InFORM 2017

Integrated Foodborne Outbreak Response Management Conference

November 6–9, 2017
Hyatt Regency Orange County
Garden Grove, CA

Conference Program
# Schedule at a Glance

## Monday, November 6 • Day 1

<table>
<thead>
<tr>
<th>Event</th>
<th>Time</th>
<th>Location</th>
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<tbody>
<tr>
<td>Registration</td>
<td>12:00 pm – 7:00 pm</td>
<td>Royal Registration</td>
</tr>
<tr>
<td>Posters Available</td>
<td>1:00 pm – 8:30 pm</td>
<td>Grand A–D</td>
</tr>
<tr>
<td>Open Sessions</td>
<td>1:00 pm – 3:00 pm</td>
<td>Various Rooms</td>
</tr>
<tr>
<td>Break</td>
<td>3:00 pm – 3:30 pm</td>
<td>Grand A–D</td>
</tr>
<tr>
<td>Open Sessions</td>
<td>3:30 pm – 5:30 pm</td>
<td>Various Rooms</td>
</tr>
<tr>
<td>Break</td>
<td>5:30 pm – 6:00 pm</td>
<td>Grand A–D</td>
</tr>
<tr>
<td>Welcome and Keynote</td>
<td>6:00 pm – 7:30 pm</td>
<td>Royal Ballroom</td>
</tr>
<tr>
<td>Reception (Cash Bar)</td>
<td>7:30 pm – 8:30 pm</td>
<td>Royal Foyer</td>
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## Tuesday, November 7 • Day 2

<table>
<thead>
<tr>
<th>Event</th>
<th>Time</th>
<th>Location</th>
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<tbody>
<tr>
<td>Registration</td>
<td>7:15 am – 5:00 pm</td>
<td>Royal Registration</td>
</tr>
<tr>
<td>Posters Available</td>
<td>8:15 am – 5:00 pm</td>
<td>Grand A–D</td>
</tr>
<tr>
<td>Sponsor Displays</td>
<td>9:45 am – 4:45 pm</td>
<td>Grand A–D</td>
</tr>
<tr>
<td>Sunrise Sessions</td>
<td>7:30 am – 8:15 am</td>
<td>Grand/Garden Rooms</td>
</tr>
<tr>
<td>Combined Session I</td>
<td>8:15 am – 10:00 am</td>
<td>Royal Ballroom</td>
</tr>
<tr>
<td>Break</td>
<td>10:00 am – 10:30 am</td>
<td>Grand A–D</td>
</tr>
<tr>
<td>Combined Session II</td>
<td>10:30 am – 12:00 pm</td>
<td>Royal Ballroom</td>
</tr>
<tr>
<td>Lunch</td>
<td>12:00 pm – 1:30 pm</td>
<td>Grand A–D</td>
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<tr>
<td>Poster Session 1</td>
<td>12:30 pm – 1:00 pm</td>
<td>Grand A–D</td>
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*Vendor Tables, Tech Expo, Program Tables, Demos*

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<thead>
<tr>
<th>Event</th>
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<tr>
<td>Combined Session III</td>
<td>1:30 pm – 3:00 pm</td>
<td>Royal Ballroom</td>
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<tr>
<td>Break</td>
<td>3:00 pm – 3:30 pm</td>
<td>Grand A–D</td>
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<tr>
<td>Combined Session IV</td>
<td>3:30 pm – 5:30 pm</td>
<td>Royal Ballroom</td>
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<tr>
<td>Awards Ceremony</td>
<td>5:30 pm – 6:00 pm</td>
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### Wednesday, November 8 • Day 3

<table>
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<tr>
<th>Event</th>
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<tbody>
<tr>
<td>Registration</td>
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<td>Royal Registration</td>
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<tr>
<td>Posters Available</td>
<td>8:15 am – 5:00 pm</td>
<td>Grand A–D</td>
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<tr>
<td>Sponsor Displays</td>
<td>9:45 am – 4:45 pm</td>
<td>Grand A–D</td>
</tr>
<tr>
<td>Sunrise Sessions</td>
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<td>Various Rooms</td>
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<tr>
<td>Concurrent Sessions I</td>
<td>8:30 am – 9:30 am</td>
<td>Various Rooms</td>
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<tr>
<td>Concurrent Sessions II</td>
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<tr>
<td>Concurrent Sessions III</td>
<td>11:00 am – 12:00 pm</td>
<td>Various Rooms</td>
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<tr>
<td>Lunch (on your own)</td>
<td>12:00 pm – 1:30 pm</td>
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<tr>
<td>Norostat Meeting</td>
<td>12:00 pm – 1:30 pm</td>
<td>Pacific Room, 2nd Fl.</td>
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<tr>
<td>PulseNet Track</td>
<td>1:30 pm – 5:30 pm</td>
<td>Grand E–G</td>
</tr>
<tr>
<td>OutbreakNet/Env. Health Track</td>
<td>1:30 pm – 5:30 pm</td>
<td>Royal Ballroom</td>
</tr>
<tr>
<td>Poster Session 2</td>
<td>5:45 pm – 6:15 pm</td>
<td>Grand A–D</td>
</tr>
<tr>
<td>Reception</td>
<td>5:45 pm – 7:00 pm</td>
<td>Grand A–D</td>
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### Thursday, November 9 • Day 4

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<td>Registration</td>
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<tr>
<td>Posters Available</td>
<td>8:00 am – 12:30 pm</td>
<td>Grand A–D</td>
</tr>
<tr>
<td>PulseNet Track</td>
<td>8:00 am – 12:30 pm</td>
<td>Grand E–G</td>
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<tr>
<td>Environmental Health Track</td>
<td>8:00 am – 12:30 pm</td>
<td>Terrace Room</td>
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<tr>
<td>OutbreakNet Track</td>
<td>8:00 am – 12:30 pm</td>
<td>Royal Ballroom</td>
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Funding for this conference was made possible in part by the Centers for Disease Control and Prevention. The views expressed in written conference materials or publications and by speakers and moderators do not necessarily reflect the official policies of the Department of Health and Human Services, nor does the mention of trade names, commercial practices or organizations imply endorsement by the US Government.
Introduction and Welcome

Welcome to InFORM 2017! This is more than just a catchy acronym. The Integrated Foodborne Outbreak Response and Management conference is an opportunity for microbiologists, epidemiologists and environmental health specialists to join forces to enhance foodborne disease surveillance, outbreak detection, response and prevention. Today’s food safety issues are complex, varied and global. By strengthening our partnerships across agencies and disciplines we can strategically respond to food safety challenges.

InFORM 2017. Since the 2015 meeting, we have made great strides in building the capacity to create and use next generation sequencing data in food safety programs. This conference highlights the ways this exciting technology is advancing the accuracy and sensitivity of public health investigations. Even as we celebrate the past two decades of achievements by the PulseNet, FoodNet and NARMS surveillance systems, we must turn to the future and work together to harness the potential of this transformative technology. You will also notice a focus on the important role of communications in outbreaks, helping the public, industry and other partners understand what can be done to improve food safety.

Sponsors and Support. Thank you to the many sponsors and supporters who made InFORM 2017 possible. InFORM received sponsorship and planning support from the Centers for Disease Control and Prevention (CDC), the Food and Drug Administration (FDA), the US Department of Agriculture’s Food Safety and Inspection Service (USDA–FSIS), the Association of Public Health Laboratories (APHL), the Council for State and Territorial Epidemiologists (CSTE), the National Environmental Health Association (NEHA), the Association of Food and Drug Officials (AFDO) and the National Association of County and City Health Officials (NACCHO). We are especially indebted to APHL for coordinating the facilities, logistics and registration for InFORM 2017. Finally, we extend our appreciation to the companies listed in this program that are providing financial support for InFORM 2017.

We hope you will find the information, discussions and issues presented at InFORM 2017 to be very stimulating and informative. Just as important, we hope you will expand and enhance your partnerships across disciplines and agencies, and have fun doing so.

Robert V. Tauxe, on behalf of the InFORM Steering Committee, including representatives from:

AFDO       CDC, NCEZID
APHL       CSTE
CDC, NCEH   FDA

NACCHO
NEHA
USDA, FSIS
InFORM’s Legacy
InFORM is a conference held every two years that integrates and builds upon the success of an important legacy:

• Since 1996, CDC and APHL have sponsored annual PulseNet Update meetings for laboratory staff who participate in the national network of PulseNet certified laboratories.

• Since 2005, annual OutbreakNet meetings were held for health department epidemiology staff involved in foodborne disease surveillance and outbreak detection and response. These meetings were sponsored by CDC and either APHL (in conjunction with the annual PulseNet meeting) or CSTE (in conjunction with the annual CSTE meeting). USDA–FSIS became an additional sponsor in 2008.

• InFORM 2013 served to integrate the PulseNet and OutbreakNet meetings, and add greater representation from the environmental health discipline.

InFORM 2017 Steering Committee
AFDO: Carrie Rigdon
APHL: Jennifer Adams, Kristy Kubota, Shari Shea
CDC, NCEH: Laura Brown, Erik Coleman, Vince Radke, Amy Freeland
CDC, NCEZID: Gwen Biggerstaff, Laura Whitlock, Sam Crowe, Peter Gerner-Smidt, Kelley Hise, Dale Morse, Frances Roldan, Ashley Sabol, Don Sharp, Rob Tauxe, Eija Trees
CSTE: Thuy Kim, Kirk Smith
FDA: Travis Goodman, Susan Lance, Sherri McGarry, Brett Weed, Lauren Yeung
NACCHO: Amy Chang, Aimee Eberly, Jennifer Li
NEHA: Elizabeth Landeen
USDA, FSIS: Kristin Holt, Glenn Tillman

NEW this Year — InFORM Has a Mobile App!
We’ve added the InFORM Conference to the APHL Meetings App. Access the schedule and all details about sessions, posters, exhibitors, speakers and sponsors at your fingertips before the meeting and onsite. Plan your experience with the My Show feature and personalize your schedule. Receive alerts, real-time program changes and reminders onsite. Create and export notes.

Download the App
Search for APHL in the Apple App or Google Play stores, or go to www.aphl.org/app in your device’s browser. Download the APHL Meetings app and then select the “2017 InFORM Conference” from the list.

Consent to Use Photographic Images
Registration and attendance at or participation in APHL meetings and other activities constitutes an agreement by the registrant to APHL’s use and distribution (both now and in the future) of the registrant’s or attendee’s image or voice, without compensation, in photographs, videotapes, electronic reproductions and audiotapes of such events and activities.
Sponsors

THANK YOU to our sponsors for their generous support of our breaks, lunch and reception! Please visit with them on Tuesday, November 7 from 9:45 am to 4:45 pm in Grand Ballroom A–D.

