer poultry production chain and continuous active monitoring of viral loads and viral strains at LPMs to minimize the risk of HPAI in both poultry and human are needed in Vietnam

Acknowledgement

We acknowledge the technical consultations from FAO in Vietnam, and the financial support from USAID for this work.

Keywords: Active surveillance, Avian influenza, Live poultry market, Vietnam

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Focus on pandemic prone pathogens
Abstract No: 15190

A FRAMEWORK FOR PREVENTING LASSA VIRUS SPILLOVER INTEGRATING RISK ANALYSIS, CRITICAL CONTROL POINTS AND OUTCOME MAPPING IN LIBERIA

Diafuka Saila-Ngita*[1] ; Mildred Harris[2] ; Kemah Tegli[2] ; Tracy Pency[2] ; Alex Mulbah[2] ; Benjamin Blamo[2] ; Elaine Faustman[3] ; Jill Falman[3] ; Julius Nyangaga[4] ; Esther Kihoro[4]
[1]Infectious Disease and Global Health/ Tufts University, Cummings School of Veterinary Medicine/ United States, [2]University of Liberia/ Africa One Health University Network / Liberia, [3]School of Public Health/ University of Washington/ United States, [4]Consultancy/ Rigth Track Africa/ Kenya

Introduction and Objectives or Purpose
Lassa fever is endemic in West Africa and is expanding across and within countries. The most important Lassa virus reservoir is Mastomys natalensis, a species of rodent difficult to control. The purpose of the study is to demonstrate a One Health approach to address Lassa virus spillover. This study is conducted under the Strategies to Prevent Spillover funded by the U.S. Agency for International Development.

Methods
We integrate risk analysis, hazard analysis and critical control points (HACCP), and participatory Outcome Mapping (OM) approaches to co-design interventions and research to address virus spillover at the human-rodent interface. Disease risk mitigation involves addressing hazard exposure and its impact. Risk factors can be identified along the exposure pathways. For instance, housing design deficiency may facilitate rodent access to homes resulting in contamination of food and water with rodents' feces and urine, and poor waste management facilitates rodent proliferation. Weaknesses at border points of entry allow movements of infected humans and rodents. On the impact mitigation side, disease continues to spread without vaccine and biosafety measures. Ribavirin treatment campaigns are ineffective due to poor diagnostics. Using the OM with 55 participants from across sectors, we identified five critical control points where potential interventions could reduce the risk of spillover and spread. These include: rodent invasion of homes and storage, waste management, preventive human vaccination, treatment, and laboratory diagnostics. We also identified 13 critical partners whose involvement will drive spillover risk mitigation and who will co-design interventions and research through four One Health Working Groups.

Results or Focus
The study focuses on the mitigation of zoonotic viral spillover at the human-rodent interface.

Conclusion or Scope
This approach facilitates control of diseases at the origin and accounts for the vulnerability and resilience of communities. The study could be extended to include virus spillover interfaces along the wildlife value-chain with pandemic potential.

Keywords: Lassa virus spillover; Critical Control Points; Outcome Mapping; Risk Analysis; Zoonotic diseases

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Focus on pandemic prone pathogens
Abstract No: 15266

PREVALENCE AND GENETIC DIVERSITY OF CORONAVIRUSES IN HUMAN IN PRE-PANDEMIC PERIOD AT HIGH-RISK HUMAN-ANIMAL INTERFACE IN BANGLADESH.

Shusmita Dutta Choudhury[*1 2] ; Ariful Islam[1 2] ; Josefina Abedin[1 2] ; Emily Hagan[2] ; Shahnaj Shano[1 2] ; Mohammed Ziaur Rahman[3] ; Tahmina Shirin[4] ; Peter Daszak[2] ; Meerjady Sabrina Flora[5] ; Jonathan H Epstein[2]
[1]EcoHealth Alliance Bangladesh Programs/ Institute of Epidemiology, Disease Control and Research (IEDCR)/ Bangladesh (□□□□□□□□), [2]Emerging Infectious Disease Research/ EcoHealth Alliance/ United States, [3]One Health Laboratory/ International Centre for Diarrhoeal Disease Research (icddr,b)/ Bangladesh (□□□□□□□□), [4]Director and Professor, Department of Virology/ Institute of Epidemiology, Disease Control and Research (IEDCR)/ Bangladesh (□□□□□□□□), [5]Directorate General of Health Services/ Ministry of Health and Family Welfare/ Bangladesh (□□□□□□□□)

Introduction and Objectives or Purpose

Coronavirus (CoV) has caused three epidemics and pandemics in past decades, resulting in a substantial impact on human and animal health and the global economy. This study aimed to screen pre-pandemic human samples to detect and molecularly characterize known and novel coronaviruses in humans at high-risk animal-human interfaces in Bangladesh.

Methods

The study was conducted as a part of One Health biological-behavioral surveillance prior to COVID-19 pandemic period. We conducted 862 interviews regarding behavioral risk practices and collected biological specimens from three district communities and one tertiary hospital, twice a year (dry and wet seasons) between 2017 and 2019. We tested samples using consensus PCR targeting RNA-Dependent RNA Polymerase (rdrp) gene. Positive PCR products were confirmed by sequencing.

Results or Focus

Overall CoV were positive in 13 (95% CI: 0.8-2.5) participants; 7 CoV-OC43, 4 CoV-HKU1, and 2 CoV-222E were detected. We found 3 CoV in respondents having influenza-like illness (n=372), 4 in fever of unknown origin (n=103), and 6 in apparently healthy participants (n=295). Detecting CoVs was not associated with age or gender of participants; however, virus detection was associated with samples collected in the dry season (p= <0.001). The study revealed that HCoV-OC43 was circulated in diverse locations, whereas HCoV-229E and HCoV-HKU1 were detected in Madaripur and Dhaka, respectively. Phylogenetic analysis demonstrated that HCoV-229E was closely similar to CoV strains detected in China, HCoV-HKU1 in the USA and Thailand, and HCoV-OC43 in France and China. However, we did not find any novel coronavirus, including SARS-CoV-related virus, in the pre-pandemic studied samples.

Conclusion or Scope

This study demonstrates diverse strains of CoVs are circulating in pre-pandemic studied samples. Our research reports molecular characterization of human CoV strains in Bangladesh. However, using One Health approach, coronavirus surveillance is recommended to better understand the CoV viral diversity and serological assays to determine the spillover events at human-animal interfaces in Bangladesh.

Keywords: Epidemiology, Molecular characterization, Coronavirus, Interface, Diversity.

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Focus on pandemic prone pathogens
Abstract No: 15369

ENVIRONMENTAL SURVEILLANCE FOR SARS-COV-2 IN KARACHI: CORRELATING SEWAGE SARS-COV-2 RNA CONCENTRATION AND REPORTED INCIDENCE OF COVID-19 FROM AN URBAN DISTRICT

Farah Khalid*[1] ; Nadia Ansari[1] ; Waqasuddin Khan[1] ; Amyn Abdul Malik[1] ; Joshua Warren[1] ; Furqan Kabir[1] ; Usma Mehmood[1] ; Saad Bin Omer[1] ; Fyezah Jehan[1] ; Mohammad Imran Nisar[1]
[1]Paediatrics / Aga Khan University Hospital/ Pakistan (پاکستان)

Introduction and Objectives or Purpose

Wastewater-based surveillance has been used around the globe to track the presence and temporal patterns of the SARS-CoV-2 virus in communities. From the time of infection until 33 days later, the virus is shed in feces whereas a considerable percentage of COVID-19 cases remain asymptomatic and are not included in clinical estimates. Viral RNA particle detection in wastewater samples can indicate the beginning of an outbreak within a catchment area well in advance of clinical surveillance. We describe the feasibility of using a sewage network to monitor the trend of SARS-CoV-2 in an urban district in Karachi, Pakistan.

Methods

We identified 4 sites draining into the Lyari River, the main open sewer in District East, Karachi, for the collection of raw sewage samples. Early morning samples were collected twice weekly from each site between June 10, 2021, and January 17, 2022. We used a distributed lag negative binomial regression model within a hierarchical Bayesian framework to describe the relationship between wastewater RNA concentration and COVID-19 cases from the catchment area.

Results or Focus

Using the bag-mediated filtration system (BMFS), we collected 151 raw sewage samples. In total, 123 (81.5%) sewage samples tested positive for the N1, N2, or E gene using reverse transcription polymerase chain reaction (RT-PCR). The average cycle threshold (Ct) value of the positive samples was 32. The average sewage RNA concentrations at each lag (1-14 days prior) were associated with current day's cases/daily cases, with a peak association observed on lag day 10 (RR: 1.15; 95% CrI: 1.10 – 1.21).

Conclusion or Scope

Wastewater-based surveillance can provide a considerable lead time over the rise in cases in a catchment area and can be used for monitoring the temporal trend of SARS-CoV-2 in the community. Local public health systems can utilize the information to plan mitigation measures for disease containment.

Keywords: Environmental Surveillance, Sewage, SARS-CoV-2 ,RNA Concentration

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Focus on pandemic prone pathogens
Abstract No: 15378

PRIORITIZING OF GREATEST NATIONAL CONCERN ZOONOTIC DISEASE IN INDONESIA

Nuryani Zainuddin*[1] ; Nancy Dian Anggraeni[2] ; Tjahjani Widiastuti[1] ; Ichwan Muslih[3] ; Arif Wicaksono[1] ; Lulu Agustine[3] ; Sitti Ganefa Pakki[4] ; Endang Burni Prasetyowati[4] ; Endang Widuri Wulandari[5] ; Farida Camalia Zenal[6]
[1]Directorate General of Livestock and Animal Health Services/ Ministry of Agriculture/ Indonesia, [2]Deputy of Disease Control and Management/ Coordinating Ministry of Human Development and Cultural Affair/ Indonesia, [3]Directorate General of Natural Resource and Ecosystem Conservation/ Ministry of Environment and Forestry/ Indonesia, [4]Directorate General of Disease Prevention and Control/ Ministry of Health/ Indonesia, [5]Surveillance/ WHO Indonesia/ Indonesia, [6]ECTAD/ FAO Indonesia/ Indonesia

Introduction and Objectives or Purpose

Zoonoses and emerging infectious diseases are increasing threats to human health, animal health, environmental health, and global health security. Overcoming the threat of zoonotic diseases requires coordination, collaboration, and communication through a multi-sectoral approach from local, national and global scales known as the One Health approach. On November 8-11, 2021, the Indonesia Ministry of Agriculture, Ministry of Health, Ministry of Environment and Forestry, and Coordinating Ministry of Human Development and Culture held a workshop to prioritize zoonotic diseases of greatest national concern using One Health Zoonotic Disease Prioritization (OHZDP) tool using equal input from representatives of human, animal, and environmental health sectors.

Methods

Prioritizing zoonotic disease was conducted using a semi-quantitative method with an analytic hierarchi process to rank the criteria in the OHZDP tool. During the workshop five criteria for ranking the zoonotic diseases were developed from economic, social, & ecological impact, pandemic and epidemic potential, public health impact (mortality and morbidity), one health intervention capacity and bioterrorism potential.

Results or Focus

Government of Indonesia executive leadership was provided with a summary of the workshop outcomes and discussed continued efforts to advance One Health in Indonesia and address the priority zoonotic diseases. The OHZDP workshop resulted in a prioritized list of six zoonotic diseases of greatest national concern which was agreed upon by voting members.

Conclusion or Scope

The six prioritized zoonotic diseases for Indonesia are Zoonotic Influenza Viruses (avian and swine influenza), Anthrax, Zoonotic Coronaviruses (COVID-19 and Middle East Respiratory Syndrome [MERS]), Rabies, Zoonotic Tuberculosis, Leptospirosis. Action plans were also developed and focused on the following thematic areas like One Health coordination, laboratory, surveillance, outbreak response, preparedness planning, prevention and control and workforce development.

Keywords: One Health Zoonotic Disease Prioritization Tool, Zoonotic Priority Disease, Indonesia

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Focus on pandemic prone pathogens
Abstract No: 15378

PRIORITIZING OF GREATEST NATIONAL CONCERN ZOONOTIC DISEASE IN INDONESIA

Nuryani Zainuddin*[1] ; Nancy Dian Anggraeni[2] ; Tjahjani Widiastuti[1] ; Ichwan Muslih[3] ; Arif Wicaksono[1] ; Lulu Agustine[3] ; Sitti Ganefa Pakki[4] ; Endang Burni Prasetyowati[4] ; Endang Widuri Wulandari[5] ; Farida Camalia Zenal[6]
[1]Directorate General of Livestock and Animal Health Services/ Ministry of Agriculture/ Indonesia, [2]Deputy of Disease Control and Management/ Coordinating Ministry of Human Development and Cultural Affair/ Indonesia, [3]Directorate General of Natural Resource and Ecosystem Conservation/ Ministry of Environment and Forestry/ Indonesia, [4]Directorate General of Disease Prevention and Control/ Ministry of Health/ Indonesia, [5]Surveillance/ WHO Indonesia/ Indonesia, [6]ECTAD/ FAO Indonesia/ Indonesia

Introduction and Objectives or Purpose

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Keywords: One Health Zoonotic Disease Prioritization Tool, Zoonotic Priority Disease, Indonesia

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Focus on pandemic prone pathogens
Abstract No: 15382

Characteristics (or Attributes) of actors involved in the live trading of poultry in Bangladesh

Md.Helal Uddin[*1] ; Jinnat Ferdous[2] ; Anne Conan Yvonne[3] ; One Health Poultry Hub and CVASU and UQ Consortium Uddin[2 1 4 5 6] ; Lorraine Chapot[7] ; Mahmudul Hasan[8] ; Rashed Mahmud[1] ; Fournie Guillaume[7] ; Md Ahasanul Hoque[1] ; Joerg Henning[2]
[1]Department of Medicine And Surgery/ Chattogram Veterinary And Animal Sciences University/ Bangladesh (□□□□□□□□□), [2]School of Veterinary Science/ The University of Queensland/ Bangladesh (□□□□□□□□□), [3]City University of Hong Kong/ City University of Hong Kong/ Hong Kong (□□), [4]Department of Medicien And Surgery/ Jhenaida Govt Veterinary College/ Bangladesh (□□□□□□□□□), [5]Institute of Epidemiology, Disease Control & Research (IEDCR), Dhaka/ Institute of Epidemiology, Disease Control & Research (IEDCR), Dhaka, Bangladesh / Bangladesh (□□□□□□□□□), [6]CP Bangladesh LTD/ CP Bangladesh LTD., Hilly Branch, Dinajpur/ Bangladesh (□□□□□□□□□), [7]Department of Pathobiology and Population Sciences/ Royal Veterinary College, London, UK/ United Kingdom, [8]Animal health Division/ Bangladesh Livestock Research Institute (BLRI), Savar, Bangladesh/ Bangladesh (□□□□□□□□□)

Introduction and Objectives or Purpose

Poultry trading practices play an important role in the spread of zoonotic food-borne pathogens. Thus, understanding the role of actors involved in live poultry trading in Bangladesh are of utmost importance to reduce the zoonotic diseases transmission.

Methods

A survey was conducted in five districts of Bangladesh between August 2020 and February 2021. Semi-structured interviews were conducted with poultry market managers (N=48), stalls owners trading poultry (N=412), mobile poultry traders (N=172) and feed and poultry dealers (N=157). Network analysis was applied to describe the connections between actors trading poultry. Networks were then compared between different chicken production systems and the spatial extend of poultry movements was explored

Results or Focus

Significance differences ($p<0.05$) were observed for the type of markets in regard to the number of stalls present, staffs employed, middlemen operating, volume of poultry sold per day, contacts between chicken types and species of poultry, presence of dogs and the mixing of newly supplied birds with unsold birds. In contrast, 100% of wholesale stall had unsold poultry at the end of the day but mostly the mixed stalls (59.6%) kept the unsold and the new chickens together at a place. Mobile poultry traders mostly supplied birds to vendors in markets but mainly purchased birds from farmers through poultry feed dealers. We explored 683 trading chains for exotic broiler and 617 for sonali. The most common chain for both types (56.2% exotic broiler; 47.0% sonali) were farm to feed dealers to mobile traders to retailers.

Conclusion or Scope

The study provided the sampling frame for next steps in which poultry traders are followed during their daily trading activities and movements are recorded with a customized App. Data generated in this project provide important insights into how poultry trading may influence the risk for disease occurrence and distribution in poultry and human populations in Bangladesh.

Acknowledgement

UKRI GCRF OHPH

Keywords: live poultry trading, poultry disease, Bangladesh

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Focus on pandemic prone pathogens
Abstract No: 15421

SEQUENCING WASTEWATER TO IDENTIFY CIRCULATING SARS-COV-2 VARIANTS OF CONCERN IN THE COMMUNITY

TONIMA RAHMAN*[1]
[1] Infectious Diseases Division/ Icddr,b/ Bangladesh (□□□□□□□□)

Introduction and Objectives or Purpose

SARS-CoV-2 mutates to create variants that may escape the current vaccine protection. Therefore, it has become essential to sequence clinical samples to identify the variants of concern to inform future vaccine designs. Sequencing many clinical samples are cost prohibitive. Hence, we sequenced wastewater samples and characterized all the variants of SARS-CoV-2 to build a longitudinal comprehensive landscape of circulating VOCs in the community.

Methods

We sequenced 319 wastewater samples, a subset of samples from an ongoing ES study in Bangladesh, collected between November 2021 to July 2022 that were positive for SARS-CoV-2 by RT-qPCR with Ct ≤ 32. The libraries were prepared using Illumina COVIDSeq with ARTIC v.4 primers and sequenced on MiSeq and NextSeq 500/550 systems. The raw data was QCed using Trimalore, and high-quality reads were aligned to SARS-CoV-2 Wuhan-Hu-1 (MN908947.3). The iVar was used for variant calling, followed by depth-weighted demixing by Freyja. Additionally, 215/319 (67%) samples were tested by in-house developed VOC-qPCR to evaluate the performance of sequencing.

Results or Focus

Out of 319 samples, two samples (0.6%) were no reads. The remaining 317 samples showed genome coverage ranging from 0.5 to 99.9%, of which 263/317 (83%) samples yielded ≥50% genome coverage. Our sequencing yielded 100% (173/173) concordant variant calls compared to VOC-qPCR for the ≥50% genome coverage samples. While the <50% genome coverage samples showed 78% (33/42) concordant. Our sequencing data showed that the most prevalent variant circulating was Delta from November to December 2021, followed by Omicron in January 2022. The BA.2 sub-lineage predominated from late January to the middle of May, and BA.5 sub-lineage took over from late May to July 2022.

Conclusion or Scope

In a setting where sequencing lots of clinical samples is not feasible, sequencing wastewater can be a cost-effective way to detect and characterize the VOCs circulating in the community.

Acknowledgement

AUTHORS: Suporn Pholwat, Hardik Parikh, Md. Ohedul Islam, Rashidul Haque, and Mami Taniuchi.

Keywords: Discovery and Surveillance, SARS-CoV-2 and other emerging pathogens, Neglected tropical diseases Vector-borne diseases Digital-aided events based on syndromic and genomics surveillance

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 14675

Addressing the challenge of Antimicrobial Resistance in Cameroon: The University leadership in capacity building at in-service and pre-service levels, from a One Health perspective.

Denis Zofou*[1] ; Felicite Djuikwo Teukeng[2] ; Arouna Njayou Ngapagna[3] ; Jane-Francis Akoachere[1] ; Moctar Mouiche Moulium[4] ; Edie Gregory Halle Ekane[5] ; Ernest L Molua[6] ; Marcellin Ngowe Ngowe[7] ; Jean Pierre Mvondo Awono[8] ; Jeanne Ngogang[2] ; Irene Naigaga; Christian K. Tiambo; Janetrix Hellen Amuguni
[1]Medical Research and Applied Biochemistry Laboratory/ University of Buea/ Cameroon (Cameroun), [2]Health Program/ Universite des Montagnes/ Cameroon (Cameroun), [3]Cameroon Office/ AFROHUN/ Cameroon (Cameroun), [4]School of Veterinary Medicine and Sciences/ University of Ngaoundere/ Cameroon (Cameroun), [5]Dean's Office, Faculty of Health Sciences/ University of Buea/ Cameroon (Cameroun), [6]Department of Agribusiness, Faculty of Agriculture and Veterinary Medicine/ University of Buea/ Cameroon (Cameroun), [7]Faculty of Medicine and Pharmaceutical Sciences/ University of Douala/ Cameroon (Cameroun), [8]Dean's Office, Faculty of Agriculture and Veterinary Meidicine/ University of Buea/ Cameroon (Cameroun)

Introduction and Objectives or Purpose

Antimicrobial drug resistance constitutes an enduring challenge which has drastically limited disease control efforts in Cameroon as in other sub-Saharan African countries. Responding to this global public Health threat, Universities have been at the forefront of workforce development, from situational analysis through in-service and pre-service, with support from the Africa One Health University Network through its USAID-funded One Health Workforce Project.

Methods

In a five-step process, an in-service manual was developed and tested for a multi-sectoral audience from 2017 to 2021: (i) A situational analysis was undertaken, with a KAP field investigation, targeting human, animal and environmental health professionals. (ii) Findings from this step informed the curriculum development process, by identifying gaps and training needs, for an in-service training program. This curriculum covers a total period of six months, alternating three indoor workshop and two field practicums. (iii) The manual developed was piloted, folowed by (iv) impact assessment, and (v) deriving the continue training program into an academic offer.

Results or Focus

A total of 21 professionals benefited from the pilot training in 2019. have been selected and three workshops have been conducted to test and improve the manual. The manual elaborated is a contribution towards improvement on GHSA indicators for AMR, better health, and support government efforts to fight AMR. The training designed attracted a strong adhesion and appropriation by the Cameroon government, notably, and received a strong support from partners. The achievements inspired develoipment of a Masters' Degree curriculum to be implemented by the University of Buea for a sustainable workforce development to adress AMR in Cameroon.

Conclusion or Scope

This story reveals the key role academia is called to play in the fight against AMR, particularly in resource-limited countries.

Acknowledgement

The process described was conducted under the USAID funded OHW and OHW-NG projects of the Africa One Health University Network, AFROHUN in Cameroon.

Keywords: AMR, in-service, pre-service training, Cameroon.

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 14762

Gendered asymmetry of access to knowledge for brucellosis control among pastoral communities in North-West Côte d'Ivoire

Yoro Stéphane Alain Babo[*1 2] ; Gilbert Fokou[2 3] ; Brou Richard Yapi[2 4] ; Coletha Mathew[5] ; Arnaud Kevin Dayoro[1] ; Rudovick Kazwala[5] ; Bassirou Bonfoh[2]
[1]Sociology/ Université Félix Houphouët Boigny, / Ivory Coast, [2]Governance, society and economic development/ Centre Suisse de Recherches Scientifiques en Côte d'Ivoire/ Ivory Coast, [3]Anthropology/ Human Sciences Research Council/ South Africa, [4]Epidemiology/ Centre d'Entomologie Médicale et Vétérinaire, Université Alassane Ouattara, / Ivory Coast, [5]Veterinarian sciences/ Sokoine University of Agriculture/ Tanzania, United Republic of

Introduction and Objectives or Purpose

Brucellosis is an infectious zoonotic disease considered as a threat to public health and for pastoralist livelihoods. Symptoms of the disease can lead to gender specific ailments such as abortions in women and orchitis in men. Pastoralists and their families are at high risk of contracting the disease. Access to health information reinforces existing knowledge and contributes to disease prevention. However, in developing countries, interventions for knowledge sharing on zoonotic diseases predominantly target men. This study aimed to describe mechanisms of knowledge production and transfer on brucellosis according to gender, by assessing the way knowledge affects behaviours of pastoral communities. A community-based cross-sectional survey was conducted among a pastoral community of the Folon region in North-West Côte d'Ivoire.

Methods

The study included transhumant pastoralists, sedentary livestock owners, shepherds and their wives. By using mixed methods, 26 semi-structured interviews were conducted, and 320 questionnaires were completed. Statistical analysis with Chi-square ($\chi 2$) comparison tests was performed to compare variables between men and women. Findings were interpreted through the concept of specialization of the social exclusion theory.

Results or Focus

We found that gender influences access to information on brucellosis and transfer of knowledge on brucellosis appeared gender-biased, especially from veterinarians toward men in the community. The social labour division and interventions of veterinarians through awareness, reinforce the knowledge gap on brucellosis between men and women. Regarding risk exposure, men and women consume raw milk, while only men in general handle animal discharges with bare hands.

Conclusion or Scope

To improve the control of brucellosis, knowledge on best practice should be shared with pastoral communities using the One health approach that encourages mutual learning. Innovative strategies based on gender daily tasks such as safe dairy processing by women and safe animal husbandry to expand their herd for men can be the entry point for the prevention of brucellosis.

Acknowledgement

The authors acknowledge support from the DELTAS Africa Initiative [Afrique One-ASPIRE/DEL-15-008]. Afrique One-ASPIRE is funded by a consortium of donors including the African Academy of Sciences (AAS) Alliance for Accelerating Excellence in Science in Africa (AESA), the New Partnership for Africa Development Planning and Coordinating (NEPAD) Agency, the Wellcome Trust [107753/A/15/Z] and the UK government.

Keywords: Knowledge production, Gender, One Health, dairy, zoonosis

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 14771

ADAPTIVE BEHAVIORAL IMMUNE SYSTEM DURING THE EMERGENCE OF COVID-19 VARIANTS: CONCERN AND PREVENTATIVE HEALTH BEHAVIORS AMONG ADULTS IN NCR, PHILIPPINES

Daniella Grace Grecia*[1] ; Anna Althea Articona*[1] ; Kenisha Averyl Cheng*[1] ; Alexandra Janine Foronda*[1] ; Vincent Enrico Ong*[1] ;
Dana Izabel Rivera*[1] ; Clarenz Sarit Concepcion[1]
[1]Medical Technology/ University of Santo Tomas/ Philippines

Introduction and Objectives or Purpose

The adaptive behavioral immune system is a complex network of behavioral mechanisms that involves the cognitive and affective system of the body to prevent contact and transmission of infectious pathogens. This descriptive correlational quantitative study aimed to investigate the relationship between the adaptive behavioral immune system and COVID-19 variants in terms of concerns and preventative health behaviors of National Capital Region residents aged 18-65 years old.

Methods

Data on socio-demographics, COVID-19 exposure, behavioral immune system, COVID-19 variants concerns, and COVID-19 preventative health behaviors were collected from 517 respondents through an online survey. Descriptive statistics, Spearman ranking correlation, and p-value determination were used as statistical tools.

Results or Focus

Results show that respondents demonstrate a high germ aversion and a low perceived infectability and majority exhibit concern and engage in preventative health behaviors. The correlation and p-value determination of germ aversion, perceived infectability, COVID-19 variants concern, and preventative health behaviors all share a positive weak but significant relationship, in contrast to previous studies. The positive weak correlation between germ aversion and perceived infectability with COVID-19 variants concern and preventative behaviors may be due to the increased vaccine coverage, increasing complacency of Filipinos, implementation of less-restrictive protocols, and previous studies being mostly conducted during the peak of the pandemic.

Conclusion or Scope

Furthermore, the results of the study may be used to allow professionals to consider the behavioral immune system as another factor in implementing the appropriate response measures in managing community movement, establishing information materials, and developing implementing guidelines for the general public regarding COVID-19 variants.

Keywords: Behavioral Immune System;Germ Aversion;Perceived Infectability;COVID-19 Variants Concern;Preventative Health Behaviors

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 14778

A system of indicators to account for the contributions of green infrastructure to the One Health approach

FERNANDO MAYOR-VITORIA*[1] ; DANIEL JATO-ESPINO[1] ; VANESSA MOSCARDO GARCIA[1] ; FABIO M CAPRA RIBEIRO[1] ; JONATHAN ROLDAN[1] ; MANUEL LOPEZ MARTINEZ[1] ; LETICIA ELISA BARTOLOME DEL PINO[1]
[1]GREENIUS Research Group/ Universidad Internacional de Valencia - VIU/ Spain (España)

Introduction and Objectives or Purpose

The aim of this study is to develop a system of indicators to measure the contributions of green infrastructure to achieving One Health. This included the design of a Multi-Criteria Decision-Making (MCDM) methodology to process the proposed indicators.

Methods

First was conducting a literature review on One Health-related indicators using the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) statement, which enabled systematizing the revision and subsequent analysis of publications. The outcomes of this process led to the definition of a series of indicators to account for the impact of green infrastructure on One Health. The processing and aggregation of indicators involved the selection of a MCDM model suitable to the specifics of this investigation.

Results or Focus

The main output is a list of indicators to determine the impact of land cover on One Health, with emphasis on the role played by green infrastructure. In this sense, the shortlisted indicators include factors such as thermoregulation capacity, ecological connectivity, forest availability, species distribution or population density, amongst others. The results also comprised the characterization of these indicators, which stemmed from either values found in the literature or calculations based on distance analysis, geoprocessing tasks and others. The MCDM methods suggested to combine the indicators were the Entropy and TOPSIS (Technique for Order of Preference by Similarity to Ideal Solution) techniques.

Acknowledgement

The main barrier endangering the achievement of One Health lies in land cover changes caused by urbanization, whose expansion has boosted the risk of zoonotic diseases due to increased contact between humans and animals. The proposed system of indicators enables determining the potential of green infrastructure to mitigate this situation by providing different ecosystem services aligned with the One Health initiative. As such, it can be used by decision-makers and planners seeking for tools to support the protection of public health.

Keywords: green infrastructure; One Health; multicriteria; PRISMA; MCDM;

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 14811

WEB-BASED COVID-19 RISK COMMUNICATION BY RELIGIOUS AUTHORITIES IN UGANDA: A CRITICAL REVIEW

Andrew Marvin Kanyike*[1] ; Etheldreda Leinyuy Mbivnjo[2] ; Ephraim Kisangala[3] ; Justine Nabukeera[4] ; Denis Kimbugwe[5] ; Tian Dennis Okucu[6]
[1]Internal medicine/ Mengo Hospital/ Uganda, [2]Nursing/ Biaka University Institute of Buea/ Cameroon (Cameroun), [3]Obstetrics and Gynecology/ Kairos Hospital/ Uganda, [4]Internal medicine/ Lynwood Medical Centre/ Uganda, [5]Faculty of Medicine/ Gulu University/ Uganda, [6]Internal medicine/ Africa Inland Church (AIC) Litein Hospital/ Kenya

Introduction and Objectives or Purpose
To explore the content of web-based communication on COVID-19 by religious authorities (RAs) in Uganda and to assess their level of integration into the Uganda Ministry of Health (MoH) and World Health Organization (WHO) COVID-19 risk communication guidelines.

Methods
A grey literature review was conducted by searching the websites of intra- and inter-religious bodies licensed by the Uganda registration services bureau (URSB) for the terms “COVID-19” and “coronavirus”. We included statements on COVID-19 in English by a RA published between December 2019 and June 2020 on official letterhead or the RA website. Statements from unrecognized RAs by URSB, and any third-party report on a RA COVID-19-related statement were excluded. The authority, accuracy, coverage, objective, date, and significance (AACODS) checklist was used to appraise the RA statements critically. Thematic analysis was used to assess the content of RA statements which were also mapped to the items of the MoH and WHO statements.

Results or Focus
Fifteen RA websites with COVID-19 content were included. Most websites (9/15) released a series of statements and two-thirds (10/15) published at least one message. All RA statements were actionable (what to do or not to do was clearly stated) and in plain English, suitable for lay readers. RA communications were centered on COVID-19 description and management; the need to adhere to established guidelines; and the adoption of health-protective behaviors, notably, social distancing and avoidance of misinformation. RAs also discussed the effects of COVID-19 and its control measures on the population and spoke against pandemic-aggravated injustices (gender-based violence and embezzlement). The RA messages incorporated the WHO statement to a greater extent than the MoH statement

Conclusion or Scope
RAs played a critical role in delivering public health messages in Uganda during the COVID-19 pandemic, a position that should be maximized by public health authorities for effective communication during emergencies.

Keywords: COVID-19, Risk communication, Religious Authority

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 14878

COVID-19 preparedness and response capacity in Sri Lanka: Implications for future pandemics

Asela Gunawardena[*1] ; Sridharan Sathasivam[2] ; Upul Senarath[3] ; Lakshmi Somatunga[4] ; Sunil De Alwis[5] ; Lal Panapitiya[6] ; Manuj Weerasinghe[3] ; Suganya Yogeswaran[7] ; Malki Kathriarachchi[8] ; Farzana Khan[7]
[1]Director General of Health Services/ Ministry of Health/ Sri Lanka (□□□□ □□□□□□), [2]Deputy Director General (Management, Development and Planning Unit)/ Ministry of Health/ Sri Lanka (□□□□ □□□□□□), [3]Department of Community Medicine/ Faculty of Medicine, University of Colombo/ Sri Lanka (□□□□ □□□□□□), [4]Additional Secretary (Public Health Services)/ Ministry of Health/ Sri Lanka (□□□□ □□□□□□), [5]Additional Secretary (Medical Services)/ Ministry of Health/ Sri Lanka (□□□□ □□□□□□), [6]Deputy Director General (Medical Services I)/ Ministry of Health/ Sri Lanka (□□□□ □□□□□□), [7]Freelance/ Freelance Consultant/ Sri Lanka (□□□□ □□□□□□), [8]Medical Unit/ Sri Jayewardenepura General Hospital/ Sri Lanka (□□□□ □□□□□□)

Introduction and Objectives or Purpose

To assess how the country's pandemic preparedness and response capacity expanded during COVID-19 pandemic, and to examine how this capacity could be efficiently embedded in the routine healthcare system.

Methods

Focus Group Discussions were conducted with COVID-19 operational teams from preventive, primary, secondary and tertiary care health facilities of the state sector, and private hospitals. Interviews were also held with health managers and citizens. Pandemic preparedness and response capacity of 3 levels of hospitals were assessed using a multi-item scale with 10 pillars.

Results or Focus

Ministry of Health has developed Sri Lanka COVID-19 Strategic Preparedness and Response Plan consisting of 10 pillars, and disseminated circulars and guidelines for the prevention and management of COVID-19. Three-layered clinical management was in operation: (i) Intermediate care centers (ii) Designated Divisional/Base hospitals with consultant cover; (iii) Designated Specialized/ Tertiary Care Hospitals with High Dependency Units and Intensive Care Units. Home-based care was introduced subsequently.

Overall, planning and coordination, operational support, and logistics were satisfactory at all 3 levels, however, there was no written preparedness plan at individual institutions. Data communication mechanisms had their specific deficiencies and challenges despite having electronic data systems. Triage system was in place at OPD. The commitment and dedication of health staff at all levels were noticeable. Infrastructure facilities for waste management were inadequate at primary care facilities. In contrast to 2019, there were significant declines in OPD attendance and admissions during 2020-21. All target populations were protected with at least one dose of vaccine, 85% with 2 doses, and 40% with the 3rd dose by March 2022.

Conclusion or Scope

Carefully designed preparedness plan based on scientific evidence, robust data, and expert consultations is essential for pandemic response. Well-coordinated health system with surveillance, RCCE, laboratory services, patient care services, and vaccination is critical for successful outcomes.

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Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 14879

NATIONAL ONE HEALTH PLATFORMS: STRENGTHENING PREPAREDNESS AND RESPONSE IN ZOONOTIC AND HUMAN DISEASES IN AFRICA

Omer T Njajou[1] ; Wilson Ashimwe[2] ; Winyi Kaboyo[3] ; Aristide Dionkounda[4] ; Sara Eyangoh[5] ; Elodie Brandamir[6] ; Jeffrey Mecaskey[7] ; Nicole DeCastro[*8]
[1]Tackling Deadly Diseases in Africa Programme / DAI/ Cameroon (Cameroun), [2]Tackling Deadly Diseases in Africa Programme/ DAI/ Belgium, [3]Tackling Deadly Diseases in Africa Programme/ DAI/ Uganda, [4]Tackling Diseases in Africa Programme/ DAI/ CÃ´te d'Ivoire, [5]Mycobacteriology/ Centre Pasteur du Cameroun (CPC)/ Cameroon (Cameroun), [6]Tackling Deadly Diseases in Africa/ DAI/ France, [7]Tackling Deadly Diseases in Africa/ DAI/ Germany (Deutschland), [8]Global Health/ DAI/ United States

Introduction and Objectives or Purpose

There is consensus on One Health's (OH) importance in how we prevent, detect and manage epidemics. The challenge is translation into national policy, systems and mechanisms to coordinate intelligence and action. National One Health Platforms (NOHP) are multi-stakeholder mechanisms for coordination across the three OH Sectors--animal, environmental and human health. Experience across three countries in Central, East and West Africa provides evidence and insight on the institutionalisation of NOHP.

Methods

Political Economy Analysis carried out in Cameroon, Côte d'Ivoire and Uganda highlight the institutions, interests and incentives framing the context of health security and effective collaboration across OH sectors. A stakeholder-led process for establishing consensus on vision, aims and objectives, captured in a One Health Assessment for Planning and Performance (OH-APP) approach, defined a maturity model for considering structures, scope and priorities for strengthening OH coordination across sectors.

Results or Focus

Cameroon: initial assessment highlighted that although a NOHP was established, restructuring was necessary to improve its functionality and inclusion across OH sectors. Priority activity then focused on restructuring the NOHP in close collaboration with the prime minister's office as well as One Health sectors.

Côte d'Ivoire: priority was placed on clarifying key functions and priorities for capacity building leading to its official launch by Prime Minister.

Uganda: priority was placed on improving the effectiveness of procedures for data sharing and operational coordination through regular quarterly meetings, and on the process of decentralising the NOHP to the districts for better coordination at the operational level.

Conclusion or Scope

A road-block in institutionalising NOHP was maintaining coordination across the three sectors. TDDA supported stakeholders to adapt evidence-informed practice to country context. Insights on process, import of contextualisation, and building shared understanding across sectors can bring great value to strengthening surveillance, preparedness and response to zoonotic and other emerging infectious diseases.

Keywords: Preparedness; Policy; Coordination; Political Economy Analysis; Surveillance

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 14881

DEVELOPMENT OF THE ASEAN REGIONAL STRATEGIC PLAN FOR PREVENTING TRANSMISSION OF ZOONOTIC DISEASES FROM WILDLIFE TRADE USING A ONE HEALTH APPROACH

Mary Elizabeth G. Miranda[8] ; Agnes Agunos[8] ; Dhannan Sunoto; Noel Miranda; Nicole DeCastro[*8]
[8]Global Health/ DAI/ United States

Introduction and Objectives or Purpose

Southeast Asia continues to experience the long-term implications of COVID-19 on its economy, health care systems, and food security. To prevent future pandemics and enable countries in Southeast Asia to detect and respond to zoonotic and emerging infectious diseases associated with the wildlife trade with pandemic potential, a regional strategy is essential.

Methods

ASEAN leaders recognized the urgent need to strengthen public health emergency response capacities by adopting a “Whole-of-ASEAN” approach. The purpose of this presentation is to describe the development of an ASEAN Regional Strategic Plan for Preventing Transmission of Zoonotic Diseases from Wildlife Trade. The conceptualization and framework development involved an iterative and consensus-building process between the technical team (veterinarians and epidemiologists), PROSPECT team, developmental partners, and ASEAN designates. A review of the literature was conducted to determine the “State of science” on One Health governance, epidemiology of zoonotic diseases in wildlife animals, and interventions. Relevant ASEAN documents were also consulted to identify existing and agreed strategies, plans of action, or mechanisms (concerning the forestry, environment, agriculture, and wildlife laws and diversity) that could complement the regional strategy.

Results or Focus

From this review, a matrix was developed that comprised 10 components/priority areas with overarching domains on governance (designation of lead sectoral bodies, sectors with primary oversight), operationalization (Multisectoral One Health Coordination systems, funding system, and engagement), and technical (surveillance and research, laboratory, inspection systems). A monitoring and evaluation plan will be developed to measure the stage of implementation and the success and achievement of the Plan.

