

Day 1: APEC Food Safety Cooperation Forum PTIN WGS Workshop for Food Safety Experts and Policymakers Zoom Chat Transcript

From Kelly.McCormick@fda.hhs.gov : WELCOME

- Please keep yourself MUTED for the duration of the event.
- Type any questions you may have into the Zoom CHAT function. You may wish to wait to enter your query until shortly before each Session's Q&A to ensure it is not addressed by presentations delivered in the interim.
- Most presentations, as well as a recording of the workshop, will be made available on Agrilinks and SPSCourses.com following the event conclusion.

From Kelly.McCormick@fda.hhs.gov : Final Agenda and Bios:

From SENASICA MX Fabiola Hernandez : Question for Eric Stevens

It is becoming less frequent for a work team to close genomes. What is your opinion of the regional references? Do you consider them valuable?

From Jay Chatterjee : Question for Eric: Does this sequencing strategy can identify (rare) transmission of genetic material between host and a pathogen (plant or animal hosts)? Or will such exchange be considered "errors"?

From USA - Eric Stevens : typically what we do is several iterations using different reference genomes available at NCBI to try and get a reference genome that is about 100 - 200

From USA - Eric Stevens : SNPs away and then use that reference genome for the final analysis

From USA - Eric Stevens : so i think, if i understood your question correctly, that using regional references that are available is fine

From USA - Eric Stevens : which is a benefit of sharing sequences since it is becoming more likely that someone out there has already fully closed a genome that is reasonably closely related to the genomes you are working with

From SENASICA MX Fabiola Hernandez : Great, thanks Eric

From USA - Eric Stevens : re: Jay; just to make sure i understand, are you asking about detecting contaminated reactions where you are sequencing both microbial and human DNA or are you asking about detecting about extraneous DNA that was taken up and incorporated into the microbial genome?

From Jay Chatterjee : Eric: Sorry for not being clearer. I am not asking for contamination during DNA isolation. But actual transfer of DNA from one organism to another (e.g. plant plastids were actually DNA sequence from bacteria- long ago). There are many such examples (although it's very, very rare events even in terms of natural mutations)

From Jay Chatterjee : lateral gene transfer

From Kelly.McCormick@fda.hhs.gov : A reminder again,

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From USA - Eric Stevens : if you are talking about detecting non-microbial DNA that originated from another species but was incorporated into the microbial genome, then it would likely depend on both the sequencing method chosen and whether a reference genome was used. If long read sequencing was used then you would have a better shot at reconstructing the full genome (including what came through lateral gene transfer) than if you used shorter read sequencing but only denovo reassembly (without a reference) would enable you to reconstruct the full sequence. The use of a reference sequence limits your reconstruction to what is contained in the reference genome (because you are using it as a guide). Hence why long read sequencing with denovo assembly would be your best shot

From Jay Chatterjee : Thanks Eric!

From USA - Eric Stevens : i loved your slides, Magaly. Totally going to ask to borrow some of your graphics!

From Magaly Toro : Sure Eric

From USA - Eric Stevens : (and your science is SO cool. makes me want to sample the streams in my neighborhood to see what is out there!)

From Magaly Toro : Hi Kelly, the pop up chart is very distracting for the speakers!

From Kelly.McCormick@fda.hhs.gov : We are on a 10-minute BREAK. Please be back at your computers by 21:40 EST.

From Magaly Toro : well, for me

From Magaly Toro : we had so many Salmonella!

From Kelly.McCormick@fda.hhs.gov : Welcome back!

From Cathy Carrillo : Nigel: How do you think campylobacter would spread through the feed network? I wouldn't think it would survive in feeds?

From npfrench : I agree Cathy, I think its unlikley to persist in feed, but I think it may be a proxy for the movement of vehicles and personnel between farms, associated with suboptimal biosecurity

From Kelly.McCormick@fda.hhs.gov : Please type any questions you may have into the Zoom CHAT function!

From Yohanes_ASAHI_JAPAN : Question for Dr. Magaly Toro or Dr. French:
Thank you for your presentations.

1. In practice, between cgMLST and wgSNP, which method would you prefer to investigate an outbreak (from the point of database availability, bioinformatics tool, data resolution, etc)?

From Cathy Carrillo : Eric: Do you think transition to Nanopore only sequencing is going to happen sometime soon for food-pathogen tracking?

From Kelly.McCormick@fda.hhs.gov : Also - all speakers from this session are welcome to add on to responses provided.

From Marc Allard : Has Nigel worked with other regions to solve global outbreaks in real-time. This would require global data sharing otherwise howdto they see the linkages between the various genomes publicly available. or are they doing surveillance of the publicly available data and reach out to any matches

From SENASICA MX Fabiola Hernandez : Talking about harmonization and quality standards. What do all speakers think about the arrive of the ISO/DIS 23418 Microbiology of the food chain Whole genome sequencing for typing and genomic characterization of foodborne bacteria-General requirements and guidance. <https://www.iso.org/standard/75509.html>

From JinHon : Would someone in the speakers panel can share insights on the overall trend of taking up WGS in foodborne outbreak investigations among APEC member economies? Ideally the insight can touch infrastructure (equipment, coordination, bioinformatics), skills requirements, and cost and benefits.

From Yohanes_ASAHI_JAPAN : cgMLST and whole genome SNP(wgSNP)

From Kelly.McCormick@fda.hhs.gov : 2 minute warning!

From USA - Eric Stevens : really happy you touched on that Magaly. you described that so much better than i did!

From Emma Aspell - USDA FAS : Hello everyone, If you'd like to remove the chat screen from your window, please refer to the down arrow in the top left of the chat box. Once you click on

the arrow, you will be able to select close. If you have any other questions regarding zoom functionality, please don't hesitate to ask.

From Yohanes_ASAHI_JAPAN : Thank you Dr. Toro

From Kelly.McCormick@fda.hhs.gov : Thanks everyone for staying a bit late! We'll see you tomorrow for Day 2. We have another excellent team of speakers and moderators for you. Please remember that the Zoom link for tomorrow is not the same as the one for today.