**Applied Maths, Inc.**

**Sponsor and Poster Reception**

11940 Jollyville Rd., Suite 115N, Austin, TX 78759, 512.482.9700

**www.applied-maths.com**

Applied Maths, a bioMérieux company, develops cutting-edge software for the biosciences. Our flagship software, BioNumerics, is the only software platform that offers integrated analysis of all major applications in Bioinformatics: 1D electrophoresis gels, MALDI-TOF, chromatographic and spectrometric profiles, phenotypic characters, Sanger sequences to whole genomes. BioNumerics has developed into a comprehensive platform combining database and analysis technologies for bacterial genomics, characterization, surveillance and molecular typing. The cornerstones of the Applied Maths successes are the broad expertise in all areas of microbial bioinformatics and the competence of designing powerful and innovative algorithms. BioNumerics is implemented in many prestigious international projects, networks and mission-critical applications including PulseNet and CaliciNet.

**Illumina, Inc.**

**Sponsor**

5200 Illumina Way, San Diego, CA 92122, 858.202.4500

**www.illumina.com**

Illumina is a leading developer, manufacturer and marketer of life science tools and integrated systems for large-scale analysis of genetic variation and function. These systems are enabling studies that were not even imaginable just a few years ago, and moving us closer to the realization of personalized medicine.

**Palantir Technologies, Inc.**

**Sponsor**

100 Hamilton Ave., Palo Alto, CA 94301, inquiries@palantir.com

**www.palantir.com**

Palantir Technologies designs, develops and deploys the Palantir Platform: commercially available software for data integration, management and analysis at enterprise scale.

**PerkinElmer**

**Sponsor**

710 Bridgeport Ave., Shelton, CT 06460, 800.762.4000

**www.perkinelmer.com**

PerkinElmer is a global leader focused on improving the health and safety of people and the environment. Our innovative detection, imaging, software, reagents and services solutions accelerate discovery in core areas of research, including: next generation DNA sequencing, featuring our chemagen technology, epigenetics, genomics, cellular research, quantitative pathology, in vivo imaging, biotherapeutics and informatics.

**QIAGEN**

**Sponsor**

19300 Germantown Rd., Germantown, MD 20874, 301.944.7713

**www.qiagen.com**

As the world’s leading provider of complete Sample to Insight solutions that unlock valuable molecular information from biological samples, QIAGEN offers a broad range of products that address the diverse needs of our global customers, whether conducting academic research or implementing routine healthcare applications. Our product portfolio addresses needs and challenges in molecular microbiology, immunology and infectious disease research and diagnostics, and covers every workflow step, from sample stabilization to results interpretation. QIAGEN quality, efficient solutions and innovative bioinformatics tools help researchers uncover the secrets of the invisible world.
Program Tables and Representatives

Association of Public Health Laboratories (APHL)
Kirsten Larson (APHL), Shari Shea (APHL)

Council to Improve Foodborne Outbreak Response (CIFOR) News and Updates
Thuy Kim (CSTE)

CryptoNet
Dawn Roellig (CDC), Michele Hlvasa (CDC)

CDC Division of Foodborne, Waterborne and Environmental Diseases (DFWED) Communications
Laura Whitlock (CDC)

FDA Coordinated Outbreak Response and Evaluation Network (CORE)
Jennifer Beal (FDA)

FDA Rapid Response Team (RRTs) Program
Travis Goodman (FDA)

Integrated Food Safety Centers of Excellence (CoEs) Product Demos and Updates
Rachel Jervis (CO)

National Center for Environmental Health (NCEH): National Environmental Assessment Reporting System (NEARS) and Environmental Health Specialists Network (EHS-Net)
Erik Coleman (CDC)

National Surveillance Team (NST)
Karen Wong (CDC)

New York State: CoE, OutbreakNet Enhanced (OBNE), and EHS-Net
Paula Pennell-Huth (NY)

PulseNet Communications
Jeny Concepcion-Acevedo (CDC)

System for Enteric Disease Response, Investigation, and Coordination (SEDRIC)
Lyndsay Bottichio (CDC)

T-cube WebPortal
Aphrodite Douris, (USDA-FSIS), Dave Boxrud (MN)

United States Department of Agriculture — Food Safety and Inspection Service (USDA–FSIS)
Doug Noveroske (USDA–FSIS), William Lanier (USDA-FSIS)

FoodNet Fast
Ellyn Marder (CDC)

National Outbreak Reporting System (NORS)
Karunya Manikonda (CDC), Mary Wikswo (CDC)
P.A.C.E.® and CPH Continuing Education Credits Available

APHL is an approved provider of continuing education programs in the clinical laboratory sciences through the American Society of Clinical Laboratory Science (ASCLS) P.A.C.E.® program. Attendees have the opportunity to earn up to 20.5 contact hours by attending the entire conference. Attendance rosters must be signed in each attended session for which credit is requested and the P.A.C.E.® certificate must be signed and certified by APHL staff at the registration desk before you leave the conference.

APHL is an approved provider of Certified in Public Health (CPH) Recertification Credits through the National Board of Public Health Examiners (NBPHE). Attendees have the opportunity to earn up to 19.0 hours of credit by attending the entire conference. APHL will not issue certificates of attendance. Attendees are responsible for keeping track of their hours.

Accreditation and Disclosure Statement

Continuing education for this activity is pending. See final announcement in addendum for details.

Disclosure

In compliance with continuing education requirements, all presenters must disclose any financial or other associations with the manufacturers of commercial products, suppliers of commercial services, or commercial supporters as well as any use of unlabeled product(s) or product(s) under investigational use.

CDC, our planners, presenters and their spouses/partners wish to disclose they have no financial interests or other relationships with the manufacturers of commercial products, supplier of commercial services or commercial supporters with the exception of Dr. Hannes Pouseele and he wishes to disclose that he is an employee of Applied Maths NV (commercial).

Planning committee reviewed content to ensure there is no bias.

Content will not include any discussion of the unlabeled use of a product or a product under investigational use. The Centers for Disease Control and Prevention, United States Department of Agriculture, Food Safety and Inspection Service, Food and Drug Administration, Council of State and Territorial Epidemiologists, Association of Public Health Laboratories, National Environmental Health Association, Association of Food and Drug Officials and the National Association of County and City Health Officials are jointly providing the CNE for this activity.

*CDC did not accept commercial support for this continuing education activity.*

To receive continuing education (CE):

1. Complete the activity.
2. Complete the evaluation at www.cdc.gov/TCEOnline.

FEES: There are no fees for CE.
Welcome and Keynote Speakers

Matthew Zhan, MD, Medical Director, Epidemiology
Orange County Health Care Agency

Dr. Zahn currently serves as Medical Director of the Division of Epidemiology and Assessment for the Orange County Health Care Agency. Dr. Zahn received his doctorate in medicine from St. Louis University School of Medicine. From 2004 through 2011, he served as Medical Director for the Louisville Metro Department of Public Health and Wellness. During that time, he also served as an Assistant Professor of Pediatric Infectious Disease at the University of Louisville School of Medicine. He has served on multiple national public health committees, including currently serving as the National Association of County and City Health Officials (NACCHO) liaison to the CDC’s Advisory Committee on Immunization Practices.

Brenda Fitzgerald, MD, Director, CDC, and Administrator, ATSDR
Centers for Disease Control and Prevention

Brenda Fitzgerald, MD, was appointed as the 17th Director of the Centers for Disease Control and Prevention and as the Administrator of the Agency for Toxic Substances and Disease Registry on July 7, 2017.

Dr. Fitzgerald, a board-certified obstetrician-gynecologist, has practiced medicine for three decades. As Georgia DPH Commissioner from 2011 to 2017, Dr. Fitzgerald oversaw various state public health programs and directed the state’s 18 public health districts and 159 county health departments. Prior to that, Dr. Fitzgerald held numerous leadership positions. She served on the board and as president of the Georgia OB-GYN Society and she worked as a health care policy advisor with House Speaker Newt Gingrich and Senator Paul Coverdell. She has served as a Senior Fellow and Chairman of the Board for the Georgia Public Policy Foundation.

Dr. Fitzgerald holds a Bachelor of Science degree in Microbiology from Georgia State University and a Doctor of Medicine degree from Emory University School of Medicine. She completed post-graduate training at the Emory-Grady Hospitals in Atlanta and held an assistant clinical professorship at Emory Medical Center. As a Major in the US Air Force, Dr. Fitzgerald served at the Wurtsmith Air Force Strategic Air Command (SAC) Base in Michigan and at the Andrews Air Force Base in Washington, DC.

Carmen Rottenberg, JD, Acting Deputy Under Secretary for Food Safety
United States Department of Agriculture

Carmen Rottenberg was appointed Acting Deputy Under Secretary for the US Department of Agriculture’s Office for Food Safety in August 2017. In this position, Ms. Rottenberg oversees development, implementation and enforcement of all of FSIS’ regulations, policies and programs. This appointment follows nearly six years in leadership roles in the Food Safety and
Inspection Service’s (FSIS’) Office of the Administrator, including serving as the Chief of Staff, the Chief Operating Officer and, most recently, the Deputy Administrator.

In those leadership roles, Ms. Rottenberg executed a budget of over $1 billion, prioritizing resources and resolving disputes, advancing the Agency’s vision and goals, and leading innovative solutions to challenges in FSIS. She has spearheaded strategic planning at FSIS and implemented numerous initiatives to strategically move the agency forward. She implemented two major reorganizations leading to a more streamlined, efficient agency, better positioned to carry out its food safety mission. Through her leadership and oversight, an early governance process matured into an established systematic approach to agency decision-making, resulting in more deliberative, science-based decisions that consider enterprise-wide risks and benefits.

Ms. Rottenberg holds a BA in Political Science and Philosophy from Hope College in Holland, MI and a JD degree from American University’s Washington College of Law.

**Stephen Ostroff, MD, Deputy Commissioner for Foods and Veterinary Medicine**

United States Food and Drug Administration

Stephen Ostroff, MD, is the Deputy Commissioner for Foods and Veterinary Medicine, a position he assumed in May 2016. In that role, he oversees the food and animal health activities of FDA, including FDA’s responsibilities in the areas of food safety and nutrition, food labeling, food and color additives, cosmetics, dietary supplements, animal drugs and animal feed, and research to support the food and veterinary medicine mission of FDA.

