PulseNet: A Network with a Glorious Past and a Bright Future

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Branch Chief

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6/7/2016
The Outbreak That Started It All

1993 Jack-in-the-Box *E. coli* O157 Outbreak

- Outbreak detected
- 732 ill, 4 deaths
- 39 days

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Laboratory Investigation of a Multistate Food-Borne Outbreak of *Escherichia coli* O157:H7 by Using Pulsed-Field Gel Electrophoresis and Phage Typing

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Two hundred thirty-three isolates of *E. coli* O157:H7 were analyzed by both pulsed-field gel electrophoresis (PFGE) and bacteriophage typing. All 23 isolates from persons whose illness was associated with a recent outbreak of *E. coli* O157:H7 (sesame linked to the consumption of undercooked hamburgers and all 27 isolates from uncooked lots of hamburger meat had the same phage type and the same PFGE pattern. Twenty-two of 74 J. E. O157:H7 isolates from Washington State and 58 of 77 isolates from other states obtained during the 4 months before the outbreak had the same phage type as the outbreak strain, but only 1 isolate had the same PFGE pattern. PFGE thus appeared to be a more sensitive method than bacteriophage typing for distinguishing outbreak and non-outbreak-associated strains. The PFGE patterns of seven non-outbreak sporadic isolates and five sporadic isolates from the outbreak period differed from that of the outbreak strain by a single band, making it difficult to identify these isolates as outbreak or non-outbreak related. Phage typing and PFGE with additional enzymes were helpful in resolving this problem. While not as sensitive as PFGE, phage typing was helpful in interpreting PFGE data and could have been used as a simple, rapid screen to eliminate the need for performing PFGE on unrelated isolates.
The Stars Had To Align

WHO-sponsored international collaborative study to evaluate methods for subtyping *Listeria monocytogenes*: restriction fragment length polymorphism (RFLP) analysis using ribotyping and Southern hybridization with two probes derived from *L. monocytogenes* chromosome

B. Swaminathan\textsuperscript{a,\*}, Susan B. Hunter\textsuperscript{a}, P.M. Desmarchelier\textsuperscript{b}, Peter Gerner-Smidt\textsuperscript{c}, L.M. Graves\textsuperscript{a}, Susan Harlander\textsuperscript{a}, Romeo Hubner\textsuperscript{d}, Christine Jacquet\textsuperscript{e}, Britta Pedersen\textsuperscript{f}, Kristin Reineccius\textsuperscript{g}, Anne Ridley\textsuperscript{h}, N.A. Saunders\textsuperscript{i}, John A. Webster\textsuperscript{j}

Genomic fingerprinting of 80 strains from the WHO multicenter international typing study of *Listeria monocytogenes* via pulsed-field gel electrophoresis (PFGE)

Roland Brosch\textsuperscript{a,\*}, Maggie Brett\textsuperscript{b}, Benedicte Catimel\textsuperscript{c}, John B. Luchansky\textsuperscript{a}, Bente Ojeniyi\textsuperscript{d}, Jocelyne Rocourt\textsuperscript{e}

Computerized Analysis of Restriction Fragment Length Polymorphism Patterns: Comparative Evaluation of Two Commercial Software Packages

P. Gerner-Smidt\textsuperscript{a,\*}, L. M. Graves\textsuperscript{b}, Susan Hunter\textsuperscript{c,\*}, and B. Swaminathan\textsuperscript{d}

Department of Gastrointestinal Infections, Statens Seruminstitut, Copenhagen, Denmark; and Foodborne and Diarrheal Diseases Branch, Division of Bacterial and Mycotic Diseases, Centers for Disease Control and Prevention, Atlanta, Georgia
Early Meetings And Trainings
Early Meetings And Trainings
Rapid Pulsed-Field Gel Electrophoresis Protocol for Typing of *Escherichia coli* O157:H7 and Other Gram-Negative Organisms in 1 Day

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Received 23 April 1997/Returned for modification 30 June 1997/Accepted 28 July 1997