Conclusion or Scope

Consultation meetings with ASEAN leaders, relevant international organizations, and development partners are forthcoming. This engagement represents the building blocks of effective regional collaboration and coherence for zoonotic disease reduction.

Keywords: COVID-19; Southeast Asia; Wildlife; Trade; Coordination

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 14882

ONE HEALTH APPROACH WITHIN THE ASEAN PUBLIC HEALTH EMERGENCY COORDINATION SYSTEM: COMMAND, COORDINATION, COLLABORATION, COMMUNICATION, AND CAPACITY DEVELOPMENT

N Miranda[8] ; J Mitchell[8] ; I Neu[8] ; D Sunoto[1] ; Nicole DeCastro[*8]
[8]Global Health/ DAI/ United States [1]Partnership for Regional Optimization with the Political-Security and Socio-Cultural Communities / DAI/ Thailand (□□□)

Introduction and Objectives or Purpose

The leaders of the Association of Southeast Asian Nations (ASEAN) are developing an ASEAN Public Health Emergency Coordination System (APHECS) to become a “Whole-of-ASEAN” multisectoral coordination mechanism to (i) better prepare and respond to public health emergencies and (ii) synchronize or harmonize relevant initiatives on public health emergencies, to improve the efficiency of regional collective response efforts.

Methods

To enable a One Health approach, the initial phase was to understand existing ASEAN PHE arrangements. The proposed model envisages how APHECS could be structured, including an outline for functional sections, multi-stakeholder roles, overall mandate, scope, and authority during health emergencies. Thirdly, multisectoral coordination and collaboration were enabled to define cross-sectoral linkages and decision-making structures.

Results or Focus

ASEAN has started to reform traditional operational structures by separate sectoral bodies, for example, the establishment of the ASEAN Coordinating Council Working Group on Public Health Emergencies (ACCWG-PHE), which sees broader integration of non-health sectors in PHE strategies.

Next steps will incorporate existing mechanisms and expertise, and experiences from other international organizations and entities. APHECS will require seamless multi-sectoral coordination and collaboration, with consideration of a multi-sectoral task force comprising select members of sectoral bodies and/or entities as well as a parallel coordinating committee among relevant ASEAN Secretariat desk officers.

Conclusion or Scope

To move APHECS forward, ASEAN Member States (AMS) will require the development of a formal ASEAN instrument similar to and in alignment with the ASEAN Agreement on Disaster Management and Emergency Response (AADMER). Functioning through the ASEAN Center for Public Health Emergencies and Emerging Diseases (ACPHEED), the PHE response governance and oversight structure would be centralized to facilitate decision-making, and support the institutionalization of One Health coordination, capacity building for joint surveillance and outbreak response, sharing of data and best practices, risk communication and public awareness, and joint strategic planning and preparedness across the ASEAN region.

Keywords: ASEAN; Surveillance; Coordination; Public Health; Outbreak response

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 14902

Gendered asymmetry of access to knowledge for brucellosis control among pastoral communities in North-West Côte d'Ivoire

Yoro Stéphane Alain Babo*[1 2] ; Gilbert Fokou[2]
[1]Sociology/ Université Félix Houphouët Boigny/ Ivory Coast, [2]Gouvernance, société développement économique/ Centre Suisse de Recherches Scientifiques en Côte d'Ivoire/ Ivory Coast

Introduction and Objectives or Purpose
Brucellosis is an infectious zoonotic disease considered as a threat to public health and for pastoralist livelihoods. Symptoms of the disease can lead to gender specific ailments such as abortions in women and orchitis in men. Pastoralists and their families are at high risk of contracting the disease. Access to health information reinforces existing knowledge and contributes to disease prevention. However, in developing countries, interventions for knowledge sharing on zoonotic diseases predominantly target men. This study aimed to describe mechanisms of knowledge production and transfer on brucellosis according to gender, by assessing the way knowledge affects behaviours of pastoral communities

Methods
A community-based cross-sectional survey was conducted among a pastoral community (PC) of the Folon region in North-West Côte d'Ivoire. The study included transhumant pastoralists, sedentary livestock owners, shepherds and their wives. By using mixed methods, 26 semi-structured interviews were conducted, and 320 questionnaires were completed. Statistical analysis with Chi-square ($\chi 2$) comparison tests was performed to compare variables between men and women. Findings were interpreted through the concept of specialization of the social exclusion theory.

Results or Focus
We found that gender influences access to information on brucellosis and transfer of knowledge on brucellosis appeared gender-biased, especially from veterinarians toward men in the community. The social labour division and interventions of veterinarians through awareness, reinforce the knowledge gap on brucellosis between men and women. Regarding risk exposure, men and women consume raw milk, while only men in general handle animal discharges with bare hands.

Conclusion or Scope

To improve the control of brucellosis, knowledge on best practice should be shared with pastoral communities using the One health approach that encourages mutual learning. Innovative strategies based on gender daily tasks such as safe dairy processing by women and safe animal husbandry to expand their herd for men can be the entry point for the prevention of brucellosis.

Acknowledgement
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Keywords: Brucellosis, One Health, dairy, milk, zoonosis

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 14941

IDENTIFICATION OF RABIES OUTBREAK ISSUE IN BALI USING COLLABORATIVE ONE HEALTH APPROACH

Ni Nyoman Sri Budayanti[1 2] ; Ni Komang Semara Yanti[*1] ; Ida Bagus Ngurah Swacita[3] ; Made Indra Wijaya[4] ; Denni Rajagukguk[5] ; Nabila Yasminuljannah Rahmani[5] ; Gede Padmanabha[1] ; I Ketut Puja[3]
[1]Udayana One Health Collaborating Center/ Udayana University/ Indonesia, [2]Faculty of Medicine/ Udayana University/ Indonesia, [3]Faculty of Veterinary Medicine/ Udayana University/ Indonesia, [4]Faculty of Medicine and Health Sciences/ Warmadewa University/ Indonesia, [5]Bali / Australia Indonesia Health Security Partnership/ Indonesia

Introduction and Objectives or Purpose

Bali Province has been declared a rabies outbreak since 2008. The revocation of the Outbreak status is still not possible because the situation of rabies in the last 3 years has increased. The increase in rabies in animal transmitting rabies increased from 102 cases in 2020 to 239 cases in 2021. Meanwhile, the death rate due to rabies in humans increased sharply to 8 people by the end of May 2022. This situation caused Rabies to become one of the major problems in Bali. This study aims to identify issues in persistent rabies outbreaks in Bali and develop recommendations using One Health approach.

Methods

This study uses the Focus Group Discussion method with parties related to the Rabies outbreak in Bali Province. The conclusion of the FGD is also accompanied by a literature study to produce well-rounded results.

Results or Focus

The FGD and literature study found that most cases of death due to rabies in Bali had a history of not receiving Anti-Rabies Vaccine/Serum after bites. Most of the dogs that were positive for rabies also did not receive the vaccine even though the dogs have owners. Public awareness about proper dog maintenance and management of dog bites is also low. In addition, the management of rabies outbreak is still addressed separately by each sector and makes it difficult to eradicate rabies in Bali.

Conclusion or Scope

This study recommends expansion of vaccination coverage, population control, socialization and education, active community involvement, and application of the One Health concept in handling rabies issues. Application of the One Health concept can lead to integrative collaborative efforts from various disciplines that work across institutions. The communication, collaboration and coordination across sectors will give maximum results if it can be applied properly and involves all relevant sectors.

Acknowledgement

Keywords: Rabies; Vaccination; Population Control; One Health Concept

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 14946

MULTISECTORAL COLLABORATION IN THE RESPONSE AGAINST ZOONOSES IN BURKINA FASO: EXAMPLE OF A JOINT INVESTIGATION ON FISH AND CATTLE MORTALITY

Rahim Kebe*[1] ; Romain Touhouri*[1] ; Micol Stock; Caitlin Madevu-Matson; Stephanie Watson-Grant; Pierre Yameogo; Boukary Ouedraogo; Issaka Sawadogo; Cyrille Kouassi
[1]Country Health Information Systems and Data Use (CHISU)/ Country Health Information Systems and Data Use (CHISU)/ Burkina Faso

Introduction and Objectives or Purpose

In 2017, the government of Burkina Faso, a country vulnerable to zoonotic diseases, organized a One-Health Zoonotic Disease Prioritization with equal input from human, animal and environmental health. A list of five priority zoonotic diseases was identified.

Methods

This study follows an action research approach where the researcher is participating as a change agent.

Results or Focus

The study focuses on the multisectorial collaboration between Ministries of Health, Animal Resources and Fisheries, and of Environment Green Economy and Climate Change involved in the OH approach to ensure an effective zoonotic diseases surveillance and response using a new approach based on system strengthening and implementation of an interoperable multi-sectoral information system. It describes how the OH approach led to joint investigations following reports of serious health events.

Conclusion or Scope

In July 2021, a significant mortality of fish and cattle was reported in the Boucle du Mouhoun region which brought to a joint investigation led by the OH technical secretariat bringing together actors from the human health, animal resources and environment sectors who visited the site and carried out investigations.

The laboratory analyzes of water samples and dead animals, demonstated that the cause was the presence of cyanide spilled into the Mouhoun River by gold panners.

Recommendations approved by the three ministries were sent to the population concerned. In the past, this type of event would have been managed separately by the ministries concerned. The joint investigation has proven to be a good multi sectoral and multidisciplinary practice. It demonstrates that the OH approach is an integrated and holistic approach to identify public health issues. Through the mortality of fish and livestock, the OH approach brought together specialists from several ministerial departments to analyze and determine the factors that led to this incident.

Keywords: One Health; Burkina Faso; zoonoses; surveillance

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 14989

Improving prevention and preparedness to arboviral infections: a community-based One Health model

Claudia Robbiati[*1] ; Alessia Milano[1] ; Silvia Declich[1] ; Maria Grazia Dente[1]
[1]Global Health/ Italian National Institute of Health/ Italy (Italia)

Introduction and Objectives or Purpose

The past five decades have seen an unprecedented emergence of epidemic arboviral diseases, a type of vector-borne diseases caused by viruses transmitted by infected arthropods. Communities are main actors in vector prevention and control strategies, and they could play a major role in preparedness activities (including surveillance and early warning). However, they are rarely considered integral part of a coherent strategy at institutional level. In the last years it became clearer how critical it is to develop preparedness plans with a One Health (OH) perspective, enhancing prevention-preparedness synergic systems which should involve all the relevant stakeholders, including communities. Evidence about the design, processes and outcomes of these inclusive systems need to be gathered and shared with decision-makers.

Methods

A rapid literature review about community-based surveillance and early warning systems for Arbovirus infections is being carried out according to three domains: design (steps, stakeholders, indicators, tools etc), processes (procedures, costs, challenges etc) and outcomes (effectiveness, sustainability, scalability, integration within the institutional systems, acceptability etc). To consolidate the results, an online consultation process with stakeholders of the MediLabSecure Network (www.medilabsecure.com) will be performed to explore existing or planned community-based surveillance and early warning systems for Arbovirus infections with a OH perspective .

Results or Focus

A OH model describing design, processes and outcomes of community-based surveillance and early warning systems for Arbovirus infections will be elaborated to guide the development and implementation of these systems and their integration within institutional plans and preparedness systems.

Conclusion or Scope

The OH model will guide disease control programmes and relevant stakeholders to plan and pilot integrated community-based surveillance and early warning systems for Arbovirus infections. A set of practical and actionable evidence-based recommendations will support MediLabSecure country institutions and other countries, to integrate OH community-based systems in institutional prevention and preparedness systems.

Acknowledgement

MediLabSecure is funded by the European Commission (DEVCO: IFS/2018/402-247)

Keywords: Arboviruses; One Health; Community; Preparedness;Model

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 14995

THE NIGERIAN MILITARY PUBLIC HEALTH RESPONSE TO COVID-19: A 14-MONTH APPRAISAL

Ojor Ayemoba[1] ; Usman Adekanye[*1] ; Michael Iroezindu[2] ; Ikenna Onoh[3] ; Yakuba Adamu[2] ; Laura Chittenden[2] ; Nathan Okeji[1]
[1]Research Unit/ Nigerian Ministry of Defence Health Implementation Programme/ Nigeria, [2]Clinical Research Centre/ United States Army Medical Research Directorate-Africa/Nigeria/ Nigeria, [3]Health Emergency Preparedness and Response/ Nigeria Centre for Disease Control/ Nigeria

Introduction and Objectives or Purpose

The COVID-19 pandemic has caused significant morbidity and mortality globally. The Nigerian government responded to the pandemic by inaugurating the Presidential Task Force on COVID-19 to coordinate resources while Nigeria Centre for Disease Control (NCDC) led the country's public health response. The Nigeria Ministry of Defence Health Implementation Programme (NMODHIP) in partnership with the US Army Medical Research Directorate – Africa/Nigeria (USAMRD-A/N) responded by coordinating the military response.

Methods

NMODHIP established a COVID-19 public health emergency operations center (PHEOC) and activated it at level 3. The multidisciplinary PHEOC consisted of both military and civilian professionals. The PHEOC utilized the WHO Incident Management System with 5 functional units and 6 pillars. The pillars include risk communication, surveillance, case management, infection prevention and control (IPC) amongst others. Each pillar had its terms of reference to guide response. All Pillar leads were integrated into the NCDC national COVID-19 EOC to ensure synergy of efforts.

Results or Focus

COVID-19 awareness and prevention measures were instituted in all military formations. IPC measures including administrative and engineering controls were emplaced. Surveillance data were collected and transmitted using Surveillance Outbreak Response Management and Analysis System (SORMAS). Military laboratories were integrated into the national COVID-19 laboratory network. Treatment centres were established and Rapid Response Teams deployed to support high burden states. The Logistics pillar supplied response consumables to sites. The research pillar used data to guide ongoing response and inform future activities.

Conclusion or Scope

The traditional combat role of the military was redirected to complement this public health emergency response. In support of civilian authorities, gaps, opportunities, and lessons were identified to improve future engagements. Dedicated funding and multisectoral collaborations with other key stakeholders are needed to strengthen military public health emergency preparedness and response.

Acknowledgement

Ismail Lawal[2], Aminu Suleiman[2], Samuel Joshua[1], Amos Ogundeji[2], Dooshima Ugandem-Okonkwo[2], Funmilayo Owolabi[1], Mary Atang[1], Goodluck Nwagbara[1], Yahaya Musa[1], Sunday Odeyemi[2], Abiodun Amosu[1], Ifeanyi Okoye[2], Yusuf Ahmed[2], Joshua Nalazai[1], Zubairu Elayo[2], Taiwo Adelanwa[1], Thomas Monday[1], Eddie Bloom[2], Emmanuel Benyeogor[3]

Keywords: COVID-19, Epidemic management/response, Public health preparedness/response

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 14997

CONTRIBUTION OF THE ONE HEALTH APPROACH TO STRENGTHENING HEALTH SECURITY IN UGANDA: A CASE STUDY

Herbert Bakiika*[1] ; Ekwaro Obuku[1] ; Martha Achan[1] ; Robert Aruho; Maureen Nabatanzi[1] ; Robert Mwebe; Lydia Nakiire[1] ; Issa Makumbi[1] ; Immaculate Nabukenya[1] ; Mohammed Lamorde [1] ; Justine Bukirwa
[1]Global Health Security Department/ INFECTITIOUS DISEASE INSTITUTE, MINISTRY OF HEALTH UGANDA/ Uganda

Introduction and Objectives or Purpose

The One Health approach is one of the tenets of implementing International Health Regulations (IHR, 2005) and the Global Health Security Agenda (GHSA). Uganda is signatory to the IHR 2005 and in 2017, the country conducted a Joint External Evaluation (JEE) that guided development of the National Action Plan for Health Security (NAPHS) 2019 – 2023.This study assessed the contribution of the One Health approach to strengthening health security in Uganda.

Methods

A process evaluation was conducted between 25th Spetember - 5th October 2020,using a mixed–methods case study design. The participants were SMEs from MDAs, IPs and NoHP members. Five FGDs were conducted covering each of the 5 TAs (workforce development, real-time surveillance, zoonotic diseases, national laboratory systems and emergency response operations), spanning 18 indicators and 96 activities.

Results or Focus

Full funding was available for 36.5% of activities and 22.9% were not funded at all. 65% of the activities were still in progress and14.2% were not yet done. In workforce development, FETP trainings and 21 DOHTs' trainings. Real Time Surveillance was achieved through incorporating animal health events reporting in the electronic integrated disease surveillance and response platform. In addition, the MoH weekly epi-bulletin included PZDs. The animal health national reference laboratory and 10 regional vet lab were assessed for capacity to conduct zoonotic disease diagnostics, two of which were integrated into the national specimen referral and transportation network. Multisectoral planning for emergency response and the actual response to PZD outbreaks was done jointly.

Conclusion or Scope
This study demonstrates the contribution of 'One Health' implementation in strengthening Uganda's health security. Investment in the funding gaps will reinforce Uganda's health security to achieve the IHR 2005. Future studies could examine the impacts and cost-effectiveness of One Health in curbing prioritized zoonotic disease outbreaks.

Keywords: One Health, International Health Regulations, Global Health Security, National Action Plan for Health Security

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15131

Swiss-Chinese collaboration towards integrated surveillance-response systems for the prevention of future pandemics

Jakob Zinsstag*[1 2] ; Xiao-Nong Zhou[1] ; Guojing Yang[2] ; Juerg Utzinger[1 2]
[1]Epidemiology and Public Health/ Swiss Tropical and Public Health Institute/ Switzerland (Schweiz), [2]Faculty of Science/ University of Basel/ Switzerland (Schweiz) [1]Centre for Tropical Diseases Research/ Shanghai Jiao Tong University School of Medicine/ China (□□) [2]Deans office/ Hainan Medical University/ China (□□)

Introduction and Objectives or Purpose

The National Institutes of Parasitic Diseases (NIPD) and Swiss TPH have a longstanding collaboration since 2008. The successful collaboration focused on parasitic zoonoses, such as schistosomiasis. A series of bi-annual international symposia on Surveillance-Response Systems leading to tropical diseases elimination have been organized successfully since 2012. Switzerland and China are currently building up and strengthen their One Health research and development capacity. The Covid-19 pandemic is a case-in-point in this regard and warrants substantial engagements of both partners and their associated institutions like the Hainan Medical University (Dr. Guojing Yang) in China and Academic institutions in Switzerland.

Methods

Facing the prevention and control of COVID-19, China and Switzerland are in a normative dilemma of preventing new outbreaks at the cost of economic hardship for millions of consumers, farmers and other economic actors. Governments and experts alone cannot solve this dilemma. All actors having their stakes need to be involved in a societal consensus to jointly enhance biosecurity, without compromising economic activities.

Results or Focus

What a nation is prepared to engage in the prevention of new outbreaks through better biosecurity has to be negotiated in every context independently. There are no blueprints, but the engagement of academic and non-academic actors in a transdisciplinary process has a high potential to find locally adapted solutions. This approach is recommended by the Organization for Economic Co-operation and Development (OECD) in a policy document. As evidenced by the COVID-19 pandemic, efforts have to move even beyond combining the surveillance of human and animal infections, but to also to integrate the surveillance of non-communicable diseases. Furthermore, without citizen engagement and a specific focus on the social sciences, it will not be possible to achieve broad acceptance of integrated surveillance-response measures. The COVID-19 pandemic is full proof of the transdisciplinary breadth required.

Keywords: One Health, integrated surveillance-response systems, transdisciplinarity

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15132

One Health approach to zoonosis control and response in legislation

Katherine Ginsbach*[1] ; Carmen Bullon [2] ; David Sherman[3] ; Kelsey Galantich[3] ; Stefania Negri [4] ; Alison Durran[1]
[1]Center for Transformational Health Law / O'Neill Institute for National and Global Health Law/ United States, [2]FAO Development Law Service / Food and Agriculture Organization of the United Nations/ Italy (Italia), [3]Capacity Building Department / The World Organisation for Animal Health / France, [4]International Law / UNISA School of Law / Italy (Italia)

Introduction and Objectives or Purpose
To identify and discuss potential entry points to introduce a One Health approach into national legislation on zoonosis management in order to improve legal preparedness to face pandemics.

Methods
The GHSA Legal Preparedness Action Package was established to develop a solid foundation and understanding of the competencies necessary for strengthening public health emergency legal preparedness. The LPAP includes a sub-working group to analyse how countries can improve zoonosis-related legislation to improve legal preparedness. Based on the questions developed and research conducted by this sub-working group, the benefits and entry points in legislation to effectively regulate zoonosis from a One Health perspective are being analysed.

Results or Focus
National legal frameworks include a variety of sectoral legislation that is relevant for the One Health approach to zoonosis control and prevention. These include public health, food safety, sustainable wildlife management, environment legislation, biodiversity, and animal health. Of particular importance in that over 70% of the newly emerging human diseases in recent decades have originated as animal infections. A One Health approach to zoonosis management requires that veterinary authorities have the policies, legal authorities, intersectoral collaborations and resources in place to detect and mitigate zoonotic disease threats. This paper will explore how a One Health approach could be mainstreamed into zoonosis-related legislation by establishing the entry points and references to relevant legal instruments. It will address the challenges and opportunities of setting up multisectoral One Health institutional frameworks that provide coordination and sustainable action to One Health governance and to the regulation of zoonosis specifically.

Conclusion or Scope
A One Health approach to zoonosis control and response is necessary to protect human, animal and environmental health from the dangers posed by zoonosis. In legislation, this requires a holistic approach and recognizes the interdependencies between different legal areas. Institutional coordination requires legal frameworks that ensure multisectoral collaboration in a sustained manner.

Keywords: Global Health Security Agenda; Legal Mapping; Zoonosis; Detect and Respond; Legal Preparedness

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15140

SPATIOTEMPORAL PATTERNS AND EVOLUTIONARY DYNAMICS OF HIGHLY PATHOGENIC AVIAN INFLUENZA H5N1 OUTBREAKS IN BANGLADESH, 2007-2022

Ariful Islam[*1] [1] ; Tasnim Ara[1] ; Emama Amin[1] ; Shariful Islam[1] ; Tahmina Shirin[4] ; Mohammad Mahmudul Hassan[2] ; Marcel Klaassen[1] ; Jonathan H Epstein[7]
[1]Centre for Integrative Ecology, School of Life and Environmental Science/ Deakin University/ Australia, [1]EcoHealth Alliance Bangladesh Program/ Institute of Epidemiology, Disease Control and Research (IEDCR)/ Bangladesh (□□□□□□□□) [4] Department of Epidemiology/ Institute of Epidemiology, Disease Control and Research (IEDCR)/ Bangladesh (□□□□□□□□) [2]Queensland Alliance for One Health Sciences, School of Veterinary Science/ The University of Queensland/ Australia [7]Vice President, Science and Outreach Program/ EcoHealth Alliance/ United States

Introduction and Objectives or Purpose

Understanding disease clustering and dissemination pathways can lead to better disease control and prevention efforts. Hence, we conducted this study to describe the epidemic characteristics spatiotemporal patterns, identify clusters of highly pathogenic avian influenza (HPAI) H5N1 outbreaks, and explore the evolutionary changes of H5N1 over time and species in Bangladesh.

Methods

We used Global Moran's I, and Global Getis Ord Gi to analyze the spatiotemporal patterns, clusters, hotspots, and kernel density of H5N1 outbreaks. Further, we applied the space-time permutation model to detect spatiotemporal clusters. We conducted a Bayesian phylogenetic analysis to generate time-scaled maximum clade credibility (MCC) tree.

Results or Focus

Our study revealed 10 HPAI H5N1 epidemic waves between 2007 and 2020. After the H5N1 vaccination in 2012, the temporal distribution of HPAI H5N1 outbreaks occurrence significantly decreased; however, the continuous shedding of the H5N1 virus is reported in surveillance all year-round. We identified seven space-time clusters of outbreaks intense from 2007-to 2012, most of which were in and around Dhaka. The Bayesian phylogenetic analysis depicts that since 2007, there have been four H5N1 clades identified in Bangladesh, with only clade 2.3.2.1a continuing to circulate since 2011. The most current reassorted clade 2.3.2.1a was identified in all reported species after 2012. The HA gene of H5N1 clade 2.3.2.1a has been reassorted into at least nine subgroups (R1-R9). After 2016, the first eight groups disappeared, and only R9 subgroups predominately circulated in all poultry species

Conclusion or Scope

Spatiotemporal patterns and the evolution of H5N1 outbreaks are critical for developing targeted control and prevention measures for AIV. We recommend improving farm biosecurity practices along with vaccinating commercial poultry to control HPAI outbreaks in Bangladesh better.

Keywords: Outbreaks; Space-time; Phylogenetic; Clade; Poultry

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15164

ANALYSIS OF COMMUNITY BEHAVIOR COVID-19 PREVENTION IN MEDAN. INDONESIA

Rina Amelia*[1] ; Arlinda Sari Wahyuni[1] ; Isti Ilmiati Fujiati[1] ; Juliandi Harahap[1] ; Putri Chairani Eyanoer[1]
[1]Department of Community Medicine/Public Health Sumatera Utara, Faculty of Medicine. Universitas Sumatera Utara/ Universitas Sumatera Utara/ Indonesia

Introduction and Objectives or Purpose

Introduction. In dealing with the COVID-19 pandemic, several strategies and steps have been made by the government to control the transmission of COVID-19, namely by applying the health protocol regulation that consists at least wearing appropriate facial masks, washing hands, and social distancing. The purpose of this study is to analyze the behavior of preventing COVID-19 in the community in the Selayang Health Center. Medan.

Methods

Methods. This study was an analytical research method with a cross-sectional research design carried out in June 2020. The study population was the community member of the Medan Selayang Health Center who was> 17 years old and willing to participate in this study. The study sample was 100 people recruited with a consecutive sampling method. Data collection was carried out using a valid questionnaire which was filled in via google form. Before filling out the questionnaire, respondents were asked to provide informed consent. Data analysis was performed using the Chi-square test ($p<0.5$) using the SPSS.

Results or Focus

The results showed that the COVID-19 prevention behavior in the Medan Selayang public health center was good for as many as 92 people (92%), and there was a relationship between education level and covid-19 prevention behavior, while age, gender, and work status were not related to COVID-19 prevention behavior.

Conclusion or Scope

Education is essential to improve public knowledge so they can do prevention measures independently.

Acknowledgement

I want to thank all the respondents who participated in the research and the medical faculty dean of medical faculty, Universitas Sumatera Utara, for the research’s convenience.

Keywords: prevention behavior; covid-19; wearing masks;washing hands; social distancing

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15216

ONE HEALTH: MULTI-SECTORAL APPROACH FOR HUMAN CASE SEARCH IN AVIAN INFLUENZA OUTBREAKS IN NIGERIA; JANUARY 29th to JUNE 15th, 2021

Daniel Kolade*[1] ; Sikiru Badaru [1] ; Motunrayo Fagbola[1] ; Mairo Kachalla[2] ; Jafiya Abubakar[1] ; Gbetsere Aghogbo[3] ; Salome Bawa [2] ; Oyeladun Okunromade[1]
[1]Surveillance and Epidemiology/ Nigeria Centre for Disease Control/ Nigeria, [2]Public Health / Federal Ministry of Agriculture and Rural Development / Nigeria, [3]Pollution Control & Environmental Health Services/ Federal Ministry of Environment / Nigeria

Introduction and Objectives or Purpose

Influenza infection can be seasonal, zoonotic, and/or pandemic. An outbreak of avian influenza started on 25th January 2021 from a backyard farm in Kano where multiple species of birds were found sick and dead. Consequently, a national one health (OH) Rapid Response Team from the Nigeria Centre for Disease Control, was deployed to the affected states to investigate and control the zoonotic and human-to-human transmission of the highly pathogenic avian influenza (HPAI) virus. We investigated the outbreak through a national OH incident management structure to demonstrate possible zoonotic transmission of HPAI.

Methods

A cross-sectional study was conducted on human contacts with infected birds. Response activities were managed through activation of an Emergency Operation Centre. Influenza-like Illness and Severe Acute Respiratory Infection were used as case definitions to search for more cases. Individuals exposed to sick and/or dead birds were followed up for 14 days for case detection. Nasopharyngeal and oropharyngeal swabs collected from exposed individuals at the farms and Live Bird Markets in 4 outbreak states. Swabs were subjected to RT-PCR testing and positive samples shipped to the United States WHO collaborating centre for confirmation and sequencing.

Results or Focus

83 exposed people in total were followed up. Majority (98.7%) were asymptomatic and 1 had catarrh. Only Seven (10.9%) were positive for Flu A (CT value :34.9 – 38.4), 6 (7.2%) were subtype A/H5 while 1 (1.2%) was unsub-typable. Upon further analysis of the 7 positive samples, 5 (71.4%) were positive for Flu A, and A/H5 (CT value, 36.3 – 43.8), 2 (28.6%) were positive for both A/H5 and A/H9 (39.2 – 40). Only 3 (42.9%) had sequence clade 2.3.4.4b like that of HPAI H5.

Conclusion or Scope

Most contacts were negative to HPAI. A coordinated OH approach for early detection and response to HPAI outbreaks is critical to mitigate and prevent transmission in humans.

Acknowledgement
Thank you

Keywords: One-Health; Avian-Influenza; EOC; Epidemiology

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15277

Evaluation of Brunei's digital pandemic management system for COVID-19: an empirical study of perceived usefulness and usability

Muhammad Ali Rosledzana*[1] ; Yuan Wei[2] ; Jane Tey[2] ; Fathi Alikhan[3] ; Justin Wong[1 4]
[1]Disease Control Division/ Ministry of Health/ Brunei, [2]EVYD Research Program/ EVYD Technology Limited/ Singapore, [3]Public Health/ EVYD Technology Limited/ Brunei, [4]PAPRSB Institute of Health Sciences/ Universiti Brunei Darussalam/ Brunei

Introduction and Objectives or Purpose

To support Brunei's COVID-19 response, a comprehensive digital pandemic management system (DPMS) was developed in May 2020 comprising a digital workstation integrating the centralized national electronic patient records database (BruHIMS), patient geo-location data, and other socio-demographic information of cases and contacts. This was supported by a front-facing public mobile application, the BruHealth app.

This study aims to evaluate the usability and usefulness of the DPMS workstation in three response areas: (1) contact tracing, (2) quarantine monitoring of contacts, and (3) triage and home recovery for confirmed cases. Each response area was supported by a dedicated team and DPMS-specific tools.

Methods

A 12-item questionnaire was adapted from predictors of technology adoption to evaluate the ease of using DPMS ('usability' – 6 items) and whether it helps complete tasks ('usefulness' – 6 items) scored on a five-point likert scale with 1 being least usable/useful and 5 being most usable/useful. The questionnaire was distributed to all staff who operated the workstation. We calculated the mean score for each item measured and used the Kruskal-Wallis test to assess differences in responses between the three teams and Spearman's test for correlation between the domain of usefulness and usability. All analysis was performed on SPSS version 26.

Results or Focus

96 of the 230 invitees responded (response rate=41.7%). The aggregate mean score across all respondents was 3.96 for usability, and 4.07 for usefulness. There was no significant difference on the mean scores between the 3 teams for both usability ($p=0.146$) and usefulness ($p=0.051$). There is a positive correlation between usability and usefulness $r=.688$, $p=<0.001$.

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15279

Patterns of date palm sap harvesting and trading practices and risk of Nipah virus transmission at communities in Bangladesh

Abdul Khaleque Md. Dawlat Khan[*1] ; Shusmita Dutta Choudhury[1] ; Md. Zulqarnine Ibne Noman[1] ; Nabila Nujhat Chowdhury[1] ; Sarah Munro[2] ; Maryska Kaczmarek[2] ; Meerjady Sabrina Flora[3] ; Tahmina Shirin[4] ; Jonathan H. Epestein[2] ; Ariful Islam[1 2]
[1]EcoHealth Alliance Bangladesh Program / Institute of Epidemiology, Disease Control and Research (IEDCR) / Bangladesh (□□□□□□□□□), [2]Emerging Infectious Disease Research/ EcoHealth Alliance/ United States, [3]Directorate General of Health Services/ Ministry of Health and Family Welfare / Bangladesh (□□□□□□□□□), [4]Director and Professor, Department of Virology / Institute of Epidemiology, Disease Control and Research (IEDCR) / Bangladesh (□□□□□□□□□)

Introduction and Objectives or Purpose

Bangladesh has been experiencing a nearly annual Nipah virus (NiV) outbreak through drinking contaminated raw or fermented date palm sap (RDPS) with bat excreta since 2001. RDPS harvesting practices and trading patterns have not been explored extensively. Hence, we conducted a study to understand RDPS collection, consumption, and selling practices and the risk of NiV spillover at the community level.

Methods

We performed an explorative qualitative study in two NiV outbreak districts, Rajbari and Naogaon, between 2021 and 2022. We recorded participant observations (n=14) and conducted ethnographic interviews (n=31) with RDPS collectors (Gacchi) on collecting and selling practices and using diversity of protective apparatus. The interview data were analysed using coding and thematic analysis based on the grounded theory approach.

Results or Focus

Gachi prefers selling RDPS more than making molasses due to time consumption, fuel costs of preparing it, and the high demand for consuming RDPS. They informed RDPS selling is not limited to their local community and sale distends location of non-harvesting areas based on customer demand through a middleman, which increases the transmission risk of NiV and other bat-borne diseases in wider geographical areas. We observed, and participants reported that Pteropus and non-Pteropus bats and rodents visited the trees and drank RDPS. They are replacing clay pots with discarded plastic pots, due to the free cost. They also prefer to use non-conventional protective apparatuses like jute bags, plastic bags, and nylon nets due to the time and resources to prepare bamboo skirts. Moreover, they reported that bats scratched out bamboo skirts and trunks to lick sap.

Conclusion or Scope

We recommend adopting a culture-sensitive intervention, including efficacy tests of bat access protection on several apparatuses with economic outcomes of the date palm sap harvesting practices to prevent spillover of NiV and other bat-borne emerging viruses in Bangladesh.

Keywords: spillover, protective apparatus, interventions, NiV

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15296

VETERINARY HUMAN RESOURCE CAPACITY BUILDING: INDONESIA'S EXPERIENCE IN THE FIELD EPIDEMIOLOGY TRAINING PROGRAM FOR VETERINARIANS

Purnama Martha Oktavia Simanjuntak*[1] ; Karoon Chanachai[2] ; Riana Arief[3] ; Irpansyah Batubara[1] ; Nuryani Zainuddin[1] ; Farida Camalia Zenal[3] ; Luuk Schoonman[3]
[1]Directorate of Animal Health, DGLAHS/ Ministry of Agriculture Republic Indonesia / Indonesia, [2]Bangkok-based Regional Development Mission for Asia/ USAID/ Thailand (□□□), [3]Emergency Center for Transboundary Animal Diseases/ Food Agricultural Organization/ Indonesia

Introduction and Objectives or Purpose

Epi-surveillance is an important competency for Veterinary Services. Skill-based training, such as the Field Epidemiology Training Programme for Veterinarians in Indonesia (PELVI) is needed to improve the capacity of government veterinarians in detection, reporting, and response to animal diseases with other sectors. This study was conducted to determine the ability of PELVI's trainees in surveillance, outbreak investigation, and other related skills, and to identify gaps that need to be improved in future training programs.

Methods

This study was conducted using a questionnaire survey where 11 PELVI mentors were asked to assess 17 trainees from the first cohort of intermediate-level PELVI training. Additionally, 6 trainees were interviewed to collect more information. Data collected include current knowledge, special knowledge needs, and skills possessed by trainees. Data analysis was carried out using a qualitative deductive thematic approach.

Results or Focus

Good skills and knowledge in designing and implementing surveillance, outbreak investigations, and can to work effectively with other sectors are the main skills recognized in the first cohort of PELVI. The study identified that more training time was needed to develop the ability to advocate, design epidemiological studies, spatial analysis, and use epidemiological software. However, trainees stated that the PELVI training helped them become more confident and the knowledge acquired supported their activities in preventing and controlling animal diseases in the field and advancing their institutions.

Conclusion or Scope

This study recommends adding exercises on certain topics for the next cohort of intermediate level PELVI training to achieve better uniformity in trainees' basic skills. Refresher training or additional thematic training can be conducted to maintain and improve the skills of alumni.

Acknowledgement

We are very grateful to all PELVI mentors and participants who have contributed, and to the Director of Animal Health and FAO ECTAD Indonesia who have supported this research.

Keywords: FETPV; PELVI; field epidemiology; capacity building

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15298

LESSONS IDENTIFIED FROM AN AFTER-ACTION REVIEW OF RAPID RISK ASSESSMENT PROCESSES FOR EMERGING INFECTIOUS AGENTS WITH ZOONOTIC POTENTIAL

Cat McGillycuddy*[1] ; Tharindu Premachandra[2] ; Michael Reynolds[3] ; Helen Roberts[2]
[1]Global Health Security/ UK Health Security Agency/ United Kingdom, [2]Exotic Disease Policy Team/ Defra/ United Kingdom,
[3]Emerging Infections and Zoonoses/ UK Health Security Agency/ United Kingdom

Introduction and Objectives or Purpose

Rapidly produced, multi-sectoral informed and evidenced based risk assessment is an essential component of preparation, prevention, detection, response and recovery (PPDRR) from zoonotic hazards for domestic and global health security.

In November 2020, a SARS-CoV-2 variant in mink with the perceived potential to hamper COVID-19 intervention efforts emerged in Denmark. In response, a rapidly produced qualitative assessment of the risk that SARS-CoV-2 infection in UK Mustelidae populations presents to humans was undertaken by the Human Animal Infection and Risk Surveillance (HAIRS) group. An after-action review (AAR) of the rapid risk assessment process (RRAP) was undertaken to describe good practices, identify issues and actions for improvement, and to promote individual and collective learning on RRAP.

Methods

A de-brief type AAR was undertaken with key members of the RRAP team informed by the WHO Guidance for After Action Review.

Results or Focus

The RRAP was performed successfully with some challenges. The commitment and contribution of experts with limited notice and tight deadlines was testament to the high-level government support, established relationships and ways of working by the HAIRS group. Improving the flexibility of the RRAP to address complex risk questions was identified as a priority action

Conclusion or Scope

Effective hazard management hinges on the ability to accurately and effectively identify, characterise and assess the risk presented by a hazard. Such processes can inform appropriate mitigation strategies to reduce downstream impacts, but also advise upon upstream actions that may prevent or moderate the likelihood or impact of the threat under review. This makes risk assessment, and investment in systems to monitor, evaluate and improve such processes, fundamental to the entire sequence of PPDRR from hazards. AAR should be viewed as a useful monitoring and evaluation tool to support improvements to individual components integral to PPDRR, as well as whole responses, to strengthen national and global health security.

Keywords: risk assessment; after action review; monitoring and evaluation; emerging infections; zoonoses

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15313

Understanding the Demand for Veterinary Services in Cambodia to Strengthen Animal Health Systems

Justin McKinley*[1] ; Barbara McPake[1] ; Katherine Gilbert[1] ; Suon Sothoeun[2] ; Has Phalmony[3] ; Sreytouch Vong[1]
[1]Nossal Institute for Global Health/ The University of Melbourne/ Australia, [2]GDAHP/ General Directorate of Animal Health and Production/ Cambodia (□□□□□□□), [3]NIPH/ National Institute of Public Health/ Cambodia (□□□□□□□)

Introduction and Objectives or Purpose

Strong animal health systems are imperative in improving zoonotic disease outbreak responses. In Cambodia, veterinary services are often inaccessible and rarely used by smallholder livestock producers. This study aims to provide evidence to strengthen the animal health system in Cambodia by identifying accessibility and the frequency of use of animal health services by smallholders, determining the roles that different veterinary service providers play in animal health, and investigating factors that contribute to smallholders' decisions to use animal health services

Methods

We conducted 30 key informant interviews and 1,528 household surveys with smallholder livestock producers across ten provinces of Cambodia to investigate access and patterns of use of different animal health service providers, namely, village animal health workers (VAHWs) and veterinarians. We expect these providers are substitutes, so we used a multivariate probit model to allow for correlations across the smallholders' choices of service provider use.