Dr. Ostroff has also served as the acting FDA Commissioner on two occasions, from April 2015 to late February 2016 and again from January to May 2017.

Dr. Ostroff served as the FDA’s Chief Scientist starting in February 2014. The Office of the Chief Scientist works closely with FDA’s product centers, providing strategic leadership and support for FDA’s regulatory science and innovation initiatives.

Dr. Ostroff joined FDA in 2013 as Chief Medical Officer in the Center for Food Safety and Applied Nutrition and Senior Public Health Advisor to FDA’s Office of Foods and Veterinary Medicine.

Prior to that, he served as Deputy Director of the National Center for Infectious Diseases at the Centers for Disease Control and Prevention (CDC). At CDC Dr. Ostroff focused on emerging infectious diseases, food safety, and coordination of complex outbreak response. He retired from the Commissioned Corps of the US Public Health Service at the rank of Rear Admiral (Assistant Surgeon General). Dr. Ostroff was also the Director of the Bureau of Epidemiology and Acting Physician General for the Commonwealth of Pennsylvania and has consulted internationally on public health projects in South Asia and Latin America.

Dr. Ostroff graduated from the University of Pennsylvania School of Medicine in 1981 and completed residencies in internal medicine at the University of Colorado Health Sciences Center and preventive medicine at CDC.
Frank Yiannas, Vice President, Food Safety
Walmart

As Vice President of Food Safety, Frank Yiannas oversees all food safety, as well as other public health functions, for the world’s largest food retailer, Wal-Mart, serving over 200 million customers around the world on a weekly basis. Frank’s scope of responsibilities includes food safety oversight of Wal-Mart’s stores, Neighborhood Markets, and Sam’s Clubs. Training and education of Associates, food safety oversight of thousands of food suppliers, and a number of critical regulatory compliance issues also come under his purview.

Prior to joining Wal-Mart in 2008, Frank was the Director of Safety & Health for the Walt Disney World Company, where he worked for 19 years. In 2001, under his tenure, Walt Disney World received the prestigious Black Pearl Award for corporate excellence in food safety by the International Association for Food Protection.

As a frequent speaker at national and international conferences, Frank is known for his ability to build partnerships and for his innovative approaches to food safety. In 2008, Frank was given the Collaboration Award by the U.S. Food and Drug Administration. He is the 2007 recipient of the NSF International Lifetime Achievement Award for Leadership in Food Safety and the 2015 Industry Professional Food Safety Hero Award by STOP Foodborne Illness. Frank is also a Past President of the International Association for Food Protection (IAFP) and a Past Vice-Chair of the Global Food Safety Initiative (GFSI). He is also an adjunct Professor in the Food Safety Program at Michigan State University.

He is the author of the books, Food Safety Culture, Creating a Behavior-based Food Safety Management System, and Food Safety = Behavior, 30 Proven Techniques to Enhance Employee Compliance, by Springer Scientific.

Frank is a Registered Microbiologist with the American Academy of Microbiology. He holds memberships with several professional associations, including the National Environmental Health Association, the American Society of Microbiology, and the Institute of Food Technologists. He received his BS in Microbiology from the University of Central Florida and his Master of Public Health (MPH) from the University of South Florida.

Michael Beach, PhD, Associate Director for Healthy Water, National Center for Emerging, Zoonotic Infectious Diseases; Deputy Director, Division of Foodborne, Waterborne, and Environmental Diseases
Centers for Disease Control and Prevention

Michael Beach, PhD, is associate director for healthy water, a program he originated at CDC. He is also Deputy Director of the Division of Foodborne, Waterborne and Environmental Diseases at CDC’s National Center for Emerging and Zoonotic Diseases. An epidemiologist and laboratorian with extensive experience in parasitic and other waterborne diseases, Dr. Beach leads a worldwide program to ensure access to safe drinking water, adequate sanitation, and basic hygiene to protect people from waterborne illnesses.
CONFERENCE SCHEDULE

MONDAY, NOVEMBER 6, 2017

12:00 PM – 7:00 PM • Royal Registration

Registration

1:00 PM – 8:30 PM • Grand A–D

Posters

OPEN SESSIONS

1:00 PM – 3:00 PM • Grand E

SEDRIC Basic Training with NEW Line List Editor

SEDRIC is a secure, web-based platform that combines epidemiologic, laboratory, and traceback data in real time for easier collaboration in outbreak investigations. This training will orient users to a new and updated line list editor, dashboard, and basic queries in object explorer.

Trainers: Lyndsay Bottichio (CDC), Rashida Hassan (CDC)

1:00 PM – 3:00 PM • Grand F

PulseNet Data Analysis Using BioNumerics and NCBI’s Pathogen Detection Pipeline

588-839-17, 2.0 P.A.C.E contact hours

At the conclusion of this session, the participant will be able to:

• Describe data analysis tools, interpretation and data management of sequence-based data within BioNumerics and other software applications developed for the PulseNet Network

This session will discuss the following topics: analyzing and managing PFGE data in BioNumerics v. 6.6; analyzing and managing sequence data in BioNumerics v. 7.6; interpreting hqSNP/wgMLST trees; creating cluster/outbreak reports for epidemiologists; and utilizing the NCBI Pathogen Detection Pipeline.

Moderators: Molly Leeper (CDC) and Beth Tolar (CDC)
Monday, November 6

1:00 PM – 3:00 PM • Grand G

Communications

Working with the Media and Your Public Information Officer (Part I)

During the first part of this session, speakers will discuss strategies for collaborating with your public information officer or communications specialists to be best prepared in outbreak investigations; what the news media need from public health officials and how to work with them most effectively; how to develop and use press announcements and talking point documents to proactively promote public health messages during an outbreak or recall situation; and practical techniques for conducting successful media interviews, answering questions, and bridging to key messages.

Part I Moderators: Brittany Behm (CDC), Natasha Dowell (CDC), Siobhan DeLancey (FDA), Michelle Catlin (USDA-FSIS)

Best Practices for Communicating with Companies Involved in Outbreaks (Part II)

During the second part of this session, speakers will discuss different processes federal agencies use to communicate with companies involved in outbreaks and available resources to use when communicating with companies during local, state, and multijurisdictional outbreaks.

Part II Moderators: Laura Whitlock (CDC), Siobhan DeLancey (FDA), RADM David Goldman (USDA-FSIS)

1:00 PM – 3:00 PM • Garden 1 & 2

What’s New with NORS

During the NORS session, speakers will provide a demonstration of recent NORS interface enhancements; present and discuss progress towards a NORS public data download website (expanded FOOD Tool); and discuss current reporting challenges and opportunities to address those challenges to improve reporting to NORS.

Moderators: Aron Hall (CDC), Sam Crowe (CDC), Katie Fullerton (CDC)

1:00 PM – 3:00 PM • Garden 3

Capacity Building in Action

This session will consist of presentations from FDA’s Rapid Response Teams (RRTs) and CDC’s Foodborne Centers for Outbreak Response Enhancement (FoodCORE), OutbreakNet Enhanced (OBNE), and Integrated Food Safety Centers of Excellence (CoEs). Each program will describe their goals, accomplishments, and products they’ve created to improve surveillance, outbreak investigations, and team collaboration. At the end of the session, there will be a panel discussion with participants from all four programs.

Moderators: Gwen Biggerstaff (CDC), Dale Morse (CDC), Brett Weed (FDA)

Speakers: Anna Newton (CDC), Elizabeth Sillence (CDC), Travis Goodman (FDA)
3:00 PM – 3:30 PM • Grand A–D

Break

3:30 PM – 5:30 PM • Grand E

SEDRIC Advanced Training with Whole Genome Sequence Trees

SEDRIC is a secure, Web-based platform that combines epidemiologic, laboratory, and traceback data in real time for easier collaboration in outbreak investigations. This training will include more advanced object explorer functions, mapping, finding questionnaires and whole genome sequencing trees, text cloud, and traceback diagrams.

Trainers: Lyndsay Bottichio (CDC), Rashida Hassan (CDC)

3:30 PM – 5:30 PM • Grand F

WGS Wet Lab Troubleshooting
588-840-17, 2.0 P.A.C.E contact hours

At the conclusion of this session, the participant will be able to:

• Describe whole genome sequencing laboratory methods used within the PulseNet Network

This session will discuss the following topics: troubleshooting problematic Illumina MiSeq runs based on the observed run parameters and sequence quality metrics; SAV demos of problematic runs; and best practices in the wet lab workflow, including preventing contamination and obtaining an optimal insert size.

Moderators: Ashley Sabol (CDC), Daniel Schoeffner (Illumina), Eija Trees (CDC)

3:30 PM – 4:30 PM • Grand G

Learn More About PFGE Before It’s Too Late!
588-882-17, 1.0 P.A.C.E. contact hours

At the conclusion of this session the participant will be able to:

• Describe pulsed-field gel electrophoresis (PFGE) laboratory methods used within the PulseNet Network

During this session, speakers will provide guidance on improving PFGE quality including protocol reminders, cost saving tips, and establishing an efficient PFGE workflow. Speakers will also discuss lab-specific PFGE topics (i.e., common and uncommon troubleshooting issues, data interpretation, etc.)

