8 September 2025

Asia PGI Webinar: Field-deployable methods for genomic surveillance of high-risk viruses and animal hosts – Q&A with Dr. Anna S. Fomsgaard

1. How do you ensure proper observance of biosafety and biosecurity measures when in the field? What measures do you take when you are able to detect a pathogenic virus during surveillance? Do you undergo quarantine since you have been exposed to an infected animal?

   We talked about this in the Q&A but briefly, biosafety and biosecurity are ensured through adherence to PPE protocols and proper training. Training in donning and doffing procedures ensures that personal protective equipment (PPE) is worn and removed correctly. We follow the risk-based PPE approach, adjusting the level of protection depending on the nature of the animal, the likelihood of zoonotic pathogen exposure, and the procedures performed (e.g., necropsy vs. non-invasive sampling).

2. Could you shed light on how you select the area for surveillance?

   That is a wonderful question that I myself am very occupied with. But to keep my answer as short as possible, I'll answer from my presentation where we are surveilling at live bird markets in Cambodia. We select this "area" because it is an established human-animal interface, and although it is important for economic realities, cultural practices, and food security in the region, we are aware that there are potentials for zoonotic spillovers. Here's a paper from 2022 about live bird markets and InfA exposure in Cambodia to highlight why we should surveil in this "area" https://doi.org/10.1111/zph.13009 .

3. What is the difference between metagenomic approach and the approach you developed in terms of wet lab workflow and data analysis? And why choose this approach over metagenomics?

   We talked about this in the Q&A but briefly, panviral sequencing is a semi-targeted method that uses broadly primers to amplify conserved regions across entire virus families or genera, striking a balance between sensitivity and breadth. This approach enhances detection of both known and non-hypothesised viruses while reducing background noise from host or environmental nucleic acids which you will get in metagenomic datasets.

4. What handheld air filter device did you use for your sampling campaign?

   We are currently testing various air filter devices. In the talk the Aerocollect was featured https://aerocollect.dk/

We are also using https://www.fishersci.com/shop/products/aerosolsense-airborne-pathogen-detection-solution/2900AA for comparison.

5. Have you tried the new Mk1D Minion and does it deal with tropical temperatures better?

   Yes, Mk1D MinION is used with the field-deployable laboratory. It performs in tropical climate, I have not had an issue with it.

6. Is there any freely available bioinformatics platform for Nanopore data analysis?

   Many bioinformatic data analysis tools are free, so it depends on what you want to do. ONT has their own Whats-In-My-Pot (WIMP) analysis for example. I talked about Basestack and Mytax2 software. There is also https://usegalaxy.org/ or Github for bioinformatic scripts.

7. Could you speak more about the real-time bioinformatics pipeline? What kind of internet requirements does it take to run? What kind of IT infrastructure requirements (laptop/workstation)? Is the bioinformatics tool downstream from MinKnow open-source and does it work offline (if internet connection drops)?

   I believe we talked about this in the Q&A but briefly, the Basestack Mytax2 pipeline is offline, works on a laptop, is not linked to MinKNOW software. It takes the fastq_pass files and assign the reads in real-time.

8. How is PiiP designed for selected targets?

   We talked about this in the Q&A but briefly, panviral primers for a virus genus are designed to target highly conserved regions shared across all (or most) members of that genus. This allows a single primer set to amplify multiple viral species or strains within the same genus.

9. Are the PiiP primer sequencing primers available to the public?

   Thank you for the interest, they will be available to the public this year when we publish.

10. May I know how we can request for access to your mentioned pan viral primers?

    Thank you for the interest, I'd be happy to share when we have published. Thank you for understanding.

11. My team specializes in wastewater surveillance research. Are there potential collaboration opportunities to advance technologies in both wet and dry lab domains?

I would be happy to hear more about what you are working on specifically and your approach to wastewater pathogen surveillance. We are also working on similar things at the Virology Unit at Institut Pasteur du Cambodge.