Results or Focus

Less than half of respondents reported having access to any service provider, and only 18.5% reported using any service provider in the last year. We find that VAHWs are more active in preventive procedures than veterinarians, who are more involved in curative treatments. Specific determinants of whether or not to seek care only slightly varied between VAHWs and veterinarians. Households with access to credit, raising cattle and having access to multiple service providers were all more likely to use any veterinary services. Conversely, raising poultry made households less likely to use veterinary services.

Conclusion or Scope

Cambodian Smallholders have low access to and use of veterinary services. The use of technology and VAHWs can play an essential role in filling the gap in access, particularly in preventive care and disease surveillance to mitigate future zoonotic disease outbreaks.

Acknowledgement

Funding - Australian Centre for International Agricultural Research and the Australian Department of Foreign Affairs and Trade Indo-pacific Centre for Health Security

Keywords: Animal health; Cambodia; Demand; Health systems strengthening; Zoonoses

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15328

Sniffing disease: a change of paradigm in outbreak management?

Anne-Lise Chaber*[1] ; Penny Conor[2] ; Tom Dodd[3]
[1]Pathobiology and Population Health/ University of Adelaide/ Australia, [2]Critical Care/ Lyell McEwin Hospital/ Australia, [3]Clinical/ South Australia Pathology/ Australia

Introduction and Objectives or Purpose

Rapid and reliable screening tools are needed to effectively prevent or manage outbreaks. PCR and Rapid Antigen Tests (RAT) fail to combine those characteristics. We have previously demonstrated that COVID-19 detector dogs (CDDs) can detect Volatile Organic Compounds in the perspiration of persons infected with SARS-CoV2 and accurately discriminate between SARS-CoV-2 infected and non-infected individuals with an overall Diagnostic Sensitivity (DSe) of 96.2% (95%CI: 94.9%-97.3%) and an overall Diagnostic Specificity (DSp) of 98.8% (95%CI: 98.49%-99.0%) in controlled settings.

Methods

Here, we evaluate the fitness-for-purpose of CDDs in two deployment settings: Adelaide airport using axillary perspiration on 2 minutes gauzes and Lyell McEwin Hospital via live detection. We estimated CDDS' ancillary attributes (i.e. invasiveness, ease-of-use, throughput capacity, turn-around time) and public acceptance (the number of people who opt-in vs opt-out). In both settings, four dogs were conditioned to give a sit and stare response when finding a patient with an active infection of SARS-CoV2 regardless of the presence or absence of symptoms. Testing and quarantine regimes, at the airport and hospital, by PCR and/or RAT tests, were not altered by CDDs' results.

Results or Focus

12% of the passengers at the airport and 94.29% of the hospital's patients opted-in. CDDs' response was immediate in both settings, but turn-around time exceeded 10 minutes at the airport. Live screening at the hospital was fast, and non-invasive but required a high level of dog training and expertise from dog handlers to maintain CDD's accuracy and focus. Samples' collection and management made the screening process unfit for purpose at the airport.

Conclusion or Scope

Ancillary attributes of CDDs make this tool fit-for-purpose to screen individuals live. CDDs' diagnostic accuracy and precision in comparison to RAT and PCR tests are the focus of another study but maintaining dogs' stamina and diagnostic accuracy while performing a repetitive task required constant work in both settings.

Keywords: Disease screening tool, COVID detector dogs, ancillary attributes

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15353

ONE HEALTH APPROACH TO NIPAH VIRUS OUTBREAK INVESTIGATION AMIDST OF COVID-19 PANDEMIC IN BANGLADESH, 2021-2022

Ariful Islam[*1 2] ; Shariful Islam[1] ; Shusmita Dutta Choudhury[1 2] ; Md Abu Sayeed[1 2] ; Sarah Munro[2] ; Maryska Kaczmarek[2] ; Mohammed Ziaur Rahman[3] ; Ahmad Raihan Sharif[4] ; Tahmina Shirin[4] ; Jonathan H Epstein[1]
[1]EcoHealth Alliance Bangladesh Program/ Institute of Epidemiology, Disease Control and Research (IEDCR)/ Bangladesh (□□□□□□□□) [2]Emerging Infectious Disease Research/ EcoHealth Alliance/ United States [3]One health Laboratory/ International center for diarrheal disease research (icddr,b), / Bangladesh (□□□□□□□□) [4] Department of Epidemiology/ Institute of Epidemiology, Disease Control and Research (IEDCR)/ Bangladesh (□□□□□□□□) [1]Vice President, Science and Outreach Program/ EcoHealth Alliance/ United States

Introduction and Objectives or Purpose

Nipah virus (NiV) is an emerging bat-borne virus causing fatal encephalitis outbreaks. Until 2020, Bangladesh reported 319 NiV cases with >70% mortality. Amidst the COVID-19 pandemic, A multidisciplinary team investigated four suspected NiV spillover events in three districts of Bangladesh between 2021 and 2022 to identify the source, behavioral risk practices, and environmental exposures.

Methods

We investigated and collected epidemiological, behavioral, and ecological data from communities and biological specimens of bats. We sampled 60 bats per outbreak and environmental pool urine samples (N=314) from seven bat roosts within 10km radius of outbreak's epicenter. The bat samples were tested for NiV by real-time RT-PCR and consensus PCR assay targeting RDRP genes of paramyxovirus (PMV) to detect known and novel PMV and to screen serum using multiplex Luminex assay for henipavirus panel.

Results or Focus

We did not detect NiV in real-time RT-PCR in bat samples; however, we found 04 urine samples positive for Nipah henipavirus and Hendra henipavirus in consensus PCR assay. In Luminex assay, results stated the seroprevalence of NiV was 15.18% (34, CI: 10.74%-20.56%), and Hendra virus was 1.3% (3/224), Cedar 13% (3/224), Mojiang 0.9% (2/224) and Kumasi virus 1.3% (3/224). The behavioral investigation showed that participants have habit of drinking raw date palm sap 73.06% (CI: 67.04%-78.51%), eating half-eaten fruits 17.96% (CI: 13.36%-23.35%). Moreover, around 47% of the respondents have date palm trees in their household; 74.78% are nursing.

Conclusion or Scope

Serological and virological data showed diverse henipavirus circulating Pteropus medius bats. The high density of date palm trees and having habits of drinking raw sap and eating half-eaten fruits in the outbreak communities; drinking contaminated raw sap was possibly the source of NiV infection. We recommend stringent one health surveillance and awareness campaigns in high-risk communities to reduce human-bat interactions and minimize spillover of bat-borne virus to humans.

Keywords: spillover, prevent, Genetic diversity, Henipavirus

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15358

Building the One Health Workforce through Competency-based Education to Prevent and Respond to Outbreaks and Related Emergencies

Getachew Kassa*[1] ; Susan Michaels-Strasser[1] ; Claire Raether[1] ; Fatima Tsiouris[1] ; Irene Naigaga[1] ; Vipat Kuruchittham
[1]ICAP/ Columbia University/ United States

Introduction and Objectives or Purpose

Background: The ability to prevent, detect, and respond to emerging public health threats requires a focus on One Health competencies. As countries struggle to respond to the ever-increasing number of complex emergencies, competency-based education (CBE) and training models grounded in One Health (OH) principles are increasingly necessary to ensure health worker efficacy and interdisciplinary work. Despite its significance, educational institutions have limited CBE systems and capacity.

Objectives: To demonstrate an OH CBE, training and assessment program using experiential learning strategies including simulations that require application of OH approaches.

Methods

ICAP at Columbia University, in collaboration with the secretariats of Africa OH University Network (AFROHUN) and Southeast Asia OH University Network (SEAOHUN), facilitated two regional workshops in May 2022. The four-day training of trainers (TOT) curriculum included the use of backward design curriculum development; competency-based assessments; stage-based maturity models; and hands-on experiential learning and assessment through simulation-based exercises. The TOT targeted faculty members to advance OH CBE. University-specific action plans were developed to guide future assessment of CBE implementation. Kirkpatrick's Model was used to evaluate the training program.

Results or Focus

Forty-three participants, 21 from 8 Africa and 22 from 7 Southeast Asia attended the training. 93% (n=40) of participants who completed pre-and post-tests showed a significant increase in knowledge (t-test, $p<0.00$. Of 34 (79%) participants who completed the training survey, 30 (88%) of them strongly agreed that the training was relevant or very relevant to their daily responsibilities, and 32 (94%) reported that they were somewhat or extremely likely to apply the learning in their current setting.

Conclusion or Scope

There was a significant increase in knowledge and clear motivation to implement CBE by the end of the TOT. We will assess progress on CBE implementation across the networks. Future efforts to assess the outcome and impact of OH-specific CBE are encouraged given emerging global health threats.

Keywords: CBE, OH, Experiential Learning, simulation exercises

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Improving outbreak response
Abstract No: 15381

Investigation of Suspected Cutaneous Anthrax outbreak in Northern part of Bangladesh, July-August, 2022

Sabrina Mohona*[1] ; Rabeya Sultana[1] ; Immamul Muntasir[1] ; Tahmina Shirin[1] ; Nazneen Akhter[1] ; Mahbubur Rahman[1] ; Nawroz Afreen[1]
[1]Field Epidemiology/ Institute of Epidemiology, Disease Control & Research/ Bangladesh (□□□□□□□□)

Introduction and Objectives or Purpose

Cutaneous Anthrax (CA) is reported sporadically in Bangladesh. In July 2022, 9 suspected human-cases of CA following slaughtering of a sick cow were reported from a sub-district of Northern Bangladesh which is not under Anthrax surveillance. An outbreak response team was deployed to identify risk exposures, determine magnitude of outbreak and recommend effective control and prevention strategies.

Methods

A descriptive epidemiological survey conducted from 17th July-10th August 2022 among those involved in slaughtering and receiving portions of infected raw meat. Cases were identified through hospital record and active community search. Suspected case was defined as resident of reporting sub-district having cutaneous lesions (e.g., papule, vesicle, or eschar) between 6th July-10th August 2022. Suspected-cases were confirmed positive for Bacillus anthracis by RT-PCR. The risk exposure and knowledge assessed through a semi-structured questionnaire. Swab and blood specimens collected from cases and tested.

Results or Focus

Among 265 exposed persons, 11 suspected cases (male 56%). Attack rate was 4%. Median age of suspected-cases was 32 (Range:23-60) years. Epidemic curve indicates single point-source exposure which coincide with 6th July 2022 (disease cow was slaughtered). Median incubation period was 6 days (Range:1-11days). Seven (64%) cases were exposed during raw meat handling. Eschar found in 9(82%) cases, mostly distributed in upper-limb (45%). Laboratory results revealed that 36% (4/11) were PCR positive for B. anthracis. Eight (73%) cases were treated with antibiotics. Slaughtered cow and other cattle of the area found non-vaccinated. No history of heavy rainfall or flood found before outbreak.

Conclusion or Scope

The investigation finding indicated that the outbreak may cause by handling raw meat of a non-vaccinated cow in bare-hand. We recommended awareness program, ring vaccination, extensive reservoir study both in animal and environment in “One Health approach”. Inclusion of sub-district in ongoing Anthrax surveillance is also needed to prevent future Cutaneous Anthrax outbreak.

Keywords: Anthrax, Bangladesh, Descriptive

Topic: One Health Science (OHS):Pandemic Preparedness: detect, prevent and respond

Abstract No: 15404

KNOWLEDGE OF ACADEMICS TOWARDS ONE HEALTH APPROACH

Siti Shofiya Novita, Firdausy Kurnia Maulana[1], Niken Salindri[3], Muhammad Atoillah Isfandiari[2], Atik Choirul Hidajah[2], Fedik Abdul Rantam[145], Annisa Vivianti[1],

Introduction and Objectives or Purpose:

Today's the world face health complex problems like antimicrobial resistance, pollution, food security, biosafety, biosecurity, and emerging and reemerging infectious diseases. In response, a transdisciplinary approach among human, animal, plant, and environmental health disciplines, described as One Health, has gained support and visibility because of its capacity to synergistically address these challenges. As the One Health approach is increasingly accepted globally, the role of academics in training future students is very important in building prospective leaders who are able to increase synergies in various sectors in improving health status. This study aimed to determine differences in knowledge of one health approach before and after participating workshop.

Methods:

The participants were academics (N=20) in various universities in Surabaya. They filled out the 10 item questionnaire (10 score for each question) before and after the workshop with the same set questions concerning one health concept. The workshop was conducted by presenting material and training on the one health approach by trainer from Indonesia One Health University Network (INDOHUN) and health problem analysis by trainer from Faculty of Public Health Universitas Airlangga. Only participant with both pre and post tests were included in the analysis (N=15). Using paired sample t-test, the differences between pre and post tests were examined for statistical significance ($p<0.05$). The workshop was funded by USAID.

Results or Focus:

The minimum and maximum pre-test scores were 10 and 70, and minimum and maximum score of post-test were 60 and 90. The pretest average result was 47.33 while the post test average result was 73.33. The knowledge after participated the workshop was significant with $p=0.000$ ($p<0.05$). Therefore, there is differences between pre and post test results.

Conclusion or Scope:

There was a workshop effect on increasing the knowledge of academics in one health approach. We recommend that this workshop can be developed at the national level to raise awareness of infectious diseases with one health approach.

Acknowledgement: - USAID - SEAOHUN - Ministry of Education and Culture of Indonesia

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Sharing of pathogens, resources and data
Abstract No: 14829

HOW TO CONDUCT AN IPD-MA OF AN EMERGING PATHOGEN. A TOOLKIT.

Lauren Maxwell [1] ; Brooke Levis[2] ; Mabel Carabali[3] ; Priya Shreedhar[*1]
[1]Heidelberg Institute of Global Health (HIGH)/ Heidelberg University/ Germany (Deutschland), [2]Centre for Clinical Epidemiology, Lady Davis Institute for Medical Research/ Jewish General Hospital/ Canada, [3]Département de Médecine Sociale et Préventive, École de Santé Publique/ Université de Montréal/ Canada

Introduction and Objectives or Purpose

Individual participant data meta-analyses (IPD-MAs) have a number of benefits over standard aggregate data meta-analyses, including the consideration of additional participants and follow-up time as well as joint consideration of study- and subject-level heterogeneity for improved diagnostic and prognostic model development and evaluation. However, IPD-MAs are resource-intensive and require careful budgeting of time from data contributing groups, a dedicated management team, a diversity of expertise, clearly documented data sharing and authorship agreements, as well as consistent and clear communication. In addition, compared to IPD-MAs of well-described pathogens, IPD-MAs conducted in response to emerging or re-emerging pathogens i.e., COVID-19, Zika, and Ebola, are especially challenging given the higher levels of heterogeneity in study enrollment, exposure and outcome definitions as well as ascertainment of the exposure, confounders, and outcomes. To help with the management of IPD-MAs of emerging pathogens, we present a toolkit that contains a suite of templates that cover the entire IPD-MA process from study recruitment to retrospective harmonization and publication.

Methods

The toolkit was developed and refined through our work over the last 15 years on multiple multinational IPD-MA projects, including the DEPRESSD, Zika Virus Individual Participant Data, and ReCoDID Consortia. The toolkit's templates have been published and are downloadable from OSF (DOI: 10.17605/OSF.IO/3FXVY).

Results or Focus

The toolkit contains budget and Gannt chart templates, job announcement templates, adaptable data sharing and authorship agreements and surveys, email templates, project management and data harmonization-related spreadsheets, as well as standard operating procedures for IPD-MA-related tasks including harmonization (Figure 1).

Conclusion or Scope

The elements of the toolkit are meant to provide a starting point for many common IPD-MA tasks and should be adapted according to the IPD-MA's specific research question, context and outcome(s) of interest. Our hope is that the toolkit will help to expedite the development and management of future IPD-MAs of emerging pathogens.

Acknowledgement

NA

Keywords: individual participant data meta-analysis; IPD-MA; toolkit; templates; IPD-MA management

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Sharing of pathogens, resources and data
Abstract No: 14905

Ties that bind: Operationalizing the One Health approach for zoonoses management in an Indian context

Festus Asaaga*[1] ; Aditi Sriram [2] ; Irfan Shakeer*[1] ; Juliette Young [2] ; Bethan Purse
[1]Biodiversity / UK Centre for Ecology & Hydrology / United Kingdom, [2]NA/ Centre for Disease Dynamics, Economics & Policy/ India
[1]NA/ Ashoka Trust for Research in Ecology and the Environment/ India [2]NA/ Agroécologie, INRAE, Institut Agro, Univ. Bourgogne/ France

Introduction and Objectives or Purpose

The emergence and re-emergence of zoonoses in the last decade has brought to the fore of global health policy discourses the importance of advancing cross-sectoral collaboration as a plausible pathway for effective disease prevention and control. Within this purview, the One Health approach is widely recognised as a useful conceptual vehicle to foster collaborative relationships between institutional networks and actors operating at the human-animal- environmental interface. There is widespread recognition that the operationalisation of One Health approach is fraught with several challenges, particularly in LMICs. Despite this, there is dearth of empirical research on the institutionalisation processes and networks, which govern decision-making with respect to zoonotic diseases and how the vicissitudes of power dynamics in disease system shape outcomes in terms of cross-sectoral collaboration and ultimate disease control measures.

Methods

Through a qualitative network analysis of published sources on OneHealth stakeholders and multi-scale (national-state-district level) key-informant interviews (n=25) with policymakers, disease managers and experts, this paper characterises the institutional networks involved in the surveillance, control and management of zoonoses in India, and considers how issues of structure and agency vary across scales.

Results or Focus

A subsequent analysis of the stakeholder power within the human-animal-environment interface underscores the misconceptions of considering cross-sectoral collaboration under One Health as a technical matter involving the navigation of trade-offs and calls for renewed focus on the political aspects of One Health institutionalization.

Conclusion or Scope

Altogether our findings highlight the importance of prioritising the underlying institutional, socio-cultural barriers (including power-laden professional hierarchies) in a bid to overcome entrenched public-health centered, top-down zoonoses management hegemonies that limit cross-sectoral OneHealth implementation in practice.

Keywords: OneHealth; Zoonoses management; Cross-sectoral Collaboration; India

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Sharing of pathogens, resources and data
Abstract No: 14998

ONE HEALTH GENOMIC SURVIELLANCE IN AUSTRALIA: USING RETROSPECTIVE DATA TO SHAPE FUTURE EFFORTS

Anne Watt*[1] ; Max Cummins[2 3] ; Angeline Ferdinand[1] ; Steven Djordjevic[2 3] ; Benjamin Howden[1]
[1]Peter Doherty Institute for Infection & Immunity/ Microbiological Diagnostic Unit, Public Health Laboratory/ Australia, [2]University of Technology Sydney/ Australian Institute for Microbiology and Infection/ Australia, [3]University of Technology Sydney/ The Australian Centre for Genomic Epidemiological Microbiology/ Australia

Introduction and Objectives or Purpose

The increasing inclusion of One Health principles in public health agendas in Australia raises the urgent need for integrated national microbial genomic surveillance. However, the independent operation of human health, animal health and environmental sectors precludes simple harmonised and collaborative surveillance. Escherichia coli is a quintessential One Health organism that colonises and infects humans, animals and contaminates food and natural environments. We collated a retrospective cross-sectoral dataset to demonstrate the value of such a surveillance system and inform the development of a One Health national platform for E. coli genomic epidemiology.

Methods

A genomic dataset comprising 4,891 E. coli isolates from Australia were collated from in-house datasets and public databases. Predominantly of human origin, samples from livestock, companion animals, wild animals, environmental, and food sources were also represented. Following genome assembly and quality control protocols, in-silico genotypic and phylogenomic analyses were used to characterise the genomes and identify inter and intra-sectoral themes.

Results or Focus

This dataset provides a surrogate for, and allows us to examine the utility of, an established multisectoral One Health genomic surveillance system. Genotypic analysis provided baseline data on antimicrobial resistance gene carriage while phylogenetic analysis highlighted inter-source transmission events. While important insights have been gained, notable biases influence the wider applicability, such as the over-representation of clinical isolates. Limited sampling from environmental, food and waste sources potentially hinder a deeper understanding of associations concerning community acquired infections and comprehensive understanding of antimicrobial resistance, pathogen evolution and zoonoses. Addressing these knowledge gaps will enable formulation of a framework to improve prospective genomic surveillance.

Conclusion or Scope

The results of this study will contribute to the development of a multisectoral prospective national One Health surveillance system in Australia. Stakeholder engagement with a participatory approach will ensure the creation of a framework that it is of benefit to all, safeguarding a sustainable and healthy future.

Acknowledgement
The authors would like to thank all data contributors.

Keywords: Genomic Surveillance; E. coli; Genomic Epidemiology

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Sharing of pathogens, resources and data
Abstract No: 15005

The need for a Global One Health Intelligence System

Madhur Dhingra*[1] ; John Weaver[1] ; Andrea Capobianco Dondona[1] ; Andrea Carvelli[1] ; Daniel Donachie; Sharon Calvin[1] ; Fernanda Dorea[1] ; Charlotte Hicks; Fairouz Larfaoui[1] ; Jas Mantero[1]
[1]Animal Production and Health Division/ Food and Agriculture Organization of the United Nations/ Italy (Italia)

Introduction and Objectives or Purpose

The One Health Intelligence Scoping Study (OHISS), has been conducted by the Quadripartite alliance (FAO, UNEP, WHO, WOAH) to identify opportunities to strengthen operational One Health Intelligence (OHI), ensuring that all relevant intelligence information from the ecosystem, animal and human health is effectively shared to improve global health security.

Methods

OHISS conducted several foundational activities, including: (i) a literature review of OHI systems or networks available globally, and their contributing lessons (ii) an identification of OHI systems or best practices ongoing or under development at national level (iii) an assessment of OHI systems within the Quadripartite organizations (iv) a hazard analysis to provide a rapid and high-level illustration of the risk landscape.

Results or Focus

A set of requirements for global OHI were proposed, to design a technical framework for a joint Quadripartite approach to operational OHI– the Global One Health Intelligence System (GOHIS). Once implemented, GOHIS will connect, add value to existing data, and make specific outputs available for different objectives. In the modular architecture proposed, dedicated, fit-for-purpose applications will drive the connection to existing processes. The development of the framework, one application at a time, focusing on the operational needs of specific OHI activities, will provide a data-fed, needs-driven development approach. A flexible architecture is proposed to ensure that the system is viable in the long term, capable of evolving to changing stakeholder needs, and allows for collaborations with external initiatives or countries.

Conclusion or Scope

GOHIS aims to amplify existing OHI capabilities and facilitate their connection, rather than replacing or creating new silos of information. Improved technical harmonization of Quadripartite activities provides opportunities for improved collaboration on OHI and hence will contribute to current efforts to improve early warning to global health threats.

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Catherine McGillycuddy , Petra Muellner, Uli Muellner, Karl Schenkel, Dubranka Selenic Minet, Lauren Weatherdon, Emilie Perone, Paula Caceres-Soto, Keith Sumption

Keywords: Global One Health Intelligence; Early warning; Quadripartite; ecosystem, animal and human health; global health security

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Sharing of pathogens, resources and data
Abstract No: 15008

CHARACTERIZING THE RISK LANDSCAPE (RISKSCAPE) FOR GLOBAL ONE HEALTH INTELLIGENCE

Sharon Calvin*[1] ; Cat McGillycuddy[2] ; Andrea Carvelli[1] ; Fernanda Dorea[1] ; Jas Mantero[1] ; Petra Muellner[1] ; Uli Muellner[1] ; John Weaver[1] ; Madhur Dhingra[1]
[1]Animal Health/ Food and Agriculture Organization of the United Nations/ Italy (Italia), [2]Global Health Security/ UK Health Security Agency/ United Kingdom

Introduction and Objectives or Purpose
The scope of One Health (OH) is large and different sectors will approach it with different perspectives and priorities. The needs of OH intelligence users will relate to the hazards and associated risk questions they must address. While this may be specific to certain jurisdictions and sectors, a shared understanding of the riskscape of OH will provide a foundation to improve intersectoral exchange of information and build appropriate intelligence systems.

Methods
As part of the Quadripartite OH Intelligence Scoping Study (OHISS), key OH hazard categories were identified and analyzed using an all-hazards approach. Four example categories were then chosen from those considered a high priority by the Quadripartite organizations, and a multidisciplinary method was tested for mapping risk pathways and associated drivers, impacts, vulnerabilities, and critical monitoring points. In June 2022, 273 subject matter experts were gathered in a series of workshops to provide a rapid and high-level illustration of this method using risk bowtie diagrams.

Results or Focus
The Quadripartite identified 17 categories of OH hazards, including those that are biological, chemical/radiological, meteorological/hydrological, and environmental. Categories were broad enough to include unknown hazards. Bowtie diagrams were completed on four categories: 1) epidemic and emerging zoonotic diseases, 2) antimicrobial resistant micro-organisms, 3) contamination of water and soil from chemical fertilizers/pesticides, and 4) non-zoonotic animal diseases affecting food security. Many critical monitoring points (e.g., human/animal waste, wildlife health) and barrier breakdowns (e.g., lack of biosecurity, poor vaccination) were identified along the pathways, as well as links between bowties.

Conclusion or Scope
The ideal operational OH intelligence system needs to have the flexibility to support multiple different risk questions related to different types of hazards, including unknown hazards. Those looking to gather and use OH intelligence should follow a risk-based, iterative process of defining the problem and determining critical monitoring points and associated data sources.

Keywords: risk landscape; hazards; intelligence; bowtie; monitoring points

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Sharing of pathogens, resources and data
Abstract No: 15023

EXPERIENCES AND CHALLENGES IN DEVELOPING GENOMIC SURVEILLANCE, INFRASTRUCTURE AND DATA SHARING IN AN ACADEMIC SETTING FROM AN LMIC

Waqasuddin Khan*[1] ; Furqan Kabir[1] ; Samiah Kanwar[1] ; Fatima Aziz[1] ; Sehrish Muneer[1] ; Adil Kalam[1] ; Mehdia Ali[1] ; Nadia Ansari[1] ; Fyezah Jehan[1] ; Imran Nisar[1]
[1]Pediatrics and Child Health/ The Aga Khan University/ Pakistan (پاکستان)

Introduction and Objectives or Purpose

Next Generation Sequencing (NGS) is being used for genomic surveillance to identify the variants of SARS-CoV-2 circulating in communities at a particular time. Consistently accumulated genomic sequences on open-access global platforms are utilized by the research community to infer comparative analysis for effective genomic examination of the evolving SARS-CoV-2 strains. This is crucial to understand how SARS-CoV-2 variants may impact public health. Socioeconomic inequalities substantially impact the ability to sequence SARS-CoV-2 strains and undermine a developing country's pandemic preparedness, quickly and continuously. In particular, the LMICs face additional challenges in the establishment, maintenance, and expansion of genomic surveillance.

Methods

We present our experiences of establishing a genomic surveillance system at country's largest private hospital. Despite being at a leading health sciences research institute, we encountered major challenges while establishing technological frameworks in-house. These were related to the collection of standardized contextual data for SARS-CoV-2 samples, procurement of sequencing reagents and consumables, challenges with library preparation, sequencing, consensus genome generation and submission of high-quality SARS-CoV-2 genomes. CZ ID consensus genome pipeline was implemented to analyze sequenced samples. High-quality SARS-CoV-2 genomes were submitted to INSDC and GISAID. Phyllosurveillance map was deployed on Nextstrain to monitor the genomic epidemiology of SARS-CoV-2 in Pakistan.

Results or Focus

During the implementation of bioinformatics pipeline, several technical roadblocks ensued which were discussed and resolved by collaboration with the Public Health for Genomic Epidemiology (PHA4GE) consortium. All genome sequences were then deposited on open-access platforms in line with the best practices. Subsequently, these efforts culminated in deploying the first SARS-CoV-2 phyllosurveillance map of Pakistan as a Nextstrain build (updated after every 2-3 weeks).

Conclusion or Scope

Our experience offers lessons for the successful development of Genomic Surveillance Infrastructure in resource-limited settings struck by a pandemic.

Keywords: SARS CoV2, Metadata, Bioinformatics pipeline, Phylosurveillance, Open access

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Sharing of pathogens, resources and data
Abstract No: 15053

The One Health Surveillance Readiness and Requirements Tool (OHSRRT): Establishing the Groundwork for Successful Multi-sectoral Surveillance Systems

Karen Meidenbauer*[1] ; Shraddha Patel[1]
[1]Applied Physics Laboratory/ Johns Hopkins/ United States

Introduction and Objectives or Purpose

The Tripartite (WHO, WOAH, and FAO) recognizes that many determinants of health outcomes are outside of the human health sector. The implementation of coordinated multi-sectoral One Health surveillance solutions to support timely data sharing between sectors is essential to rapidly identify disease events. Data from human, animal, environmental and other relevant sectors should be included in a coordinated surveillance system to support disease prevention, detection, response and mitigation.

Methods

Challenges for countries seeking to adopt a coordinated One Health surveillance system include determining how to structure the proposed system and determining if quality data exists within the individual sectors that can be utilized for coordinated surveillance. Many countries also struggle to determine best methods to establish a system that is sustainable within their government organization and funding structure.

The One Health Surveillance Readiness and Requirements Tool (OHSRRT) was developed to determine country readiness and gather requirements to develop a One Health surveillance system based on defined critical success factors.

Results or Focus

The prototype of OHSRRT was successfully piloted in Uganda in July 2018. The tool includes a stakeholder engagement guide and questionnaire, data collection and characterization sheet, and a landscape assessment. The tool is structured so the results collected can be used to determine functional requirements for an operational One Health surveillance system.

Conclusion or Scope

Multi-sectoral information exchange is essential to build capacity, enhance situational awareness, and support Global Health Security while building trusted relationships and improving communication and collaboration across disciplines. Building upon the OHSRRT tool's initial success, and the recommendations and findings from the joint Tripartite Surveillance and Information Sharing Operational Tool (SISOT) working group, the Johns Hopkins Applied Physics Laboratory plans to evolve the existing OHSRRT prototype into an open-source, electronic tool that countries can easily access and utilize to help establish a functional coordinated surveillance solution.

Keywords: One Health, surveillance, zooneses, multi-sectoral, tripartite, requirements, data, system

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Sharing of pathogens, resources and data
Abstract No: 15113

Avian Influenza Surveillance in Live Bird Markets in the Lao People’s Democratic Republic – 2022

Leo Loth*[1] ; Phouvong Phommachanh[2] ; Phetlamphone Meeduangchanh[2] ; Vilakone Luangmanyvongkhao[2] ; Chanthana Senaphanh[2] ; Khaophone Saphangthong[2]
[1]Emergency Centre for Transboundary Animal Diseases (ECTAD) / Food and Agriculture Organization of the United Nations (FAO)/ Lao People’s Democ. Rep., [2]National Animal Health Laboratory/ Department of Livestock and Fisheries/ Lao People’s Democ. Rep.

Introduction and Objectives or Purpose

After the first human infection of avian influenza A subtype H5N6 virus was reported in Lao People’s Democratic Republic (PDR), in 2021, Avian Influenza (AI) surveillance in Live Bird Markets (LBM) was scaled up. The surveillance objectives were (1) to monitor subtypes and genetic characterization of AI viruses circulating across the country, (2) to detect potential zoonotic AI viruses, and (3) to identify potential pandemic viruses at the wildlife-livestock-human interface.

Methods

From January till July 2022, monthly sampling was conducted in 1 LBM in 12 high risk provinces of the 18 provinces in the Lao PDR. A total of 4,920 oropharyngeal swabs from poultry and environmental swabs were screened for influenza A viruses by real-time reverse-transcriptase polymerase chain reaction (rRT-PCR). Virus isolation was attempted on selected samples, of which hemagglutinin (HA) and neuraminidase (NA) genes were sequenced.

Results or Focus

During the sampling period, avian influenza A was detected in 8 of the 12 provinces. Subtype H5N1 was detected 88 times (prevalence 1.8%) in all 8 provinces. Subtype H9 was detected 26 times (prevalence 0.5%) in 2 provinces. Subtype H5N6 was diagnosed 6 times (prevalence 0.1%) in one province, bordering the People’s Republic of China. Virus isolation and sequencing is ongoing.

Conclusion or Scope

The prevalence of HPAI viruses detected in LBMs in Lao PDR was not significantly different from that previously reported in neighboring countries. Despite numerous attempts to reduce public health threat from HPAI H5N1 and H5N6, the viruses are maintained in the poultry population. To minimize the risk of HPAI in both poultry and humans, we recommend continuous monitoring of viral loads and viral strains in the environment, safer value and production chains, and research on more effective antigenic vaccines.

Acknowledgement

We hereby acknowledge the dedicated work of the animal health professionals collecting the diagnostic specimens each month.

Keywords: Avian Influenza ; Surveillance ; Live bird market ; Zoonotic ; Pandemic

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Sharing of pathogens, resources and data
Abstract No: 15161

Captive wildlife management survey in Vietnam, 2015 – 2021

Nhữ Thu[*1] ; Pawin Padungtod[1] ; Newman Scott[2]
[1]Emergency Center for Transboundary Animal Diseases/ Food and Agricultural Organization of the United Nations/ Vietnam (Việt Nam), [2]Regional Office for Asia and the Pacific/ Food and Agricultural Organization of the United Nations/ Thailand (□□□)

Introduction and Objectives or Purpose

In Vietnam, breeding and raising a wide range of wildlife species in captive wildlife facilities (CWFs) are common practices.

Methods

We conducted surveys and developed software to create a captive wildlife facilities management (CWFM) system. This database provides up-to-date information on the distribution of CWFs, the number of species, and individuals according to the level of protection outlined by the government and the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) categories

Results or Focus

CWFs were located in all provinces and regions, but differed in distribution, number of species and individual animals. The Mekong River Delta region recorded the highest number of CWFs (35.3%) and the highest number of animals (43.1%). In 2021, 95 species in the CITES Level 1 protection group were being raised at 1,824 CWFs; 137 species in 4,554 CWFs in Level 2; and 139 species in 1,499 CWFs in Level 3. The overall number of CWFs in 50 provinces decreased by a negative compound annual growth rate of -7.2%. It is crucial to continue to monitor the changing dynamics of CWFs to manage and trace animal origins, generate more evidence to understand and develop guidelines for breeding and raising practices, facilitate market connections for registered CWFs, reduce fraudulent practices, and assess the risk of disease transmission from zoonoses originating from wildlife to minimize public health impact.

Conclusion or Scope

We recommend periodic compulsory reporting of CWF activities using the CWFM system. We also suggest that information about CWFs needs to be shared publicly so that community members are aware of CWF activities and can participate in monitoring them.

Acknowledgement

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Keywords: Captive Wildlife farming; Management Software; Breeding; Vietnam

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Sharing of pathogens, resources and data
Abstract No: 15398

Investigating differences in drinking water quality among drinking water sources, and pathogen sharing(Campy, E.coli) in rural communities in Rwanda

Benjamin Ndayambaje*[1] ; Dan Snow[1] ; Arindam Malakar[1] ; Andromede Uwase[1] ; Elizabeth VanWormer[1]
[1]Natural Resources/ University of Nebraska/ United States

Introduction and Objectives or Purpose

Water contaminants including bacteria and heavy metals can adversely impact animal and human health. Heavy metals can be toxic to aquatic organisms and humans and can accumulate in food chains. Bacterial contamination from human and animal waste in water sources also poses health threats to humans and animals. To understand potential exposure to contaminants in drinking water sources, and shared pathogens. We examined water quality in drinking water sources, and investigated pathogen sharing at the human-animal-environment interface in rural communities of Rwanda.

Methods

We collected 47 water samples from these sources in Karongi District in August 2021, and January 2022. We measured basic water quality parameters (PH, temperature, conductivity, TDS, and salinity) in the field using a portable water quality meter. Using Colilert test kits, we assessed total coliform bacteria and E. coli in water. Heavy metals, nitrates, and trace metals were analyzed. Fecal and water sample culturing for shared zoonotic pathogens (Campylobacter, E.coli, and Salmonella).

Results or Focus

Non-metallic compounds and most trace metals across water sources were below WHO and U.S. Environmental Protection Agency potable water safety guideline values. However, iron and manganese levels exceeded recommended values across sites. High coliform bacteria detected in surface water samples (53.33%), followed by household water samples (20%). No fecal indicator bacteria were detected in public taps. 90% of livestock & water samples were positive for E.coli and Campy by culture.

Conclusion or Scope

Our results highlight the need to investigate the sources of high iron and manganese and DNA whole genome sequencing (WGS) from isolates to define population structures of shared pathogens. Furthermore, promote outreach on bacterial contamination in drinking water sources and home storage containers in rural Rwanda.

Acknowledgement

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Keywords: Water quality; trace metals; nitrate-nitrite; bacteria; E. coli; shared pathogens

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Systems for collecting clinical data
Abstract No: 14692

Diagnostic and reporting practices of human brucellosis in health facilities in Arusha region, northern Tanzania

AbdulHamid Lukambagire*[1 2] ; GABRIEL SHIRIMA[3] ; DAVIS SHAYO[4] ; COLETHA MATHEW[1] ; RICHARD YAPI[5] ; CHRISTOPHER KASANGA[1] ; BLANDINA MMBAGA[2] ; RUDOVICK KAZWALA[1] ; JO HALLIDAY[6]
[1]VETERINARY MEDICINE AND PUBLIC HEALTH/ SOKOINE UNIVERSITY OF AGRICULTURE/ Tanzania, United Republic of, [2]KILIMANJARO CLINICAL RESEARCH INSTITUTE/ KILIMANJARO CHRISTIAN MEDICAL CENTRE/ Tanzania, United Republic of, [3]LIFE SCIENCES AND BIOENGINEERING/ THE NELSON MANDELA AFRICAN INSTITUTION FOR SCIENCE AND TECHNOLOGY/ Tanzania, United Republic of, [4]EPIDEMIOLOGY, MONITORING AND EVALUATION/ REGIONAL MEDICAL OFFICE, ARUSHA/ Tanzania, United Republic of, [5]CENTRÉ D'ENTOMOLOGIE MÉDICALE ET VÉTÉRINAIRE/ UNIVERSITÉ ALASSANE OUATARRA/ Ivory Coast, [6]INSTITUTE OF BIODIVERSITY, ANIMAL HEALTH AND COMPARATIVE MEDICINE/ UNIVERSITY OF GLASGOW/ United Kingdom

Introduction and Objectives or Purpose

The One Health strategic plan in Tanzania highlights limited data on the burden of human brucellosis. Brucellosis is expected to be more prevalent in rural, pastoralist communities given the disease transmission patterns. This study sought to collect data on the testing and reporting practices of brucellosis at district health facilities in Arusha region, northern Tanzania.

Methods

A total of 24 health facilities in Arusha region were included in the study. Retrospective data were extracted from facility record logbooks for every month from January 2012 to May 2018. A standard questionnaire was administered to capture information on: test procurement, costs and performance at health facilities. Generalised linear mixed models were used to evaluate associations between brucellosis testing, brucellosis positivity and fixed variables, with a significant p value of ≤ 0.05.

Results or Focus

The probability of testing for brucellosis in health facilities was significantly associated with an interaction between the year of testing and facility ownership. The probability of brucellosis positivity among the tested population was significantly associated with the type of health facility, mainly hospitals and the district where testing was done. Five different Febrile Brucella Agglutination Test (FBAT) kits sourced from private distributors were used in all facilities. Testing protocols were highly variable across facilities as was kit use in different facilities, based on availability.