Moderators: Lavin Joseph (CDC), Molly Freeman (CDC)
3:30 PM – 5:30 PM • Garden 1 & 2

**Food Code for Non-Environmental Health Professionals**

*During this session, speakers will review the food code, the main body of regulations governing retail food establishments, focusing on the strengths and limitations for preventing foodborne illnesses; review the process for controlling a foodborne illness outbreak (regulatory actions that can be taken); and discuss the process involved in developing the Food Code with scientific rationale.*

**Moderators:** Larry Ramdin (Salem Board of Health), Michele DiMaggio (Contra Costa County)

**Speakers:** Richard Ramirez (FDA), Larry Ramdin (Salem Board of Health), Michele DiMaggio (Contra Costa County, CA)

3:30 PM – 5:30 PM • Garden 3

**Environmental Health Specialists Network (EHS–Net): Contributions to Foodborne Illness Outbreak Investigation and Prevention**

*For this session, state and local food safety program staff funded by CDC’s EHS-Net cooperative agreement will discuss past and current EHS-Net projects that inform foodborne illness outbreak investigation and prevention. They will also discuss how these projects demonstrate the important roles environmental health plays in outbreak investigation and prevention.*

**Moderator:** Laura Brown (CDC)

**Speakers:** Lauren DiPrete (Southern Nevada HD), David Nicholas (NYSDOH), D. J. Irving (TN), Joyce Tuttle (CA), Daniel O’Halloran (NYC)

3:30 PM – 5:30 PM • Garden 4

**Outbreak Investigation from Detection to Action: The USDA–FSIS Perspective**

*Speakers from various FSIS Offices will present on the FSIS perspective on an outbreak investigation, from surveillance to intervention; FSIS advances in information exchange and collaboration between public health partners; using FSIS investigatory and enforcement tools to protect public health; and applying lessons learned from outbreaks to improve FSIS food safety policy.*

**Moderators:** Doug Noveroske (USDA–FSIS), William Lanier (USDA–FSIS)

**Speakers:** Bonnie Kissler (USDA–FSIS), Mark Crowe (USDA–FSIS), Louis Tate (USDA–FSIS), Stephanie Defibaugh-Chavez (USDA–FSIS), Chau Vu (USDA–FSIS), Melanie Abley (USDA–FSIS)
6:00 PM – 6:45 PM • Royal Ballroom

Welcome

Matthew Zhan, MD, Medical Director, Epidemiology
Orange County Health Care Agency

Brenda Fitzgerald, MD, Director, CDC, and Administrator, ATSDR
Centers for Disease Control and Prevention

Carmen Rottenberg, JD, Deputy Under Secretary for Food Safety — Acting
United States Department of Agriculture

Stephen Ostroff, MD, Deputy Commissioner for Foods and Veterinary Medicine
United States Food and Drug Administration

6:45 PM – 7:30 PM • Royal Ballroom

Keynote

Mega Trends in Food Safety

Never before in history has the responsibility to provide safe and affordable food to so many rested on the shoulders of so few. And never before in history, have the consequences for not doing so been greater. It is difficult to overstate the difference in our food system today compared to just a century ago, when many of our food safety approaches were first being developed. At the dawn of the 20th century, a majority of consumers worldwide were still living in a pre-industrialized era, living off the land, with most people still involved with food production in some way, shape, or form. Fast forward a mere hundred years and the transformation that has occurred in food production is nothing short of amazing. Today, the way we get our food from farm to fork, the food system, has evolved into an increasingly complex network interdependent on many businesses, stakeholders, and individuals. Although there is no question that the emergence of today’s modern food system has provided consumers with a more diverse food supply and convenient source of prepared, economical, and ready-to-eat meals, these trends have resulted in both benefits and additional risks. This session will provide an overview of global food safety trends, emerging food system issues, and the actions needed to ensure consumers worldwide have access to an abundant supply of safe, affordable, and sustainable food.

Frank Yiannas, MPH, Vice President, Food Safety & Health
Walmart Stores Inc., Bentonville, AR, USA

7:30 PM – 8:30 PM • Grand Foyer & Grand A-D

Welcome Get Together

View Posters — Cash bar
TUESDAY, NOVEMBER 7, 2017

7:15 AM – 5:00 PM • Royal Registration

Registration

8:15 AM – 5:00 PM • Grand A–D
Posters available for viewing

9:45 AM – 4:45 PM • Grand A–D
Vendor Displays

SUNRISE SESSIONS

7:30 AM – 8:15 AM • Grand E

CIFOR Needs Your Feedback

Staying true to CIFOR’s “bottoms up approach,” the purpose of this session is to solicit feedback from those in the field to identify any new barriers to rapid outbreak detection and response that CIFOR could address through new projects. Session objectives include: 1. Introduce CIFOR’s new strategic plan and structure. 2. Brainstorm ideas for new projects. 3. Gain feedback from end users on the revisions of the CIFOR website, Guidelines, and Toolkit, and plans to create a CIFOR app.

Moderators: Kirk Smith (MN), Don Sharp (CDC)

7:30 AM – 8:15 AM • Garden 4

Information Sharing Between FDA and State, Local, Tribal, and Territorial Officials: Commissioning and 20.88 Agreements

This session will describe how commissioning and 20.88 agreements allow FDA to share commercial confidential, pre-decisional and trade secret information with state, local, tribal, and territorial governments to support outbreak investigations and other food protection activities.

Moderator: Travis Goodman (FDA)

Speakers: Patrick Clouser (FDA), Lauren DiPaola (FDA)
7:30 AM – 8:15 AM • Garden 3

**WGS of Non-PulseNet Organisms: Expectations in the Lab, Reporting, etc.**

This session will provide the latest updates on various AMD programs and activities in addition to states sharing their experience with whole genome sequencing of non-PulseNet organisms. Session topics may include discussion on laboratory methods, establishing quality standards and development of pipelines for the analysis of non-PulseNet pathogens.

**Moderator:** Pamela O’Brien (HI)

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7:30 AM – 8:15 AM • Garden 1 & 2

**Integrating Traditional and Next Generation Methods for Salmonella Serotyping**

Whole Genome Sequencing (WGS) is transforming the public health microbiology workflows for enteric pathogens. Currently, public health laboratories perform both traditional and molecular methods to serotype Salmonella isolates for surveillance and outbreak detection. The availability of open source tools for downstream analysis of genomic data are enabling laboratories to streamline traditional workflows into a single WGS workflow for bacterial reference identification, serotyping and virulence characterization. This roundtable will provide a forum for microbiologists and other interested scientists to discuss current issues related to the transition of traditional Salmonella serotyping methods to WGS and its utility in outbreak detection and surveillance.

**Moderator:** Patricia Fields (CDC)

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7:30 AM – 8:15 AM • Grand F

**Evaluation of Food and Environmental Samples from Non-Federal Sources: Chain of Custody, Sample Integrity and Other Considerations**

This session will provide the latest FSIS and FDA food and environmental sampling chain of custody techniques and describe Federal agency communications with State and other non-Federal laboratories testing food and environmental samples that may impact regulatory decision-making. Session objectives include: 1. Gain a better understanding of the techniques for and the importance of maintaining chain of custody of samples from sample collection, transit, and through laboratory analysis. 2. Learn how Federal and State agencies communicate when non-Federal labs test food and environmental samples during outbreak investigations. 3. Learn how FDA and FSIS evaluate laboratory results from non-Federal sources in order to make regulatory decisions.

**Moderator:** Bonnie Kissler (USDA-FSIS)

**Speakers:** Louis Tate (USDA-FSIS), Stephanie Defibaugh-Chavez (USDA-FSIS), Terri McConnell (FDA-ORA), Nellie Dumas (New York State Department of Health, Wadsworth Center)
Day Two

588-883-17, 6.5 P.A.C.E. contact hours

At the conclusion of today, the participant will be able to:

• Describe the changing food safety, epidemiologic and laboratory practices for enteric disease surveillance, outbreak detection and response
• Discuss lessons learned from Shiga toxin-producing *E. coli* outbreak investigations as it relates to foodborne infections and outbreak detection
• Identify key roles laboratory, epidemiology and environmental health play in outbreak investigations
• Describe how next generation sequencing technologies have transformed public health surveillance, outbreak detection and response
• Describe how culture-independent diagnostics tests are affecting current foodborne outbreak investigations and surveillance

8:15 AM – 8:30 AM • Royal Ballroom

Welcome

Michael Beach, PhD, Deputy Division Director, Division of Foodborne, Waterborne, and Environmental Diseases, Centers for Disease Control and Prevention

COMBINED SESSION I

8:30 AM – 10:00 AM • Royal Ballroom

Then & Now: The Changing Landscape of Enteric Disease Surveillance, Outbreak Detection & Response

This session will examine changes in the landscape of enteric disease surveillance, outbreak detection, and response in the past 20 years. It will present a case study from the 1998 outbreak of listeriosis linked to Bil Mar Foods ready-to-eat meats and discuss the federal food safety agencies’ vision and goals for the future. This session will discuss new/ongoing challenges to food safety such as: changes in
our food production and supply, including more imported foods; changes in the environment leading to food contamination; better detection of multistate outbreaks; new and emerging bacteria, toxins, and antibiotic resistance; changes in consumer preferences and habits; and changes in the tests that diagnose foodborne illness.

Moderators: Ian Williams (CDC), RADM David Goldman (USDA-FSIS), Michael Beach (CDC)

Speakers: Rob Tauxe (CDC), Brian Sauders (NY), Janell Kause (USDA-FSIS), Paul Kiecker (USDA-FSIS), Stic Harris (FDA)

10:00 AM – 10:30 AM • Grand A–D
Break

COMBINED SESSION II

10:30 AM – 12:00 PM • Royal Ballroom
Lessons Learned from Shiga Toxin-Producing E. coli Outbreak Linked to Flour

Flour has been a suspected vehicle for Shiga toxin-producing E. coli (STEC) infections since a 2009 multistate outbreak of STEC O157:H7 infections was linked to prepackaged cookie dough. Flour was never confirmed as the source of the cookie dough outbreak or in subsequent STEC outbreaks where flour was an exposure of interest. In 2016, however, a team of federal, state, and local officials investigated an outbreak of STEC O121 and O26 infections that was ultimately linked to contaminated flour from a single US producer. This complex investigation involved multiple partners working through numerous challenges to implicate flour as the source of the outbreak. There was a clear benefit from close collaboration with the affected industry. This session will include speakers addressing this and similar outbreaks from multiple perspectives, including CDC, FDA, state health officials, industry, and the Public Health Agency of Canada.

