PulseNet Track: Session 1

Adapting Workflows for WGS: Where are we now and what's to come?

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Overview

- Brief discussion from select laboratories
  - Small group discussions
  - Large group discussion
  - Wrap-up

Questions to think about

- **Do you receive primary samples and/or isolates for sequencing, and in about what proportion for each organism?**
- Does your workflow incorporate CIDT's (Pros, Cons, How to improve run)? Reflex culturing for CIDT positive assays?
- **Does your laboratory workflow allow for a 7 working TAT (Yes (How), No (Why), and improvements)?**
- How do you deal with too few samples to fill a standard MiSeq reagent kit in order to meet TAT? Do you use Micro or Nano reagent kits?
- **Do you employ V2 or V3 chemistry or both?**
- Are you considering using Nextera DNA Flex library for library prep?
- **Do you use, or would you consider using a NextSeq for sequencing large batches (about 80 Salmonella genomes on one run and uses 2X150 chemistry)?**
- Do you use robotics for extraction and/or library prep and how does it impact cost and TAT?
- **Aside for $$, are there other issues preventing your lab from conducting real-time surveillance (what support/ideas would be required to improve it)?**
- How is your laboratory prioritizing sequencing all salmonella samples? Decision criteria? Continuing PFGE to determine what to sequence? # and % PFGE v WGS
- **How do you handle repeat sequencing results from the CDC and how does it impact your workflow? Do you start from extracting the isolate or somewhere else in the workflow?**
- Did your laboratory go through any reorganization to support WGS?

Wrap-up

- Questions and/or concerns?
  - Final thoughts?

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  - APHL
  - PulseNet
  - (Special presenters ??)