Conclusion or Scope

A range of commercially sourced FBAT kits were routinely used for brucellosis testing in all the health facilities included in the study. The performance and quality assurance of these tests was done using varied protocols in different facilities, complicating the comparison and interpretation of test results and case reporting. This study highlights the need for development of a standardised brucellosis testing scheme in Tanzania.

Keywords: Brucellosis, “health facilities”, diagnosis, reporting, Tanzania

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Systems for collecting clinical data
Abstract No: 14742

REALIZATION OF THE IMPACT OF FRONTLINE IN SERVICE APPLIED VETERINARY TRAINING IN HANDLING HEALTH ISSUES AT COMMUNITY LEVEL

Daniel Mdetele*[1] ; Makungu Selemani[1] ; Michael Madege
[1]Directorate of Veterinary Services/ Ministry of Livestock and Fisheries/ Tanzania, United Republic of

Introduction and Objectives or Purpose

Frontline In-Service Applied Veterinary Epidemiology Training (ISAVET) aiming at improving animal health workforce, is a four-month programme with 75% applied and 25% classroom training. Applied training is a home-based field work which has a three-month duration. The trainings lay foundation for theoretical and practical framework focusing on preparedness and response to diseases.

Methods

Tanzania rolled out three training cohorts, cohort II carried from 29th September and concluded on 31st March 2022, had total of 25 participants where 15 were men and 10 females coming from local government authorities, Veterinary investigation stations, animal health training institutions, Wildlife conservation authorities and Livestock research institutions. Field study topics chosen by trainee based on relevance to trainee's workstation after consultation with their line supervisors. Where, three Bacterial diseases, eleven viral diseases, two antimicrobial residues, four mycoplasmas, one Endoparasite and four Protozoan diseases topics were chosen.

Results or Focus

Studies showed, data collected at field level were useful in describing health issues. Analysis and interpretation of the disease information were helpful in taking informed decision on control measures, which was helpfully on early detection, rapid response and limited diseases spreading. Recorded anthrax case in human, livestock and wildlife, the seasonality of outbreaks and the distribution of diseases in wards of Ngorongoro district showed the potential of handling data in collaboration among different specialties as it has value for both human, animal, and environmental health. Evidence of drug residues in meat and milk, level of community awareness among livestock keepers was realized. Incidences of dog bites which has positive correlation with rabies were observed and indicated the need for information sharing among health sectors for proper follow up, case managements and designing measures that can be used to minimize human rabies.

Conclusion or Scope

It was learned that handling health issues holistically, using a One Health approach is inevitable in the current world.

Keywords: Frontline In-Service Applied Epidemiology Training

Topic: One Health Science (OHS): Pandemic Preparedness: detect, prevent and respond: Systems for collecting clinical data
Abstract No: 15289

Dynamic BAHIS – development of a flexible information management system for animal health in Bangladesh

Eric Brum*[1] ; Mikolaj E. Kundegorski[1] ; Taifur Rahman[1] ; Motahara Tasneem[1]
[1]Emergency Centre for Transboundary Animal Disease (ECTAD) / FAO/ Bangladesh (□□□□□□□□)

Introduction and Objectives or Purpose

Animal health epidemiology in Bangladesh is principally based on aggregate monthly reporting from upazila (sub-district) livestock offices. The aggregation of data at country level is an extensive process significantly reducing accuracy and timeliness. Paper-based reporting is not only a large burden for government veterinarians, but also provides little support in accessing and linking relevant data. Introduction of disease monitoring and surveillance programs requires additional reporting. Integrated reporting is not possible and data analysis is difficult.

Methods

The Bangladeshi Animal Health Intelligence System (BAHIS) was developed for the Department for Livestock Services in 2019 with funding from USAID and technical support from FAO’s Emergency Centre for Transboundary Animal Diseases. It consists of a desktop data-entry application and a server application for configuration, data access and visualizations. This modular open-source solution integrates with lab information management systems (LIMS) and enables Application Programming Interface (API), data exporting, and dashboarding. BAHIS allows deploying any number of modules, integrating with other solutions, including human health systems. Using the popular data platform KoBoToolbox and state-of-the-art application framework Electron.js, BAHIS builds on a wide expertise of the software community.

Results or Focus

BAHIS is designed around the concept of configurable projects allowing gradual movement of all reporting duties of veterinary services into the system without disrupting usual operations. Projects are built using multiple linked forms with connection to master data and external (e.g. laboratory) data. Currently, BAHIS provides patient registry, event investigation, biosecurity assessments, and environmental surveillance modules, demonstrating a wide range of applications. It is deployed in all 495 upazila livestock offices. Data gathered by BAHIS enabled the first identifications of both lumpy skin disease and goat pox in the country.

Conclusion or Scope

Many data gathering solutions are available, however BAHIS’ extendable configuration, focused on One Health, can uniquely accelerate digitalisation and integration of animal health surveillance in many countries.

Keywords: Animal health; BAHIS, Disease Monitoring and Surveillance

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Clinical, epidemiology and molecular drivers of disease susceptibility
Abstract No: 15072

SEROPREVALENCE OF Q FEVER AND ITS RISK FACTORS AMONG WORKERS ENGAGED IN LIVESTOCK HYGIENE AND QUARANTINE IN KOREA

Byung Chul Chun[*1] ; Soo Kwon Rho[2] ; Kyung Won Hwang[3] ; Soojin Kim[1] ; Ho Sung Lee[3] ; Trishna Kisiju[1] ; Jeong Ran Kwon[3] ; Een Suk Shin[3] ; Ji Yeon Lee[3] ; Byeong Cheol Gil[2]
[1]Department of Preventive Medicine/ Korea University College of Medicine/ Korea, Rep. (□□□□), [2]Division of Bacterial Disease/ Korea Disease Control and Prevention Agency/ Korea, Rep. (□□□□), [3]Division of Zoonotic and Vector Borne Disease Control/ Korea Disease Control and Prevention Agency/ Korea, Rep. (□□□□)

Introduction and Objectives or Purpose

This study was aimed to estimate the seroprevalence of Q fever and to identify the risk factors among workers who engaged in livestock hygiene and quarantine in Korea.

Methods

Of 879 workers in Korean Livestock Hygiene and Quarantine Center, 616 were selected in proportion to the number of local workers. From February to April 2022, total 616 sera of workers were collected, and Q fever antibodies (IgM and IgG in each Phase I and II) were measured by IFA method. For 80 cases with 1:32 or higher in the first test, the second sera were collected 3 weeks later. Presenting illness including medical history, detailed working history in farms and slaughterhouses, frequency of exposure to each livestock, and attitude & practice for Q fever prevention were also asked and surveyed at the same time. The diagnosis based on antibody titer followed the standards of Korean Disease Control and Prevention Agency

Results or Focus

Of the 616 workers tested for serum, 522 (84.7%) were male and 94 were female. The mean age was 36.7(±8.0) years. Confirmed acute Q fever cases were 4 (0.6%) by over 4 folds increasing of second titer. Suspected Q fever (acute or chronic) cases were 43 (7.0%). The seropositive rate was higher in males (8.7%) than in females (1.1%), and increased significantly with increasing age ($p<0.001$). The higher the contact frequency with goats, the higher the Q fever antibody positivity rate ($p=0.047$), but this was not the case with cattle and pigs. Multiple logistic regression shows the working history of goat slaughterhouse (OR=14.0, 95%: 4.6,42.7), treatment of by-products from aborted animals (OR=2.8, 95%CI 1.3, 5.8) were significantly associated with confirmed and suspected Q fever.

Conclusion or Scope

In Korea, continuous monitoring and epidemiological investigations of goat slaughterhouses and goat farms are required to prevent Q fever among livestock workers.

Keywords: zoonosis, Q fever, risk factors, seroepidemiology, surveillance

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Clinical, epidemiology and molecular drivers of disease susceptibility
Abstract No: 15306

Epidemiology and characteristics of Monkeypox cases and their contacts, Singapore

Andrew Phua*[1] ; Jayne Lim[1] ; Sae-Rom Chae[1] ; Kee Leng Chua[1] ; Christopher Neoh[1] ; Phoebe Lee[1] ; Cheryl Tang[1] ; Lin Cui[2] ; Marc Ho[1] ; Vernon Lee[1]
[1]Communicable Diseases Division/ Ministry of Health Singapore/ Singapore, [2]National Public Health Laboratory/ Ministry of Health Singapore/ Singapore

Introduction and Objectives or Purpose

This analysis describes the epidemiology and characteristics of the 2022 monkeypox outbreak and public health response in Singapore.

Methods

Suspect cases were notified to the Ministry of Health, assessed by infectious disease clinicians and confirmed by polymerase chain reaction. Symptomatic individuals were isolated, clinically managed, and positive samples sequenced. Contact tracing was performed to prevent further community transmission. Close contacts were quarantined and lower-risk contacts placed on phone surveillance.

Results or Focus

Singapore has recorded 15 monkeypox cases in the current outbreak, all men aged 25 to 59 years (median 36). Of these, 5 were imported and 10 were community cases with 9 being unlinked and one a close contact of another case. Of 60 close contacts quarantined, two turned positive. No lower-risk contacts became cases.

Time from symptom onset to laboratory confirmation ranged from 2 to 14 days (median 6). Presenting symptoms included rash (n=9; 60.0%), fever (n=4; 26.7%), headache (n=1; 6.7%), and anal discomfort (n=1; 6.7%). All cases eventually developed skin lesions and the majority developed fever (n=13; 73.3%). Less frequent symptoms included asthenia, lymphadenopathy, headache, and anal discomfort. All cases had at least one dermatologic or rectal specimen test positive and all were confirmed as West African clade; genome sequencing showed local case sequences were closely related.

Conclusion or Scope

In Singapore, all monkeypox cases were mild and occurred in men. Most community cases were epidemiologically unlinked, indicating possible transmission within the local community, and additional cases are expected over time.

This highlights the need for greater outreach and engagement of high-risk populations, focusing on case detection and disease prevention. Concurrently, awareness must be raised in the general and healthcare communities to better understand monkeypox and its spread, address stigmatization of high-risk groups while reinforcing that anyone can be infected.

Acknowledgement

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Keywords: monkeypox; epidemiology; risk factors; virus; contact tracing

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Clinical, epidemiology and molecular drivers of disease susceptibility
Abstract No: 15395

Epidemiological surveillance of influenza A viruses at pig slaughterhouses in Cambodia

Dina KOEUT[*1] ; Arata Hidano[*1] ; Sothyra Tum[1]
[1]General Directorate of Animal Health and Production/ National Animal Health and Production Research Institute/ Cambodia
(□□□□□□□)

Introduction and Objectives or Purpose

The emergence of Influenza A viruses (IAV) with pandemic potential from pig populations is of public health concern. A rapid transformation in the swine industry, international pig movements, and the presence of multispecies farming in Southeast Asian countries may heighten such risks. The 'PigFluCam+' project aims to better understand influenza dynamics at the swine-human interface. Here we present findings from ongoing slaughterhouse surveillance in Cambodia, where IAV circulation in pigs has been poorly characterized.

Methods

Fourteen slaughterhouses were recruited from four provinces in Cambodia, with monthly sampling since May 2020. Using a pre-calculated sample sizes for different pig batch sizes, nasal swab and serum samples were collected from randomly selected pigs from all batches (a group of pigs from the same origin) that were present at the time of each visit. Information regarding pig origin was obtained using structured questionnaires. Nasal swabs were tested by real-time PCR, and positive samples subjected to sequencing and phylogenetic analyses. Logistic regression was conducted to identify factors associated with batch-level positivity.

Results or Focus

As of February 2022, 56 (1.7%) out of 3,402 individual pigs, corresponding to 37 (6.2%) of 597 sampled batches, tested PCR-positive for IAV M-gene. Batches from smallholders were less likely to test positive compared to those from commercial farms (Odds ratio: 0.15, 95% CI: 0.02 – 0.81, $p = 0.04$). Findings from ongoing genetic and serological analyses will also be presented and discussed from a One Health perspective.

Conclusion or Scope

Pig sector intensification could have substantial impacts on IAV ecology and evolution in Cambodia. A cross-national and sector-wide approach, including engagement of commercial pig companies, is required to integrate IAV surveillance into routine activities in countries considered a hotspot for IAV circulation. We will share the lessons learnt through our One Health project, and discuss challenges and opportunities.

Acknowledgement
The project or effort depicted was or is sponsored by the United States Department of the Defense, Defense Threat Reduction Agency.

Keywords: One Health, Influenza A virus, swine, zoonosis, slaughterhouse surveillance

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 14797

SEROPOSITIVITY AND SEROCONVERSION TO ENDEMIC ZOONOTIC PATHOGENS AMONG MARKET VENDORS IN THE LAO PDR

Nilandone Senvanpan[1, 2] ; Vilayouth Phimolsarnnousith[1] ; Sayaphet Rattanavong[1] ; Stuart Blacksell[1, 3, 4] ; Mayfong Mayxay[1, 3, 5] ; Daniel Reinharz[6] ; Mathieu Pruvot[7] ; Paul Newton[1, 3, 4] ; Matthew Robinson[*1, 3]
[1]Microbiology Laboratory, Mahosot Hospital/ Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit (LOMWRU)/ Lao People's Democ. Rep., [2]./ Lao Tropical & Public Health Institute/ Lao People's Democ. Rep., [3]Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine/ University of Oxford/ United Kingdom, [4]Faculty of Tropical Medicine, Mahidol University/ Mahidol-Oxford Tropical Medicine Research Unit (MORU)/ Thailand (□□□), [5] Institute of Research and Education Development/ University of Health Sciences,/ Lao People's Democ. Rep., [6]Département de Médecine Sociale et Préventive/ Université Laval/ Canada, [7]./ Wildlife Conservation Society/ United States

Introduction and Objectives or Purpose

Interactions between humans and animals in the process of hunting, selling and consuming wild animal meat raises public health concerns, yet perception of health risks is often low. In Lao markets 23% of wildlife meat vendors said their produce could transmit disease, and 86% did not consider their health was at risk from their occupation. To understand the risks associated with exposure to wild animal meat, we conducted a one-year longitudinal serosurvey of market vendors to characterise the frequency of seropositivity and seroconversion to three endemic zoonotic bacterial pathogens in Laos: Rickettsia typhi, Orientia tsutsugamushi, and Leptospira spp.

Methods

150 vendors in three markets, selling vegetables, farmed meat or wildlife meat (and combinations thereof) consented to provide a blood sample up to three times between March 2017 and June 2018. Samples were tested for the presence of IgG against the target pathogens.

Results or Focus

Twenty individuals (13.3%; 95% CI: 8.5–20.1) sero-converted for at least one pathogen during 15 months. The prevalence of anti-Leptospira IgG across all occasions was 12.0% (95% CI: 7.5-18.6), whilst against R. typhi was 24% (95% CI: 17.6-31.8) using ELISA and 12.7% (95% CI: 8.0-19.3) by IFA. Anti-O. tsutsugamushi IgG prevalence was 20% (95% CI: 14.1-27.5) using ELISA and 12% (95% CI: 7.5-18.6) using IFA, and significantly differed between vendor types (p=0.047), with vegetable and wild meat vendors (21.7% and 27.3%, respectively) having higher prevalence than farmed meat vendors (8.5%).

Conclusion or Scope

A significant number of vendors seroconverted (~10% per year) for key endemic zoonotic bacterial pathogens, which are often detected in wild vertebrates. The pattern of seropositivity suggests links with what the vendor sells and warrants further investigation to identify transmission pathways between wildlife and humans, and the risk attributable to wildlife trade and consumption and different practices along the supply chain.

Keywords: wildlife; market; Rickettsia; Leptospira; scrub typhus; Laos

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 14798

Consumption of raw date palm sap and human exposure to bats in Bangladesh; the risk of Nipah

Ireen Shanta[*1] ; Stephen Luby[2] ; Kamal Hossain[1] ; James Heffelfinger[3] ; A. Marm Marm Kilpatrick[4] ; Najmul Haider[5] ; Syed Ahmed[1 6] ; Juliet Pulliam[7] ; Erin Kennedy[3] ; Emily Gurley[8]
[1]Infectious Diseases Division/ Icddr,b/ Bangladesh (□□□□□□□□), [2]Infectious Diseases/ Stanford University/ United States, [3]Division of Global Health Protection/ Centers for Disease Control and Prevention (CDC), Atlanta, USA/ United States, [4]Dept. Ecology & Evolutionary Biology/ University of California/ United States, [5]The Royal Veterinary College/ University of London/ United Kingdom, [6]Department of Epidemiology and Public Health/ Sylhet Agricultural University/ Bangladesh (□□□□□□□□), [7]South African DSI-NRF Centre of Excellence in Epidemiological Modelling and Analysis (SACEMA)/ Stellenbosch University/ South Africa, [8]Infectious Disease Epidemiology/ Johns Hopkins Bloomberg School of Public Health/ United States

Introduction and Objectives or Purpose

Pteropus medius fruit bats, the reservoir host of Nipah virus can directly contaminate the raw date palm sap with their saliva and urine. Fresh raw date palm sap consumption early in the morning in the winter is a common practice in rural Bangladesh. In 2011, the government of Bangladesh recommended that people not drink raw date palm sap. We aimed to assess the pattern, frequency and trend over time of raw date palm sap consumption and bat exposure in Bangladesh.

Methods

During 2013-2016, we conducted repeated cross-sectional surveys of a nationally representative sample of 10,002 households from 1,001 randomly selected urban and rural communities. Household members were interviewed about consumption of raw date palm sap and their exposures to bats in the past month.

Results or Focus

Throughout the country, 7% of respondents (7.5% in rural areas, 5% in urban areas) reported that at least one household member consumed raw date palm sap in the past month in the winter (November-April). The highest consumption was reported during January (16%) and February (12%). Date palm sap consumption was higher in Khulna (17%; p<0.001) and Rajshahi (13%; p<0.001) compared to other divisions (1.6%-5.6%). The proportion of households in which at least one person reported drinking raw date palm sap during 2013-14 was 11%, 5.5% during 2014-15 and 4.6% during 2015-16 (χ^2=52 for trend test, p<0.001); a decrease was observed in most divisions. Fifty-two percent of households reported observing bats close to their households and 0.5% reported direct contact with bats.

Conclusion or Scope

Date palm sap consumption decreased throughout Bangladesh from 2013 to 2016, although the reasons for the year-to-year changes in sap consumption remain poorly understood. This reduction would decrease the risk of human Nipah infections. Continued monitoring of sap consumption could guide interventions to further reduce risk, including targeting interventions toward those areas with highest consumption.

Keywords: Date palm sap,bats, Bangladesh, Nipah

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 14857

ASSESSING BEHAVIORAL RISK FACTORS DRIVING ZOONOTIC SPILLOVER AMONG HIGH-RISK POPULATIONS IN MYANMAR

Su Yadana[*1] ; Marc Valitutto[1 2] ; Ohnmar Aung[2] ; Lee-Ann Hayek[3] ; Jennifer Yu[2] ; Theingi Win Myat[4] ; Moh Moh Htun[4] ; Hlaing Myat Thu[4] ; Leilani Francisco[5] ; Suzan Murray[2] ; Htin Lin
[1]Program/ EcoHealth Alliance/ United States, [2]Global Health Program/ Smithsonian's National Zoological Park and Conservation Biology Institute/ United States, [3]National Museum of Natural History/ Smithsonian Institution/ United States, [4]Department of Medical Research/ Ministry of Health/ Myanmar (Burma) (□□□□□□), [5]Research/ Henry M. Jackson Foundation for the Advancement of Military Medicine/ United States

Introduction and Objectives or Purpose

Zoonotic disease outbreaks regularly occur within Myanmar and at its borders partly due to insufficient knowledge of behavioral risks, hindering participatory surveillance and reporting. To explore behavioral mechanisms of spillover in Myanmar, we aimed to 1) evaluate the details around animal contact and types of interaction, 2) assess the association between self-reported unusual symptoms (i.e., any illness or sickness that is not known or recognized in the community or diagnosed by medical providers) and animal contact activities, and 3) identify the potential risk factors including behavioral practices of self-reported illness.

Methods

Participants were enrolled at two community sites in Southern Myanmar (n = 708). A behavioral questionnaire was administered to understand participants' animal exposures, behaviors, and self-reported illnesses.

Results or Focus

Compared to participants who did not have any unusual symptoms, participants who had unusual symptoms in the past year were significantly more likely to have sold dead animals (OR = 13.6, 95% CI: 6.8-27.2), raised animals (OR = 3.4, 95% CI: 2.3-5.0) and eaten sick animals (OR = 4.4, 95% CI: 3.0- 6.4) in the same year. The association remained significant when adjusted for age, education and primary livelihood activities. Females had higher odds of reporting self-reported unusual symptoms than males, and those involved in crop production, animal production and other animal-involved occupations are more likely to have reported unusual illness than those in non-animal related occupations.

Conclusion or Scope

We reported the significant associations between self-reported unusual symptoms among participants and participants' animal contact activities as well as evidence of potential risk factors of self-reported unusual symptoms. The largest part of surveillance data in the region have been focusing on virological results while epidemiological and behavioral investigations have been lacking and poorly understood. Our findings contribute to much needed human behavioral data for targeted interventions and strategies to prevent zoonotic disease transmission at human-animal interfaces.

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 14891

Potential zoonotic bacteria identified from reticulated python (Malayopython reticulatus) and environmental samples in a python slaughterhouse and wet markets in Indonesia

Sugiyono Saputra[1] ; Herjuno Ari Nugroho[*1] ; Syaiful Rizal[1] ; Yohanna Yohanna[2] ; Amir Hamidy[2] ; Agmal Qodri[2] ; Sylvia Laatung[3] ; Patrick Mileto[4] ; Matthew Neave[4] ; Frank Y K Wong[4]
[1]Research Center for Applied Zoology/ National Research and Innovation Agency (BRIN)/ Indonesia, [2]Research Center for Biosystematics and Evolution/ National Research and Innovation Agency (BRIN)/ Indonesia, [3]Faculty of Animal Sciences/ Sam Ratulangi University/ Indonesia, [4]Australian Centre for Disease Preparadness (ACDP)/ The Commonwealth Scientific and Industrial Research Organisation (CSIRO)/ Australia

Introduction and Objectives or Purpose

The reticulated python (Malayopython reticulatus) is a non-venomous snake species in Indonesia harvested from the wild for their meat and skins. Poor sanitation and absent biosafety and biosecurity management in processing facilities and wet markets may expose handlers and the interface environments to transmission of zoonotic pathogens. Our study aims to identify zoonotically important bacterial pathogens by isolation as well as screen other potentially pathogenic bacteria through a metagenomic approach.

Methods

Animal and environmental sampling were conducted twice during 2019 in python slaughter houses in Palembang, South Sumatera and once in 2022 in several wet markets in North Sulawesi. A total 35 samples were collected, and 10 samples were positive using Salmonella Isolation Transwab (Medical Wire, UK).

Results or Focus

Out of this, seven bacterial isolates were respectively identified as Salmonella enterica subsp. enterica serovar Typhimurium (n=2), Salmonella enterica subsp. enterica serovar Typhi (n=1), Citrobacter freundii (n=1), Citrobacter europaeus (n=1), Citrobacter murliniae (n=1), and Edwardsiella hoshinae (n=1) based on 16S rRNA gene sequencing. The fourth sampling in several wet markets will be conducted in September 2022 and along with other samples obtained , the microbial community in python and environmental samples will be analysed through Nanopore 16S rDNA amplicon sequencing to screen for zoonotic bacteria.

Conclusion or Scope

Detecting the presence of pathogenically important bacteria will contribute to the understanding of the potential for transmission of zoonotic pathogens from wildlife, and inform on improved processing and food safety practices in the bushmeat trade.

Keywords: Zoonotic Bacteria; Reticulated Python; Bushmeat Trade; Zoonoses

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 14958

AN INVESTIGATION OF RISK FOR EXPOSURE TO ZOONOTIC VIRUSES AT THE HUMAN-ANIMAL INTERFACE IN RURAL INDIA

Ava Sullivan*[1] ; Harjeet Singh Maan[2] ; Shannon Ball[1] ; Emily Hagan[1] ; Simon Anthony[3] ; Leilani Fransisco [4] ; Rajesh Bhatia[1] ; Peter Daszak [1] ; Jonathan Epstein[1]
[1]Research/ EcoHealth Alliance/ United States, [2]Gandhi Medical College/ State Virology Laboratory/ India, [3]Department of Pathology, Microbiology Immunology / University of California at Davis/ United States, [4]Data Coordinating and Analysis Center / Henry M. Jackson Foundation/ United States

Introduction and Objectives or Purpose
India is a hotspot for emerging zoonoses. The USAID-funded PREDICT-2 project was designed to develop capacity in EID hotspots for detection of known and potentially zoonotic viruses in wildlife, livestock, and people, and to better characterize risk of human exposure to these viruses. Through targeted sampling for viruses with zoonotic potential at human-animal interfaces, the project sought to understand risks and drivers for transmission.

Methods
Sixty-five patients from the Primary Health Centre (PHC) in Maharajganj district, Uttar Pradesh, a northern state of India, were purposively enrolled, based on the clinical presentation of unexplained acute encephalitis, severe acute respiratory illness, or hemorrhagic fever. We collected clinical specimens (blood/nasal swab) and administered a pre-validated behavioral questionnaire. Specimens were tested using broadly reactive, family-level consensus PCR protocols for five viral groups: paramyxoviruses, filoviruses, coronaviruses, influenza viruses and flaviviruses, and the questionnaire collected information on demographics, health beliefs and behaviors, animal contact, and travel.

Results or Focus
We detected six known viruses from 129 samples of 65 participants, including Coronavirus 229E (6 individuals), Human parainfluenza virus 1 (11), 2 (3) and 3(6), Influenza A (22), and West Nile virus (3), including instances of co-infection. Participants commonly had contact with rodents, birds, dogs, cats, and bats in the home, and with cattle around the home. Participants reported seeking medical treatment from both hospitals and indigenous medicine, as well as uncertainty about the potential cause of their illness.

Conclusion or Scope
All viruses detected were known human pathogens, and though West Nile is zoonotic, our study was not designed to understand risk factors for vector-borne viruses. Nonetheless, this study sheds light on behaviors associated with animal contact in rural Uttar Pradesh that could increase the risk of exposure to zoonotic viruses. Better understanding exposures can inform future studies and intervention design, contributing to early detection of spillover and prevention of zoonotic disease threats.

Keywords: Emerging infectious diseases, India, zoonosis, human-animal interface, surveillance

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 14970

Longitudinal survey of potential zoonotic viruses from wildlife and environmental samples at high-risk human-animal interfaces in Indonesia

Sugiyono Saputra*[1] ; Herjuno A. Nugroho[1] ; Syaiful Rizal[1] ; Anik B. Dharmayanthi[2] ; Masrukhin Masrukhin[2] ; Meis J. Nangoy[3] ; Ancy Joseph[4] ; Patrick Mileto[4] ; Matthew Neave[4] ; Frank Y. K. Wong[4]
[1]Research Center for Applied Zoology/ National Research and Innovation Agency (BRIN)/ Indonesia, [2]Research Center for Biosystematics and Evolution/ National Research and Innovation Agency (BRIN)/ Indonesia, [3]Faculty of Animal Science/ Sam Ratulangi University/ Indonesia, [4]Australian Centre for Disease Preparedness (ACDP)/ The Commonwealth Scientific and Industrial Research Organisation (CSIRO)/ Australia

Introduction and Objectives or Purpose

Indonesia is recognised as one of the hotspot countries for emerging infectious diseases (EID) and potential zoonotic diseases (PZD). The intersection of trade and food value chain interactions at the livestock, wildlife and human interface is one of the main drivers of spillovers of zoonotic diseases. Bushmeat trade and encroachment of peri-urban development into wildlife habitats also contribute to increased risks. Many studies have linked wildlife to viral disease outbreaks in people at such interfaces, which also impact global animal and human health and national economic security. We describe here a pilot wildlife and eDNA EID surveillance study to investigate the viromic landscape and to monitor the risks of transmission and dissemination of potential EIDs and PZDs.

Methods

We conducted longitudinal wildlife and environmental sample surveys in several wet markets in North Sulawesi and bird markets in East Java, Indonesia. Sampling will be performed at the same sites four times per year with the second such sampling completed to date in 2022, the first year of study. Targeted wildlife have included bats, rodents, wild and domesticated pigs, and wild birds that have been traded live or freshly slaughtered for bushmeat or other trade value at such wet markets.

Results or Focus

A total >250 samples are currently underway for diagnostic screening to known pathogenic viruses, including animal coronavirus, influenza virus, lyssavirus, paramyxovirus and hantavirus using pan-family PCR assays. Additionally, representative sample subsets will analysed for the development of NGS-based, EID-targeted, metaviromic and bioinformatics pipelines.

Conclusion or Scope

This study will contribute to baseline viromic profiles of the targeted wildlife interface samples and inform strategies for early detection of viral pathogens and assessing risks for EIDs and PZDs, critical for strengthening global preparedness against future pandemics.

Acknowledgement

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Keywords: emerging infectious diseases (EID); potential zoonotic diseases (PZD); wildlife; human-animal interfaces; wet markets

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 15231

INVESTIGATING THE SALE OF BUSHMEAT ON SOCIAL MEDIA

Georgia Moloney *[1] ; Koffi Jules Gossé[2] ; Sery Gonedelé BI[2] ; Philippe Gaubert[3 4] ; Anne-Lise Chaber[1]
[1]School of Animal and Veterinary Sciences/ The University of Adelaide/ Australia, [2]Laboratoire de Biotechnologie, Agriculture et Valorisation des Ressources Biologiques, UFR Biosciences/ Université Félix Houphouët-Boigny d'Abidjan-Cocody/ Ivory Coast, [3]Laboratoire Evolution et Diversité Biologique (EDB), IRD/CNRS/UPS/ Université Toulouse III Paul Sabatier / France, [4]Centro Interdisciplinar de Investigação Marinha e Ambiental (CIIMAR)/ Universidade do Porto/ Portugal

Introduction and Objectives or Purpose
Social media provides a platform through which wildlife crime syndicates can readily access a global consumer-driven market. Whilst studies have uncovered the online trade in wildlife, the availability of bushmeat has not been assessed.

Methods
To investigate the sale of bushmeat online, 563 posts published between 2018 and 2022 from six West African Facebook pages were evaluated.

Results or Focus
Across 1,511 images and 18 videos, we visually identified 26 bushmeat species-level taxa including mammals (six Rodentia, five Artiodactyla, four Carnivora, two Lagomorpha, two Pholidota, one Primate, one Hyracoidea), aves (three Galliformes) and reptiles (two Squamata), predominately sold as smoked (63%) or fresh (30%) whole carcasses or portions. Whilst most of the species advertised were classified as Least Concern according to the IUCN Red List, four were Near Threatened, Vulnerable or Endangered. Species representing all three CITES Appendices were also identified. Additionally, some species recognised have previously been associated with infectious pathogens, such as coronaviruses. A number of taxa identified through images and text, including pangolin, crocodile, bats and hornbill, are protected from game hunting in West Africa, however their advertisement on the surface web indicates weak policy enforcement. Comparatively, when 'bushmeat' was input into the deep web browser Tor, no results were generated suggesting bushmeat vendors have no need to hide their activities online.

Conclusion or Scope
Our study provides a baseline for bushmeat trade activity through Facebook and encourages the need for further research into the role of social media in facilitating the internationalisation of the illegal wildlife trade, which could have devastating biodiversity and public health impacts. We highlight the accessibility endorsed by social media has revolutionised the sale of wildlife and expedites the exploitation of threatened species worldwide whilst enhancing the threat of zoonotic spillover events. We conclude that enhanced policy enforcement is essential locally and online to combat the sale of bushmeat.

Keywords: Biosecurity; Bushmeat; Conservation; Social media; Zoonotic spillover

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 15249

UNDERSTANDING LAND PRACTICES AND POTENTIAL EXPOSURES TO PLASMODIUM KNOWLESI AMONG OIL-PALM PLANTATION WORKERS IN LANGKAT DISTRICT, NORTH SUMATERA, INDONESIA

Ivana Alona*[1] ; Indo Siregar[1] ; Sunny Sanderson[2] ; Mossadeq Al Qorny[3] ; Inke Lubis*[1] ; Mat Grigg[2]
[1]Faculty of Medicine/ Universitas Sumatera Utara/ Indonesia, [2]School of Health Research/ Menzies/ Australia, [3]Faculty of Public Health/ Universitas Sumatera Utara/ Indonesia

Introduction and Objectives or Purpose

Agricultural expansion and deforestation have resulted in land use change linked to altered dynamics and distribution of malaria. P.knowlesi (Pk) is underestimated in Indonesia due to limited molecular diagnostic tools. A study related to agricultural and forest land types, expansion, and deforestation from satellite data suggested that the areas with reduced human malaria cases potentially increase the emergence of Pk. We aimed to understand the agricultural and land use practices in plantations and how this may increase the possible risks of Pk's vector exposure to communities in Salapian, a subdistrict in Langkat, North Sumatera, Indonesia.

Methods

This was a qualitative study conducted in Langkat from July-August 2022. The study included local farm or plantation workers. An open-ended semi-structured interview was conducted with each participant. We used triangulation of observative data, pictures, field notes, and transcribed interviews. The transcriptions were coded and analyzed using thematic analysis.

Results or Focus

Ten interviews were conducted in this study and 5 themes emerged. The oil plantation workers in Salapian perceive that oil palm commodity is more profitable than the others. Long tailed-macaques presence is normal in the community. The workers ignore mosquito protection while the exposure exists. Working on the plantation is a priority despite being ill. Community knowledge, treatment, and prevention of malaria are not adequate.

Conclusion or Scope

The altered agricultural land to oil palm plantation in Salapian is related to the existence and behavior of long-tailed macaques. Inadequate knowledge of malaria and ignoring mosquito bites prevention will increase the plantation workers' risks of experiencing the burden of malaria. Given the economic importance of the plantations and the abundance of Pk reservoir hosts, it is essential that forest, agricultural, macaque conservation, public health, and health departments collaborate to identify pertinent interventions to control Pk infection thoroughly.

Acknowledgement

This study was funded by Australian Center for International Agricultural Research (ACIAR)

Keywords: land use practice; P. knowlesi; macaques; mosquitos; oil-palm plantation

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 15357

Human animal contact to inform zoonotic disease risk across gradients of agricultural land use change in rural The Gambia

Aliyu Nuhu Ahmed[*1] ; Kris Murray[1] ; Takuya Iwamura[2] ; Kimberly Fornace[3]
[1]Disease Control and Elimination/ Medical Research Council Unit The Gambia/ Gambia, [2]Forest Ecosystems & Society/ Oregon State University/ United States, [3]Disease Control/ London School of Hygiene and Tropical Medicine/ United Kingdom

Introduction and Objectives or Purpose

My research focuses on better understanding which landscape and livelihood factors influence the likelihood of human-animal contact (zoonotic disease reserviours) events in rural communities in The Gambia. My hypothesis is that land use change for agriculture influences the likelihood of direct and indirect contact between humans and zoonotic disease reserviours.

Methods

My project integrates biological surveys of animal samples (wild and domestic), animal biodiversity analytics using soundscape analysis, and individual-level behavioral factors, and integrate landscape-level ecological factors to weigh risks to human health.

Results or Focus

Preliminary results of questionnaire interviews have revealed that human animal interaction patterns are frequent and diverse with about 22 different animals involved in these contacts. The majority, approximately 80% of respondents have at least one 1 contact with an animal reservoir within the past 1 month. The most prevalent wildlife contact was with monkeys 68% and the most frequent domestic animal contact reported is for cattle 50%. Most participants are farmers and forest activities were common in rural settings. About 70% of the household had livestock, mostly goats housed within the household with both people and livestock sharing the same surrounding. We also documented reports of domestic/livestock-wildlife contacts. Knowledge and attitude towards zoonoses was poor, with 44% reporting that they do not think they can get disease directly from animals. Use of personal protective clothing when handling animals or their products was also poor, with 52% having never worn any.

Conclusion or Scope

Results from the pilot study so far have demonstrated a frequent and diverse contact with a variety of zoonotic disease reserviours and a lack of adequate knowledge about zoonoses and precautionary measures. This result will guide the continued ongoing investigation of the project moving forward and identify areas of intervention.

Acknowledgement

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Keywords: Land use change, Human animal contact, Zoonoses, Disease risk

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 15359

Healthy lives from sustainable food systems - Lessons learnt from the 2022 Uppsala Health Summit

Karin Artursson*[1]

[1]Dept of Biomedical Sciences and Veterinary Public Health/ National Veterinary Institute and Swedish University of Agricultural Sciences/ Sweden (Sverige)

Introduction and Objectives or Purpose

To provide healthy food for everyone is a huge challenge. To produce the food in a sustainable way is even more challenging. That is why this year´s Uppsala Health Summit focus on “Healthy lives from sustainable food systems”. Unfortunately, the number of undernourished people in the world continues to increase, and the progress towards the Sustainable Development Goals is slow, ensuring access to safe, nutritious, and sufficient food for all people and eradicating all forms of malnutrition. Conflicts, climate shocks, low productivity and inefficient food supply chains push up the cost of nutritious foods and increase the unaffordability of healthy diets.

Methods

Uppsala Health Summit is a recurring international policy arena for dialogue on challenges for health and healthcare, and how we can overcome them. Personally invited decision-makers, opinion-makers and experts participate in active dialogue in thoroughly prepared workshops and plenum sessions.

Results or Focus

A Pre-conference report will be published during early autumn. This can be found at https://www.uppsalahealthsummit.se. During the 2022 Uppsala Health Summit, October 25-26, solutions for a more sustainable food production that produce healthy foods, affordable and accessible to everyone, will be presented and discussed with a One Health view. The outputs will be guidance and roadmaps to support such initiatives. Areas that will be highlighted during the summit are Sustainable animal production, Effects on health and Consumer behaviour. Food security and Food safety are among the aspects discussed. The perspective is From farm to fork!

Conclusion or Scope

Results and conclusions will be summarized in a Post conference report. The outcome will be presented at the meeting.

Keywords: Food security;Food safety;Health;Zoonoses;Antimicrobial resistance;

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 15370

Joint Risk Assessment Of Avian Influenza Subtype H9N2 Transmission In Live Bird Market And Layer Farms In East Java Province

Gunawan Setiaji*[1] ; Shinta Dewi[1] ; Nurhayati ; Ichwan Muslih ; Romadona Triada ; Achmad Badiq Qolbi Shober; Bambang Hari Rusiyanto; Endang W Wulandari; Farida C Zenal ; Ali R Arasyi
[1]Directorate of Veterinary Public Health/ Directorate General of Livestock and Animal Health Services, Ministry of Agriculture, Jakarta/ Indonesia

Introduction and Objectives or Purpose
Avian Influenza (AI) subtype H9N2 is an enzootic poultry disease with low pathogenicity, but important economic impact due to production loss. The virus caused 95 confirmed human cases in several countries from 1998-2021. The H9N2 virus was first detected in poultry in Indonesia in 2017, however no case was reported in human. The joint risk assessment (JRA) was conducted to determine the risk of H9N2 transmission from poultry to humans and develop risk mitigation measures.

Methods
This qualitative risk assessment was used the Tripartite Zoonosis Guide-JRA Operational Tool, and involved multisector across ministries and provincial government sectors

Results or Focus

The likelihood of at least one person in a live bird market or layer chicken farm in East Java province to be infected by AI subtype H9N2 through direct or indirect contact with poultry or the environment is HIGH and the impact is MINOR. The uncertainty of this assessment is LOW. The high likelihood was determined based on the large layer chicken population in East Java, the surveillance results which identified H9N2 subtype as the dominant virus found in 2019-2021 in poultry farm and live bird markets. The minor impact was determined based on the fact that H9N2 subtype virus can cause economic loss in poultry, particularly layer chickens, however there is no known human case in Indonesia and the fatality of any known human case is low. Reliable information on the virus is available, therefore the uncertainty level is low.