Moderators: Matthew Wise (CDC), Beth Melius (WA)

Speakers: Karen Neil (CDC), Nereida Corral (CO), Brooke Whitney (FDA), Scott Hood (General Mills), Laura Whitlock (CDC), Lorelee Tschetter (PHAC)

12:00 PM – 1:30 PM • Grand E–G
Lunch
(Vendors Tables, Tech Expo, Program Tables, and Demos, Poster Session I)

Tech Expo and Vendor Tables:

Table 1: Palantir Technologies  Table 4: Illumina
Table 2: PerkinElmer  Table 5: Qiagen
Table 3: Applied Maths
Program Tables:

Table 6: Council to Improve Foodborne Outbreak Response (CIFOR) News / Updates
Table 7: CryptoNet
Table 8: FDA Coordinated Outbreak Response and Evaluation Network (CORE)
Table 9: FDA Rapid Response Teams (RRTs) Program
Table 10: Integrated Food Safety Centers of Excellence (CoEs) Product Demos / Updates
Table 11: CDC Division of Foodborne Waterborne Environmental Diseases (DFWED)
Table 12: National Center for Environmental Health (NCEH) - National Environmental Assessment Reporting System (NEARS) and Environmental Health Specialists Network (EHS-Net)
Table 13: National Surveillance Team (NST)
Table 14: New York State CoE, OBNE and EHS-Net
Table 15: PulseNet Communications
Table 16: System for Enteric Disease Response, Investigation, and Coordination (SEDRIC)
Table 17: T-cube WebPortal
Table 18: United States Department of Agriculture — Food Safety and Inspection Service (USDA–FSIS)
Table 19: FoodNet Fast
Table 20: National Outbreak Reporting System (NORS)
Table Near Registration: Association of Public Health Laboratories (APHL)

12:30 PM – 1:00 PM • Grand A–D
Poster Session I and Meet the Authors

12:30 PM – 1:30 PM • Pacific Room
NHGQ Epi Info Database Demo and Q&A

• Demonstrate the features of the new national hypothesis-generating questionnaire (NHGQ) Epi-Info database
• Describe how ORPB will be utilizing this database to collect data during multistate cluster investigations via the web survey
• Demonstrate how local and state users can create local NHGQ (or modified NHGQ) databases for local outbreak investigations
• Answer questions from users about the national database and local/state implementation of the database

Facilitator: Rashida Hassan (CDC)
COMBINED SESSION III

1:30 PM – 3:00 PM • Royal Ballroom

Navigating Whole Genome Sequencing and Its Utility in Foodborne Surveillance, Outbreak Detection, and Response

This session will provide attendees with an overview of the implementation, coordination and use of whole genome sequencing to identify and respond to foodborne outbreaks. International, federal and state speakers will discuss implementation from an epidemiological and laboratory perspective. The US federal agencies’ approach using the Genomics in Food and Feed Safety (Gen-FS) working group to coordinate communications, standardize methods, and provide training will be presented. International partners will present approaches to WGS in food safety in their countries. This session will also highlight the use of whole genome sequencing by a state public health department for cluster detection and outbreak investigation as well as progress and limitations to implementing WGS in a state public health laboratory.

Moderators: John Dunn (TN), Heather Carleton (CDC), David Melka (FDA), Cesar Morales (USDA-FSIS)

Speakers: Chris Braden (Gen–FS), Carlota Medus (MN), Kiera Glasgow (Australia), Vishnu Chaturvedi (CA)

3:00 PM – 3:30 PM • Grand A–D

Break

COMBINED SESSION IV

3:30 PM – 5:30 PM • Royal Ballroom

Culture-Independent Diagnostic Tests (CIDTs): Changing the Landscape of Surveillance

This session will provide a background on currently available CIDTs on the marketplace and national efforts addressing public health laboratory testing and their impact to current surveillance activities. Additionally, speakers from local and state health departments will provide examples on how CIDT test results are affecting current foodborne outbreak case investigations.

Moderators: Carlota Medus (MN), Kristy Kubota (APHL)

Speakers: Peter Gerner-Smidt (CDC), Ellyn Marder (CDC), Dave Boxrud (MN), Dana Eikmeier (MN), David Young (SC), Anna Carlson (NE), Ryan Jepson (IA), David Nicholas (NY)
Tuesday, November 7

5:30 PM – 6:00 PM • Royal Ballroom

Awards Ceremony

OutbreakNet Bill Keene Award for Excellence in Epidemiology

PulseStar Award for Outstanding Achievement in PulseNet

Kati Kelley Award for Exceptional Service to PulseNet

John J. Guzewich Environmental Health Public Health Team Award
SUNRISE SESSIONS

7:30 AM – 8:15 AM • Garden 1 & 2

Partnerships for Food Protection (PFP) Food Emergency Response Resources

This session will review key resources developed through the Partnership for Food Protection (PFP) for use in foodborne illness outbreaks and food-related investigations, including: 1. PFP Overview - The Partnership for Food Protection (PFP) is the structure used to bring together and coordinate the efforts of regulatory and public health officials to achieve a national Integrated Food Safety System (IFSS). The function of the PFP is to promote communication and integration between all jurisdictions and provide resources, risk-informed insight, and best practices to improve the system that partners can utilize to inform and enhance their work to protect public health; 2. Quick Start Food Emergency Response Job Aid – A tool to facilitate communication, coordination, and planning amongst programs and agencies early on in a food emergency event; 3. Best Practices for Use of FoodSHIELD during a Food/Feed Incident – Best practice guidance for using FoodSHIELD as a tool to enhance real-time communication amongst stakeholders during food emergencies; and 4. An overview of projects currently in progress including, the PFP Capacity Building and Mentorship Program for Rapid Response Teams (RRTs), and Improving Information Sharing.

Moderators: Priscilla Neves (FDA), Travis Goodman (FDA)

Speakers: Priscilla Neves (FDA), Carrie Rigdon (MN Ag), and Travis Goodman (FDA)

7:30 AM – 8:15 AM • Pacific Room

FDA Coordinated Outbreak Response and Evaluation Network (CORE) Updates and Highlights

The purpose of this session will be to provide updates and highlights from FDA’s Coordinated Outbreak Response and Evaluation (CORE) Network. The main learning objective of this session is to familiarize the audience with specific facets of outbreak investigations coordinated by CORE and to share summaries of high impact post-response activities related to past outbreaks. Specific topic areas will include: firm calls
Wednesday, November 8

(what to expect and what to share); factors that FDA considers regarding traceback and update on informational traceback process and applications; and an overview of CORE post-response examples of post-response initiatives for high profile outbreaks.

Moderators: Jennifer Beal (FDA), Susan Lance (FDA), Lauren Shade (FDA)

Speakers: Karen Blickenstaff (FDA/CORE), CDR Kari Irvin (FDA/CORE), Angela Fields (FDA/CORE), Diane Gubernot (FDA/CORE)

7:30 AM – 8:15 AM • Garden 4

Current Issues In Antimicrobial Resistance Surveillance and Impact on Outbreak Response

This sunrise session will provide a forum to discuss current issues in antimicrobial resistance surveillance for outbreaks. Topics will include the use of resistance data in outbreak investigations (including predicted resistance from whole genome sequencing), and the development of a Scary Isolate Response Initiative to guide public health response to patients infected with pathogens that have very concerning resistance patterns (e.g., colistin resistance mediated by mcr-1 or azithromycin resistance in Salmonella). Discussants will share examples of success stories and challenges in outbreak response using NARMS surveillance data. Representatives from partner organizations will be invited to discuss strategies to improve resistance surveillance and to optimize partner involvement and outcomes.

Discussants: Meseret Birhane (CDC), Louise Francois Watkins (CDC), Cindy Friedman (CDC)

7:30 AM – 8:15 AM • Garden 3

Analytical Tools for WGS: Bioinformatic Pipelines, Cloud Computing and the Dark Arts as Practiced by Your State Public Health Bioinformaticians (STAPH–B)

This session will include a panel of state public health bioinformaticians that are currently utilizing NGS and bioinformatics for microbial identification and outbreak detection. This session will highlight the tools, workflows, and resources available to state public health laboratories and how to implement them effectively.

Moderator: Joel Sevinsky (CO)

Panelists: Joel Sevinsky (CO), Dave Boxrud (MN), Kevin Libuit (VA), Kelly Oakeson (UT)
7:30 AM – 8:15 AM • Terrace Room

**Updates on Efforts for Controlling *Listeria monocytogenes* (**Lm**) in Retail Delicatessens**

*Efforts to enhance knowledge, skills, and abilities to control *Listeria monocytogenes* (*Lm*) in Retail Delicatessens are on-going. Learn the most up-to-date information on regulatory and industry efforts aimed at *Lm* control in retail delicatessens.*

**Moderator:** Michele DiMaggio (Contra Costa County Health Services, CA)

**Speakers:** Kristin Holt (USDA-FSIS), Larry Ramdin (Board of Health, Salem, MA), John Burnett (Purdue University), Liza Frias (Orange County Health Care Agency, CA)

8:15 AM – 8:30 AM • Grand A–D

**Break**

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### CONCURRENT SESSIONS OVERVIEW

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### CONCURRENT SESSIONS I

8:30 AM – 9:30 AM • Garden 1 & 2

**The Changing Landscape of Norovirus: From Detection to Surveillance**

588-884-17, 1.0 P.A.C.E contact hour

At the conclusion of this session, the participant will be able to:

- Describe new laboratory methods for norovirus and epidemiological trends in restaurant associated norovirus outbreaks

*This session will describe recent advances in genotyping and in vitro culture of norovirus, describe workflow processes and methods for detection of norovirus in foods, and describe an exemplary outbreak investigation that utilized new norovirus diagnostic methods.*

**Moderator:** Aron Hall (CDC)

**Speakers:** Jan Vinje (CDC), Toni Morales (FDA), Amy Saupe (MN)
Wednesday, November 8

8:30 AM – 9:30 AM • Garden 3

WGS and Epi Integration Part I
588-885-17, 1.0 P.A.C.E contact hour

At the conclusion of this session, the participant will be able to:

- Describe methods for integration of epidemiological and whole genome sequencing data for surveillance and outbreak detection of foodborne diseases

During this session, presenters will discuss ways WGS and epidemiological data is integrated in their jurisdiction. The presenters will also discuss how epidemiological data or lack thereof affect the interpretation of the WGS data. Case studies will be presented.

Moderators: Katie Garman (TN), Kelley Hise (CDC), Eija Trees (CDC)

Speakers: Laboratory and Epi Data Integration in SEDRIC, Rashida Hassan (CDC)
Implementation to Integration: DCLS’s Phased Approach to Sharing Molecular Subtyping Data with Epidemiologists, Lauren Turner (VA DCLS)

WGS Tree Presentations:
Salmonella Anatum Infections Associated with Imported Papaya, Colin Schwensohn (CDC), Molly Leeper (CDC)
Salmonella Heidelberg Linked to Contact with Cattle, Lauren Stevenson (CDC), Morgan Schroeder (CDC)
Salmonella Saintpaul Investigation, Beth Tolar (CDC)

8:30 AM – 9:30 AM • Garden 4

Dr. Strangevehicle: How I Learned to Stop Worrying and Love the Unsolved Outbreaks
588-886-17, 1.0 P.A.C.E. contact hour

At the conclusion of this session, the participant will be able to:

- Identify strategies for conducting investigations with partners from different disciplines and agencies for coordinated outbreak response

This session will describe recent unsolved outbreaks and how partners can collaborate to find new vehicles, handle difficult situations with multiple agencies, use technology to assist investigations, and have partners work together for solutions and improvements in food safety.

