The Use of Whole Genome Sequencing in the PulseNet Network

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Outline

- Overview of PulseNet and WGS Implementation
- Impact of COVID on PulseNet
- Use of WGS in Outbreak Detection
- New Paradigms of Molecular Surveillance: Reoccurring, Emerging, and Persisting (REP) Strains
- New ways to View PulseNet Data: BEAM dashboard

87 labs participate:
- All state health departments
- City health departments
- FDA & USDA laboratories

Links with:
- PulseNet Canada
- PulseNet International

- Standard laboratory methods
- Results submitted to national database
- All participants can search for matches

Every year PulseNet saves at least half a billion dollars in medical costs and lost productivity.

$1 spent = $70 saved!

PulseNet: Detection outbreaks with molecular data

Public health labs generate molecular fingerprints using WGS

Data from pathogens are transmitted to centralized database at CDC in Atlanta, Georgia

PulseNet Monitors for clusters of illnesses with the same molecular “fingerprint”

Then tells epidemiologists about clusters to investigate

Bacteria with the same molecular “fingerprint” are more likely to come from a common source
PulseNet by the Numbers: Overall Submissions to PulseNet, Human and Non-Human

Submissions to PulseNet USA, 1996-2021

* Transition from PFGE to WGS July 15, 2019
†March 11, 2020, COVID-19 declared pandemic
PulseNet Submissions during COVID

Human STEC Uploads

Human Salmonella Uploads

Human Listeria Uploads

Human Campylobacter Uploads

Human Uploads to PulseNet, 5-yr average compared to 2020/2021, by month

Notes: 5-year average calculated from 2015-2019; fully transitioned from PFGE to WGS July 15, 2019

*March 11, 2020, COVID-19 declared pandemic
Impact of WGS Implementation on Foodborne Outbreak Surveillance

- Smaller, more numerous potential outbreaks identified
- More available data to evaluate
  - Genetic analyses, historical, food/environmental, international
- Can apply novel methodologies and technologies to aid outbreak investigations
- Can identify new trends in data and link historic isolates with more precision
Using WGS to Link Clinical Cases with Outbreak Source

Listeria monocytogenes outbreak associated with cheese (2013)

= epi-related clinical cases
= historical isolates from cases (same PFGE pattern)
= environmental isolates
= closely genetically related

www.cdc.gov/listeria/outbreaks/cheese-07-13/index.htm
WGS analysis of a representative sample of isolates belonging to a *Salmonella* Newport cluster associated with melons

- Isolates with earlier isolation dates formed one clade
- As the outbreak continued, isolates with later isolation dates formed a new clade
- Ultimately, all isolates were included in the outbreak investigation and found to be linked to melons
- Epi info indicated a common supplier for the melons and traceback info from FDA indicated a single farm

WGS analysis can be used to compare strains from the region over time.
WGS helps identify challenges beyond outbreaks: Reoccurring, Emerging, and Persisting (REP) Strains

- **Reoccurring Strain**: Strain that periodically causes a substantial number of illnesses, typically in outbreaks, separated by periods when it is not isolated from people or it causes very few illnesses.

- **Emerging Strain**: Strain that causes illnesses that have increased in frequency, or have the potential to increase in frequency, over time.

- **Persisting Strain**: Strain that causes illnesses consistently over time, although the frequency of illnesses may fluctuate.
How Are REP Strains Identified?

- Outbreak investigations
- Identifying pathogens in foods, production environments, or growing regions
- Searching for groups of genetically related clinical isolates in whole genome sequence databases
Investigating REP Strains

- Repeated/ongoing identification of the same strain suggests that there is an “upstream” contributor or reservoir likely at play

- Traditional outbreak control measures like product recalls may fail to address the underlying contributors to the problem

- Additional investigational approaches are needed for REPs beyond what is used in typical outbreak investigations
  - Collaboration with external partners: other federal agencies, academia, industry, etc.
  - Special/targeted epidemiologic studies
  - Other novel approaches
    - Source attribution studies
    - Long-term prevention measures
Potential Importance of REP in Reducing Disease Incidence

- Only a small fraction of illnesses are linked to an outbreak
  - Most illnesses reported through PulseNet are not linked to a source
  - ~90% of isolates are not identified as part of an outbreak

- REP strains could represent a larger fraction of illnesses than traditional outbreaks

- Driving down incidence of enteric and other foodborne pathogens requires better understanding of seemingly “sporadic” illness

- WGS provides new opportunities to attribute contamination source to “sporadic” illnesses
Utility of REP Strains

- Have identified over 20 REP strains of *Salmonella, STEC, Listeria*, and *Campylobacter*
- Continue to identify new REP strains and modify as needed definitions of existing REPs as strains evolve
- Applying new tools including accessory genome analysis to better characterize REP strains
- Coming soon – website about REP strains as well as more specific information on individual REP strains
Improving Accessibility of PulseNet Data: BEAM (Bacteria, Enterics, Amoeba, and Mycotics) Dashboard

- Tool to make actionable data from PulseNet readily accessible
- Power BI dashboard to visualize trends in PulseNet data
- Initially displaying PulseNet Salmonella data, in the future will include additional pathogens and AMR data
- Coming soon at: https://www.cdc.gov/ncezid/dfwed/BEAM-dashboard.html
Conclusions

- WGS creates new opportunities for:
  - Data sharing
  - Identifying new types of strains: REP strains
  - Data visualization on BEAM dashboard
Thank you!

For more information:
https://www.cdc.gov/ncezid/dfwed/edlb/index.html
https://www.cdc.gov/pulsenet/index.html
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The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.