Conclusion or Scope

Based on the JRA results, existing surveillance activities should be enhanced through integrated surveillance and recommended risk mitigation measures including biosecurity implementation in farms, collectors, and live bird market, vaccination in layer farms and risk communication along poultry market chain to reduce transmission risks between human and poultry. This flag the importance of one health joint risk assessment for zoonotic diseases interface.

Keywords: joint risk assessment;Avian Influenza; East Java

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Drivers of spillover and reverse zoonosis
Abstract No: 15384

Canine rabies vaccination and community sensitization in Tororo: A demonstration of the efficacy of One Health approaches

Elicana Nduhuura*[1] ; Agwe Ahmed[2] ; Muyomba Robert[3] ; Peninah Nsamba[4]
[1]Community Health/ Mbarara University of Science and Technology/ Uganda, [2]Humanities and Social Science/ Makerere University/ Uganda, [3]District Veterinary Offices/ Tororo District Local Government/ Uganda, [4]School of Public Health/ Makerere University/ Uganda

Introduction and Objectives or Purpose

In Uganda, rabies (caused by lyssavirus family) is an endemic but fatal zoonotic disease which is notifiable In Tororo district; a multi-disciplinary team of university students conducted a rapid community assessment, and prioritized dog-bites as a public health challenge in the community. This prompted students together with the community to conduct rabies sensitization and canine vaccination exercise.

To demonstrate significance of collaborative multidisciplinary health interventions through vaccination of dogs and cats

Methods

Mobilization of the community with the social scientists taking lead; veterinary students were actively participating in vaccination of the pets using vaccine provided by government at no cost, while sensitisation messages were prepared with scientific inputs from medical, veterinarian and wildlife students.. During home visits, perceptions of canine rabies vaccination by the community were sought.

Results or Focus

Factors affecting previous vaccination efforts included limited household coverage attributed to ineffective mobilization, few veterinarians, or poor compliance of the community due to ignorance and political beliefs. However, during this activity, three vaccination sites Ojolowendo, Kajarao and Totokidwe within the above parishes a total of 103 dogs and 10 cats were vaccinated. During the sensitization, community members raised concerns about rabies disease such as (i) Why rabies vaccination is not prioritized to humans (ii) Whether the pets would be able to get a second dose. Gender aspects that arose during the discussions were that male children took pets for vaccination and were responsible for their care

Conclusion or Scope

Community engagement by a multi-disciplinary team of students improved community response rabies disease control in Tororo district, as well as promoting teamwork, leadership. We also addressed dangerous practices such as game hunting, consumption of poisoned birds and unhygienic wound management from dog bites

Acknowledgement

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African One Health University Network

Tororo District Local Government

Keywords: Rabies;vaccination;commuinity; multidisciplinary;intervention

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Molecular epidemiology and evolution
Abstract No: 14852

Enzootic circulation of potentially zoonotic highly pathogenic avian influenza viruses in wild birds in Germany

Anne Pohlmann*[1] ; Jacqueline King[1] ; Christian Grund[1] ; Martin Beer[1] ; Timm Harder[1]
[1]Institute of Diagnostic Virology (IVD)/ Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health (FLI)/ Germany (Deutschland)

Introduction and Objectives or Purpose

Highly pathogenic avian influenza viruses (HPAIV) of clade 2.3.4.4b of the H5 goose/Guangdong lineage have repeatedly emerged in Germany since 2016. The 2020-2021 and 2021-2022 HPAIV winter seasons exceeded previously recorded epizootics in Germany in terms of number of avian cases, genetic diversity, and duration.

Methods

Genome analyses were used to map the routes of introduction of HPAIV H5 to Germany, to track the spread of viruses through Europe and onward to North America. Special focus was put on HPAIV H5 detected in scavenging terrestrial mammalian carnivores infected presumably by ingesting infected avian prey.

Results or Focus

Between October 2020-2022 six different subtypes (H5N1, H5N2, H5N3, H5N4, H5N5, H5N8) were detected as of July 2022. They show different segment composition and indicate several incursions into Germany and an unprecedented capability to reassort. In addition, the year-round detection of these viruses signals the risk of an enzootic situation as infections with HPAIV were also reported in wild birds and sea mammals during the summer of 2021 and HPAIV H5N1 infections were detected in wild birds in summer 2022 causing devastating losses particularly in colony-breeding sea birds.

The potential zoonotic properties of circulating strains became apparent when human cases infected with H5N8 viruses in Russia in 2020 and H5N1 viruses in England and the United States in 2022, respectively, were reported after contact to infected poultry. Contingency to infect mammalian species is also emphasized by cases in terrestrial carnivores in Germany including several harbor seals in August 2021, and H5-infected foxes and martens throughout 2022.

Conclusion or Scope

The trend of a genetically flexible HPAIV H5 strain evolving into multiple genotypes is continued unbrokenly. The current developments bear the risk of an enzootic HPAIV situation with severe consequences for avian wildlife, significantly increased and extended incursion risks for poultry holdings, and the looming risk of zoonotic virus emergence.

Keywords: HPAIV; Influenza;

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Molecular epidemiology and evolution
Abstract No: 14866

Characterisation Of Salmonella Weltervreden Isolates From Humans, Food, Wild Birds And Environment In Singapore

Yen Ching Lim*[1] ; Wei Ching Khor[1] ; Khar Hui Ong[1] ; Swaine Chen[2] ; Wei Ling Tan[1] ; Joanne Chan[1] ; Angela Li[1] ; Kyaw Thu Aung[1]
[1]National Centre for Food Science/ Singapore Food Agency/ Singapore, [2]Laboratory of Bacterial Genomics/ Genome Institute of Singapore/ Singapore

Introduction and Objectives or Purpose

Salmonella Weltevreden is among the top five serovars contributing to human salmonellosis in Singapore and is predominantly found in Southeast Asia. As S. Weltevreden is commonly reported in seafood and aquatic environment, the relatively high consumption of fish and seafood in Singapore may pose food safety concerns. To better understand the molecular epidemiology and characterize the antimicrobial resistance of S. Weltevreden isolates in Singapore, we performed whole genome sequencing (WGS) and antimicrobial susceptibility testing on the isolates collected from humans, food chain, and wild birds representing a part of the larger environment.

Methods

Eighty-nine S. Weltevreden isolates were collected from human, food chain and wild birds between 2010 and 2017. WGS was performed on the isolates, followed by bioinformatic analyses for serotype, MLST, and resistance genes predictions. To obtain the phenotypic antimicrobial resistance profile, antimicrobial susceptibility testing was performed against 31 antimicrobials, belonging to 13 antimicrobial classes.

Results or Focus

All 89 S. Weltervreden isolates belonged to ST365, attributing to 56.2% from humans, 30.3% from food (including chicken and seafood), 2.2% from farm and slaughterhouse and 4.4% from wild birds. Out of 89 isolates, only 6 (6.74%) were resistant to at least one antimicrobial, and 4 demonstrating resistance to at least three antimicrobials. Relatively higher resistance rate was seen against Tetracycline (4/6,66.67%), while 1 food isolate was resistant against Colistin. Genomics analysis showed that 6 isolates carried at least 1 antimicrobial resistant gene, with Beta-lactam and folate pathway antagonist resistant genes each detected in 3 isolates. WGS analysis revealed the closed relatedness of selected isolates from different sample types.

Conclusion or Scope

Although the relative low occurrence of antimicrobial resistance suggests the viability of antimicrobial treatment options for salmonellosis related to S. Weltevreden, the high prevalence of this serovar in various sources highlights the need to constantly monitor S. Weltevreden in various sources.

Acknowledgement

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Keywords: Salmonella Weltevreden; antimicrobial resistance; molecular epidemiology; human; food chain

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Molecular epidemiology and evolution
Abstract No: 14996

Evolutionary history and phylogeographic analysis of dog rabies virus in Cameroon

Jocelyne Noel Sowe Wobessi*[1] ; Richard Njouom[1] ; Serge Sadeuh-Mba[1] ; Jean-Luc Bailly[2]
[1]Virology/ Centre Pasteur du Cameroun/ Cameroon (Cameroun), [2]Laboratoire Génome Micro-organisme et Environnement (LMGE)/ Universite de Clermont Auvergne/ France

Introduction and Objectives or Purpose

Rabies is a widespread zoonosis that estimated 60,000 human deaths each year. Nearly all human rabies cases are caused by bites from a rabid dog. The etiological agent of rabies, the Rabies Lyssavirus (RABV) belongs to the genus Lyssavirus and family Rhabdoviridae. RABV has been repeatedly detected and reported in dog populations in Cameroon with a co-circulation of the sub-clades Africa 1a and 1b of the Cosmopolitan clade as well as the Africa-2 clade which is less prevalent. Phylodynamic studies coupled with epidemiological data have been shown to provide a better understanding of the factors that promote the spread and maintenance of rabies virus and an evaluation of the impact of different intervention measures. However, no study has been conducted to investigate the origin of the RABV isolates detected in dog populations in Cameroon and the dynamics of the spread of the canine rabies virus in the regions of Cameroon. The aim of this study was to determine the evolutionary history of RABV from the N, P, M and G genes.

Methods

The time-scale Markov chain Monte Carlo (MCMC) phylogenetic tree was estimated with BEAST 1.10.4 software, using the General Time Reversible model with proportion of invariable sites plus gamma-distributed rate heterogeneity (GTR+G+I), and an uncorrelated relaxed molecular clock. The latitude and longitude of the detected isolates was used to perform phylogeographic analyses, in combination with the phylogeny of the different sequences, to estimate the spread of RABV in Cameroon.

Results or Focus

Overall, phylogeographic analyses showed that the city of Yaoundé was the main focus of RABV infection and that RABV spread between cities near and far in Cameroon through the movement of infected dogs, facilitated by human movement.

Conclusion or Scope

These results are very important as they inform on the need to implement appropriate and effective control and elimination measures.

Acknowledgement

Not applicable

Keywords: Rabies virus, Dog, phylodynamic, phylogeographic

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Molecular epidemiology and evolution
Abstract No: 15030

SPIKE-INDEPENDENT INFECTION OF HUMAN CORONAVIRUS 229E IN BAT CELLS

Marcus Mah[1] ; Martin Linster[1] ; Dolyce Low[*1] ; Yan Zhuang[1] ; Firdaus Samsudin[2] ; Foong Ying Wong[1] ; Peter Bond[2] ; Ian Mendenhall[1 3] ; Yvonne Su[1] ; Gavin Smith[1 4 3 5]
[1]Emerging Infectious Diseases/ Duke-NUS Medical School/ Singapore, [2]Bioinformatics Institute/ Agency for Science, Technology and Research (A*STAR)/ Singapore, [3]SingHealth Duke-NUS Global Health Institute/ Duke-NUS Medical School/ Singapore, [4]Centre for Outbreak Preparedness/ Duke-NUS Medical School/ Singapore, [5]Duke Global Health Institute/ Duke University/ United States

Introduction and Objectives or Purpose

The order Chiroptera (bats) is a reservoir for many viruses. Bats harbor coronaviruses closely related and ancestral to SARS-CoV, MERS-CoV, and SARS-CoV-2. Similarly, human coronavirus 229E diverged from 229E-like bat viruses about 130 years ago. Little is known about virus adaptation during cross-species transmission of coronaviruses from bats to humans, partly impeded by the lack of relevant bat cell lines to support this research.

Methods

To identify possible evolutionary pathways at the bat-human interface, we conducted “reverse evolution” experiments by serially passaging 229E in Rhinolophus lepidus kidney (Rhileki) cell line established in our laboratory. The aim was to adapt human 229E isolates to the primordial bat host and determine mutations that allowed ancestral 229E prior to diverge, jump species barriers and adapt to humans. We passaged six clinical isolates and performed next-generation sequencing (NGS).

Results or Focus

Surprisingly, we observed extensive deletions in the spike and ORF4 regions that halt expression of the spike protein, while observing sustained replication throughout ten passages in Rhileki cells. The deletions ranged from 324–3,656 nt and were present in five out of six tested isolates and appeared in two isolates as early as passage one. The consensus of the truncated viruses comprised ≥97.4% of the NGS reads. We confirmed loss of spike protein at intermediary passages in western blot analyses.

Conclusion or Scope

The results suggest spike-independent replication of coronaviruses as an alternative mechanism of infection in the absence of a spike-receptor match that may be exclusive to bat cells. A non-specific mode of entry could be a common feature in bats that might precede the acquisition of a spike gene for canonical spike-receptor interaction, thereby facilitating cross-species transmission.

Acknowledgement

Jayanthi Jayakumar

Keywords: evolution; pandemic; receptor usage; zoonotic; spike

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Molecular epidemiology and evolution
Abstract No: 15241

First Molecular Detection of Influenza D virus in Cattle from Commercial farm in Nigeria, Sub-Saharan Africa

AbdulAzeez Anjorin*[1] ; Gideon Moronkeji[1] ; Omolade Maiyegun[1] ; Kabiru Akinyemi[1]
[1]Microbiology (Virology Research)/ Lagos State University/ Nigeria

Introduction and Objectives or Purpose

Although influenza D virus (IDV) was first detected in pigs in the US in April 2011, further studies have demonstrated that IDV is more prevalent in cattle than in swine. But in Nigeria, no work has been done on IDV despite the manifestation of influenza-like illness in cattle. Therefore, this study carried out molecular surveillance of IDV in sick and healthy cattle in Lagos.

Methods

Prospective epidemiological surveillance was initiated in Kara, a large commercial farm where animals of different ages in open pens are reared, sold, and butchered under poor hygienic conditions without adequate biosecurity measures. A total of 80 nasopharyngeal swabs were collected between October and November 2021. The samples were extracted using RNA purification kit (NIMR, Nigeria). RNA extracts were amplified following a two-step PCR with an initial cDNA conversion using FIREScript RT cDNA synthesis kit (Solis Biodyne, Estonia), followed by PCR amplification using OneTaq Quick-load 2x master-mix with standard buffer (NEB, UK) in a Rotor-Gene thermocycler (Qiagen, Germany). Amplicons were detected using a 1.5% Gel electrophoresis.

Results or Focus

IDV was detected in 26/80 (32.5%) cattle from a commercial farm. Sick animals recorded a higher 65% (17/26) molecular prevalence compared to the healthy population with 34.6% (9/26). Based on clinical presentations, the highest molecular prevalence of 65% (17/26) was detected in cattle having nausea and diarrhoea, while animals with typical clinical symptoms of diarrhoea-only recorded 57.69% (15/26), and those with nausea-only had 7.69% (2/26). Age prevalence showed 62.23% (18/26) highest detection in cattle of 4 years old, followed by 23.07% (6/26) in 5years old, while the lowest 7.69% (2/26) was recorded in 3 years old.

Conclusion or Scope

This study showed the first molecular detection of IDV in Nigeria and West Africa sub-region to the best of our knowledge. It underscores the need for continuous surveillance of IDV at the animal-human interface.

Keywords: Influenza D virus (IDV); molecular surveillance; PCR; Cattle; One health

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Molecular epidemiology and evolution
Abstract No: 15283

High proportion of Plasmodium knowlesi infection in Mursala Island, North Sumatra, Indonesia

Inke Nadia Diniyanti Lubis*[1] ; Ranti Permatasari[2] ; Lambok Siahaan[3] ; Rycha Dwi Syafutri[1] ; Monica Nadya Sinambela[1] ; Irbah Rea Alvieda Nainggolan[1] ; Meliani [2] ; Matthew Grigg[4]
[1]Pediatrics/ Universitas Sumatera Utara/ Indonesia, [2]Clinical Pathology/ Universitas Sumatera Utara/ Indonesia, [3]Parasitology/ Universitas Sumatera Utara/ Indonesia, [4]NA/ Menzies School of Health Research/ Australia

Introduction and Objectives or Purpose

There has been an increase in incidence of the zoonotic malaria in Southeast Asia, and in Indonesia, it has been reported in Sumatra and Kalimantan. The knowlesi infection has most commonly been misdiagnosed by microscopy as either P. falciparum or P. vivax, and increased reported numbers of cases of either species affecting the assessment of malaria control programs to eliminate human malaria. We aimed to determine the incidence of zonotic malaria in Mursala island, in the southern part of the North Sumatra province.

Methods

A cross-sectional survey on healthy population of Mursala island was conducted in September 2019. Finger-pricked blood was collected for rapid diagnostic test as point-of-care testing, as well as for blood slide, and into DNA/RNA shield tube for microscopy examination and molecular analysis at Universitas Sumatera Utara. Sensitive and specific molecular methods to detect human and zoonotic malaria were performed. Clinical, demographic and epidemiological data were collected.

Results or Focus

Sixty-four individuals were screened, of them nine were positive for malaria. None of the RDTs and microscopy results were positive for malaria. But using highly sensitive molecular methods, one case was detected as P. vivax, five as P. knowlesi, two mixed infections of P. vivax and P. knowlesi, and one could not be speciated.

Conclusion or Scope

Ultra-sensitive PCR detection method is necessary to detect knowlesi malaria. Further understanding on knowlesi malaria transmission including the the behaviour of the vectors and macaque hosts and the risk factors for individual are required, to inform the Indonesian NMCP and to enable tailored control measures to all malaria species.

Keywords: Malaria, Plasmodium knowlesi, Plasmodium vivax, Indonesia

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Molecular epidemiology and evolution
Abstract No: 15318

Understanding Zoonotic Disease Emergence From Bats in Vietnam

My Ngoc Kha*[1] ; Truong Son Nguyen[2] ; Dinh Thong Vu[2] ; Hongying Li[3] ; Marc Valitutto[3] ; Kendra Phelps[3] ; Cadhla Firth[3] ; Peter Daszak[3] ; Guy E. Thwaite[1 4] ; Thanh Duy Pham[1 4]
[1]Molecular Epidemiology/ Oxford University Clinical Research Unit/ Vietnam (Việt Nam), [2]Animal/ Institute of Ecology and Biological Resources/ Vietnam (Việt Nam), [3]NA/ EcoHealth Alliance/ United States, [4]Centre for Tropical Medicine and Global Health/ Oxford University/ United Kingdom

Introduction and Objectives or Purpose

Vietnam is located on the eastern margin of the Indochinese peninsula, with high mountains and limestone karsts spreading from the north to the south, coastal islands, and complex river systems, which combine to create habitats conducive to a high diversity of bat species. The emergence of SARS-CoV-2 has recently highlighted the need for research into the geographic and taxonomic distribution of bats and bat-borne viruses in the Southeast Asian region.

The proposed project has two objectives: (1) to characterize bat diversity in different ecological settings in Northern Vietnam; and (2) to identify coronaviruses with known or predicted zoonotic potential.

Methods

We sampled bats from the limestone mountain region in northern Vietnam ~120-160km from Yunnan province in China, which is known to contain relatives of SARS-CoV and SARS-CoV-2. Bat species were identified using traditional morphological techniques in combination with polymerase chain reaction (PCR)-based barcoding. Coronavirus detection was performed on fecal samples and/or rectal swabs using conventional PCR-based assays, followed by Sanger sequencing.

Results or Focus

A total of 346 bats were sampled from 2 provinces in Vietnam: Vinh Phuc and Tuyen Quang. A total of 18 bat species have been identified. Coronaviruses were found in ~30% of bats tested, with Rhinolophus spp. (~61%) and Hipposideros spp. (~30%), most frequently associated with CoV presence. Phylogenetic analysis indicates a high diversity of CoVs circulating in bat populations in Northern Viet Nam, some of which are closely related to those known to cause disease in domestic animals, including pigs.

Conclusion or Scope

Despite the small sample set analyzed, the identification of a range of new and known CoVs in bats inhabiting the limestone karst region of northern Vietnam suggests that these populations may harbor a rich diversity of coronaviruses. Further work will be required to assess the risk of zoonotic and enzootic disease emergence associated with CoVs circulating in this region.

Keywords: CoV; Zoonotic Diseases; Bats in Vietnam

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Pathogenesis and modes of transmission
Abstract No: 14684

Role of Poultry Trade Network on the Avian Influenza A Viruses Environmental Contamination Patterns at Live Bird Markets, Dhaka, Bangladesh

Shovon Chakma*[1] [2] ; Muzaffar G Osmani[3] ; Philip P Mshelbwala[1] ; Mohammed Abdus Samad[4] ; Eric Brum; Ricardo J. Soares Magalhães
[1]Spatial Epidemiology Laboratory, School of Veterinary Science/ The University of Queensland/ Australia, [2]Emergency Centre for Transboundary Animal Diseases (ECTAD)/ Food and Agriculture Organization of the United Nations/ Bangladesh (□□□□□□□□□), [3]Department of Livestock Services, Dhaka, Bangladesh/ Ministry of Fisheries and Livestock, Government of Bangladesh/ Bangladesh (□□□□□□□□□), [4]Bangladesh Livestock Research Institute/ Ministry of Fisheries and Livestock, Government of Bangladesh/ Bangladesh (□□□□□□□□□)

Introduction and Objectives or Purpose

An increased probability of environmental contamination with avian influenza A viruses at live bird markets (LBMs) in Dhaka's metropolitan presumably linked to the network of poultry movements in Bangladesh. This study aimed to characterize the Dhaka metropolitan area's LBM poultry trade network by the source of poultry purchase and quantify the association between the selected market characteristics and year-long avian influenza A viruses (H5 and H9) environmental contamination patterns at the LBMs of Dhaka metropolitan, Bangladesh.

Methods

We screened the market-level source of poultry purchase data of 108 Dhaka metropolitan area LBMs (collected in Jan-Mar 2016) and summarized the characteristics of the market trade network, such as degree centrality, closeness centrality and betweenness centrality, k-core. We performed univariable multinomial logistic regression to quantify the association between the selected market characteristics and the year-round (Jan-Dec 2016) market level avian influenza A(H5H9) environmental contamination patterns.

Results or Focus

The poultry trade networks (market-market, market-district, district-district) of Dhaka metropolitan area LBMs are highly connected within Dhaka and widely connected across the country (Figure 1). The LBM-level avian influenza A(H5) and A(H9) environmental contamination patterns were associated with risk factors such as market type, market location, season, and several estimates of LBM network connectivity.

Conclusion or Scope

This study showed the need for routine evaluation of LBM-based avian influenza surveillance by the market-level source of poultry purchase network data to improve avian influenza A viruses detection system for humans and animals population, and contamination in the environment.

Acknowledgement

We are thankful to the Department of Livestock Services, Bangladesh Livestock Research Institute, Emergency Centre for Transboundary Animal Diseases of FAO, Dhaka North and South City Corporations for providing support in the Dhaka LBM census and AIV surveillance activities. Surveillance in LBM was funded by the USAID through FAO. The University of Queensland provided PhD scholarship to Shovon Chakma.

Keywords: live bird market; network analysis; avian influenza; environmental contamination; Bangladesh

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Pathogenesis and modes of transmission
Abstract No: 14688

Evidence of Exposure to NIPAH Virus among Domestic and Peridomestic Animals Living in Human Outbreak Sites in Bangladesh

Ausraful Islam*[1] ; CL Deborah[2] ; MZ Rahman[3] ; SU Khan[4] ; JH Epstein[5] ; P Daszak[6] ; SP Luby[7] ; JM Montgomery[8] ; JD Klena[9] ; ES Gurley[10]

[1]PEI, IDD, icddr,b/ Ausraful Islam/ Bangladesh (□□□□□□□□□), [2]Centers for Disease Control and Prevention/ CL Deborah/ United States, [3]Centers for Disease Control and Prevention/ MZ Rahman/ Bangladesh (□□□□□□□□□), [4]BlueDot/ SU Khan/ Canada, [5]EcoHealth Alliance/ JH Epstein/ United States, [6]EcoHealth Alliance/ P Daszak/ United States, [7]Department of Medicine, Division of Infectious Diseases & Geographic Medicine, Stanford University/ SP Luby/ United States, [8]Centers for Disease Control and Prevention/ JM Montgomery/ United States, [9]Centers for Disease Control and Prevention/ JD Klena/ United States, [10]Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health/ ES Gurley/ United States

Introduction and Objectives or Purpose

A previous study has reported the exposure of domestic animals to NiV-like viruses in Bangladesh, although their role in transmission in Bangladesh remains unclear. Our objective was to detect infections among domestic and peri-domestic animals living in close proximity to bat roosts associated with human NiV cases in Bangladesh.

Methods

From Oct-13 to Oct-15 in six confirmed human Nipah outbreak sites, we collected bat roost urine and collected blood samples from animals along with their feeding habits. All animal serum samples were sent to the CDC, Atlanta, where a human IgG ELISA was adapted and optimized to test animal sera by using alternative positive and negative control sera and horseradish peroxidase-conjugated Pierce Recombinant Protein A/G.

Results or Focus

Of the five bat roosts sampled, roost urine from four had NiV RNA. No animal deaths were reported nearby human cases. We sampled 604 domestic (cattle, sheep, goat) and 552 peridomestic (rat, shrew, dog, cat) animals from 369 households. Cattle (3/274; 1%), dogs (5/189; 3%), and cats (4/85; 5%) had evidence of antibodies to NiV in their serum. 33% of cattle (91/274) and goats (110/330) were fed dropped fruit; two cattle with antibodies were fed dropped fruit.

Conclusion or Scope

NiV spillovers occur in ruminants and carnivores without obvious increases in mortality which may allow opportunities for the virus to evolve and transmit in other species. Surveillance for spillovers should include multiple species to truly understand the ecology of NiV and risks for transmission.

Acknowledgement

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Keywords: Nipah virus, domestic animals, peri-domestic animals, antibody

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Pathogenesis and modes of transmission
Abstract No: 14720

Carcass disposal practices of small scale livestock farmers in rural Bangladesh

Ireen Shanta[*1] ; Syed Ahmed[6] ; Melissa Kadzik[1] ; Antonio Vieira[2] ; Kamal Hossain[1] ; Taifur Rahman[1] ; Rita Traxler[2] ; Sk Islam[2] ; Erin Kennedy[3] ; Johanna Salzer[2]
[1]Infectious Diseases Division/ Icddr,b/ Bangladesh (□□□□□□□□), [6]Department of Epidemiology and Public Health/ Sylhet Agricultural University/ Bangladesh (□□□□□□□□) [1]National Center for Emerging and Zoonotic Infectious Diseases/ Centers for Disease Control and Prevention (CDC), Atlanta, USA/ United States [2]Bacterial Special Pathogens Branch/ Centers for Disease Control and Prevention (CDC), Atlanta, USA/ United States [2]Infectious Diseases/ Stanford University/ United States [3]Division of Global Health Protection/ Centers for Disease Control and Prevention (CDC), Atlanta, USA/ United States

Introduction and Objectives or Purpose

Anthrax is a global zoonotic disease caused by the spore-forming bacterium Bacillus anthracis. In Bangladesh, outbreaks are periodically reported among people and livestock, with approximately 4,000 reported suspected human cutaneous anthrax between 2009-2020. Improper disposal of anthrax infected carcasses can contaminate grazing land with spores that may survive for years and infect healthy animals. Understanding carcass disposal practices of small-scale livestock farmers in rural Bangladesh can guide anthrax control and prevention strategies.

Methods

We enrolled 1,620 households, 800 from outbreak and 820 from non-outbreak areas. We conducted a cross-sectional survey from October 2017 to March 2018 in four districts with the highest number of suspected human cases and four districts having never reported cases. We randomly selected 10-11 villages per district; totaling 81 villages. From each village, 20 households with at least one domestic animal (cattle/buffalo/goat/sheep) were randomly enrolled and the primary raiser was interviewed to understand the practices of carcass disposal.

Results or Focus

Among 1,382 households with cattle/buffalo, 85 reported unexpected animal deaths within the last 12 months. Among them, 78% of households reported burying carcass (non-specific depth), 11% disposed in open field, 8% disposed in a water body, 2% gave the carcass to cobbler, and 1% disposed in the jungle. Among 1,007 households with goat/sheep, 336 reported unexpected deaths of animals within the past 12 months. Among them, 62% reported burying carcass, 21% disposed in open field, 12% disposed in a water body, and 6% disposed in jungle. The burial practice was found higher in cattle/buffalo than goat/sheep ($p=006$). However, there were no significant ($p>0.05$) differences in carcass disposal practices among outbreak and non-outbreak areas.

Conclusion or Scope

Most of the households reported the burial of livestock carcasses. However, educational intervention about deep burial (minimally 6 feet), its feasibility in flooded areas, and potential alternatives for carcass disposal in the region should be assessed.

Keywords: Carcass disposal, livestock farmers, Bangladesh

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Pathogenesis and modes of transmission
Abstract No: 14772

Understanding SARS-CoV-2 transmission, host infection and susceptibility in minks

Vinaya Venkat*[1] ; Thanakorn Niamsap[1] ; Kirsi Aaltonen[1] ; Jenni Virtanen[1] ; Rasmus Malmgren[1] ; Kristel Kegler[1] ; Tanu Chawla[2] ; Lara Leal Ambrosio Dutra[1] ; Eng Eong Ooi[2] ; Tarja Sironen[1]
[1]Department of Veterinary Medicine and Department of Virology/ University of Helsinki/ Finland (Suomi), [2]Emerging Infectious Diseases/ Duke NUS Medical School/ Singapore

Introduction and Objectives or Purpose

The emergence of SARS-CoV-2 has ravaged human and animal health, collectively damaging global economies. Minks are farmed for their fur and appear highly susceptible to SARS-CoV-2 infection. Infection dissemination has been controlled through mass culling, which is costly to the fur industry. Understanding the transmission of SARS-CoV-2 in minks and the outcome of infection could provide insights on infection countermeasures to reduce the economic burden.

Methods

Infection patterns in male and female minks were studied separately. Several intranasally infected minks were also held in the same environment as naïve minks and observed for infection for seven and 10/11 days, respectively. Saliva, aerosol, and surface samples were analysed daily by RT-PCR and cell culture. At the end of each experiment, various tissue samples were collected for histopathological analysis.

Results or Focus

RT-PCR of saliva samples showed that more male than female minks became infected following intranasal virus inoculation. Significantly more viable viruses were detected in aerosols collected from the males compared to the females, which can explain the RT-PCR positive findings in environmental samples. Consistently, we observed virus transmission from infected males to naïve males but not from infected to naïve females. Histology of the lungs from the males indicated the formation of syncytial cells, hyaline and pneumocyte changes, vasculitis and alveolar oedema, suggesting SARS-CoV-2 infection. Histology of the female lungs, in-situ hybridisation, and immunohistochemistry are yet to be performed.

Conclusion or Scope

These findings suggest gender is a susceptibility factor to SARS-CoV-2 infection in minks and that the viral burden that develops following infection increases their likelihood as sources of transmission. Host response investigations into these gender-based differences in infection susceptibility could be insightful into the determinants of SARS-CoV-2 infection in minks.

Acknowledgement

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Keywords: SARS-Cov-2, mink, omicron, transmission

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Risk assessment of emerging pathogens in animal models
Abstract No: 14695

Emergency Preparedness and Risk Assessment for Animal Epidemic Prone Diseases in Nigeria

Ahmad I Al-Mustapha[*1 2 3] ; Hamza Ibrahim[4] ; Oluwaseun Adeolu Ogundijo; Muftau Oyewo[3 5] ; Ahmed Tijani Abubakar[6] ; Folashade Onatola[5] ; Victoria Adetunji[2] ; Emmanuel J Awosanya[2] ; Annamari Heikinheimo[1]
[1]Department of Food Hygiene and Environmental Health/ University of Helsinki/ Finland (Suomi), [2]Department of Veterinary Public Health and Preventive Medicine/ University of Ibadan/ Nigeria, [3]Department of Veterinary Services/ Kwara State Ministry of Agriculture and Rural Development/ Nigeria, [4]Department of Veterinary and Pest Control Services/ Federal Ministry of Agriculture and Rural Development/ Nigeria, [5]Nigeria Field Epidemiology and Laboratory Training program/ African Field Epidemiology Network/ Nigeria, [6]Division of Disease Control and Prevention/ Africa Center for Disease control and Prevention/ Ethiopia

Introduction and Objectives or Purpose

Growth in the livestock sector is associated with a heightened risk for epidemic diseases. In Nigeria, the animal healthcare system is characterized by lack of reliable evidence-based data, poor surveillance activities, and poor preparedness for epidemic-prone diseases.

Methods

We conducted an online cross-sectional survey of all Directors of state veterinary services in Nigeria (n=37) to evaluate their risk assessment (RA) status and their emergency preparedness plans in April 2022.

Results or Focus

Our findings showed that 25 of the 37 states (67.5%) in Nigeria have never conducted RA for any EPD whereas seven (18.9%) and four (10.8%) states have conducted RA for ASF and HPAI respectively. Only 11 (30.0%) states had ever adopted the existing national contingency plans during an outbreak. Unfortunately, most of the plans neither included public awareness and risk communication strategy nor did they have established organizational arrangements stating specific duties to be executed by each “stakeholder” during an outbreak. In addition, only 15 states (42.1%) had sufficient surveillance kits, none of them had conducted a simulation test for any EPD, nor have budgetary provisions for compensation, active surveillance, or rapid response following the outbreak of an EPD. In the same vein, states do not enforce movement restrictions even during the outbreak of an EPD, have no holding quarantine facilities, and could not enforce the compulsory culling of all affected animals (where necessary) to curtail the spread of an EPD. Only ten (n=27.0%) states have a functional “local one-health multi-sectoral consultative committee”.

Conclusion or Scope

These findings necessitate the urgent need to implement the “Risk Assessment for Animal Epidemic Prone Diseases” project (RA-4-AEPD) in Nigeria. The project aims to train states with several generic RA tools, develop SOP for important EPD, assess the incursion risk of multiple infectious animal diseases into a state, and enable states plan and effectively respond to outbreak of EPDs.

Keywords: Risk Assessment, Epidemic-prone diseases, Nigeria, ASF, HPAI, RVF, Anthrax, FMD, CBPP

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Risk assessment of emerging pathogens in animal models
Abstract No: 14728

Evidence based on One Health Index for Performance Assessment of a key Indicator of One Health—Zoonoses in Sub-Saharan Africa

Kokouvi Kassegne[*1] ; Han-Qing Zhao[1] ; Si-Wei Fei[1] ; Jing-Xian Yin[1] ; Qin Li[2] ; Tian-Ge Jiang[1] ; Xiao-Xi Zhang[1] ; Yi Zhang[2] ; Xiao-Kui Guo[1] ; Xiao-Nong Zhou[1 2]
[1]School of Global Health, Chinese Center for Tropical Diseases Research, One Health Center, Shanghai Jiao Tong University-The University of Edinburgh/ Shanghai Jiao Tong University School of Medicine/ China (□□), [2]Department of Vector Borne Tropical Diseases/ National Institute of Parasitic Diseases at Chinese Center for Disease Control and Prevention (Chinese Center for Tropical Diseases Research)/ China (□□)

Introduction and Objectives or Purpose

Zoonoses are public health threats that cause severe damages worldwide and, constitute a key indicator of One Health (OH). The OH approach is being applied for control programmes of zoonotic diseases. In a very recent study, we have developed an evaluation system for OH performance through global OH index (GOHI). This study applied GOHI to evaluate OH performance for zoonoses in sub-Saharan Africa.

Methods

Framework for OH index on zoonoses (OHIZ) was constructed including five indicators, 15 sub-indicators and 28 datasets. Publicly available data were referenced to generate OHIZ database which included both qualitative and quantitative indicators for all sub-Sahara African countries (n=48). GOHI algorithm was referred to estimate scores for OHIZ. Indicators weight was calculated by adopting the fuzzy analytical hierarchy process.

Results or Focus

Overall, five indicators associated with weights were generated as follows: source of infection (23.70%), route of transmission (25.31%), targeted population (19.09%), capacity building (16.77%), and outcomes/case-studies (15.13%). Following the indicators, a total of 37 sub-Sahara African countries aligned with OHIZ validation, while 11 territories were excluded for unfit or missing data. The OHIZ average score of sub-Saharan Africa was estimated at 53.67/100. The highest score was 71.99 from South Africa, while the lowest score was 40.51 from Benin. It is also worth to be mentioned that Sub-Sahara African countries had high performance in many sub-indicators associated with zoonoses, e.g., surveillance and response, vector and reservoir interventions, and natural protected areas, which suggests this region had a certain capacity in control and prevention or responses to zoonotic events.

Conclusion or Scope

This study reveals that it is possible to perform the OH evaluation for zoonoses in sub-Saharan Africa by OHIZ. Findings from this study provide preliminary research information in advancing knowledge of the evidenced-risks to strengthen strategies for effective control of zoonoses and to support the prevention of zoonotic events.

Keywords: One Health index; One Health performance; zoonoses; sub-Saharan Africa

Topic: One Health Science (OHS): Risk Factors Driving Zoonotic Infections: Risk assessment of emerging pathogens in animal models
Abstract No: 15110

Variegated squirrel bornavirus -1 (VSBV-1) animal models

Kore Schlottau*[1] ; Daniel Nobach[2] ; Friederike Feldmann[3] ; Christiane Herden[2] ; Heinz Feldmann[3] ; Donata Hoffmann[1] ; Martin Beer[1]
[1]Institute of Diagnostic Virology/ Friedrich-Loeffler-Institute/ Germany (Deutschland), [2]Institute of Veterinary Pathology/ Justus-Liebig-University/ Germany (Deutschland), [3]National Institute of Allergy and Infectious Diseases/ National Institutes of Health/ United States

Introduction and Objectives or Purpose

Variegated squirrel bornavirus 1 (VSBV-1) is a zoonotic virus and caused fatal encephalitis in squirrel breeders and zoo keepers in Germany. It is assumed that kept exotic squirrels represent reservoir hosts. Screening approaches revealed positive animals within the subfamilies Sciurinae (S. variegatoides and S. granatensis) and Callosciurinae (C. prevostii, C. finlaysonii, T. swinhoei). Virus phylogeny linked to squirrel trade analysis showed the introduction of a common ancestor of known current VSBV-1 isolates into captive exotic squirrels in Germany, most likely by Prevost's squirrels, which are indigenous to Southeast Asia.

The aim of this study was to test the susceptibility of different rodent and non-human primates for VSBV-1, to characterize the course of disease and thereby to establish infection models, representing either dead-end host or reservoir host, which could provide deeper insights into transmissions pathways, pathogenesis and countermeasure development.

Methods

VSBV-1 infection studies were done with different rodents (rats, bank voles, mice, gerbils, guinea pigs and Swinhoe's striped squirrels (T. swinhoei) in addition to rhesus macaques. Laboratory rodents were infected with VSBV-1 by intracerebral, intranasal or subcutaneous infection. Rhesus macaques and T. swinhoei were inoculated either by the intracerebral route or by multiple routes (intranasal, conjunctival, intramuscular and subcutaneously; reflecting possible natural infection routes). All animals were monitored for signs of disease and virus shedding.

Results or Focus

None of the rodents showed any clinical disease and no virus shedding was observed. Despite that, some intracerebrally infected animals were susceptible to infection as shown by high viral loads in their brains. All intracerebrally infected monkeys developed severe neurological signs. The VSBV-1 infected animals developed symptoms after 8-12 weeks and the disease duration was up to one month.

Conclusion or Scope

Macaques intracerebrally infected with VSBV-1 develop a human-like disease and may serve as a surrogate model for human bornavirus infection and Swinhoe's striped squirrels could represent reservoir hosts.