Moderators: Jennifer Beal (FDA), Lyndsay Bottichio (CDC), Zachary McCormic (NH)

Speakers: Lyndsay Bottichio (CDC), Amanda Conrad (CDC), Brooke Whitney (FDA), Vasuda Reddy (NYC), D’Ann Williams (MD), Quyen Phan (CT), Christina Turner (CT)
8:30 AM – 9:30 AM • Terrace Room

**In the Heat of an Outbreak: Different Perspectives on Regulatory Communication**
588-887-17, 1.0 P.A.C.E. contact hour

At the conclusion of this session, the participant will be able to:

- Describe different approaches and lessons learned regulatory agencies have with communication among partners during outbreak investigations

The goal of the session is to reach shared understanding of different entities’ needs and limitations around communication during an outbreak. This session will explore recent outbreaks as case studies to demonstrate how to incorporate lessons learned from one outbreak to another, and how that affects outbreak outcomes. USDA–FSIS will discuss the Salmonella I 4,[5],12:i:- outbreaks of 2015 and 2016, associated with whole roasting pigs, and the session will foster discussion about the timeline of communications. FDA will discuss the frozen strawberries and frozen tuna hepatitis A investigations, and the SoyNut Butter E. coli investigations as instances where communications were either successful or challenging, and discuss innovative ways to work around communication challenges that the FDA regularly faces as a regulatory agency.

**Moderators:** Karen Becker (USDA–FSIS), Ian Williams (CDC)

**Speakers:** Aaron Lavallee (USDA–FSIS), Beth Melius (WA), Siobhan DeLancey (FDA)

9:30 AM – 9:45 AM • Grand A–D

**Break**

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**Concurrent Sessions II**

9:45 AM – 10:45 AM • Garden 1 & 2

**Linking Environmental and Epidemiological Data on Restaurant-Related Norovirus Outbreaks**
588-888-17, 1.0 P.A.C.E. contract hour

At the conclusion of this session, the participant will be able to:

- Describe how recent data from norovirus outbreak epidemiology and environmental investigations can inform norovirus outbreak investigation and prevention.

*CDC content experts will discuss how recent data from norovirus outbreak epidemiology and environmental investigations can inform norovirus outbreak investigation and prevention.*

**Moderator:** Laura Brown (CDC)

**Speakers:** Aron Hall (CDC), Amy Freeland (CDC), Laura Brown (CDC)
Wednesday, November 8

9:45 AM – 10:45 AM • Garden 3

**WGS and Epi Integration Part II: Finding a Needle in a Haystack — Using WGS to Identify Clusters with Common PFGE Patterns**

588-889-17, 1.0 P.A.C.E. contact hour

At the conclusion of this session, the participant will be able to:

- Describe analytical methods and approaches for whole genome sequence-based data

During this session, presenters will discuss how WGS and analysis is conducted in their jurisdiction. Case studies will be presented to exhibit how WGS identified outbreaks that would not have been detected using PFGE alone. We will also describe the use of WGS to determine next steps in the outbreak investigation.

**Moderators:** Katie Garman (TN), Kelley Hise (CDC), Eija Trees (CDC)

**Speakers:** Lisha Constantine-Renna (TN), Hope Dishman (GA), Katherine Marshall (CDC)

9:45 AM – 10:45 AM • Garden 4

**Epidemiologic Methods: New and Old Tools to Investigate Foodborne Outbreaks**

588-890-17, 1.0 P.A.C.E. contact hour

At the conclusion of this session, the participant will be able to:

- Describe the use of old and new tools for the investigation of foodborne outbreaks

Methods commonly used for formal analytic studies, such as community based case-control studies or using credit card receipts to identify restaurant patrons, are increasingly difficult to conduct. This session will focus on the use of innovative epidemiologic methods to determine the source of foodborne and other enteric disease outbreaks. Federal, state, and local investigators will present brief case studies on experiences using some of these methods and the benefits and challenges of using such methods. Session objectives include: novel methods to recruit controls or generate exposure comparison data, using the binomial comparison of proportions for hypothesis generation, venue/event-based investigations, options for case-finding or finding controls in restaurant and other outbreaks, and best approaches to ingredient-specific analytic studies.

**Moderators:** Carlota Medus (MN), Matthew Wise (CDC), Kerri Brown (CO)

**Speakers:** Leslee Warren (Tri-County HD, CO), Cindy Burnett (UT), Josh Rounds (MN), Peter Ruestow (Chicago)
9:45 AM – 10:45 AM • Terrace Room

One Health Approach to Farm-to-Table: Importance of On-Farm Investigations During Outbreaks
588-891-17, 1.0 P.A.C.E. contract hour

At the conclusion of this session, the participant will be able to:

• Discuss the importance of a One Health approach to investigating outbreaks involving human, animal and environmental factors

This concurrent session has three primary aims: 1. to raise awareness of the importance of a One Health approach to outbreak investigations including human, animal and environmental elements; 2. to share strategies for conducting joint investigations with partners in the agriculture sector; and 3. to foster discussion around challenges presented by on-farm investigations

Moderators: Megin Nichols (CDC), Alice Green (USDA-FSIS)

Speakers: Misha Robyn (CDC), Tony Halsted (Hoover Hatchery), Donald Sockett (WI Veterinary Diagnostic Laboratory), Jason Lombard (USDA-APHIS)

10:45 AM – 11:00 AM • Grand A–D

Break

Concurrent Sessions III

11:00 AM – 12:00 PM • Garden 1 & 2

Developing Collaboration to Enhance Investigation of Antimicrobial Resistance in Food Pathogen of Animal Origin Involved in Outbreaks
588-892-17, 1.0 P.A.C.E. contact hours

At the conclusion of this session, the participant will be able to:

• Describe methods used to investigate foodborne illnesses caused by antimicrobial resistance bacteria

This session will provide examples of how state and federal partners work together to investigate foodborne outbreaks caused by antimicrobial resistant bacteria.

Moderators: Nkuchia M’ikanatha (PA), Heather Tate (FDA), Louise Francois Watkins (CDC), Alice Green (USDA-FSIS)

Speakers: Vivian Leung (CT), Samir Hanna (TN), Kelly Kline (PA)
Wednesday, November 8

11:00 AM – 12:00 PM • Garden 3

**Whole Genome MLST Databases**
588-893-17, 1.0 P.A.C.E. contact hours

At the conclusion of this session, the participant will be able to:

• Discuss best practices for ensuring quality whole genome sequencing data for PulseNet

During this session, speakers will discuss how wgMLST schemes have been developed and how they are being validated, interpreting results and defining thresholds for relatedness of strains for PulseNet surveillance. Also, speakers will highlight the genotyper tools being developed for use in BioNumerics, updates on WGS nomenclature development, and the status of wgMLST for non-PulseNet organisms.

**Moderator:** Steven Stroika (CDC)

**Speakers:** Heather Carleton (CDC), Rebecca Lindsey (CDC), Hannes Pouseele (Applied-Maths)

11:00 AM – 12:00 PM • Garden 4

**Retrospective Outbreak Investigations: Leveraging Food and Environmental Data to Protect Public Health**

This session will revisit the topic of Retrospective Outbreak Investigations (first introduced at the 2015 INFORM conference), which begins when a product or environmental isolate is linked by WGS to clinical isolates. The purpose of this session is to build upon that introduction and give participants an update on the status of this approach using a case study involving a smoked fish manufacturer in NY. The session will then conclude with a brief overview of current activities at FDA and CDC relative to standardizing procedures for evaluating these types of clusters, prioritizing which ones to investigate, and describing the unique challenges and opportunities for this approach.

**Moderators:** Susan Lance (FDA), Ian Williams (CDC)

**Speakers:** Matthew Wise (CDC), Amanda Conrad (CDC), Jennifer Beal (FDA), Leslie Hintz (FDA)

11:00 AM – 12:00 PM • Terrace Room

**Late Breaker**

This late breaker session will highlight several recent outbreaks and investigations. In this dynamic “rapid-fire” session each author will give a 5-minute oral presentation followed by 5 minutes for questions and discussion.

**Moderators:** Michael Jhung (CDC), Justin Henderson (MI)

**Speakers:** TBD
12:00 PM – 1:30 PM
Lunch (on your own)

12:00 PM – 1:30 PM • Pacific Room
NoroSTAT Meeting

Day Three Afternoon
588-894-17, 3.5 P.A.C.E contact hours
At the end of this afternoon, the participant will be able to:
• Describe lessons learned for transitioning laboratory workflows for the integration of whole genome sequencing within the PulseNet laboratories
• Discuss best practices for tracking and integrating culture independent diagnostic test specimens within public health laboratory workflows

INDIVIDUAL TRACKS

1:30 PM - 5:30 PM • Grand E–G
PulseNet Track
(See page 31 for the OutbreakNet and Environmental Health Track)

1:30 PM – 3:00 PM • Grand E–G
Transitioning Workflows for PulseNet: Perspectives from the PulseNet Laboratories
Moderators: Julia Wolfe (CAOC), Karim George (KY), Molly Freeman (CDC)

CDC’s Experience with CLIA Validation of WGS Wet-Lab and Analytical Tools, Rebecca Lindsey (CDC)

Single-Molecule Real-Time Sequencing Technology (SMRT): Validation and Implementation of Long-Read Sequencing at the Microbial Diseases Laboratory of the California Department Public Health, Rituparna Mukhopadhyay (CA)

Lessons Learned: Integrating Automated Workflows for PulseNet, Roxy Meek (WA)

Lessons Learned: Validation of SeqSero and Establishing a WGS Workflow for Salmonella Serotyping, Jisun Haan (MN)

3:00 PM – 3:15 PM • Grand E–G
Discussion and Q/A
Wednesday, November 8

3:15 PM – 3:45 PM • Grand A–D
Break

3:45 PM – 4:40 PM • Grand E–G
Panel Discussion 1
Tracking and Data Management of WGS and CIDTs: Sharing Best Practices
Panelists will lead a discussion of challenges and best practices that have emerged as WGS and CIDTs are integrated into public health lab workflows.

Moderators: Morgan Schroeder (CDC), Jeannette Dill (TN)
Panelists: Angie Taylor (MN), Ryan Jepson (IA), Bill Wolfgang (NY)

4:45 PM – 5:30 PM • Grand E–G
Panel Discussion 2
Addressing Quality and Contamination: From the Bench to Analysis
Panelists will discuss the use of bioinformatic tools to examine sequence quality, laboratory mitigation of sequence contamination, and CLIA validation of WGS methods.

Moderators: Lavin Joseph (CDC), Steve Dietrich (MI)

Using Bioinformatics Tools to Examine Sequence Quality, Heather Carleton (CDC), Joel Sevinsky (CO)
Laboratory Mitigation of Sequence Contamination, Lauren Turner (VA)
WGS CLIA Validation, Karim Morey (OR)

5:30 PM
PulseNet Adjourns
OutbreakNet and Environmental Health Track

1:30 PM – 3:30 PM • Royal Ballroom

Notes from the Field Part I

Speakers from local, state, and national public health agencies across multiple disciplines will discuss novel enteric outbreak investigations, surveillance activities, and new tech innovations. Presentations will be followed by an opportunity for colleagues to ask questions and discuss presentation findings.

