Next Generation Sequencing

Has Public Health found its killer technology?

Session Review
What have we learned?
I mean, what was the **MOST** important thing that we learned?
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Hot sauces and acid fruits are not prophylactic for Vibrio infections!!
Seriously:

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But:
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2. Strategic level tracking of a pathogen over time
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Under the surface, this array of experiences reveals the awesome diversity in how this technology can assist public health:

1. High resolution outbreak assessment
2. Strategic level tracking of a pathogen over time
3. More data, more accurately, more quickly, for improved TAT
In outbreak assessments of Vibrio, Campylobacter and Salmonella from Julie Haendiges and Kelly Oakeson:

-PFGE can’t tell things apart well enough for a complete understanding of outbreaks
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- Resources are limited in public health
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- changes in individual genes over time, can tell us as much about our own interventions (or lack thereof), than it does about the opponent organisms themselves
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- Again:
- Can preserve resources
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- More data
- More complete information
- Can lead to quicker outcomes
- Can lead to less ambiguity
- Again:
- Can preserve resources
- Allow resources to be more productively utilized
It doesn’t end here...
Other utilities for NGS
In New York State and CDC:

- Drug resistance assessment in Mycobacterium tuberculosis

- All the drugs / genes in a single test

- First line, second line

- Would eventually allow for strain typing, simultaneously
Replacing general bacteriology with NGS in Alameda County, CA has allowed:

- Bacterial identification
- Salmonella serotyping in real time
- Certain drug susceptibility assessments in real time
- Detailed monitoring of our CRE cases
- Resolution of possible lab error
Next Steps

• Seek ways to get this technology in wide use
  – Equipment and Software;

• Power of NGS grows exponentially, when more people use it and data is shared

• Metagenomic applications: specimens vs. isolates
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Thank you to our speakers, and to APHL for hosting this session.