Keywords: encephalitis; bornavirus; animal models

Keywords: encephalitis; bornavirus; animal models

Topic: One Health Science (OHS): Science of Climate and Ecological Change on One Health: Intervention and mitigation strategies
Abstract No: 15247

Policy, Environment, and Biosecurity (PEB)

Scott Newman[*1] ; Sonevilay Nampanya[1] ; Paolo Motta[1]
[1]Regional Office for Asia and the Pacific/ Food and Agriculture Organization of the United Nations/ Thailand (□□□)

Introduction and Objectives or Purpose

The establishment of the Animal Production and Health Commission for Asia and the Pacific (APHCA) was initiated by Asian nations at the 5th FAO Regional Conference on Animal Production in 1974. APHCA became operational through endorsement at the 60th Session of the FAO Council in December 1975. The purpose of APHCA is to promote livestock development in the Asia and Pacific region, focusing on animal health and husbandry. Membership is open to FAO member countries in the region which is home to more than two-thirds of the global domestic livestock population and more than half of the world's poor livestock keepers. There are currently 18 member states (Australia, Bangladesh, Bhutan, India, Indonesia, Iran, Lao PDR, Malaysia, Mongolia, Myanmar, Nepal, Pakistan, Papua New Guinea, Philippines, Republic of Korea, Samoa, Sri Lanka & Thailand).

APHCA supported the establishment of Dairy Asia and has traditionally focused on supporting poor peoples' livelihoods, and livestock as a source of nutrition, livelihoods, income, resilience and sustainability for livestock holders and communities. This has been achieved by promoting information-generation & exchange, providing normative guidance and coordinating joint actions among member countries and other stakeholders.

Recently, One Health, climate smart livestock production, farm biosecurity, and transboundary diseases (African Swine Fever and Lumpy Skin Disease) with direct impacts on livestock, trade, livelihoods and development have been at the forefront of regional topics of relevance. Looking ahead to the post COVID-19 era, and with a better understanding of the connectivity amongst livestock, wildlife, people and the environment, APHCA is reviewing member country and regional livestock development priorities. This presentation will highlight strategic resources available through APHCA, provide further details about APHCA membership, and touch upon how the Commission will adjust to accommodate current needs of member countries and regional priorities.

Keywords: Policy; Environment; Biosecurity; PEB

Topic: One Health Science (OHS): Vaccines and Therapeutics for Emerging Infections: Enabling equitable access
Abstract No: 14979

PUBLIC HEALTH IMPACT OF HERPES ZOSTER VACCINATION ON OLDER ADULTS IN SINGAPORE

Helen Oh*[1] ; Carol Tan[2] ; Charles Williams[3] ; Nikolaos Giannelos[4] ; Cheryl Ng[5]
[1]Department of Infectious Diseases/ Changi General Hospital/ Singapore, [2]The Good Life Medical Centre, Geriatric Medicine/ Mount Alvernia Hospital/ Singapore, [3]Medical Affairs/ GSK/ Singapore, [4]VEO Vaccines/ GSK/ Belgium, [5]Health Outcomes/ GSK/ Singapore

Introduction and Objectives or Purpose

Herpes zoster (HZ), a painful, unilateral rash, occurs upon reactivation of latent varicella-zoster virus due to immunosenescence/immunosuppression. With a rapidly ageing population at higher risk for HZ, the burden of disease on Singapore's healthcare system is increasingly significant. Vaccination can prevent HZ and its complications; in 2021, recombinant zoster vaccine (RZV) was approved locally for HZ and postherpetic neuralgia (PHN) prevention in adults ≥50 years of age (YOA). This modelling study estimated the potential public health impact of HZ vaccination in the 2021 Singapore population ≥50 YOA.

Methods

The global ZOster ecoNomic Analysis (ZONA) model was used, with local adaption to model inputs/assumptions. The model followed cohorts from year of vaccination over their remaining lifetime, exploring three vaccination scenarios, no vaccination/RZV/zoster vaccine live (ZVL), under mass vaccination (30% coverage). 82.5% second-dose compliance (RZV) was assumed. Sensitivity analysis was performed.

Results or Focus

In the 2021 population (1.51 million), 406,513 HZ (27.0%), 68,264 PHN (4.5%), and 54,949 other complications (3.6%) cases were projected without vaccination. Compared with no vaccination, the number of HZ/PHN/other complications cases avoided with mass vaccination with RZV (73,129/11,094/9,205) was 4–5 times that with ZVL (17,565/2,781/1,834). The youngest age cohort (50–59 YOA) contributed almost half of all HZ cases avoided with RZV. Overall, RZV prevented 2,827 hospitalisations and 8 deaths, versus no vaccination. Number needed to vaccinate to prevent one HZ/PHN case was lower for RZV (7/41) than ZVL (26/163). Results were robust under sensitivity analysis.

Conclusion or Scope

This analysis demonstrated reduced morbidity of HZ with vaccination, where superior public health outcomes were observed with RZV versus ZVL. RZV vaccination is an appropriate healthy ageing strategy for HZ prevention among Singapore adults ≥50 YOA, especially with early vaccination from 50 YOA. These findings serve to inform national-level vaccination strategies and clinical decision-making regarding HZ and PHN prevention in Singapore.

Acknowledgement

Funding: GlaxoSmithKline Biologicals SA.

Keywords: Herpes zoster; Immunisation; Public health impact; Recombinant zoster vaccine; Shingles

Topic: One Health Science (OHS): Vaccines and Therapeutics for Emerging Infections: Novel vaccine technology
Abstract No: 15335

PRECLINICAL EFFICACY OF A SARS-COV-2 RBD BASED VACCINE PRODUCED WITH THE THERMOPHILIC FILAMENTOUS FUNGAL EXPRESSION SYSTEM THERMOTHELOMYCES HETEROTHALLICA, C1.

Mariana Gonzalez Hernandez*[1] ; Franziska K. Kaiser[1] ; Imke Steffen[5] ; Malgorzata Ciurkiewicz[1] ; Geert Van Amerongen[3] ; Ronen Tchelet[2] ; Mark Emalfarb[2] ; Markku Saloheimo[3] ; Marilyn Wiebe[3] ; Marika Vitikainen[3] ; Irina C. Albulescu[4] ; Berend Jan Bosch[4] ; Wolfgang Baumgaertner[1] ; Bart L. Haagmans[5] ; Albert D.M.E. Osterhaus[1]
[1]Research Center for Emerging Infections and Zoonoses (RIZ)/ University of Veterinary Medicine Hannover, Foundation/ Germany (Deutschland), [5]Department of Biochemistry / Research Center for Emerging Infections and Zoonoses/ University of Veterinary Medicine Hannover, Foundation/ Germany (Deutschland), [1]Institute of Pathology/ University of Veterinary Medicine Hannover, Foundation/ Germany (Deutschland), [3]Xplore / Viroclinics / Netherlands, [2]Dyadic International, Inc/ Dyadic International, Inc/ United States [3]VTT Technical Research Centre/ VTT Technical Research Centre/ Finland (Suomi) [4]Virology Section, Infectious Diseases and Immunology Division, Department of Biomolecular Health Sciences, Faculty of Veterinary Medicine/ Utrecht University/ Netherlands [5]Department of Viroscience/ Erasmus Medical Center/ Netherlands

Introduction and Objectives or Purpose

The ongoing COVID-19 pandemic, caused by SARS-CoV-2, has resulted in more than 500 million cases and more than 6 million deaths. The emergency use of newly developed vaccines has been the most efficient way to control the pandemic. However, the emergence of SARS-CoV-2 variants of concern (VOC) has reduced the efficacy of vaccines and monoclonal antibodies currently available. The receptor-binding domain (RBD) of the SARS-CoV-2 spike protein is the main target for virus neutralizing (VN) antibodies. Here, we evaluated the immunogenicity and efficacy of a SARS-CoV-2 RBD vaccine candidate produced with the Thermothelomyces heterothallica, C1 protein expression system.

Methods

Syrian golden hamsters were immunized with different C1 based candidate vaccine combinations: SARS-CoV-2 RBD, SARS-CoV-2 RBD coupled to a nanoparticle (RBD-nano), or SARS-CoV-2 RBD with the non-coupled nanoparticle (RBD+nano), with or without adjuvant (aluminum hydroxide; alum). Hamsters injected with PBS were used as control. Hamsters received a homologous boost with the respective combination 28 days after the first injection, and at day 42 they were challenged with SARS-CoV-2 Wuhan-Hu-1. Necropsy was done 4 d.p.i., when lung and nasal turbinates were collected. RBD ELISA and virus neutralization test were used to evaluate the antibody response at day 0, 28, 42 and 46.

Results or Focus

We showed that a single dose of RBD-nano with alum, efficiently induced SARS-CoV-2 VN antibodies and to higher levels than the non-adjuvanted equivalent. Moreover, we observed a 10-to-100-fold reduction of virus titers in the lungs when using the RBD-nano without or with alum, respectively. In addition, significant reduction in viral antigen and lesions in the lungs were observed. Finally, VN antibodies neutralized SARS-CoV-2 VOCs D614G, Alpha, Beta and Gamma.

Conclusion or Scope

In conclusion, our results support the use of the C1 protein expression system to produce recombinant vaccines against virus infections that may overcome limitations associated with the use of mammalian expression systems.

Keywords: SARS-CoV-2; receptor binding domain; vaccine; Thermothelomyces heterothallica; filamentous fungus

Topic: One Health Science (OHS): Vaccines and Therapeutics for Emerging Infections: Platforms for universal vaccines and therapeutics
Abstract No: 14706

MRNA-BASED COVID-19 BOOSTER VACCINATION ELICIT HIGH LEVELS OF NEUTRALISING ANTIBODIES

Hanisah Sharif*[1] ; Hazim Ghani[1] ; Liyana Ahmad[1] ; Chee Wah Tan[2] ; Lin Naing[1] ; Justin Wong[3] ; Yuan Wei[4] ; Lin-Fa Wang[2] ; Anne Cunningham[1] ; Si Yee Chan
[1]PAPRSB Institute of Health Sciences/ Universiti Brunei Darussalam/ Brunei, [2]Programme in Emerging Infectious Diseases/ Duke-NUS (National University of Singapore) Medical School/ Singapore, [3]Disease Control Division/ Ministry of Health/ Brunei, [4]EVYD Research Pte Ltd/ EVYD Technology Limited/ Singapore

Introduction and Objectives or Purpose

There has been rapid vaccine development and approval to combat the COVID-19 pandemic. These include traditional inactivated whole viral vaccines and novel vaccine platforms using viral vectors and mRNA-based vaccines. The levels of neutralising antibodies (NAb) generated following vaccination with BBIBP-CorV (S), AZD1222 (A) and mRNA-1273 (M), with and without a booster dose of either mRNA-1273 (--M) or BNT162b2 (--P) were investigated in the Bruneian population.

Methods

A total of 2,713 participants were recruited, of which 1,376 participants received two doses of vaccination of either SS (n = 136), AA (n = 602) or MM (n = 638). Furthermore, 1,337 participants were boosted with either BBIBP-CorV (SSS, n = 10), mRNA-1273 (SSM, n = 95; AAM, n = 2; MMM, n = 258) or BNT162b2 (SSP, n = 50; AAP, n = 42; MMP, n = 880) vaccines. Percentage inhibition by NAb were assessed using cPass™ SARS-CoV-2 Neutralization Antibody Detection Kit (GenScript BioTech, China).

Results or Focus

mRNA vaccines (MM) induced higher levels of NAb compared to viral vector (AA) and inactivated vaccine (SS). A third booster dose induced significantly higher NAb inhibition in all cases. Heterologous mRNA booster doses increased the levels of NAb irrespective of the primary series. SSM/P NAb were significantly higher than SS and SSS (both, $P < 0.001$); AAM/P generated more NAb than AA ($P < 0.0001$). Participants who received MM as their primary vaccination series demonstrated a modest increase in NAb inhibition following an mRNA-based booster dose. No significant differences were observed between participants boosted with either mRNA-1273 or BNT162b2.

Conclusion or Scope

mRNA-based vaccine induced higher NAb levels compared to viral vector and whole inactivated viral vaccines. A single mRNA-based booster dose broadly increased NAb in all participants irrespective of the primary vaccination series received, highlighting the advantage of heterologous vaccination.

Keywords: COVID-19; Vaccination; Neutralising antibodies.

Topic: One Health Science (OHS): Vaccines and Therapeutics for Emerging Infections: Platforms for universal vaccines and therapeutics
Abstract No: 14903

Bat ASC2 suppresses SARS-CoV-2-immune-complex-induced inflammasome activation

Vivian Chih-Wei Chen*[1] ; Adrian Eng Zheng Kang[1] ; Pui San Kong[1] ; Wei Lun Ng[1] ; Lan Huong Nguyen[1] ; Wan Rong Sia[1] ; Qi Su[1] ; Linh Chi Dam[1] ; Matae Ahn[1] ; Lin-Fa Wang[1] [2]
[1]Emerging Infectious Diseases/ Duke-NUS Medical School/ Singapore, [2]SingHealth Duke-NUS Global Health Institute/ Duke-NUS Medical School/ Singapore

Introduction and Objectives or Purpose
As the only flying mammal, bats are special in their longevity and ability to asymptomatically host numerous emerging viruses, including the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) – the causative agent of the COVID-19 pandemic with significant public health and economic impact for the past three years. While these viruses affect bats minimally, they are highly pathogenic and can be lethal to humans. The immunopathology induced by infection has been linked to activation of the inflammasome, an intracellular multiprotein complex of the innate immunity. Interestingly, our previous studies demonstrated dampened inflammasome components in bats, and our recent study revealed bat ASC2 as an inhibitor of the inflammasome, suggesting mechanisms for bats' ability to host deadly viruses without disease. Here we specifically focus on the effect of bat ASC2 in the context of SARS-CoV-2.

Methods
To study SARS-CoV-2-induced inflammation, human monocytes were treated with immune complexes formed by the receptor-binding domain (RBD) of SARS-CoV-2 spike protein and afucosylated/fucosylated anti-RBD monoclonal antibody. The effect of priming on SARS-CoV-2-immune-complex-mediated inflammation was studied using the TLR2 ligand Pam3CSK4. To examine the ability of bat ASC2 to block the inflammation, bat ASC2 fused with a cell-penetrating peptide was delivered intracellularly.

Results or Focus
Our data show that SARS-CoV-2 immune complex activates inflammasome in human monocytes in an NLRP3-dependent manner, and production of the proinflammatory cytokine IL-1β increases with the presence of afucosylated antibodies and/or priming. This inflammasome activation can be inhibited via intracellular delivery of bat ASC2 protein, demonstrating bat ASC2 as a potent negative regulator of the inflammasome.

Conclusion or Scope
These results reveal a SARS-CoV-2-immune-complex-mediated inflammasome activation and a bat-derived mechanism of inhibiting SARS-CoV-2-induced inflammation to reduce disease severity. Learning from bat biology has shed light on new approaches to alleviate diseases. This could lead to development of therapeutics derived from bats for infections and inflammasome-driven diseases in humans.

Keywords: Bats; inflammation; disease tolerance; SARS-CoV-2; immune complex

Topic: One Health Science (OHS): Vaccines and Therapeutics for Emerging Infections: Platforms for universal vaccines and therapeutics
Abstract No: 14981

Targeting the inflammasomes as a therapeutic approach for infectious and inflammatory diseases

Qi Su*[1] ; Wei Lun Ng[1] ; Vivian Chih-Wei Chen[1] ; Adrian Eng Zheng Kang[1] ; Lin-Fa Wang[1] [2] ; Matae Ahn[1]
[1]Programme in Emerging Infectious Diseases/ Duke-NUS Medical School/ Singapore, [2]SingHealth Duke-NUS Global Health Institute/ Duke-NUS Medical School/ Singapore

Introduction and Objectives or Purpose

We previously reported bats having reduced inflammatory response upon infections by different types of viruses, including +/- sense single-stranded or double-stranded RNA viruses, due to the dampening of their NOD-like receptor protein 3 (NLRP3) inflammasome pathway. The inflammasome pathway is critical in many inflammatory diseases including but not limited to infectious diseases. Our team recent discovered a novel bat ASC2 protein that suppresses inflammation by inhibiting the apoptosis-associated speck-like protein containing a CARD (ASC) speck formation during inflammasome activation. A recombinant human protein Hupa4, with gain-of-function mutations from bat ASC2 protein, was designed for potential therapeutics. The use of cell-penetrating peptides (CPPs) as a tool for intracellular delivery of macromolecules was proven effective in recent decades. In this work, we evaluate the use of a CPP-aided protein drug derived from bats in targeting the inflammasome pathway to reduce inflammatory response.

Methods

We designed a fusion protein between Hupa4 and the HIV-1 trans-activator of transcription (TAT) protein-derived CPP. The fusion protein was administered to human peripheral blood mononuclear cells (PBMCs) and adult primary human epidermal keratinocytes (HEKa). The NLRP3 inflammasome in PBMCs and the NLRP1 inflammasome in HEKa were subsequently stimulated with nigericin and talabostat respectively. Release of lactate dehydrogenase and IL-1β were used to evaluate the inflammatory responses. The delivery of fusion protein across the cell membrane was measured by western blot.

Results or Focus

TAT-Hupa4 fusion protein reduced NLRP3 and NLRP1 inflammasome activation in PBMCs and skin cells by reducing pyroptosis and inflammatory cytokine IL-1β secretion. The CPP successfully aided the trans-membrane delivery of Hupa4 in a dose-dependent manner.

Conclusion or Scope

The CPP-aided Hupa4 fusion protein is a viable anti-inflammatory strategy that could be applied in a great diversity of infectious and other inflammatory diseases, by modulating the host immune response. In addition, bats can provide us novel inspirations in tackling human diseases.

Keywords: Inflammasomes; Cell-penetrating peptides; Protein therapeutics;

Topic: One Health Science (OHS): Vaccines and Therapeutics for Emerging Infections: Therapeutic antibodies
Abstract No: 14700

NAb levels generated by homologous vaccines, regardless of a booster dose, do not influence the incidence of breakthrough SARS-CoV-2 infections

Liyana Ahmad*[1] ; Hazim Ghani[1] ; Hanisah Sharif[1] ; Saifuddien Bagol[2] ; Surita Taib[2] ; Yuan Wei[3] ; Linfa Wang[5] ; Anne Cunningham[1] ; Lin Naing[1] ; Justin Wong[4]
[1]PAPRSB Institute of Health Sciences/ Universiti Brunei Darussalam/ Brunei [2]Department of Laboratory Services/ Ministry of Health/ Brunei [3]EVYD Research Private Limited/ EVYD Research Private Limited/ Singapore [5]Programme in Emerging Infectious Disease/ Duke-NUS Medical School/ Singapore [4]Disease Control Division/ Ministry of Health/ Brunei

Introduction and Objectives or Purpose

Brunei controlled the first wave of the COVID-19 pandemic with strict public health measures (March-May 2020). A second wave (Deltavariant) accelerated the national vaccination programme (August-November 2021). A third wave (January 2022; mainly Omicron variant) led to more than one quarter of the population being infected. We evaluated the incidence of breakthrough infection in a cohort of the general population with known neutralizing antibodies (NAb) levels induced by either 2 doses of mRNA-1273, AZD1222, or BBIBP-CorV vaccines, or boosted with either mRNA (mRNA-1273 or BNT162b2) or BBIBP-CorV vaccines.

Methods

COVID-19 infection was self-reported via the National 'BruHealth' App (PCR or ART) according to the guidelines from the Ministry of Health. Levels of NAb in participants who tested positive for COVID-19 was compared to those who remained negative across vaccine groups and adjusted for age, sex, ethnicity, time since last dose, and pre-existing medical conditions.

Results or Focus

A total of n=609/2713 individuals tested positive (by 8thApril 2022) across all vaccine platforms. All cases were mild/moderate and none required active medical treatment. There was no association between levels of NAb, number of doses, or vaccine platform. Logistic regression demonstrated a higher risk of infection in those who had cancer and had only received two doses (17.6% higher risk, p=0.012). There was no difference in the incidence of breakthrough infection between individuals who received two or three doses (p=0.851). Those with ischaemic heart disease (IHD) had a 12.4% higher risk of infection (p=0.03). Malay ethnicity was associated with higher risk (p=0.001) while older age groups (≥60) was associated with a lower risk (p=0.002).

Conclusion or Scope

All vaccines prevented severe infection and hospitalisation in our study population. Vulnerable groups should be boosted and those with pre-existing health conditions (e.g. IHD) should take additional precautions. Other observations are likely to be behavioural.

Keywords: COVID19, vaccine, breakthrough, booster, neutralising antibodies

Topic: One Health Science (OHS): Science of Climate and Ecological Change on One Health: Intervention and mitigation strategies
Abstract No: 15403

Safe Food Fair Food: A One Health project to improve food safety in Cambodia

Hung Nguyen-Viet*[1] ; Sothyra Tum; Chhay Ty; Fred Unger; Sinh Dang-Xuan; Melissa Young; Johanna Lindahl; Rortana Chea; Delia Grace
[1]Animal and Human Health/ International Livestock Research Institute (ILRI)/ Kenya

Introduction and Objectives or Purpose

The Safe Food Fair Food for Cambodia project was implemented by the International Livestock Research Institute in partnership with Cambodian and international partners. The project aimed to reduce the burden of foodborne disease in traditional markets.

Methods

The project conducted the market survey, modelling analysis, risk profiling, intervention using a One Health approach and focusing on pork and poultry value chains and two key pathogens: Salmonella spp. and Staphylococcus aureus. The project conducted activities in traditional markets in 25 provinces across the country.

Results or Focus

The overall prevalence of Salmonella and S. aureus in 496 samples of pork and chicken was found to be 43-45% and 29-38%, respectively. These findings show foodborne disease is a major public health issue in Cambodia. A cost-of-illness assessment used data from 266 cases of foodborne illness in Phnom Penh and Siem Reap collected from hospitals show that the cost of foodborne illness was US$ 63 per case. Quantitative microbial risk assessment estimated the risk of acquiring salmonellosis after consuming contaminated pork and chicken salad show that annual incidence rates of salmonellosis estimated from consuming chicken salad, pork salad and mixtures of chicken and pork salads were found to be 11%, 4% and 15%, respectively. A Randomized Controlled Trial intervention to improve food safety that included provision of equipment (US$ 20 per retailer) and training of pork sellers on good hygiene practices using the project's handbook of five key actions was implemented. Intervention significantly reduced Salmonella prevalence in the trial group.

Conclusion or Scope

The project generated new evidence on health and economic burden of foodborne diseases in Cambodia and piloted low-cost interventions that improved food safety in traditional markets. We recommended to scale up this intervention to improve food safety in Cambodia.

Acknowledgement

LSIL, USAID, A4NH, CGIAR One Health Initiative

Keywords: Food safety, informal markets, foodborne disease, intervention

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Animal and human vaccines and other preventive interventions for pandemic preparedness: Costs, benefits and risks of animal vaccination: economics of vaccines in relation to antibiot
Abstract No: 14687

EFFECTIVENESS AND PROFITABILITY OF PREVENTIVE VETERINARY INTERVENTIONS IN CONTROLLING INFECTIOUS DISEASES OF RUMINANT LIVESTOCK IN SUB-SAHARAN AFRICA: A SCOPING REVIEW

Francis Sena Nuvey*[1 2 3] ; Jalil Arkoazi [1 4] ; Jan Hattendorf[1 4] ; Gloria Ivy Mensah[5] ; Kennedy Kwasi Addo[5] ; Günther Fink[1 4] ; Jakob Zinsstag[1 4] ; Bassirou Bonfoh[3]
[1]Epidemiology and Public Health/ Swiss Tropical and Public Health Institute/ Switzerland (Schweiz) [2]Faculty of Medicine/ University of Basel/ Switzerland (Schweiz) [3]African Science Partnership for Intervention Research Excellence/ Centre Suisse de Recherches Scientifiques/ Ivory Coast [4]Faculty of Science/ University of Basel/ Switzerland (Schweiz) [5]Department of Bacteriology/ Noguchi Memorial Institute for Medical Research, University of Ghana/ Ghana (Gaana)

Introduction and Objectives or Purpose

Agriculture in general, and livestock production in particular, serve as a livelihood source for many people in sub-Saharan Africa (SSA). In many settings, lack of control of infectious diseases hampers livestock productivity, undermining the livelihood of rural populations. This scoping review sought to identify veterinary interventions previously applied and evaluated as well as their relative effectiveness in controlling infectious livestock diseases.

Methods

To be included, papers had to be written in English, German or French, and had to describe the effectiveness and/or profitability of preventive veterinary intervention(s) against anthrax, blackleg, bovine tuberculosis, brucellosis, contagious bovine pleuropneumonia, contagious caprine pleuropneumonia, foot and mouth disease, goat pox, lumpy skin disease, pasteurellosis, peste des petits ruminants, and/or sheep pox in any SSA country.

Results or Focus

Of the 2748 publications initially screened, 84 met our inclusion criteria and were analyzed. Most of the studies (n = 73, 87%) evaluated the effectiveness and/or profitability of vaccination, applied exclusively, applied jointly with, or compared to strategies like deworming, antimicrobial treatment, surveillance, feed supplementation, culling and dipping in reducing morbidity and/or mortality to livestock diseases. The effectiveness and/or profitability of antimicrobial treatment (n = 5), test and slaughter (n = 5), and use of lay animal health workers (n = 1) applied exclusively, were evaluated in the other studies. Vaccination was largely found to be both effective and with positive return on investment. Ineffective vaccination was mainly due to loss of vaccine potency under unfavorable field conditions like adverse weather events, cold chain failure, and mismatch of circulating pathogen strain and the vaccines in use.

Conclusion or Scope

Vaccination is the most effective and profitable means of controlling infectious livestock diseases in SSA. However, to achieve effective control of these diseases, its implementation must integrate pathogen surveillance, and optimal vaccine delivery tools, to overcome the reported field challenges.

Keywords: Effectiveness; Profitability; Preventive interventions; Infectious disease; Vaccination

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Animal and human vaccines and other preventive interventions for pandemic preparedness: Costs, benefits and risks of animal vaccination: economics of vaccines in relation to antibiot
Abstract No: 14779

FACTORS AFFECTING BURNOUT IN JUNIOR DOCTORS ROTATING THROUGH ORTHOPAEDIC SURGERY DURING THE COVID-19 PANDEMIC

Rui Lee[*1] ; Si Jian Hui[2] ; Yu Han Chee[2]
[1]Family Medicine/ National University Health System/ Singapore, [2]Orthopaedic Surgery/ National University Health System/ Singapore

Introduction and Objectives or Purpose

When COVID-19 first struck Singapore, manpower was redirected to medical specialties and National Centre for Infectious Diseases (NCID), resulting in a sharp drop in manpower to surgical specialties. This paper evaluates the impact of this on newly minted House Officers (HOs) entering NUH (National University Hospital) Orthopaedics, comparing their burnout rates in Contaminiation wards housing COVID-19 patients versus that of Clean wards housing non-COVID patients, with interesting results.

Methods

The Burnout Measure, Short Version by Malachi-Pines was used to measure the burnout scores of the House Officers via an online survey. Both quantitative and qualitative data (anecdotes) were collected.

Results or Focus

16 % of House Officers (HOs) met the criteria for burnout while serving in the Clean wards versus 0% rates of burnout in the Contamination wards. 66% of HOs in the Clean wards were deemed at risk of burnout, more than twice than the percentage of 30% of HOs at risk of burnout in the Contamination wards. The lower burnout rates reported in Contamination teams was attributed to a smaller patient load, and a fixed team consultant as compared to multiple consultants in the Clean teams. Interestingly, majority of respondents did not feel they were being placed at higher risk while in contamination teams, with 91% expressing they felt safe in Personal Protection Equipment (PPE) provided by the hospital. In fact, most HOs reported the COVID wards to be a period of rest and respite compared to their usual wards.

Conclusion or Scope

Patient load and senior team structures play paramount roles and may even outweigh the stress which comes from looking after infectious patients, shedding light on what affects junior doctors’ burnout levels while they rotate through a short-staffed surgical specialty during times of crisis.

Acknowledgement
We would like to thank the House Officers who participated in the study.

Keywords: Burnout, Pandemic preparedness, COVID-19, Mental Health, Manpower, Surgery

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Animal and human vaccines and other preventive interventions for pandemic preparedness: Costs, benefits and risks of animal vaccination: economics of vaccines in relation to antibiot
Abstract No: 14899

MEASURING AND EVALUATING EPIDEMIC RESPONSE LAWS AND POLICIES WITH A ONE HEALTH APPROACH

Kashish Aneja[*1] ; Katherine Ginsbach[1] ; Sam Halabi[1] ; Katie Gottschalk[1] ; Alison Durran[1]
[1]Law/ O'Neill institute for National and Global Health Law, Georgetown University/ United States

Introduction and Objectives or Purpose

Effective pandemic response and preparedness require laws and policies to be aligned with science and respect the One Health approach. Epidemic response laws and policies can have life and death consequences and significant economic implications and must be measured, evaluated and changed to meet the evolving context.

Methods

The COVID-19 Law Lab platform enables quantitative representation of epidemic law and policies in a given country for multiple years, enabling governments and researchers to compare countries, and learn about the impacts and drivers of policy choices.

Results or Focus

The Law Lab will systematically identify and visualize laws/policies adopted around the world, by providing summaries, policies and visualizations across public health interventions, and serving as a living library of legal documents. The Law Lab is built on the WordPress platform that facilitates user-friendly contributions by individuals across the world.

Conclusion or Scope

Through the creation of new software for this legal database, we will be able to (1) serve as an open-source law library (2) index and code policies to facilitate analysis, (3) provide visualization tools to show how policies are being implemented, including interactive data analysis tools. This interface can then be connected to other platforms, facilitating analysis across issues including legislations regulating animals and environmental laws/policies, epidemics and diseases and harnessing existing data for multisectoral solutions. The law lab, inter alia, can help reconcile the difference in foundations of health-related legislation (based on the principle of scientific justification) and environmental legislation (based on the precautionary principle)

Keywords: COVID-19, PANDEMIC PREPAREDNESS AND RESPONSE, ONE HEALTH, DATABASES, LEGAL PREPAREDNESS

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Animal and human vaccines and other preventive interventions for pandemic preparedness: Optimal deployment and new strategies (e.g. oral vaccines) for vaccines
Abstract No: 14679

A “6M” framework to hospital outbreak preparedness

Jiahui Li*[1] ; Koh Cheng Thoon[1] ; Kai-qian Kam[1] ; Karen Nadua[1] ; Natalie Tan[1] ; Chia Yin Chong[1] ; Chee Fu Yung[1]
[1]Paediatric infectious disease/ KK Women’s and Children’s Hospital / Singapore

Introduction and Objectives or Purpose

The COVID-19 pandemic has demonstrated the need for a structured framework in order for healthcare systems to respond adequately to emerging infectious diseases. Here, we describe a “6M” approach that provides an overarching approach to outbreak preparedness.

Methods

The “6M”s include Man, Methods, Materials, Milieu, Medications and Message.

Results or Focus

“Man” includes manpower and training, where teams of deployable, trained healthcare practitioners are kept updated, with scheduled training programmes and cross-institutional drills. In “Methods”, both medical and logistical workflows are incorporated into every aspect of the framework, with clear delineation of tasks. “Materials” include resources for diagnostics for cases and at-risk groups, with consultation made with microbiologists for quality control, and appropriate persons for performing of such tests. Logistics of diagnostics include supply, distribution of such diagnostic material to ensure timely diagnosis.

“Milieu” considers environmental factors and containment. Appropriate isolation guidelines include isolation criteria, and suitable facilities of isolation catered to vulnerable population groups such as children and families. Personal protective equipment and transport of suspect or infected cases are important considerations in containment. “Medications” include therapeutics and vaccination. Rapid development of therapeutic guidelines by expert committees are required, along with open discussion with international counterparts. Apart from a reliable supply of vaccines, a vaccine programme that can be rapidly scaled up with trained personnel to deliver vaccines is crucial in vaccine delivery. “Message”, which constitutes the backbone of the framework, underlies communication channels that serve to effectively disseminate information to healthcare practitioners, patients and public. Information should not only be centrally communicated but also flow laterally in a timely manner. In the age of social media, proactive means to mitigate spread of misinformation is also crucial.

Conclusion or Scope

In conclusion, a “6M” approach provides a structured approach outlining essential considerations when planning for an outbreak response by a healthcare system.

Keywords: outbreak response; framework; structured

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Animal and human vaccines and other preventive interventions for pandemic preparedness: The need for transfer of technology and innovations in low resource settings
Abstract No: 15054

Metagenomic next-generation sequencing to characterize etiologies of non-malarial fever in a cohort living in a high malaria burden area of Uganda

Lusajo Mwakibete*[1] ; Saki Takahashi[2] ; Vida Ahyong[1] ; Allison Black[1] ; John Rek[3] ; Isaac Ssewanyana[3] ; Moses Kamya[4] ; Isabel Rodriguez-Barraquer[2] ; Cristina M. Tato[1] ; Bryan Greenhouse[2] ; Grant Dorsey[2] ; Prasanna Jagannathan[5]
[1]Infectious Diseases/ Chan Zuckerberg Biohub/ United States, [2]Division of HIV, ID and Global Medicine/ University of California San Francisco / United States, [3]Infectious Disease/ Infectious Diseases Research Collaboration/ Uganda, [4]Medicine/ Makerere University/ Uganda, [5]Microbiology and Immunology/ Stanford/ United States

Introduction and Objectives or Purpose
Causes of non-malarial fevers in sub-Saharan Africa remain understudied.

Methods
We used metagenomic next-generation sequencing (mNGS) to systematically investigate causes of non-malarial fever in participants of all ages enrolled in a cohort in eastern Uganda. Between December 2020 and August 2021, respiratory swabs and plasma samples were collected at 313 study visits where participants presented with fever and were negative for malaria by microscopy.

Results or Focus
Samples were analyzed using CZ ID, a web-based platform for microbial detection in mNGS data. Overall, viral pathogens were detected at 123 of 313 visits (39%). SARS-CoV-2 was detected at 11 visits; other prevalent viruses included Influenza A, RSV, and seasonal coronaviruses. Notably, 11 influenza cases occurred between May and July 2021, coinciding with the SARS-CoV-2 Delta wave.

Conclusion or Scope

This study illustrates the utility of mNGS in elucidating the multiple causes of febrile illness, which could aid in surveying and responding to pathogens circulating in a region.

Acknowledgement

We thank all study participants who took part in this study. We also thank the clinical, laboratory, and data study team and the Infectious Diseases Research Collaboration for administrative and technical support. We acknowledge sources of funding support, including from the Schmidt Science Fellows, in partnership with the Rhodes Trust; Chan Zuckerberg Biohub Investigator program; NIH/NIAID;

Keywords: non-malarial fever, metagenomic sequencing, pathogen surveillance.

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Ensuring the fit of key One Health models and innovations and their implementation into health systems.
Abstract No: 14746

OPERATIONALIZATION OF ONE HEALTH IN GERMANY'S INTERNATIONAL DEVELOPMENT COOPERATION

Lara Hollmann*[1] ; Angela Schug[2] ; Friederike Paul-Fariborz[3 4] ; Tobias Luppe[3] ; Leonie Derksen[5] ; Daniel Eibach[5]
[1]Sector Initiative One Health/ Deutsche Gesellschaft für Internationale Zusammenarbeit (GIZ) GmbH/ Germany (Deutschland), [2]Sector Initiative One Health/ Deutsche Gesellschaft für Internationale Zusammenarbeit (GIZ) GmbH/ Germany (Deutschland), [3]KfW Competence Center Social Development, Governance and Peace/ KfW Development Bank / Kreditbank für Wiederaufbau (KfW)/ Germany (Deutschland), [4]GIZ Sector Programme Global Health/ Deutsche Gesellschaft für Internationale Zusammenarbeit (GIZ) GmbH/ Germany (Deutschland), [5]Division 101 - Special Initiative on pandemics and global health, pandemic prevention, One Health/ German Federal Ministry for Economic Cooperation and Development (BMZ)/ Germany (Deutschland)

Introduction and Objectives or Purpose

The concept of the One Health approach has been extensively discussed, but implementation still lacks support. In line with the German Federal Ministry for Economic Cooperation and Development's (BMZ) 2021 One Health Strategy, Germany's investments are supporting the shift from theory to practice geared towards implementing the Sustainable Development Goals. For this BMZ is working with implementing agencies such as the Deutsche Gesellschaft für Internationale Zusammenarbeit (GIZ) and KfW Development Bank. The aim is to reduce health risks that arise at the human-animal-environment interface through preventive measures, to add value and reduce fragmentation, duplication and inefficiencies that continue to undermine progress in low and lower-middle income countries.

Methods

BMZ' One Health work is implemented in four fields of action: (i) anchoring the approach in German development cooperation; (ii) strengthening cooperation and networking; (iii) capacity development; and (iv) political agenda setting. Implementation considers the full complexity of the systems addressed, guided by evidence and sustainability principles.

Results or Focus

BMZ has funded over 60 One Health-related projects between 2016 and 2021 with more than 800 million EUR in more than 30 countries and regions. Projects focus on zoonoses, neglected tropical diseases, antimicrobial resistance, and pandemic prevention, preparedness and response (PPR). Activities aim, for example, to improve surveillance, expand roll out of digital tools and strengthen human capacity development.

Conclusion or Scope

BMZ' One Health work includes financial cooperation through multilateral, regional development banks and KfW, and technical cooperation projects across the globe with a particular focus on Africa. Additionally, BMZ builds partnerships with key stakeholders e.g., World Organisation for Animal Health, World Health Organization and the United Nations Environment Programme. As a large donor in global health, food security, water, biodiversity, and the Financial Intermediary Fund for PPR, Germany will use its position as a trailblazer to advance the One Health approach in key facilities and institutions.

Keywords: policy; implementation; partnership; One Health

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Ensuring the fit of key One Health models and innovations and their implementation into health systems.
Abstract No: 14763

Capacitating One Health in Eastern and Southern Africa (COHESA) – From Awareness to Action

Shauna Richards*[1] ; Alexandre Caron[2 3] ; Margaret Karembu[4] ; Bibiana Iraki[4] ; Hélène De Nys[2] ; Eric M Fèvre[1 5] ; Delia Grace[1 6] ; Theo Knight-Jones[1]
[1]Animal and Human Health/ International Livestock Research Institute / Kenya, [2]CIRAD/ Centre de coopération internationale en recherche agronomique pour le développment / France, [3]Faculdade de Veterinaria/ Universidade Eduardo Mondlane/ Mozambique (Moçambique), [4]./ ISAAA AfriCenter/ Kenya, [5]Institute of Infection, Veterinary and Ecological Sciences/ University of Liverpool/ United Kingdom, [6]Food and Markets Department/ Natural Resources Institute/ United Kingdom

Introduction and Objectives or Purpose

To increase awareness of One Health (OH) research and policies in Eastern and Southern Africa (ESA), enhance cross-sectoral collaboration between government entities with OH mandates and OH stakeholders across society, equip educational and research institutions to train the next generation workforce and identify solutions to tackle OH issues, and to increase capacity of the public and private sector to identify and deliver OH solutions.

Methods

COHESA is working with partners in Botswana, Ethiopia, Kenya, Malawi, Mozambique, Namibia, Rwanda, Tanzania, Uganda, Zambia, and Zimbabwe to deliver the project. Net-mapping (identifying key OH actors/institutions) and a baseline assessment has been undertaken to describe the OH landscape in each country and identify gaps to be addressed by the project. COHESA looks to build national and regional OH capacity by developing and reinforcing collaborative OH governance mechanisms with evidence based OH strategies. Future OH capacity will be enhanced through strengthening educational institutions to deliver OH courses. Delivery of solutions for a specific OH issue is planned for Ethiopia, Kenya, Mozambique and Zimbabwe, with the approach then used as a model for OH delivery.

Results or Focus

Early outputs include net-mapping of OH actors and baseline assessments of OH status across each country, which will inform on solutions that can be implemented through building cross-departmental collaboration and capacity. COHESA is working with national and regional higher education bodies to benchmark OH curricula to establish new and improved OH courses.