Moderators: Amy Robbins (NY), Justin Henderson (MI)

Food Source Information: A Food Production Wiki for Public Health Professionals, Elaine Scallan (CO SPH/CoE)

Don’t Have a Cow, Man: Calf-Associated Outbreaks of Cryptosporidiosis in New Hampshire, Zachary McCormic (NH)

Salmonella Javiana Infections Linked to a Restaurant in Maricopa County, Arizona — 2016, Heather Venkat (AZ)

Vibrio vulnificus Wound Infection After Handling Tilapia Purchased From a Live Freshwater Fish Tank, Laurie Stewart (WA)

A Rapid One Week Response: Salmonella Braenderup in Potato Salad, Melanie Harris (IA)

Shiga Toxin-Producing Escherichia coli 0157:H7 Infections After Attendance at a Cider Festival — Kansas, 2016, Daniel Neises (KS)


Outbreak of Salmonella Enteritidis Associated with a Restaurant in Kentucky, 2016, Carrell Rush (KY)

3:30 PM – 4:00 PM • Grand A–D

Break

4:00 PM – 4:45 PM • Royal Ballroom

Use of Shopper/Loyalty Card and Other Purchase Data Resources to Assist with Outbreak Investigations

Shopper/loyalty card data and other purchase data resources are increasingly being used during foodborne outbreaks to assist with hypothesis generation and product traceback of suspect food vehicles. After this session, the participant will be able gain an understanding of how this information is used during outbreak investigations in addition to available resources.

Moderators: Bonnie Kissler (USDA-FSIS), David Nicholas (NYSDOH)

Speakers: Christine Applewhite (CT), Greg Leos (TX), Julie Schlegel (NCAG)
Wednesday, November 8

4:45 – 5:30 PM • Royal Ballroom

**Implementing Statewide Foodborne Illness Complaint Systems: Successes and Challenges**

*During this session, speakers will describe various statewide foodborne illness complaint systems, describe challenges and successes in implementing a statewide foodborne illness complaint system, discuss challenges/successes when promoting a foodborne illness complaint system, and review steps taken when evaluating a foodborne illness complaint system.*

**Moderators:** Katie Garman (TN), Amy Robbins (NYS)

**Speakers:** Jane Yackley (TN), Danny Ripley (Nashville/Davidson County Metro HD), Kenny Davis (UT), Daniel Neises (KS)

5:30 PM

**OutbreakNet and Environmental Health Adjourns**

5:45 PM – 7:00 PM • Grand A–D

**Poster Reception**

*Sponsored by Applied Maths*

5:45 PM – 6:15 PM • Grand A–D

**Poster Session II and Meet the Authors**
THURSDAY, NOVEMBER 9, 2017

7:30 AM – 12:30 PM • Royal Registration

8:00 AM – 12:30 PM • Grand A–D

Posters Available for Viewing

Day Four

588-895-17, 3.5 P.A.C.E. contract hours

At the conclusion of this day, the participant will be able to:

- Describe current PulseNet USA and International activities network participants are developing for implementation of whole genome sequencing within PulseNet
- Describe the integration of regulatory and clinical data within the PulseNet Network
- Describe analytic tools and practices for sharing data at the local and state levels
- Describe current status of CDC metagenomics and isolate recovery projects
- Discuss novel approaches for culture-independent identification and characterization methods from clinical and environmental samples

INDIVIDUAL CONFERENCE TRACKS

**PulseNet Track**

(See page 35 for Environmental Health Track and page 36 for OutbreakNet Track.)

8:00 AM – 8:15 AM • Grand E–G

**PulseNet Innovation Award • Presenter:** Drew Kohlhorst, IHRC

8:15 AM – 9:15 AM • Grand E–G

**PulseNet USA and International Roadmap: Transitioning to WGS Surveillance and Outbreak Detection**

**Moderators:** Serena Giovinazzi (FLAG), Aphrodite Douris (USDA–FSIS)

**PulseNet International & USA Steering Committee Updates**, Peter Gerner-Smidt (CDC)

**Integration of Regulatory and Clinical Data: Perspectives from FDA and USDA–FSIS**, Eric Stevens (FDA), Cesar Morales (USDA–FSIS)

**Perspectives from a Food Regulatory Laboratory: FLAG’s Experience with WGS Implementation**, Serena Giovinazzi (FLAG)
State Solutions for Analysis and Reporting: Perspectives from the State Public Health Bioinformaticians (Staph-B) Workgroup

The emergence of next generation sequencing (NGS) is revolutionizing microbial identification and outbreak detection, both nationally and at the state public health level. Although implementing NGS in the state public health laboratory is a significant achievement, the greater challenge lies in the analysis and reporting of the results. This session will describe three separate state level solutions for embracing and incorporating NGS analysis into standard laboratory practice. Examples will include when to use both reference-based and reference-free bioinformatic pipelines, how to leverage cloud based computing resources at the state level, and effective communication strategies between the laboratory and epidemiologists.

Moderators: Joel Sevinsky (CO) Julia Wolfe (CAOC)

Bioinformatic Analyses of Whole-Genome Sequence Data in a Public Health Laboratory, Kelly Oakeson (UT)

Cloud Solutions for State NGS Bioinformatics and Storage, Joel Sevinsky (CO)

NGS Communication between Laboratories and Epidemiologists, Angela J. Taylor (MN)

Current Laboratory-based Strategies in Addressing CIDTs

Moderators: Eija Trees (CDC), Jeannette Dill (TN)

CIDT challenges and changes in Colorado, Emily Travanty (CO)

CIDT: An overachieving GI panel, Jeannette Dill (TN)

PanGIA: Culture-Independent Identification and Characterization of Infectious Agents Directly from Clinical and Environmental Sources, Jonathan Jacobs (MRI Global)

Development of Sequencing Methods for Direct-from-Specimen Surveillance and Subtyping, Jo Williams-Newkirk (CDC)

PulseNet Closing Remarks

PulseNet Adjourns
Environmental Health Track

8:30 AM – 10:30 AM • Terrace Room

Environmental Assessments and Root Cause

This session will explore various approaches to environmental assessments and root cause analysis when problems arise, such as harborage, contamination events or when foodborne illness is connected to a product or facility. Speakers will also describe the impact and influences of people, economics, business culture, and other considerations on an investigation.

Moderators: Steve Mandernach (IA), Kristin Holt (USDA-FSIS), Brett Weed (FDA), Vince Radke (CDC)

Speakers: Karin Hoelzer (Pew Charitable Trusts), Karen Becker (USDA-FSIS), Laura Brown (CDC), Danny Ripley (Metro Public Health Department, Nashville, TN)

10:30 AM – 11:00 AM

Break

11:00 AM – 12:30 PM • Terrace Room

Demystifying the Lab

Collecting specimens, food, or environmental samples is more than what it seems. During this session, the wonders of the laboratory will be revealed when you hear how samples are received, processed, interpreted and reported. You will also hear how EH professionals plan for sampling and use field samples to help solve outbreaks. Finally, this session will feature new tools for detecting pathogens on different surfaces that would be useful during outbreak investigations. Attending this session will provide the opportunity to clarify your questions about the hows and whys of sampling, what happens in a laboratory, and the best tools for the job.

Moderators: Michele DiMaggio (Contra Costa County), Carrie Rigdon (MN), Larry Ramdin (Salem Board of Health)

Speakers: Jan Vinje (CDC), Maria Ishida (NY), Melanie Harris (IA)

12:30 PM

Environmental Health Adjourns
Thursday, November 9

**OutbreakNet Track**

8:00 AM – 10:00 AM • Royal Ballroom

**Notes from the Field Part II**

Speakers from local, state, and national public health agencies across multiple disciplines will discuss novel enteric outbreak investigations, surveillance activities, and new tech innovations. Presentations will be followed by an opportunity for colleagues to ask questions and discuss presentation findings.

**Moderators:** William Lanier (USDA–FSIS), Thai-An Nguyen (CDC)

- **Multistate Outbreak of *E. coli* O157:H7 Infections Linked to Soy Nut Butter — United States, 2017**, Rashida Hassan (CDC)
- **International Collaboration to Identify an Unusual Source of Illness: *Salmonella* Chailey Outbreak Associated with Coconut, 2017**, Marsha Taylor (British Columbia, CAN)
- **Incubation Period for Outbreak-Associated, Non-Typhoidal Salmonellosis Cases, Minnesota, 2000–2015**, Dana Eikmeier (MN)
- **Application of Whole Genome Sequencing to Support Foodborne Disease Outbreak Detection and Investigations in Connecticut**, Quyen Phan (CT)
- **Shigella Infections with Decreased Susceptibility to Azithromycin and Association with Bacterial Sexually Transmitted Infections in New York City, 2014–2016**, Katelynn Devinney (NYC)
- **Using xTAG® Gastrointestinal Pathogen Panel (GPP) Results in Exclusion of Enteric Disease Cases from High-Risk Settings**, Amanda Shoemate (OK)
- **Use of a REDCap Database for Management and Tracking of the Tennessee FoodCORE Interview Team’s Contact Attempts and Interview Outcomes**, Stephanie Cavallo (TN)
- **The Relationship Between Food access and Reported *Salmonella* and *Campylobacter* cases in Pennsylvania: A Spatial Comparison of Urban and Rural Areas**, Erica Smith (Drexel University)

10:00 AM – 10:30 AM

**Break**
Thursday, November 9

10:30 AM – 11:15AM • Royal Ballroom

**Cluster vs Outbreak**

This session will provide participants with a better understanding of how clusters and outbreaks of illness are defined and categorized at both the national and state level. Both single state and multi-state investigations will be discussed. This session will include speakers from state public health departments as well as the CDC.

**Moderators:** Colin Basler (CDC), Colin Schwensohn (CDC), Kerri Brown (CO)

**Speakers:** Matthew Wise (CDC), Samuel Crowe (CDC), Amy Saupe (MN), Mackenzie Tewell (AZ)

11:15 AM – 12:00 PM • Royal Ballroom

**Protecting Public Health: Deciding When to Communicate About an Outbreak**

A consumer warning issued at the right time can save lives. Close collaboration is essential when creating timely and clear messages for the public during outbreaks. In this interactive dialogue session, a panel of communication and media experts will discuss making decisions and crafting messages for the public during outbreaks. Participants will also share their own successes and challenges deciding when to communicate and what to say, and pose questions to the panelists.