Genomic DNA patterns generated by pulsed-field gel electrophoresis are highly specific for different strains of an organism and have significant value in epidemiologic investigations of infectious-disease outbreaks. Unfortunately, time-consuming and tedious specimen processing is an inherent problem which limits the use of this powerful technology as a real-time epidemic investigational tool. Here, I describe a rapid method to improve the response time and provide specific bacterial strain identification for the typing of *Escherichia coli* O157:H7 and other gram-negative organisms in a single day.
Early Meetings And Trainings
Early Meetings And Trainings
Innovations In American Government Award 1999
PulseNet For Dummies
First Cost Benefit Study

Dispatches

Costs and Benefits of a Subtype-Specific Surveillance System for Identifying *Escherichia coli* O157:H7 Outbreaks

Elamin H. Elbasha,* Thomas D. Fitzsimmons,*† and Martin I. Meltzer*

*Centers for Disease Control and Prevention, Atlanta, Georgia, USA; and †Colorado Department of Public Health and Environment, Denver, Colorado, USA

We assessed the societal costs and benefits of a subtype-specific surveillance system for identifying outbreak-associated *Escherichia coli* O157:H7 infections. Using data from Colorado, we estimated that if it averted five cases annually, the system would recover all its costs.
In 2002, PulseNet was recognized as one of the fifteen most significant government initiative programs to have won the prestigious Innovations in American Government Award.

The Innovations in American Government Program had received over 23,000 applications by 2002. The award places the PulseNet program among the top 0.0007% of all the programs that have applied to the Innovations in American Government Program. Also in 2002, PulseNet was recognized as a runner-up for the Highest Public Health Impact Program Award Program for more information.

In 1999, PulseNet was inaugurated by the Vice President of the United States in a ceremony held at the White House. The Innovations in American Government Program is a significant force in identifying and promoting excellence and creativity in the public sector. PulseNet was issued the Innovations in American Government Award in 1999.

Please view the Innovations in American Government Award Program for more information.
Meetings And Trainings
Meetings And Trainings
Universal Size Standard Strain
(Salmonella ser. Braenderup H9812)

Four organism-specific standards
One standard for ALL organisms
New Methods: MLVA

Multiple-Locus Variable-Number Tandem-Repeat Analysis as a Tool for Subtyping *Listeria monocytogenes* Strains

Katharine E. Volpe Sperri, Sophia Kaitariou, Justin S. Edwards, and Leslie A. Wolf
North Carolina State Laboratory of Public Health, Raleigh, North Carolina, and North Carolina State University, Raleigh, North Carolina

Second Generation Subtyping: A Proposed PulseNet Protocol for Multiple-Locus Variable-Number Tandem Repeat Analysis of Shiga Toxin-Producing *Escherichia coli* O157 (STEC O157)

Eija Hyytia-Trees, Sandra C. Smole, Patricia A. Fields, Bala Swaminathan, and Efrain M. Ribo

Comparison of Multiple-Locus Variable-Number Tandem Repeat Analysis, Pulsed-Field Gel Electrophoresis, and Phage Typing for Subtype Analysis of *Salmonella enterica* Serotype Enteritidis

D. Boorud, K. Pederson-Gurud, J. Wotton, C. Medus, E. Lyszkowicz, J. Besser, and J. M. Bartkus
Minnesota Department of Health, Minneapolis, Minnesota, and Centers for Disease Control and Prevention, Atlanta, Georgia
PulseNet Impact

The decade's 10 biggest food-borne illness outbreaks

By Jacque Wilson, CNN
updated 11:04 AM EST, Fri Oct 14, 2011
16 New Vehicles in Outbreaks in the United States, 2006 - 2015

Data Sources: PulseNet, OutbreakNet, Foodborne Disease Outbreak Surveillance System

- Bagged spinach
- Carrot juice
- Peanut butter
- Broccoli powder on a snack food
- Dog food
- Pot pies
- Canned chili sauce
- Hot peppers
- White pepper
- Raw cookie dough
- Whole, raw papaya
- Hazelnuts
- Pine nuts
- Mechanical deboned tuna
- Cashew cheese
- Caramel apples