Conclusion or Scope

COHESA aims to embed the OH approach in ESA through building cross-discipline, and cross-sectoral collaboration to address the complex, systems-wide challenges that threaten the modern world, specifically focussing on government, education, research sectors, and OH service providers. Understanding the current state of OH across ESA and OH actors' relationships, promotion of OH evidence-based strategies and governance, and enhancing OH capacity will facilitate adoption of OH solutions.

Keywords: One Health; baseline assessment; net-mapping; cross-sectoral collaboration

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Ensuring the fit of key One Health models and innovations and their implementation into health systems.
Abstract No: 14953

Assessing food security performance from the One Health concept: an evaluation tool based on the Global One Health Index

Lefei Han*[1 2] ; Siyu Gu[1 2] ; Fumin Chen[1 2] ; Xiaoxi Zhang[1 2] ; Jingshu Liu[1 2] ; Xiaokui Guo[1 2] ; Xiaonong Zhou[1 2] ; Qinqin Hu*[1 2]
[1]School of Global Health/ Shanghai Jiao Tong University School of Medicine/ China (□□), [2]One Health Center/ Shanghai Jiao Tong University-The University of Edinburgh/ China (□□)

Introduction and Objectives or Purpose

Food systems instantiate the complex interdependencies between humans, the physical environment, and other organisms. Applying One Health approaches for agri-food system transformation is crucial to combat the threats from food security, nutrition, and food safety, as well as enhance the sustainability of food systems. This study proposes to develop a potential assessment tool, named the global One Health index – Food Security (GOHI-FS), to evaluate food security performance across countries from One Health perspective and identify relevant gaps that need to be filled urgently for ideal and sustainable food systems.

Methods

We comprehensively reviewed existing frameworks and elements of food security. The indicator framework was conceptualized following the structure-process-outcome model and confirmed by expert advisory. Publicly available data in 2020 was collected for each indicator. The weighting strategy was determined by the Fuzzy Analytical Hierarchy Process. The data for each indicator was normalized and aggregated by weighted arithmetic mean. Logit-transformed linear regressions were performed to evaluate the associations of GOHI-FS with health and social-economic indicators.

Results or Focus

The GOHI-FS includes 5 first-level indicators, 19 second-level indicators and 45 third-level indicators. There were 146 countries enrolled for evaluation. The highest average score was shown in Nutrition (69.8) and the lowest in Government support and response (31.3). There was regional heterogeneity of GOHI-FS. Higher average scores were shown in North America (76.1, 75.5-76.7), followed by Europe and Central Asia (66.5, 47.6-78.6), East Asia and the Pacific (61.3, 44.9-78.6), Latin America and the Caribbean (61.4, 54.5-71.2), Middle East and North Africa (57.1, 42.9-68.9), South Asia (49.6, 35.3-60.0), Sub-Saharan Africa (42.7, 29.5-62.5). We also found significant associations between GOHI-FS and GDP per capita, socio-demographic index, health expenditure and life expectancy.

Conclusion or Scope

GOHI-FS is a potential assessment tool to understand the gaps in food security across countries under the One Health concept.

Acknowledgement
N.A.

Keywords: Food Security, One Health, Index, indicator framework, performance assessment

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Ensuring the fit of key One Health models and innovations and their implementation into health systems.
Abstract No: 14977

COVID-19 Law Lab: Building Partnerships and Facilitating Law and Policy Surveillance for a Cross-Sectoral, Collaborative and 'One Health' Approach to Pandemic Preparedness and Response

Katherine Ginsbach*[1] ; Kashish Aneja*[1] ; Alison Durran [1] ; Katie Gottschalk[1] ; Sam Halabi[1]
[1]Center for Transformational Health Law / O'Neill Institute for National and Global Health Law/ United States

Introduction and Objectives or Purpose

The COVID-19 Law Lab initiative is designed to address the urgent need for quality legal information to support the study of how law and policy can be used to effectively manage this, and future, pandemic(s). The initiative also strives to document how governments have worked to promote public health while respecting human rights and promoting equity, especially for historically marginalized or vulnerable groups.

Methods

It is a partnership comprising the O'Neill Institute, Georgetown University, the WHO, UNAIDS, IDLO, IPU, and UNDP. The database involves individual and regional collaborations and with universities, civil society, law firms, and individuals. We have also hosted training sessions and individuals have taken ownership of research for a country.

Results or Focus

It contains over 7,000 legal and policy documents related to the COVID-19 pandemic. In-country partnerships allows us to gain valuable knowledge about data collection barriers and how these laws and policies are being implemented to help guide us in better preparedness and response for the next pandemic. The database is a publicly accessible, open-source database of COVID-19 related measures impacting health and human rights that promotes transparency and accountability by documenting countries' pandemic responses through the use of law and policy.

Conclusion or Scope

The database can facilitate law and policy surveillance and analysis, identify gaps including barriers to the 'One Health' approach across countries. Such a database will build global and regional partnerships that facilitate reforming pandemic response and preparedness laws and policies that follow a One Health approach.

Keywords: COVID-19; Pandemic Preparedness and Response; Policy Surveillance; One Health

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Ensuring the fit of key One Health models and innovations and their implementation into health systems.
Abstract No: 15097

ASSESSING EFFECTS OF THE COVID-19 PANDEMIC ON HEALTH SECURITY AND INFORMATION SYSTEMS IN THE MIDDLE EAST AND NORTH AFRICA

Derek Kunaka*[1] ; Omar Almjadalawi*; Micol Stock*[1] ; Lisa Kowalski*[1] ; Derek Kunaka*[1]
[1]USAID Country Health Systems and Data Use (CHISU) Program/ JSI / United States

Introduction and Objectives or Purpose

The U.S. Global Health Security Agenda (GHSA) has prioritized support to countries in the Middle East and North Africa (MENA) region to better prepare for future disease outbreaks. Even prior to the COVID-19 outbreak, the region experienced key challenges in effective coordination of regional efforts to monitor diseases, including the provision of datasets or evidence necessary to provide a holistic understanding of each country and of the region overall. These information sharing gaps were exacerabted by the pandemic.

With support from the WHO Eastern Mediterranean Regional Office, the USAID-funded Country Health Information Systems and Data Use (CHISU) program began a landscape analysis in 2021 of 11 MENA countries (Algeria, Egypt, Iraq, Jordan, Lebanon, Libya, Morocco, Syria, Tunisia, West Bank/Gaza, and Yemen) to understand their health information systems, platforms, and policies for disease surveillance and pandemic preparedness. The goal of the assessment was to understand the status of One Health systems in the region and to provide recommendations for improved national and regional level disease surveillance and outbreak response.

Methods
CHISU conducted a desk review and held key informant interviews with stakeholders covering the 11 study countries. Stakeholders included government representatives, donors (ex. USAID, WHO), program implementing partners, and independent experts. CHISU spoke to health experts, as well as representatives from the agriculture, environment, and zoonotic health sectors.

Results or Focus
CHISU gained an in-depth understanding of health governance and policies, human and zoonotic disease surveillance data systems, and technology tools for outbreak management.

Conclusion or Scope

The assessment identified common gaps in pandemic preparedness including political resistance to data sharing, lack of endorsement in/ capacity to adopt existing disease surveillance technology tools, and a lack of resources to formalize national and regional disease surveillance platforms. Findings will be shared with USAID, WHO, and the country governments interviewed to inform their future investments and strategies.

Keywords: HIS, disease surveillance, OneHealth, MENA, governance

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Ensuring the fit of key One Health models and innovations and their implementation into health systems.
Abstract No: 15153

Validation of a community-friendly tool to assess Patient satisfaction in Tuberculosis programme in the Covid Pandemic period; Bhubaneswar; India

Sonali Kar*[1] ; Melat Menberu[1] ; Pooja Priyadarshini[1] ; Manas Ranjan Behera[1] ; Kirti Sahu
[1]Community Medicine/ Kalinga Institute of Medical Sciences/ India

Introduction and Objectives or Purpose

Tuberculosis is a priority programme for India, one of the 20 countries with high burden of TB. Odisha (Eastern India) in 2017reported 159/lakh/year vis-à-vis national average incidence of 138.33/lakh/year. Under National Strategic Plan 2020-25, in 2021 Odisha was ranked second in country for its efforts on TB elimination. WE assess community feedback on the programmatic endeavors, by using a tool of client satisfaction.

Methods

350 consecutive subjects, adults aged 18 years and above consented among the 465 who were newly diagnosed between 5/4/21 to 5/4/22; given a prevalence of 30% TB at 5% error and 95% CI and 5% non-response. Confirmed cases were interviewed at one DOTS center in an urban city, using this pre-designed and pretested tool after taking requisite ethical permission from the institute as well as after consent from the participating subjects.

The tool had 24 items; alpha Cronbach coefficient was 0.928 (bootstrap 95% CI) overall; suggesting very good reliability.

Results or Focus

Infrastructure mean score for all 10 questions was above 4.5 ; for process it was <4.05 for a few questions and mainly these referred to Out of pocket expenditures and waiting time; outcome again for all three questions mean score was near or above 4.4. The overall score was between 5 to 10; maximally at 8.

Conclusion or Scope

Tool gave clear-cut hints at the best picture scenario, as the study was done at a single DOTS service centre in the capital city of the state, which ran effectively even in the pandemic. However, it brings out the weak points In the processes like the cost incurred to come to the centre and communication with ancillary staff. No difference in satisfaction levels were reported among pulmonary and extrapulmonary cases (ratio 8.4:1.5) in this study in covid period

Acknowledgement

NTEP programme of Odisha and my collegues

Keywords: Tuberculosis, service satisfaction, likert scale, out of pocket expenditure

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Ensuring the fit of key One Health models and innovations and their implementation into health systems.
Abstract No: 15201

AN INSTITUTIONAL CAPACITY MAP OF ONE HEALTH IN THE GREATER MEKONG SUBREGION

Angus Campbell*[1] ; Clare Strachan[1]
[1]Nossal Institute for Global Health, Melbourne School of Population & Global Health/ University of Melbourne/ Australia

Introduction and Objectives or Purpose

Understanding institutional capacity and activity is critical to One Health (OH) operationalisation and investment strategies. We conducted institutional mapping in the Greater Mekong Subregion (GMS), to identify and describe organisations operating in, or relevant to, OH.

Methods

An institutional list was compiled through virtual stakeholder consultations across the health, livestock/agriculture and environment sectors followed by a desktop review of scientific literature, reports and websites. Institutions and networks were included if they directly identified themselves having OH aims or OH activities, were key and active in public, animal or environmental health, or had cross-sectoral activity objectives. Identified institutions were categorised according to their primary sector, key activity area(s), and OH themes.

Results or Focus

Most OH institutions were from government and education/academia, with fewer from civil society or the private sector (Table 1). The relative proportion of OH institutions was similar across countries (P=0.061).

Although requiring further validation from GMS stakeholders, the most common activity was capacity building, possibly reflecting the number of education/academic institutions identified. Fewer institutions appeared to be active in leadership/management, communication, policy/advocacy/regulation, although large numbers may not be necessary in these areas.

Thematically, stakeholders most commonly were involved in preventing emerging infectious disease in humans (27%). This encompassed human disease outbreak prevention, rural development, and advancing agricultural practice. Government typically implemented these activities. Surveillance and reporting (14% of institutions) most commonly involved human infection, although some surveillance/reporting of animal pathogens occurred.

Table 1: GMS One Health institutions by country and sector (NGO: non-government organisation; CSO: civil society organisation)

Country	Government	Education/Academia	NGO	CSO	International	Inter-governmental	Private	Total
Cambodia	6	3	1		1			11
Lao PDR	7	5			1			13
Myanmar	4	3		2				9
PRC: Guangxi AR & Yunnan	27	7	1					35
Thailand	8	13		1				22
Viet Nam	35	25	1	9	2			72
Regional		1			9	12	1	23
TOTAL	87	57	3	12	13	12	1	185

Conclusion or Scope

Most OH activities in the GMS still occur within sectors, and there is little private sector representation. Increased cross-sectoral activities, especially closer coordination of sectoral disease surveillance systems, and greater inclusion of wildlife, biodiversity and environment are still required. Future studies to describe OH capacity might include developing and using direct measures of actual OH capacity, beyond implying it from descriptions of current institutional activities.

Acknowledgement

Keywords: operationalisation; coordination; joint working

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Ensuring the fit of key One Health models and innovations and their implementation into health systems.
Abstract No: 15202

BUILDING HEALTH SYSTEMS RESILIENCE THROUGH ONE HEALTH WORKFORCE DEVELOPMENT

Vipat Kuruchittham[*1] ; Parntep Ratanakorn[2 3] ; Michael Tee[3 4] ; Sudarat Damrongwatanapokin[1] ; Thị Hương Lê[3 5]
[1]Secretariat/ Southeast Asia One Health University Network/ Thailand (□□□), [2]Steering Committee/ Thailand One Health University Network/ Thailand (□□□), [3]Executive Board/ Southeast Asia One Health University Network/ Thailand (□□□), [4]Board/ Philippine One Health University Network/ Philippines, [5]Board/ Vietnam One Health University Network/ Vietnam (Việt Nam)

Introduction and Objectives or Purpose

Health workforce is fundamental to building health systems resilience. Universities, producers of health workforce, play an essential role in supplying resilient and competent health professionals to effectively prevent, detect and respond to increasing health threats such as the COVID-19 pandemic. Southeast Asia One Health University Network (SEAOHUN), established in 2011, connects and brings together over 95 member universities in 8 Southeast Asian countries to institutionalize One Health (OH) curriculum into university offerings to build the next generation of OH professionals with the right skillset and mindset, such as critical thinking, communication, collaboration, and systems thinking, to solve complex health challenges. Additionally, universities conduct OH research to support policymakers with evidence-based information, and provide innovative solutions to support governments in their surge capacity.

Methods

This case study distills lessons learned from our decade journey in fostering an extensive multi-country and multi-disciplinary network from 10 founding universities in 4 countries to become a leading regional network of over 95 universities in 8 countries on OH capacity building and research.

Results or Focus

Success factors include building trust and partnership, finding OH champions, having committed development partners, strengthening governance and operating structure, increasing visibility to advocate OH education at all levels, and diversifying our funding portfolio for organizational sustainability.

Conclusion or Scope

SEAOHUN represents academic voices often lacking at national, regional, and international forums. SEAOHUN is a member of the Global Health Security Agenda and a partner of Southeast Asian Ministers of Education Organization, ASEAN+3 Field Epidemiology Training Network, among other OH leading institutions and networks.

We strongly believe in the power of networks and multi-sectoral collaboration as we build on each other's strength in keeping our world safe from infectious disease threats. Our model can be adapted and replicated to build networks in other regions for the development of a sustainable and competent health workforce of the future.

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Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Ensuring the fit of key One Health models and innovations and their implementation into health systems.
Abstract No: 15260

A global analysis of One Health Networks: who and what is driving the proliferation of One Health collaborations?

Afifah Rahman-Shepherd[*1 2] ; Athman Mwatondo[3 4 5] ; Scott Chiossi[3] ; Lara Hollmann[3] ; Josphat Maina[4 5] ; Karishma Krishna Kurup[3] ; Osman Dar[3 6] ; Osama Ahmed Hassan[3]

[1]Saw Swee Hock School of Public Health/ National University of Singapore/ Singapore, [2]Faculty of Public Health and Policy/ London School of Hygiene and Tropical Medicine/ United Kingdom, [3]Global Health Programme/ Chatham House (The Royal Institute of International Affairs)/ United Kingdom, [4]Kenya Zoonotic Disease Unit/ Ministry of Health/ Kenya, [5]International Livestock Research Institute/ International Livestock Research Institute/ Kenya, [6]United Kingdom Health Security Agency/ United Kingdom Health Security Agency/ United Kingdom

Introduction and Objectives or Purpose

With the COVID-19 pandemic, there has been a renewed focus on threats emerging at the human-animal-environment interface and investments in One Health collaborations are expected to increase. Efforts to monitor the growth in One Health Networks (OHNs) are essential to avoid duplication and misalignment of investments. This study maps the global distribution of existing OHNs and assesses their collective characteristics to identify potential gaps and target investment more effectively.

Methods

We systematically searched PubMed, Google, Google Scholar, and relevant conference websites, and identified 184 OHNs worldwide for further analysis. We developed four case studies to illustrate key findings from our research and exemplify best practices in One Health operationalisation.

Results or Focus

While there has been growth in the number of OHNs forming in the last ten years than in the preceding decade, investment in OHNs has not been equitably distributed, with more OHNs forming and headquartered in Europe than in any other region. Emerging infections and novel pathogens are the priority for most OHNs, with far fewer OHNs focusing on other important hazards and pressing threats to health security. We found major gaps in the OHNs collaboration model in terms of the diversity of stakeholder and sector representation, which we argue impede effective and equitable OHN formation, and contribute to other imbalances in OHN distribution and priorities.

Conclusion or Scope

The increased attention to One Health post-COVID-19 presents an opportunity to better align efforts and resources where there is the most need. Analyses like ours should be used as a baseline to establish databases and repositories of OHNs worldwide. Greater attention should then be paid to understanding existing resource allocation and distribution patterns, and to help establish more egalitarian networks that truly address the breadth of One Health issues and serve communities most affected by emerging, re-emerging or endemic threats arising at the human-animal-environmental interface.

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Keywords: One Health initiatives; One Health networks; multi-sectoral collaboration

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Ensuring the fit of key One Health models and innovations and their implementation into health systems.
Abstract No: 15285

ONE HEALTH, MULTIPLE IMPACTS OF ONE HEALTH WORK IN BANGLADESH AND THE ASIAN REGION FOCUSING ON THE POULTRY INDUSTRY

Easrat Jahan Esha*[1] ; Prof. Dr. Md. Ahasanul Hoque[1] ; Prof. Robyn ALDERS[2]
[1]Department of Medicine and Surgery, Faculty of Veterinary Medicine/ Chattogram Veterinary and Animal Sciences University/ Bangladesh (□□□□□□□□), [2]Development Policy Centre/ Australian National University/ Australia

Introduction and Objectives or Purpose

Bangladesh is embracing “One Health” (OH), with a strong focus on zoonotic diseases. This study assesses the impacts and lessons learned from the implementation of OH approaches in Bangladesh and the region over the last decade. It also identifies new OH endeavors that can better support health security, especially for the poultry sector.

Methods

The scoping review protocol set inclusion and exclusion criteria for Bangladesh and selected South Asian Association for Regional Cooperation and Association of Southeast Asian Nations documents. A tailored interview guideline used with 25 key informants determined how effectively the OH approach connects to emerging diseases and antimicrobial resistance (AMR).

Results or Focus

Bangladesh is at high risk for zoonotic diseases like Avian influenza, Nipah, Rabies, Anthrax, and leptospirosis due to high human population density, human-animal interaction, and environmental degradation. Deforestation, natural disasters, and AMR encourage OH stakeholders to strategize how best to implement this approach across all sectors in a robust and efficient manner. Our review revealed that, relative to the other study countries, Bangladesh has made solid progress in institutionalizing the OH approach via an inter-ministerial steering committee and an OH secretariat. However, despite the establishment of these bodies, Bangladesh lags behind in effective OH communication between sectors and with the public. Inadequate coordination among stakeholders, incompatible funding, and minimal evidence-based research were common obstacles. Bangladesh can learn from several countries regarding more effective OH action through strengthening their inter-sectoral and public awareness communication, and establishment of local OH teams.

Conclusion or Scope

Strong coordination mechanisms, which enable multi-sectoral stakeholders to promote honest and timely knowledge sharing and management are essential. Engaging high-level government bodies that oversee frontline ministries helps overcome bureaucratic hurdles in OH implementation.

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Prof Robyn ALDERS, Honorary Professor, Development Policy Centre, Australian National University

Keywords: One Health; AMR; coordination; zoonotic

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Ensuring the fit of key One Health models and innovations and their implementation into health systems.
Abstract No: 15316

WORKING OUT HOW TO WORK TOGETHER: COMMUNICATION, COORDINATION, COLLABORATION OR INTEGRATION FOR OPERATIONALIZING ONE HEALTH

Mayank Barot [*1] ; Barbara McPake[1] ; Angus Campbell [1]
[1]One Health Unit/ The Nossal Institute for Global Health/ Australia

Introduction and Objectives or Purpose

The essential One health argument is that the human, animal and environmental health fields should work closely together. However, putting this into practice remains a major challenge. One of the key issues is the limited practical guidance and understanding on how institutions can foster and sustain cross-sectoral efforts.

Methods

Our research addresses this critical gap with a simple framework that identifies and defining four types of institutional arrangements that support the operationalization of One Health.

Results or Focus

These are communication; the sharing of information, coordination; aligning separate activities, collaboration; working together but maintaining separate entities and integration; merging entities. The framework provides four criteria to help determine which institutional arrangement is most appropriate. These criteria are the extent and distribution of specialist knowledge; if specialist knowledge is high and concentrated, then greater levels of integration will be more difficult. Each step will require greater levels of sharing such knowledge across parties. Timing considerations; if activities have time specific impacts that interact with each other, then the benefits of greater levels of integration will be greater at least to the point of ‘co-ordination’ – so that activities are timed to maximize impact. Externalities; If externalities of the activities of one party affects the other, then the benefits from greater levels of integration will be greater so that externalities are jointly managed. Economies of scope and joint production; If there is significant scope for economies of scope and joint production, then the benefits from greater levels of integration will be greater so that activities maximize economies of scope and jointly produce outputs. Examples of this framework are provided in consideration of One Health interventions tackling the issue of Leptospirosis and Anti-microbial resistance (AMR).

Acknowledgement

This work was part of an Asian Development Bank (ADB) project to Strengthen Regional Health Cooperation in the Greater Mekong Subregion.

Keywords: One Health; Multi-sectoral; Collaboration; One Health operationalization

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Ensuring the fit of key One Health models and innovations and their implementation into health systems.
Abstract No: 15350

A multi-sectorial One Health approach to Biosurveillance and Epidemic Preparedness: a Singapore case study

Kelvin Lim*[1] ; Albert Ty[1] ; Shuzhen Sim[2] ; Kyaw Thu Aung[3] ; Charlene, Judith Fernandez[1] ; Lee Ching Ng[2] ; Siow Foong Chang[1] ; Tze Hoong Chua[1] ; Him Hoo Yap[1] ; Kenneth Er[1]
[1]Animal and Veterinary Service/ National Parks Board/ Singapore, [1]Epidemiology and Disease Control Division/ Ministry of Health/ Singapore, [2]Environmental Health Institute/ National Environment Agency/ Singapore [3]National Centre for Food Science/ Singapore Food Agency/ Singapore

Introduction and Objectives or Purpose

While the world struggles with the COVID-19 pandemic and monkeypox, climate change plays an increasing role in the emergence and spread of infectious diseases. Singapore, as a city-state and entrepot, remains vulnerable to the public health impact of infectious diseases arising from climate change and other disease drivers. Climate change can create disruptions in the ecosystem causing spill-over events and disease transmission. Further, other associated human activities such as urbanisation and deforestation, and transboundary movement of people, animals (and vectors), and wildlife trade, can precipitate the emergence or spread of zoonotic diseases. This presents new challenges to the traditional and singular approach of biosurveillance and epidemic preparedness.

Although Singapore has relative successes in handling previous public health crises, challenges continue to aris. A Whole-of-Government biosurveillance strategic framework that encompasses public health, animal/wildlife health, environmental health, food safety sectoral leads is needed to identify common areas of concern, aggregrate scientific expertise and develop joint action plans.

Methods
The One Health agencies in Singapore have developed a framework which aims to identify the gaps and opportunities in the current biosurveillance and epidemic preparedness landscape.

Results or Focus
The conceptual framework comprises four strategic thrusts of scanning and early detection, management of hosts and vectors, inter-agency information integration, and science and technology. Specific actions and outcomes have been identified for each thrust. A multi=sectoral approach is needed especially for disease threats that occur at the human-animal-environment interface, as it requires joint risk assessments and analyses to ensure emerging threats are escalated to decision makers accordingly. Development of a One Health data platform for joint sense-making and risk assessment is underway, and implementation of a holistic sampling approach has come to the fore

Conclusion or Scope
Singapore adopts a One Health approach to biosurveillance and epidemic preparedness.

Acknowledgement
Authors: Wendy Sng, Kelvin Ho and WIlson Tan

Keywords: One Health; Biosurveillance framework; epidemic preparedness

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Harmonisation of regulatory standards for pandemic response or research
Abstract No: 14939

Pandemic preparedness and workplace training resilience: Innovative pedagogical methods for nurse training

Hui Luan Tan*[1] ; Hui Yen Oh[2] ; Hui Fang Delphine Tan[1] ; Boon Eng Sim[1] ; Chui Lee Eng[3] ; Kai Guo Benny Loo[4]
[1]Department of Advancing Nursing and Education/ KKH Women's and Children's Hospital/ Singapore, [2]Ward 86/ KKH Women's and Children's Hospital/ Singapore, [3]Division of Nursing/ KKH Women's and Children's Hospital/ Singapore, [4]Division of Medicine/ KKH Women's and Children's Hospital/ Singapore

Introduction and Objectives or Purpose

A game-based clinical method and a case-based learning approach are used in this study to develop effective pedagogical tools that enable nurses to develop the clinical reasoning skills they need to care for patients in acute care settings.

Methods

A separate design-based research was conducted to develop a serious game about clinical reasoning. Case-based approaches were used during face-to-face sessions to allow nurses to have a discussion guided by a facilitator after a case presentation. A variety of learning experiences are offered to nurses through this blended learning programme that combines technology-supported learning and face-to-face learning.

Results or Focus

On the clinical reasoning skills checklist, 22 participants achieved a baseline score of 70%. In August and November, third-month and six-month assessments will be conducted. The results will be compared with those from the baseline assessment.

An e-Learning Experience Questionnaire with 32 items received a score of 80.95%. On the basis of these findings of the quality of teaching in a blended context domain, a game-based clinical approach appears to enhance intrinsic motivation to maintain learning levels. A case-based learning approach promotes more active and reflective thinking during face-to-face sessions, according to the participation interaction and engagement domain.

Conclusion or Scope

Nurses played a crucial role in the diagnostic process while caring for patients. They dealt with complex tasks within a dynamic environment. In response to the COVID-19 outbreak, training around the world has postponed and cancelled in-person classes. Workplace training is becoming one of the hardest-hit activities. Nurse training cannot stall capability development. We cannot simply pause on critical workplace training even as we strive to put staff safety first. By protecting personnel, adhering to pandemic response regulations, enabling pedagogical tools and delivery, and establishing and expanding virtual live learning, this study enhances value-creating efforts.

Keywords: Workplace Training Resilience, Innovative Pedagogical Methods, Nurse Training, Game-Based, Case-Based

Topic: Pandemic Preparedness and Health Systems Resilience (PPHSR): Secondary/indirect impact to human and animal health: Harmonisation of regulatory standards for pandemic response or research
Abstract No: 15114

Accelerated Development of a Quality System Compliant Emergency Ventilator for Pandemic Use

Fiona Loke[*1] ; Judith Wong[2] ; Derrick Chan[3] ; Herng Lee Tan[2] ; Wai Chye Cheong [1] ; Jessica Quah[4] ; Shariq Khan[5] ; Biju Thomas[6] ; Ghee Chee Phua[7]
[1]Medical Technology Office/ Singapore Health Services Pte Ltd/ Singapore, [2]Children's Intensive Care Unit/ KK Women's and Children's Hospital/ Singapore, [3]Paediatric Neurology/ KK Women's and Children's Hospital/ Singapore, [4]Department of Respiratory and Critical Care Medicine/ Changi General Hospital/ Singapore, [5]Department of Anaesthesiology/ Sengkang General Hospital/ Singapore, [6]Paediatric Respiratory Medicine/ KK Women's and Children's Hospital/ Singapore, [7]Department of Respiratory and Critical Care Medicine/ Singapore General Hospital/ Singapore

Introduction and Objectives or Purpose

The Covid-19 pandemic brought a shortage of ventilators worldwide, sparking attempts both by amateur teams and professional companies to build them rapidly to meet emergency needs. In the race against the clock, it is unclear how many teams implemented quality systems during development to address safety, quality and efficacy concerns. Here, we present a case study of our team's implementation of ISO13485 quality management systems (QMS) requirements, applied to our rapid-manufacture emergency-use ventilator development effort.

Methods

Limited units of ventilators were prototyped to meet design requirements from clinical end users, verified through in-house and third-party testing, validated through preclinical studies performed by clinicians, and evaluated through a user acceptance test.

Results or Focus

It was found that the use of the QMS processes helped to ensure the design met functional and other requirements, reduced risk, and was of a consistent quality, even though the team was not seeking regulatory approval at the time.

Conclusion or Scope

The design was subsequently licensed out to an ISO13485-certified vendor partner, and a number of units were exported for emergency use. While the units would still require formal regulatory emergency-use approval by local authorities prior to use in patients, this has underscored the importance of QMS implementation, even in an emergency-use development timeline, in enabling the creation of a functionally reliable product that is acceptable to users and of consistent quality.

Acknowledgement

SG-INSPIRE was funded by KK Women's and Children's Hospital Health Services Innovation and Development grant (PI: JW and PI: DC), SingHealth Duke-NUS Academic Medicine COVID-19 Grant (PI: DC) and SingHealth Duke-NUS Academic Medicine Special Request for Urgent COVID-19 Research Funding (PI: DC).

Keywords: ventilator; ISO13485; quality management system;

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Country experience and case studies for integrating environmental perspectives into One Health
Abstract No: 14723

Aspergillus Colonization and Aflatoxin Contamination of Post-harvest Maize: Focus on the Rift-Valley Region of Kenya

Grace Gachara*[1] ; Rashid Suleiman[1] ; Beatrice Kilima[1] ; Rachid Lahlali[2]
[1]Department of Food Sciences and Agro-processing/ Sokoine University of Agriculture/ Tanzania, United Republic of, [2]Ecole Nationale d'Agriculture de Meknès/ Mohammed VI Polytechnic University/ Morocco (المغرب)

Introduction and Objectives or Purpose

Maize (Zea mays L.) is an economically important cereal crop in sub-Saharan Africa. The cereal offers a plethora of benefits including dietary provision, poverty reduction, animal feed supply and food security. Despite its numerous uses, maize production has been continually threatened by a plethora of factors, with post-harvest losses and mycotoxins, such as aflatoxins, being the most prevalent problem. Given that maize consumption is projected to increase by approximately 16% by 2027 due to the burgeoning of livestock and human populations, it is deemed crucial to promptly address the aflatoxin menace. In Kenya, major outbreaks of aflatoxicoses have been documented and they are attributed to poor pre, peri and post-harvest practices. In the study, we seek to examine the scope of the aflatoxin menace within the Rift-valley region, Kenya's bread basket and leading maize producer, but unfortunately little or no research has been undertaken to access the mycotoxin challenge.

Methods

The study focuses on two counties; Uasin Gishu and Elgeyo Marakwet. Given that maize is the staple in Kenyan diets, assessing and investigating aflatoxin contamination in high maize cultivation and producing regions is paramount. The occurrence and distribution of total aflatoxins(AFs) in stored maize and the aflatoxigenicity potential of Aspergillus flavus and Aspergillus parasiticus in stored maize in both counties will be determined. The genetic profile of both Aspergillus species will be evaluated using molecular methods by first quantifying their DNA and the conducting Next Gen Sequencing for all AF^+ samples.

Results or Focus

The study seeks to providing ample information on the adverse effects of aflatoxins in the human, animal and agricultural spheres; an aspect that further links the research to the one health theme.

Conclusion or Scope

It is anticipated that the research will emerge as an educative and enlightening read regarding aflatoxin contamination to farmers, animal nutritionists, scientists and scholars within sub-Saharan Africa.

Acknowledgement

Sokoine University

Keywords: Aflatoxins; Rift-valley; maize; Aspergillus spp.; Kenya.

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Country experience and case studies for integrating environmental perspectives into One Health
Abstract No: 15073

Climate Smart Livestock Assessment for Asia and the Pacific

Andreas Wilkes [*1] ; Sonevilay Nampanya [1] ; Hang Thi Than Pham [1] ; Hideki Kanamaru [1] ; Anne Mottet[1] ; Scott Newman[1]
[1]N/A/ New Zealand Agricultural Greenhouse Gas Research Centre (NZAGRC) Grasslands Research Centre/ New Zealand [1]Regional Office for Asia and the Pacific/ Food and Agriculture Organization of the United Nations/ Thailand (□□□) [1]N/A / Food and Agriculture Organization of the United Nations (FAO) / Italy (Italia)

Introduction and Objectives or Purpose

Livestock production in the Asia-Pacific Region is affected by climate change and is a source of greenhouse gas (GHG) emissions. This study assessed the readiness of countries in the region to implement climate smart livestock (CSL) policies and measures.

Methods

Assessment was conducted using secondary data and literature on 36 developing countries in the region. Indicators covered: (1) Vulnerability to climate change (using indicators of exposure, sensitivity and adaptive capacity adapted for livestock from the ND-GAIN food vulnerability index); (2) Livestock GHG emissions (level and growth rate 2010-2019); (3) Coherence of livestock and climate change policies, and climate smart programme implementation.

Results or Focus

(1) Livestock emissions have grown in 58% of countries. Nine of 17 countries with the largest livestock emissions have rapidly growing emissions (median growth rate 25% p.a.), 7 of which are also among the most vulnerable countries. Cattle are the largest emission source, but buffalo, chicken, swine or goats contribute significantly in 6 of these 9 countries. (2) Differences in importance of animal source foods mean livestock vulnerability may differ from overall food vulnerability. Higher livestock vulnerability results from higher exposure and sensitivity, and lower adaptive capacity. Livestock production is negatively correlated with cereal production in many countries, suggesting although livestock is vulnerable, it may sometimes buffer crop-related vulnerability. (3) Livestock is prioritized for adaptation in 36% of NDCs and 15 mention mitigation measures. Climate change is addressed in many countries' livestock-related policies and plans, but few have undertaken in-depth assessments of CSL needs and options or are implementing domestically or internationally financed CSL programmes.

Acknowledgement

FAO-RAP

Conclusion or Scope

Depending on country circumstances, support may address capacities for identifying CSL needs and options, policy development and/or investment planning. Variation in country readiness to promote CSL suggests potential for cross- and co-learning among countries in the Asia-Pacific region.

Keywords: Climate Smart Livestock; Assessment; Asia and the Pacific

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Country experience and case studies for integrating environmental perspectives into One Health
Abstract No: 15075

The Global Livestock Environmental Assessment Model-interactive (GLEAM-i): an online GHG assessment tool based on IPCC Tier 2 methodology

Anne Mottet*[1] ; Şeyda Özkan[1] ; Félix Teillard[1] ; Antonio Rota[1] ; Pierre Gerber[2]
[1]N/A / Food and Agriculture Organization of the United Nations (FAO) / Italy (Italia), [1]N/A/ International Fund for Agricultural Developmenthttps / Italy (Italia) [2]N/A/ World Bank Office/ Croatia (Hrvatska)

Introduction and Objectives or Purpose
The Global Livestock Environmental Assessment Model-interactive (GLEAM-i) is an on-line greenhouse gas (GHG) assessment tool. It has been developed by FAO and partners to support governments, project planners, producers, industry and civil society organizations. It can be used in the preparation of national GHG inventories, Nationally Determined Contributions (NDC) and in ex-ante project evaluation for estimating the climate co-benefits of technical improvements in animal husbandry, feed and manure management.

Methods
GLEAM-i is an online, IPCC Tier 2, greenhouse gas (GHG) calculator specific to the livestock sector. It brings the core functionalities of the FAO Global Livestock Environmental Assessment Model (GLEAM) to the public in a web application. The current version of GLEAM-i allows the direct comparison between Baseline and Scenario conditions and includes the 2010 background data from GLEAM 2.0 as default parameters.

Results or Focus
GLEAM-i is accessed in average by 500 users monthly. It is also used by FAO to support the GHG assessment of projects and investments in livestock in over 20 countries in support of the World Bank, the International Fund for Agricultural Development, the International Funding Corporation and the European Bank for Reconstruction and Development. GLEAM-i is also used to support capacity development of government and international funding institutions staff in GHG emissions calculations in livestock. An average of 75 professionals have been trained by FAO in the use of GLEAM-i every year.

Conclusion or Scope
Through detailed Tier 2 GHG calculations and capacity development, GLEAM-i can support a better inclusion of livestock in national climate commitments and a better accountability of climate co-benefits of improvements in livestock production. Improved capacity in countries on livestock GHG accounting can also support better access to climate finance.

Keywords: GLEAM-i; Livestock Assessment

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Country experience and case studies for integrating environmental perspectives into One Health
Abstract No: 15155

Future directions for One Health Research: Regional and Sectoral Gaps

Touseef Ahmed*[1] [2] ; Muhammad Farooq Tahir[3] ; Lisa Boden[4] ; Tigga Kingston[1]
[1]Biological Sciences/ Texas Tech University/ United States, [2]Epidemiology and Public Health/ University of Veterinary and Animal Sciences/ Pakistan (پاکستان), [3]United Nations/ Food and Agriculture Organization/ Pakistan (پاکستان), [4]Global Academy of Agriculture and Food Security/ The University of Edinburgh/ United Kingdom

Introduction and Objectives or Purpose

One Health (OH) concepts highlight the inter-relationships in health among people, animals, and the environment. It is expanding to include many new interdisciplinary research areas that were not recognized at its inception.Sectoral research gaps and regional biases in OH activities may undermine the world OH commitment.

Methods

We performed comparative analysis of abstracts presented at the 1st World One Health Congress (WOHC) and 6th WOHC to identify potential biases in OH research. Based on their content, we classified (n =1234) abstracts presented in both congresses into six sectoral research areas in OH namely: Disease Surveillance, Capacity Building and Civil Society, Public Policy and Regulation, Antimicrobial Resistance, Environmental and Ecological Issues, and Sustainable Food Systems. We classified abstracts based on corresponding author's country and regional affiliation to identify potential regional biases in OH research.

Results or Focus

In total, 302 abstracts were presented from 54 countries during the 1st WOHC, and 932 abstracts from 93 countries were presented during the 6th WOHC, reflecting a remarkable increase of 68% in abstracts submission between two congresses. At both congresses, Disease Surveillance accounted for the majority (~35%) of abstract submissions. A consistent underrepresentation of research on Environmental and Ecological Issues and Sustainable Food Systems, with (~10%) and (~5%) of the total abstracts presented at each congress. We found that authors from developed countries, who were selected for inclusion in the 6th WOHC appeared to focus mostly on Public Health Policy and Regulations, in comparison with authors from developing countries where Disease Surveillance dominated in abstracts submission categories.

Conclusion or Scope

Global One Health commitment must be ensured by timely actions that encourages global participation to address the identified new geographic-sectoral gaps in OH research. It can be achieved by working more closely with resourceless countries to enhance their ability to detect and respond locally to OH problem of global significance.

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Country experience and case studies for integrating environmental perspectives into One Health
Abstract No: 15198

THE SEASONALITY OF VARICELLA IN THE TROPICAL CLIMATES OF COLOMBIA: A STATISTICAL AND MATHEMATICAL MODELING STUDY

Laura Andrea Barrero Guevara*[1 2] ; Elizabeth Goult[1] ; Matthieu Domenech de Cellès[1]
[1]Epidemiology of Infectious Diseases/ Max Planck Institute for Infection Biology/ Germany (Deutschland), [2]Charité–Universitätsmedizin Berlin/ Institute of Public Health/ Germany (Deutschland)

Introduction and Objectives or Purpose

Every year varicella-zoster virus (VZV) causes over 70 million infections, hundred of thousand of disability□adjusted life years, and almost 15,000 deaths in children worldwide. In addition, the virus persists lifelong and can be reactivated as herpes-zoster, causing neuropathic pain. Although most severe cases and deaths are concentrated in tropical low and middle-income countries, research has focused on temperate high-income countries. In temperate regions, seasonal climate drives varicella transmissibility, peaking typically at the end of winter. However, in tropical regions, climate patterns are fundamentally different, and the drivers of varicella transmissibility are unclear. Here we characterized the seasonal incidence and explored the climatic drivers of varicella in Colombia, a tropical country with a vast diversity of climates.

Methods

We used high-resolution spatial and temporal data on reported varicella cases to the Colombian surveillance system (SIVIGILA) from 2011-2014 before the vaccine's introduction. The spatial variations in varicella seasonality were described with generalized additive models and linked to climates across Colombia using dissimilarity matrices. In addition, we developed a compartmental transmission model to test whether climatic variables can explain the seasonality of varicella in Colombia and Mexico.

Results or Focus

In contrast to most temperate regions, we found that varicella incidence in Colombia peaks twice, and its seasonality varies substantially between regions. These variations followed a latitudinal gradient and correlated with humidity and precipitation patterns across Colombia. Furthermore, including humidity in a VZV transmission model explained both heterogeneous bimodal seasonal variations of varicella in Colombia and its rigidly single-peak seasonality in Mexico.

Conclusion or Scope

Our findings indicate that seasonal variations in humidity can drive varicella transmission in the tropics, contributing to the understanding of the global seasonality of VZV. Furthermore, in a rapidly changing global climate, they illustrate the need to carefully consider within-country climatic variations to allocate effective preventive interventions for infectious diseases such as varicella.

Acknowledgement

Keywords: Varicella zoster virus infection; Environmental health; Childhood disease; Climate; Seasonality

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Country experience and case studies for integrating environmental perspectives into One Health
Abstract No: 15240

AGROECOLOGICAL ACTIONS IN PROMOTING POPULATION HEALTH IN AREAS AFFECTED BY THE COLLAPSE OF A MINING TAILINGS DAM IN BRAZIL

Luan Ritchelle Dos Anjos*[1] ; Klaisy Christina Pettan-Brewer[2] ; Silvia Dantas Costa[3]
[1]Agroecological Technical Assistance / Fundação Renova/ Brazil (Brasil), [2]Department of Comparative Medicine/ University of Washington/ United States, [3]Agroecological Technical Assistence/ Fundação Renova/ Brazil (Brasil)

Introduction and Objectives or Purpose
The collapse of the mining tailings dam owned by Vale® and BHP Billiton® in Brazil, in 2015, caused the biggest environmental disaster in national history and the biggest disaster in world history involving tailings dams, taking 62 million m³ of ore tailings to the Rio Doce and its banks, to the sea. In this process, thousands of families had their food safety and nutritional security compromised due to the impact of the tailings in the areas adjacent to the river.

Methods
In this context, the process of repairing the impact and recovering the affected areas in 5 municipalities has contributed to the health and well being of the affected families. Agroecological gardens and orchards which produce healthy and pesticide-free food for families to eat were successfully implemented. Furthermore, agroforestry systems were implemented for the production of various natural and organic products for commercialization and consumption by families, sugarcane plantations and grass were implemented in areas free of tailings for high quality animal feed and no risk of contamination, and permanent preservation areas, such as springs and riverbanks were fenced off and reforested with native trees isolating these portions for full regeneration.

Results or Focus
Wildlife fauna and flora has been protected and restored, progressively. The Agroecological Technical Assistance service has also been offered to families to capacitate rural producers in the production of organic and healthy food, both for families and for animals, through a participatory and integrative methodology.

Conclusion or Scope

Thus, families have been recovering and even expading food safety and security. One Health approaches have contributed to increase production and autonomy for the families, bringing economic viability, food security and environmental conservation to the region, especially when it comes to smallholders.

Acknowledgement

To Renova Foundation and the Organização Cooperativa de Agroecoligia (OCA) for their support.

Keywords: agroecology; food security and nutrition; autonomy; planetary health; sustainability.

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Environmental change, pathogen risk and health
Abstract No: 14838

Improving Psychosocial health of Adolescents with Diabetes (I-PAD) in KKH

Soo Ting Joyce Lim*[1] ; Kok Ann Amos Lim[1] ; Rashida Farhad Vasanwala[1] ; Xiang Feng Tan; Lois Ling’en Teo; Pei Kwee Lim; Yuen Ching Angela Hui
[1]Nursing Clinical Service/ Kk women and children hospital, Singhealth/ Singapore

Introduction and Objectives or Purpose

Mental health conditions are frequently encountered in adolescents with diabetes. Early recognition of diabetes distress, defined as negative emotions arising from daily burden of self-management, could prevent adolescents from adverse mental health conditions. Our objective are To assess the suitability of self-reported Diabetes Distress Screening (DDS) scale for adolescents with diabetes and explore the effectiveness ofpsychological intervention

Methods

This project adopted KKH’s 3-Step Quality Improvement Model with 149 adolescents pre-identified based on age 13 and above on self-reporting diabetes distress. High risk adolescents were sent for counselling in joint clinic by Advanced Practice Nurse (APN) and Psychologist. The moderate risk group will receive phone calls from Diabetes Nurse Educators (DNE). Post intervention DDS was conducted along with a feedback evaluation (8-items on patient perspective of effectiveness of Joint Clinic and DNE calls) to analyzesustainability and impact of interventions.

Results or Focus

59% (n=97) had moderate to high DDS. Among the high distress group, 17 were seen in the joint clinic and post intervention DDS significantly reduced by 70.6% ($p<0.05$). 39 in the moderate distress group received DNE phone calls and their DDS was reduced by 61.5% ($p<0.05$). From the evaluation on adolescents’ perspectives on effectiveness of both interventions, they were glad to speak to nurses about their personal matters outside of medical aspect and able to discuss solutions to their problems.

Conclusion or Scope

The screening of diabetes distress with intervention at Joint Clinic and DNE calls were effective in improving the overall adolescents’ psychosocial health. Ongoing self-reported DDS will be used at annual review clinic for early screening of distress in all adolescents with diabetes. The project closed by publishing an information booklet titled ‘Together, a healthier body and mind’ that illustrates the importance of the body, mind, spirit and heart as a holistic approach to a well-balanced and meaningful lifespan.

Acknowledgement

THank you IPRAMHO funding support.

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Environmental change, pathogen risk and health
Abstract No: 15059

THE LEVEL OF KNOWLEDGE, ATTITUDE, AND BEHAVIOR OF HEALTHCARE WORKERS REGARDING LEPTOSPIROSIS PREVENTION IN BINJAI CITY'S PRIMARY HEALTHCARE CENTERS, INDONESIA

Yolanda Hanalena[1] ; Evita Mayasari*[1]
[1]Microbiology/ Universitas Sumatera Utara, Faculty of Medicine/ Indonesia

Introduction and Objectives or Purpose

Introduction: Leptospirosis is a neglected infectious disease of public health importance concerning morbidity and mortality in humans and animals. Leptospira interrogans, the bacteria causing human leptospirosis, are found mostly in soil-contaminated urine of the reservoirs (commonly rats). Leptospirosis causes around 1030000 cases and 58900 deaths annually worldwide. Indonesia is a tropical country with high rainfall and flood-risk regions. Those regions with high populations and poor sanitation are vulnerable to a Leptospirosis outbreak. Some areas in Binjai City of North Sumatra, Indonesia, tend to be inundated with water after rainfall. Knowledge, attitude, and behavior of healthcare workers in primary healthcare centers of the vulnerable community in Binjai City are one of the keys to successful preventive measures against a Leptospirosis outbreak. Objective: We conducted this study to determine the relationship between knowledge, attitude, and behavior regarding Leptospirosis prevention among healthcare workers in Binjai City.

Methods

Methods: This is an analytical study with a cross-sectional design. We determined the level of knowledge, attitude, and preventive behavior by asking 71 healthcare workers in the Health Centers of east Binjai to complete questionnaires in September 2021. The grades for knowledge, attitude, and preventive behavior were from the percentage of correct answers. The scores of ≤55%, 56%-74%, and ≥75% are considered as having poor, moderate, and a good level of knowledge, attitude, and preventive behavior, respectively. Further, we analyzed the data statistically.

Results or Focus

Results: Twelve (16,9%) males and 59(83,1%) females, median age 45-49 years 19(26.8%), completed the questionnaires. Most healthcare workers have a good level of knowledge 67(94.4%), good attitude 62(87.3%), and good preventive behavior 64(90.1%). Pearson's correlation analyses showed relationships between the level of knowledge and preventive behavior (r=0.739) and between attitude and preventive behavior (r=0.584, a=0.05).

Conclusion or Scope

Conclusion: There was a strong positive correlation between the healthcare workers' level of knowledge and preventive behavior.

Acknowledgement

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Keywords: Leptospirosis; Prevention; Knowledge; Attitude; Behavior

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Environmental change, pathogen risk and health
Abstract No: 15107

Global perspectives on One Health for Pandemic Prevention

Jonathan Epstein[*1] ; Peter Daszak[*1] ; Meerjady Flora[*2] ; Wanda Markotter[*3] ; Sudarat Damrongwtanapokin[*4]
[1]N/A/ EcoHealth Alliance/ United States, [2]Ministry of Health, Government of Bangladesh/ Institute for Epidemiology, Disease Control & Research (IEDCR)/ Bangladesh (□□□□□□□□), [3]Centre for Viral Zoonoses/ University of Pretoria/ South Africa, [4]Thai Royal Government/ One Health Technical Advisor/ Thailand (□□□)

Introduction and Objectives or Purpose

The pathogens responsible for most emerging infectious diseases, including those that have become pandemic, originate in animals, especially wildlife, and spillover into people where human animal contact occurs. Despite this, our responses to emerging disease and pandemic risk have overwhelmingly favored interventions taken after spillover occurs, such as surveillance, drugs and, with COVID-19 and Ebola, vaccinations. Such post-spillover actions are critical but will inevitably be inadequate to control disease emergence risk as we have seen with COVID and the current monkeypox pandemic. Human disease surveillance, for example, aims to identify causative pathogens through tracing backwards from detection of unusual disease case clusters. Too often, an emerging pathogen has become more broadly established in people than the first few cases detected by the time the causative agent has been identified, making control far more difficult, or impossible as happened with SARS-CoV-2. COVID-19 and monkeypox are the latest examples of why current post-spillover approaches to disease emergence are insufficient to prevent a pandemic. To be effective and equitable, pandemic prevention must address spillover - the moment when an animal virus jumps into people, and concentrate on areas where high risk animal-human contact occurs. Despite spillover prevention's absence from many high level reports and guidance, including those developed in the wake of COVID-19, some countries have adopted a One Health approach to preventing emerging zoonotic disease outbreaks that emphasizes reducing spillover risk. This symposium, formatted as a moderated panel discussion, will feature prominent One Health leaders from the US, Africa and Asia to describe One Health in practice and show how public health systems can work in tandem with research programs to identify and reduce high-risk human activities that allow zoonotic pathogens to emerge.

Keywords: One Health; Policy; Zoonoses; Prevention; Spillover

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Environmental change, pathogen risk and health
Abstract No: 15278

Diversity and Characterization of Coronaviruses in Rodents and Shrews, Bangladesh

Shariful Islam[*1 2] ; Ariful Islam[1 2 3] ; Mohammad E. Hossain[4] ; Melinda K. Rostal[2] ; Tahmina Shirin[5] ; Meerjady S. Flora[6] ; Simon J. Anthony[2 7] ; Mohammed Z. Rahman[4] ; Peter Daszak[2] ; Jonathan H. Epstein[2]
[1]EcoHealth Alliance Bangladesh Programs/ Institute of Epidemiology, Disease Control and Research (IEDCR)/ Bangladesh (□□□□□□□□□), [2]Emerging Infectious Disease Research/ EcoHealth Alliance/ United States, [3]Centre for Integrative Ecology, School of Life and Environmental Science/ Deakin University/ Australia, [4]One Health Laboratory/ International Centre for Diarrhoeal Disease Research, Bangladesh/ Bangladesh (□□□□□□□□□), [5]Director/ Institute of Epidemiology, Disease Control and Research (IEDCR)/ Bangladesh (□□□□□□□□□), [6]Directorate General of Health Services/ Ministry of Health and Family Welfare/ Bangladesh (□□□□□□□□□), [7]Department of Pathology, Microbiology, and Immunology/ University of California-Davis/ United States

Introduction and Objectives or Purpose

Rodents are the most diverse mammalian order, along with shrews, have frequent direct and indirect contact with humans. These species are important hosts of many viruses affecting both human and animals. The current pandemic COVID-19 have sparked to explore the coronaviruses (CoVs) circulating in wildlife. Hence, the study sought to detect and characterize the known and unknown CoVs in rodents and shrews in Bangladesh.

Methods

We collected and tested oral and rectal samples from rodents and shrews twice a year, winter and summer, from 5 sites in Bangladesh from 2015-2018, using consensus PCR for CoVs and confirmed by sequencing of positive samples. We performed DNA barcoding to confirm host species.

Results or Focus

Twenty-three rodents (2.13%; n=1075) and seven shrews (3.09%; n=226) were positive for CoVs. Three CoV strains where one strain of Alphacoronavirus and two strains of genus Betacoronavirus, were identified. Wencheng Sm shrew coronavirus (WSSC; AlphaCoV) was detected in Suncus murinus (n=6). Longquan Aa mouse coronavirus (LAMV; BetaCoV) was detected in Bandicota bengalensis (n=2) and Suncus murinus (n=1). Murine coronavirus (MC; BetaCoV) was detected in Bandicota bengalensis (n=1), Bandicota cf. indica (n=1), Bandicota sp. (n=1), Mus musculus (n=2), Rattus rattus (n=14), Rattus tanezumi (n=1) and Rattus cf. tanezumi (n=1). Overall, highest CoV prevalence was found in rats belonging to the species Rattus rattus (3.9%) and in samples collected in the dry season (2.6%) and from Dinaipur district (4%). We did not detect any novel CoVs including SARS CoV-2 related virus in our study samples.

Conclusion or Scope

The study findings advance our fundamental understanding of CoVs in rodents and shrews and suggest that rodents and shrews may carry additional unrecognized CoVs in Bangladesh.

Acknowledgement

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Keywords: Coronavirus, Rodents, Shrews, Bangladesh

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Policies, interventions and novel approaches (including private sector engagement, advocacy, etc.) to address environmental drivers of disease
Abstract No: 14777

On Target: Enhancing communication for prompt behavior change during outbreaks

Olutola Bamsa[*1] ; Chris Chukwunyere[1] ; Bolutito Omotuyole[1]
[1]Public Health/ Giusta Health Foundation/ Nigeria

Introduction and Objectives or Purpose

In Nigeria, poor and delayed compliance with COVID-19 preventive measures, including vaccination, has been partly attributed to the poor engagement of trusted influencers. There is therefore need to re-appraise communication paradigms to ensure effective and speedy behavior modification during health emergencies.

Methods

We set out to discover ways to reach communities with messages that will engender prompt behaviors necessary to mitigate disease transmission during outbreaks. Using the World Health Organization literature on COVID-19 prevention and vaccines, we trained and facilitated discussions between twenty Civil Society Organization (CSO) representatives in Abuja, Nigeria, and engaged them in a three-month mobilization drive to prevent COVID-19 and improve vaccine acceptance in their communities.

Results or Focus

- The profile of influencers vary widely by communities and are affected by perceptions of transparency, integrity, empathy and an existing legacy.
- Communities in the same geographic locations differ widely by interests, vocation and lifestyles – these factors can be utilized to deliver effective messages for prompt compliance.
- Community based organizations such as Civil Society Organizations are themselves influencers who can provide clear and insightful guidance that will ensure effective risk communication in their communities.
- 9 of 18 unvaccinated CSO representatives, and 15 percent of the target population received COVID-19 vaccinations immediately after the trainings and mobilization drives. A young priest who was trained influenced the vaccination of 1500 parishioners. (All recipients attributed vaccine receipt to the trainings.)

Conclusion or Scope

For effective and speedy behavior modification, communication designs need to ensure strong community engagement to identify, map and engage trusted influencers in the planning and delivery of public health messages.

Acknowledgement

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Keywords: communication; risk communication; influencers; COVID-19 vaccine uptake; community engagement;

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Policies, interventions and novel approaches (including private sector engagement, advocacy, etc.) to address environmental drivers of disease
Abstract No: 14945

ONE HEALTH COMMUNITY OF PRACTICE - METHODOLOGICAL APPROACHES TO SHARING GOOD PRACTICES

Maximilian Möhrle*[1] ; Nadja Münstermann[1]
[1]Sector Initiative One Health/ Deutsche Gesellschaft für Internationale Zusammenarbeit (GIZ) GmbH/ Germany (Deutschland)

Introduction and Objectives or Purpose
The One Health approach has been widely discussed in recent years, however, easily accessible good practice examples that showcase the One Health methodology are still lacking. The PANORAMA One Health community (PANO-OH) offers projects worldwide the option to publish and search for good practice examples. CABI is a platform that scientifically analyses the methodology of One Health projects and publishes their results in case studies. Together, PANO-OH and CABI facilitate an exchange of lessons learned to improve and promote global accessibility to One Health projects.

Methods
On PANO-OH, case studies are documented as solutions using a standard format that identifies replicable “building blocks” (key success factors). Solutions are reviewed by the community coordinators and shared on the online platform. They are also integrated into capacity development activities and workshops. CABI One Health is an open access journal that publishes case studies in an accessible and science-based style. The case studies are submitted through a set template and go through a peer review process for quality assurance.

Results or Focus

The topics on PANO-OH and CABI include a range of conservation and sustainable development topics, including projects on pandemic preparedness, monitoring and surveillance, climate and ecological change, environmental change and health, food security and many more.

A focus for both platforms is showcasing how One Health projects can create an added value. One Health strives to ameliorate human, animal, plant and environmental health, ensure sustainability, and enhance financial saving and social resilience. This is approached through cross-sectoral collaboration between sectors and actors.

Conclusion or Scope
PANO-OH and CABI help new and existing projects to implement the One Health approach successfully and build on existing experiences. In the future, CABI and PANO-OH aim to strengthen their cooperation and coordinate activities to streamline solution sharing.

Keywords: One Health, Added Value, Community of Practice, Good Practice

Topic: Policy, Environment & Biosecurity (PEB): Environmental change and health: Policies, interventions and novel approaches (including private sector engagement, advocacy, etc.) to address environmental drivers of disease
Abstract No: 15254

Dogs - the top pets in a rural region of Sri Lanka; findings from a descriptive cross-sectional evaluation

Devarajan Rathish*[1] [2] ; Jayanthe Rajapakse [1] ; Kosala Weerakoon [3]
[1]Department of Veterinary Pathobiology/ Faculty of Veterinary Medicine and Animal Science, University of Peradeniya/ Sri Lanka (□□□□ □□□□□□), [2]Department of Family Medicine/ Faculty of Medicine and Allied Sciences, Rajarata University of Sri Lanka/ Sri Lanka (□□□□ □□□□□□), [3]Department of Parasitology/ Faculty of Medicine and Allied Sciences, Rajarata University of Sri Lanka/ Sri Lanka (□□□□ □□□□□□)

Introduction and Objectives or Purpose

Pet ownership is an important aspect of contemporary life. It delivers an eclectic array of benefits to people. However, information on pet ownership from rural regions is comparatively restricted. We report the prevalence, associated factors, and rabies vaccination for dog ownership in Anuradhapura, a rural district of Sri Lanka.

Methods

A community-based, cross-sectional study was conducted using an interviewer-administered questionnaire. Households with at least 1 adult residing in Anuradhapura for at least 5 years were included. Probability proportional to size was used to select households to represent all divisional secretariats of the district. Data on rabies vaccination within the last year was derived from the participant's verbal information. Binary logistic regression was used to find possible associations between dog ownership and the variables of interest.

Results or Focus

Out of the selected 532 households, the most common pet was the dog (41%). Households with more than one adult female and Buddhists were significantly associated with dog ownership ($p < 0.05$). Security was the most common role for dogs at home (69%). Amongst the dog owners, most were gifted with or inherited a dog (49%), owned the dog for 1-5 years (62%), fed the dog with home-made food (78%), and had their dogs outdoor in a non-specific area (68%). And, most took their dog for at least one veterinary visit (67%) and vaccinated their dogs against rabies (90%) within the last year. Further, vaccination was the most common reason for the dog's veterinary visit (97%).

Conclusion or Scope

The dog was the most common pet and had a veterinary visit and rabies vaccination within the last year. It highlights responsible pet ownership and the opportunity for research on canine companionship and human health. The findings are vital to guide future research related to one-health among people of rural regions.

Keywords: Canine companionship; One Health; Rabies vaccination

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Economic activity and One Health risk (ie. land use; domestic animals and wildlife management)
Abstract No: 14825

Drivers of self-treatment and sub-optimal antibiotic usage in humans and animals in agricultural communities of northern Tanzania

Kathrin Loosli*[1] ; Fortunata Nasuwa[2] ; Matayo Melubo[2] ; Kunda Mnzava[2] ; Louise Matthews[1] ; Stephen Mshana[1] ; Blandina Theophil Mmbaga[2 4] ; Adrian Muwonge[5] ; Alicia Davis[6] ; Tiziana Lembo[1]
[1]The Boyd Orr Centre for Population and Ecosystem Health, Institute of Biodiversity, Animal Health & Comparative Medicine, College of Medical, Veterinary & Life Sciences/ Univeristy of Glasgow/ United Kingdom [2]Kilimanjaro Clinical Research Institute/ Kilimanjaro Christian Medical Centre/ Tanzania, United Republic of [1]Department of Microbiology and Immunology/ Catholic University of Health and Allied Sciences, Bugando Medical Centre/ Tanzania, United Republic of [4]Kilimanjaro Christian Medical University College/ Kilimanjaro Christian Medical Centre/ Tanzania, United Republic of [5]The Roslin Institute, Royal (Dick) School of Veterinary Studies/ University of Edinburgh/ United Kingdom [6]School of Social and Political Sciences/Institute of Health and Wellbeing/ University of Glasgow/ United Kingdom

Introduction and Objectives or Purpose

Self-treatment with antibiotics acquired without a prescription is often considered a major driver of bacterial antimicrobial resistance (AMR) in humans and livestock, especially in low- and middle-income countries. The purpose of this study was to understand what drives such practices in Tanzanian agricultural communities, to inform targeted AMR interventions and policy update.

Methods

We conducted a mixed-method study in six rural communities, in three unique livelihood systems: pastoral, agropastoral and smallholder. Specifically, the study included a household survey (600 households) and an exit survey (790 respondents) at antibiotic dispensing facilities. In addition, we interviewed 11 local antibiotic providers and observed their antibiotic dispensing facilities. Finally, we conducted a drug bag activity involving locally purchased antibiotics which were then discussed with household members (30 households).

Results or Focus

We show that inadequate access to and quality of human and veterinary healthcare provision drive people's health seeking choices, leading to self-medication by purchasing of human and veterinary antibiotics at local pharmacies or drug stores. Such health care inadequacies include drug stockouts, long waiting times and high costs associated with public health services. A shortage of veterinary and medical professionals often makes self-treatment the only option available. Furthermore, current antibiotic dispensing practices at retail and public facilities provide patients and farmers with inadequate knowledge on how to use antibiotics appropriately. Resulting problematic practices we identified include suboptimal antibiotic use like unnecessary administration of antibiotics for non-bacterial conditions and human-animal (and vice versa) antibiotic crossover-use.

Conclusion or Scope

To address AMR, antibiotic stewardship policies should remove existing barriers preventing access to health services to address the widespread over-the-counter purchase of antibiotics. Furthermore, the quality of human and veterinary healthcare must be improved at all levels in order to reduce sub-optimal treatment practices that could lead to poor health outcomes and AMR development.

Acknowledgement

Keywords: antibiotic use; self-treatment; quality of healthcare; Tanzania; access to antibiotics

(It is not possible to to edit the keywords anymore so I am adding them here)

Keywords: antimicrobial resistance

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Economic activity and One Health risk (ie. land use; domestic animals and wildlife management)
Abstract No: 15227

Soil Coxiella burnetii positivity around a Q fever-positive dairy goat farm

A M Hasanthi Abeykoon*[1] ; Christina M Nelson[1] ; Sathya N Kulappu Arachchige[1] ; Anke K Wiethoelter[1] ; Gemma A Vincent[2] ; John Stenos[3] ; Simon M Firestone[1] ; Mark A Stevenson[1]
[1]Faculty of Veterinary and Agricultural Sciences/ University of Melbourne/ Australia, [2]Solve Consulting/ Solve Consulting/ Australia, [3]Australian Rickettsial Reference Laboratory/ Australian Rickettsial Reference Laboratory/ Australia

Introduction and Objectives or Purpose

Coxiella burnetii causes Q fever, a zoonotic disease reported in all countries of the world except New Zealand. It is an intracellular bacterium exhibiting mechanisms to sustain harsh extracellular environment. Management conditions on intensively managed dairy goat herds provide conditions suitable for C. burnetii transmission and spread if infection is present. As a result, there is the potential of infection risk to humans either working on these farms or resident nearby. Given that Q fever transmission between animals and humans occur via the environment, controlling the spread of Q fever requires approaches that are multifaceted and One Health oriented. This study assessed the level of C. burnetii environmental contamination around a Q fever-positive intensively managed dairy goat farm in Victoria, Australia.

Methods

Soil was sampled at 136 sites in a buffer zone of 1500 m diameter outside the farm boundary and tested using the IS1111 qPCR assay. It was hypothesized that soil C. burnetii positivity would be negatively associated with distance from the farm sheds, distance from waterways and have positive associations with specific land use types. After comparing spatially explicit and non-spatial regression models, a generalized linear model was fit, and related model criteria were assessed.

Results or Focus

The median distance between a sampling site and the nearest kidding shed was 3000 m (minimum 900 m; maximum 5100 m). Coxiella burnetii soil positivity was scattered and showed no clear association with distance from the farm sheds. A weak, negative trend was observed between distance from waterways and soil positivity.

Conclusion or Scope

This study demonstrates a low level of C. burnetii contamination outside an infected farm boundary. The detected (albeit weak) association was biologically plausible and could be influenced by wildlife or water runoff of deposited C. burnetii on topsoil, factors that should be investigated in future studies.

Acknowledgement

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Keywords: Q fever; environmental contamination; qPCR; One Health

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Human, social and ethical dimensions of outbreak preparedness and response efforts (ie. social and economic inequalities, public trust, moveme
Abstract No: 14820

RAPID MULTI-METHOD ASSESSMENT OF THE IMPACTS OF THE COVID-19 PANDEMIC ON WET MARKET BIOSECURITY AND FOOD SECURITY IN THE PHILIPPINES

Renzo Guinto*[1 2] ; Marianne Bongcac[1] ; Mara De los Santos[1]
[1]Planetary and Global Health Program/ St. Luke's Medical Center College of Medicine-William H. Quasha Memorial/ Philippines,
[2]Sunway Centre for Planetary Health/ Sunway University/ Malaysia

Introduction and Objectives or Purpose

In the wake of the COVID-19 pandemic, wet markets were perceived as potential sources of novel zoonotic diseases due to the sale of live animals. Meanwhile, wet markets were also heavily impacted by the pandemic due to various restrictions that were hastily enforced. This study examined the impacts of the COVID-19 pandemic on wet markets in the Philippines, specifically on biosecurity reforms and the restrictions' effect on local food security.

Methods

This exploratory qualitative research study utilized a multi-method approach consisting of media analysis, policy review, key informant interviews, and rapid ethnography in an urban and rural wet market in the Philippines. Data collected from various methods were triangulated and key findings were synthesized using thematic analysis.

Results or Focus

As part of the pandemic response, only a few additional hygiene and sanitation practices were enforced at wet markets, including the use of plastic barriers and conduct of more intense market disinfection. It was found that stakeholders were excluded during policy creation and implementation of the restrictions even as wet markets were perceived as essential services. Hence, the restrictions initially caused a chain reaction across the supply chain that unveiled underlying food system vulnerabilities, primarily the lack of financial capacity of small-scale producers. Ultimately, food prices increased, while alternative methods of food distribution emerged such as online retailing and satellite markets.

Conclusion or Scope

Despite the additional temporary hygiene and sanitation practices enforced during the pandemic, overall wet market biosecurity needs to be further improved. The restrictions greatly affected the local food supply, disproportionately impacting both small-scale producers and low-income consumers. Moving forward, there is a need to apply a proactive, whole-of-society approach to pandemic response, especially in wet markets. Different sectors must exercise greater communication and collaboration in order to mitigate the negative impacts on local food security and maximize the positive benefits of improving biosecurity.

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Human, social and ethical dimensions of outbreak preparedness and response efforts (ie. social and economic inequalities, public trust, moveme
Abstract No: 14893

Harnessing data science for risk-based targeted inspection in prevention of foodborne disease outbreaks in Singapore

Muhd Tarmidzi*[1] ; Benjamin Er[1] ; Kyaw Thu Aung[1] ; Angela Li[1]
[1]Research and Exposure Science Department/ Singapore Food Agency/ Singapore

Introduction and Objectives or Purpose

The Singapore Food Agency (SFA) routinely conducts inspections on food establishments to identify premises with food safety issues. Apart from routine inspections, ad-hoc inspections are done in response to public feedback on any food safety related issue. Public feedback data provides an early warning of a persistent food safety issue on a particular food establishment through multiple feedback over time. Feedback on alleged food poisoning is analysed to identify food establishments and food items with higher food safety risk, for targeted inspections. Data-driven targeted inspections has allowed the SFA to prioritise resources and reap time-savings and efficiency in ensuring food safety

Methods

Alleged food poisoning feedback data received from the Singapore public was extracted from an online database maintained by SFA. The extracted data was cleaned and processed using R software to extract specific information (e.g.,unique identification number of food establishment, details of address and foods consumed). The extracted data is then used to identify food establishments and foods items of higher risk of a food safety lapse using text analytics.

Results or Focus

Our analysis showed that there was a four times higher chance on average of identifying food establishments and food-business chains with food safety lapses through data-triggered inspections as compared to routine inspections. Additionally, our analysis was able to identify high-risk foods through text analytics that was corroborated by lab test results of food sample through post-market monitoring.

Conclusion or Scope

The use of data science tools and techniques has allowed the SFA to make sense of the large volume of public feedback data in ensuring food safety. Through data-triggered inspections, SFA was able to improve its operational efficiency in the detection of food establishments with non-compliance to food safety as compared to routine inspections. SFA was also able to effectively identify high-risk foods to inform its conduct of food sampling and testing operations.

Acknowledgement

Keywords: foodborne disease; data analytics; food safety; targeted inspections;

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Human, social and ethical dimensions of outbreak preparedness and response efforts (ie. social and economic inequalities, public trust, moveme
Abstract No: 15209

A game-theoretical approach to One Health: The case of rabies elimination in Africa

Jakob Zinsstag*[1 2] ; Alvar Bucher[1 2] ; Günther Fink[1 2] ; Nakul Chitnis[1 2]
[1]Epidemiology and Public Health/ Swiss Tropical and Public Health Institute/ Switzerland (Schweiz) [2]Faculty of Science/ University of Basel/ Switzerland (Schweiz)

Introduction and Objectives or Purpose
Previous research has shown that rabies can be eliminated locally, through dog mass vaccination campaigns, and thus eliminate rabies induced human lives lost. To realize the full potential of such an intervention, all 48 countries would need to simultaneously follow a One Health (OH) approach, in the form of conducting a vaccination campaign in the animal reservoir.

Methods
Through available data, an exemplary cost as well as a cost-benefit analysis of a continental rabies elimination scenario analysis for the 48 countries of mainland Africa was modeled and monetized. Through this monetization the utilities for the underlying strategies were derived which were then used for a game theoretical mapping.

Results or Focus
Our results show that the sustained presence of canine transmitted rabies corresponds to a public goods problem. As each individual countries utility ranking does not incentivize the execution of such an intervention, the equilibrium is for all countries to remain at the current status quo, which is the continuous administration of PEP. Through the inclusion of a limited PEP reach and the monetization of the human lives lost in the form of the forgone future Gross Domestic Product (GDP) contributions, we can solve the public goods problem and incentivize the countries to cooperate over 31 years.

Conclusion or Scope

The human lives lost due to canine transmitted constitute, similar as the tragedy of the commons as described by Hardin a common public-goods problem. As the effect of a successful rabies elimination is going to last for generations a strategic coordination and the forming of alliances is key to realize these benefits. This game theoretical discussion enables a political discourse which can enable a regional elimination of rabies.

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Human, social and ethical dimensions of outbreak preparedness and response efforts (ie. social and economic inequalities, public trust, moveme
Abstract No: 15332

An Engagement and Advocacy lesson for rabies prevention: Singapore's Trap-Neuter-Release-Manage Programme and mass rabies vaccination

Kelvin Ho*[1] ; Anhui Lin[1] ; Evan Lin[1] ; Hui Ling Lin[1] ; Kelvin Lim[1] ; Charlene, Judith Fernandez[1] ; Tze Hoong Chua[1] ; Siow Foong Chang[1] ; Him Hoo Yap[1]
[1]Animal and Veterinary Service/ National Parks Board/ Singapore

Introduction and Objectives or Purpose

Singapore has been rabies-free since 1953. To mitigate the risk of rabies incursion from surrounding endemic countries, Singapore launched the five-year nationwide Trap-Neuter-Release-Manage programme in 2018 that employed humane, science-based methodology to sustainably reduce the local free-roaming dog population. The annual rabies vaccination programme for pet dogs living in Singapore's coastal regions and off-shore islands also started in 2016, to ensure adequate rabies seroconversion in this at-risk population. Both initiatives require sustained engagements with relevant stakeholders to ensure seamless implementation of the programmes. The objective is to describe the success factors behind the engagement and advocacy journey for rabies prevention in Singapore.

Methods

The engagement toolkit comprises of 1) Establishing a set of clear, relevant and realistic objectives 2) Determine the relevant stakeholders and partners that are crucial to the initiatives. 3) Develop a roadmpa and operation plan, 4) Advocacy and funding, 5) Awareness building and education, 6)Celebrate early successes and project achievements.

Results or Focus

More than 3,100 stray dogs have been trapped under the programme, with more than 60% of the dogs being rehomed or fostered. Moreover, the results from the rabies vaccination study have demonstrated rabies seroconversion above 80%, reflecting the effectiveness of the programme. This is supported by strong buy-in and support from community caregivers of the dogs and local animal welfare groups. There has been over-subscribed participation from private veterinarians, and students in the annual vaccination exercises. Policy makers have signalled their support through social media publicity of these efforts.

Conclusion or Scope

The impact of rabies is primarily on human health, but disease prevention efforts need to start from the animal source through sustained Dog Population Management (DPM) interventions. A strong engagement and advocacy approach ensured the successful implementation of rabies prevention and control measures in Singapore.

Acknowledgement

Lim HweePing, Teo BoonHan, Toh Xinyu, Wang Yifan, Ng OiWing, Huangfu Taoqi, Wong WaiKwan

Keywords: engagement and advocacy for rabies prevention, Trap-Neuter-Release-Manage programmes, rabies vaccination, e

Topic: Policy, Environment & Biosecurity (PEB): Globalisation and human drivers of disease in a rapidly changing world: Social inequalities and pandemic risk
Abstract No: 15045

Stressors and coping strategies of migrant workers diagnosed with COVID-19 in Singapore: a qualitative study

Kaisin Yee[*1 2 3] ; Hui Peng Peh[1] ; Yee Pin Tan[1] ; Irene Teo[1] ; Emily U Tong Tan[1] ; Justin Paul; Mahalakshmi Rangabashyam; Mothi Babu Ramalingam; Weien Chow[1] ; Hiang Khoon Tan[1 3]
[1]-/ SingHealth COVID-19 Community Care Facilities/ Singapore, [2]Department of Global Health and Population/ Harvard TH Chan School of Public Health/ United States, [3]-/ SingHealth Duke-NUS Global Health Institute/ Singapore

Introduction and Objectives or Purpose

The health, psychological and socioeconomic vulnerabilities of low-wage migrant workers have been magnified in the COVID-19 pandemic, especially in high-income receiving countries such as Singapore. We aimed to understand migrant worker concerns and coping strategies during the COVID-19 pandemic to address these during the crisis and inform on comprehensive support needed after the crisis.

Methods

In-depth semi-structured interviews were carried out with migrant workers diagnosed with COVID-19. The participants were recruited from a COVID-19 mass quarantine facility in Singapore through
a purposive sampling approach. Interviews were transcribed verbatim and thematic analysis performed to derive themes in their collective experience during the crisis.

Results or Focus

Three theme categories were derived from 27 interviews: migrant worker concerns during COVID-19, coping during COVID-19 and priorities after COVID-19. Major stressors in the crisis included the inability to continue providing for their families when work is disrupted, their susceptibility to infection in crowded dormitories, the shock of receiving the COVID-19 diagnosis while asymptomatic, as well as the isolating conditions of the quarantine environment. The workers coped by keeping in contact with their families, accessing healthcare, keeping updated with the news and continuing to practise their faith and religion. They looked forward to a return to normalcy after the crisis with keeping healthy and having access to healthcare as new priorities.

Conclusion or Scope

We identified coping strategies employed by the workers in quarantine, many of which were made possible through the considered design of care and service delivery in mass quarantine facilities in Singapore. These can be adopted in the set-up of other mass quarantine facilities around the world to support the health and mental well-being of those quarantined. Our findings highlight the importance of targeted policy intervention for migrant workers, in areas such as housing and working environments, equitable access to healthcare, and social protection during and after this crisis.

Acknowledgement

Keywords: migrant health; pandemic response; migrant workers; mental health

Topic: Policy, Environment & Biosecurity (PEB): Science of Climate and Ecological Change of One Health: Rabies and dog
Abstract No: 15255

Family health and canine companionship: a qualitative exploration from rural Sri Lanka

Devarajan Rathish[*1 2] ; Jayanthe Rajapakse [1] ; Kosala Weerakoon [3]
[1]Department of Veterinary Pathobiology/ Faculty of Veterinary Medicine and Animal Science, University of Peradeniya/ Sri Lanka (□□□□ □□□□□□) [2]Department of Family Medicine/ Faculty of Medicine and Allied Sciences, Rajarata University of Sri Lanka/ Sri Lanka (□□□□ □□□□□□) [3]Department of Parasitology/ Faculty of Medicine and Allied Sciences, Rajarata University of Sri Lanka/ Sri Lanka (□□□□ □□□□□□)

Introduction and Objectives or Purpose

The one-health concept identifies the human-animal bond as a mode to improve mental well-being. Dog ownership is associated with positive health benefits like improved physical activity and cardiovascular health. We aim to explore owners' perceptions of their dogs' impact on family health in Anuradhapura, a rural district of Sri Lanka. Such information from rural regions is limited.

Methods

A descriptive qualitative design using in-depth interviews and observation of owner-dog interaction during the interview at the private residences of the participants. Dog owners aged 40-65 years, residing in Anuradhapura, Sri Lanka for at least 5 years, owning ≤3 dogs, and did not own other pets for the last 1 year were recruited. The wave of participants was formed using snowball sampling. Interviews were tape-recorded and transcribed and thematic analysis was performed.

Results or Focus

Data from 24 participants were collected and most shared responsibility for pet care (88%) and had only one pet dog (50%). The village dog and the German Shepherd were the most common pet dog breeds. The participants had and received an excellent level of attention towards and from their pet dogs. Also, they perceived stress reduction and mental satisfaction while interacting with pet dogs. Further, the child's preference was an important factor in owning a pet dog. However, expense and reduced travel were highlighted as concerns of dog ownership. Some have experienced grief due to the loss of a pet. Nevertheless, owners seldom experienced any health risks from their pet dogs.

Conclusion or Scope

The perceived mental well-being among dog owners will help plan out research and intervention on one health. However, concerns such as expense and reduced travel need to be addressed. The willingness to adopt village dogs should be guided by responsible pet ownership in rural regions.

Keywords: Child's preference; Mental well-being; One Health; Village dog