Data are preliminary and subject to change
PulseNet Now:
Whole Genome Sequencing (WGS): A Paradigm Shift In Public Health Microbiology
Listeria Cluster Metrics Before and After WGS

- No. of clusters detected:
  - Pre-WGS (Sept 2012–Aug 2013): 14
  - WGS Year 1 (Sept 2013–Aug 2014): 19
  - WGS Year 2 (Sept 2014–Aug 2015): 21

- No. of clusters detected sooner or only by WGS:
  - Pre-WGS: N/A
  - WGS Year 1: 6
  - WGS Year 2: 6

- No. of outbreaks solved (food source identified):
  - Pre-WGS: 2
  - WGS Year 1: 4
  - WGS Year 2: 9

- Median no. of cases per cluster:
  - Pre-WGS: 6
  - WGS Year 1: 4
  - WGS Year 2: 3

- No. of cases linked to food source:
  - Pre-WGS: 6
  - WGS Year 1: 16
  - WGS Year 2: 93

Courtesy: Brendan Jackson, Enteric Diseases Epidemiology Branch
HHS Innovates Award 2014 - Secretary’s Pick
CDC Director’s Award for Innovation 2015
PulseNet WGS Certifications

- Passed certifications as of June 2\textsuperscript{nd} 2016:
  - PNUSA: 24 labs, 23 states, 55 individuals
  - PNI: 1 lab, 1 individual

- Pending:
  - 2 complete submissions awaiting for evaluation at CDC
  - 3 partial submissions waiting for additional files to be submitted
## Projected wgMLST Database Validation and Deployment Timeline

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<td>External validation</td>
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- Listeria monocytogenes
- Campylobacteraceae & Shiga toxin-producing E. coli (STEC)
- Salmonella
- Vibrio, Shigella & other diarrheagenic E. coli
- Cronobacter & Yersinia
CIDTs Are Coming!

World’s Most Portable Molecular Diagnostics System Unveiled at AACC
GeneXpert Omni to Further Decentralize Critical TB, Virology and Ebola Tests

SUNNYVALE, Calif. and GENEVA, July 28, 2015 /PRNewswire/ -- Cepheid (Nasdaq: CPHD) and FIND today unveiled GeneXpert® Omni, the world’s most portable molecular diagnostics system enabling unprecedented access to accurate and potentially life-saving diagnosis for patients suspected of TB, HIV and Ebola in even the most remote areas of the world.

NEW xTAG® Gastrointestinal Pathogen Panel (GPP)

The evolution of GI diagnosis

Now you can test for 15 key bacteria, viruses, and parasites – all in under 5 hours

xTAG® GPP is the first diagnostic to offer detection of 15 major gastrointestinal pathogens in a single test
Results within 5 hours for timely and better patient care
Fast kon-knockdown time and sensitivity

July 28, 2015
Crisis!

Danger + Opportunity
PulseNet USA Strategy to Meet The Challenge of Culture Independent Diagnostic Methods

1. Preserve cultures
   - Surveillance by current methods (Serotyping, PCR, AR, PFGE, MLVA)

2. Prepare for the future working on pure cultures
   - Surveillance by whole genome sequencing

3. Metagenomics
   - No cultures
   - Surveillance and diagnostics by metagenomics
“That’s been one of my mantras — focus and simplicity. Simple can be harder than complex...once you get there, you can move mountains.”

-Steve Jobs
The Stool Metagenomics App & The Ultra-Portable Sequencer
No Matter Where You Go
- There You Are

Confucius / (Buckaroo Banzai)
THE FUTURE AIN'T WHAT IT USED TO BE

YOGI BERRA

BUT IT WILL BE FUN!

PETER GERNER-SMIDT
Acknowledgements

The greatest group of people to work with:

Disclaimers:

“The findings and conclusions in this presentation are those of the author and do not necessarily represent the official position of the Centers for Disease Control and Prevention”

“Use of trade names is for identification only and does not imply endorsement by the Centers for Disease Control and Prevention or by the U.S. Department of Health and Human Services.”