**Moderator:** Laura Whitlock (CDC)

**Panelists:** Brittany Behm (CDC), Natasha Dowell (CDC), Aaron Lavallee (USDA-FSIS), Siobhan DeLancey (FDA)

12:00 PM – 12:30 PM • Royal Ballroom

**OutbreakNet Closing Remarks**

12:30 PM

**OutbreakNet Adjourns**
P-001

Surveillance for Multi-State Shigellosis Person-to-Person Clusters: Lessons Learned

Authors: Elizabeth Adam, Mateusz Karwowski, Amanda Garcia-Williams, Kathleen Fullerton

Affiliation: Waterborne Disease Prevention Branch, CDC

Background: Clusters of shigellosis are usually spread through person-to-person contact rather than via a point source. Multi-state cluster investigations, identified through PFGE patterns, are triaged for CDC monitoring, while control efforts are managed by state and local health departments. To improve CDC surveillance and communication approaches, we reflect on lessons learned from state collaborations.

Methods: We assessed epidemiologic data on multi-state clusters detected by PulseNet from January to June 2017, and reviewed questions and feedback received from partners through technical assistance consultations and a roundtable discussion at the 2017 CSTE conference. We evaluated how information collected was used to guide response efforts at the state and local level.

Results: CDC monitored six multi-state clusters that ranged in size from five to 277 cases. Three clusters involved transmission among men who have sex with men (MSM), two international travel, and one childcare and community spread. Isolates from four clusters showed phenotypic resistance to treatment antibiotics azithromycin, ciprofloxacin, or ceftriaxone. Information most frequently used in state and CDC communication was data describing patient characteristics and outcomes, primarily for the purpose of better understanding antimicrobial resistant cases. Consults with states involved two main topics: 1) appropriate treatment and control strategies given particular antimicrobial resistance findings and 2) balancing economic and resource considerations with disease control strategies during childcare outbreaks. Health departments that participated in the CSTE discussion indicated a desire for standardized childcare exclusion policy guidance and expressed a need for privacy considerations when conducting investigations among MSM.

Conclusions: More work is needed to learn how surveillance data, particularly that collected during multi-state cluster investigations coordinated by CDC, can be used to better support state and local health departments to respond to shigellosis clusters.
P-002

Analysis of PFGE patterns of *Salmonella* spp. isolated from imported and domestic food products in Korea

Authors: Eun Sook An¹, Jin Hee Hwang², Seok Hwan Kim¹, Mi Ri Choi¹, Won Hee Jeong¹, In Sun Joo¹, Soon Han Kim¹, Hyo Sun Kwak¹, Jin Hwan Hong¹

Affiliations: ¹Food Microbiology Division, ²Foodborne Diseases Prevention and Surveillance Division, Ministry of Food and Drug Safety, 187 Osongsaengmyeong 2-ro, Osong-eup, Heungdeok-gu, Cheongju-si, Chungcheongbuk-do, 363-700, Republic of Korea

**Background:** *Salmonella* is a major cause of food-borne illness worldwide and commonly found in various kinds of food product, including meat, eggs, fruits, vegetables, nuts and spices. Recently, *Salmonella* in chickens imported from Brazil has been detected in Korea. As a part of the national surveillance system, we need to investigate the characteristics of *Salmonella* in the food products. In this study, we described to characterize *Salmonella* isolates from imported and domestic food samples in Korea.

**Methods:** Between January 2015 and July 2017, A total of 48 *Salmonella* spp. isolates from imported (n=10) and domestic food samples (n=38) were collected. These isolates were tested for a genetic diversity analysis with Pulsed-field gel electrophoresis (PFGE) using restriction endonuclease XbaI. The gel images were processed and analyzed by BioNumerics software.

**Results:** Ten of *salmonella* spp. isolates in chickens imported from Brazil were identified as 2 serotypes: S. Heidelberg (n=9), S. Sandiego (n=1). In PFGE analysis, the patterns of 9 strains (S. Heidelberg) showed 83.2% similarity. Also, we analyzed PFGE patterns of thirty-eight of *Salmonella* spp. isolates in domestic food samples. The similarity levels of the PFGE patterns (n=38) showed 52.8% ~ 83.2%. At the end, we analyzed 48 strains studied, the PFGE patterns of 9 isolates in Brazilian chickens and 5 isolates in domestic chickens showed 77.6 ~ 83.2% similarity.

**Conclusion:** A total of 9 *Salmonella* spp. isolates in chickens imported from Brazil showed same serotype and high similarity. These 9 isolates showed high homology with 5 *Salmonella* spp. isolates in domestic chickens. Therefore, we are planning to further studies about *salmonella* spp. isolates using alternative method such as multilocus sequence typing (MLST), whole-genome sequencing (WGS).
P-003

A multi-prefectural outbreak of *E. coli* 0157 associated with sugarcane juice in Okinawa Prefecture, Japan, 2016


Affiliations: 1 Field Epidemiology Training Program of Japan FETP-J, 2 Naha City Public Health Center, 3 Okinawa Prefectural Government, 4 Okinawa Prefectural Institute of Health and Environment, 5 National Institute of Infectious Diseases, Japan


Methods: We conducted unmatched case-control study and trace-back investigation to determine the source of EHEC O157 infection. Behavioral data used standardized questionnaire, constructed by Naha city. IS-printing, analyzed by multiplex PCR-based strain-typing methods for EHEC O157 as a screening, and multiple-locus variable-number tandem-repeat analysis (MLVA) were performed to help define cases.

Results: A total of 32 individuals met the case definition. Of 32 cases, 22 were confirmed cases, six were symptomatic cases and four were suspected case for the outbreak. All cases came from 15 prefectures, outside of Okinawa prefectures, between 20 July and 2 September 2016. Of 32 cases, 18 cases are hospitalized. Four children, aged 4-16 years, developed haemolytic uraemic syndrome, and one child had invagination of intestines.

All 32 cases visited to an amusement park. All cases and 24 of 38 controls (63.2%) consumed sugarcane juice which purchased from juice stand B in the amusement park. A subsequent case-control study supported the hypothesis that sugarcane juice was the source of the outbreak (odds ratio=24.69, 95% confidence interval (CI): 4.93–∞). All strains isolated from 25 cases were *E. coli* O157 Stx2. IS-Printing was same pattern and MLVA type was closely related for all cases.

Conclusion: We concluded that the multi-prefectural outbreak of enterohemorrhagic *E.coli* O157 might associate with consumed sugarcane juice among travelers.

Authors: Barrett, KA¹; Harrigan, M¹; Wymore, K²; LaClair, B³; Olsen, D⁴; Nicholson, C⁵; Decuir, M⁶; McMillian, M⁷; Cahoon, J⁸; Geissler, A¹

Affiliations: ¹Division of Foodborne, Waterborne, and Environmental Diseases, National Center for Emerging & Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, Atlanta, GA; ²California Emerging Infections Program, Oakland, CA; ³Georgia Department of Public Health, Atlanta, GA; ⁴Connecticut Emerging Infections Program, New Haven, CT; ⁵New Mexico Emerging Infections Program, Albuquerque, NM; ⁶Minnesota Department of Health, Saint Paul, MN; ⁷Tennessee Department of Health, Nashville, TN; ⁸Maryland Department of Health and Mental Hygiene, Baltimore, MD

Background: FoodNet conducts active laboratory-based surveillance for nine enteric pathogens. In 2012, FoodNet began including reports of positive culture-independent diagnostic tests (CIDTs), many of which are on PCR-based syndrome panels that can detect multiple pathogens. We describe polymicrobial detections (PDs) and examine changes in their frequency corresponding with the use of CIDTs.

Methods: We defined a polymicrobial detection as detection of >1 pathogen, or >1 species or serotype by culture (CX) or CIDT in specimens collected <30 days apart from patients in seven FoodNet sites during 2011–2016.

Results: During 2011–2016, we identified 1,071 persons with PDs, resulting in 2,164 (2%) cases. PDs were identified in specimens collected on the same day for 845 (79%) persons, within 1–7 days for 110 (10%), and 8–30 days for 115 (11%). Among patients with PDs, 954 (89%) had two pathogens detected, 96 (9%) had 2 subtypes of a pathogen, and 21 (2%) had ≥ 3 pathogens or subtypes. Campylobacter was the pathogen most commonly detected in PDs, paired most often with Salmonella (27%), followed by Shigella (16%), Shiga toxin-producing Escherichia coli (11%), and Cryptosporidium (11%). There were 618 persons with PDs (58%) detected by CIDTs; among these, 297 (48%) were antigen-based tests, 151 (24%) laboratory-developed PCRs, 84 (14%) syndrome panels, and 86 (14%) involved multiple types of CIDTs. Average annual incidence rates of PDs increased 73% in 2014–2016 compared with 2011–2013 (0.71 vs. 1.23 per 100,000 persons). The percentage of patients whose PDs were detected only by CIDTs increased in from 0% in 2011 to 25% in 2016, and the percentage of patients whose PDs included a CX-confirmed pathogen decreased from 77% to 30%.

Conclusions: The number of polymicrobial detections has increased since the introduction of CIDTs. PDs complicate case classification, cluster detection, and treatment decisions. Additional data and standardized recommendations are needed to inform interpretation of results and guide public health action.
**Background**: In recent years, laboratories have increasingly used culture-independent diagnostic tests (CIDTs) to detect enteric pathogens, including *Vibrio* species. In 2016, CSTE approved defining CIDT-detected *vibriosis* as probable cases. Timely data collection on *Vibrio* species and sharing with the Food and Drug Administration (FDA) and the Interstate Shellfish Sanitation Conference (ISSC) helps ensure compliance with national shellfish regulations and review progress toward illness reduction.

**Methods**: CDC revised the case report form for the Cholera and Other *Vibrio* Illness Surveillance (COVIS) system to include probable cases and incorporated state feedback on usability. CDC set up protocols for more frequent data sharing with FDA and ISSC. States helped with form changes and case definition implementation. CDC encouraged electronic case reporting. CDC also developed a weekly update on *Vibrio* activity during peak season.

**Results**: In 2017, CIDT data collection began, and states received the new COVIS case report form and guidance. As of July 20, 2017, states reported 150 cases detected by CIDT. Of those, 29 were culture-confirmed, 70 were negative for *Vibrio* by culture, and 51 had no culture results. CDC increased sharing of shellfish-related COVIS forms with FDA to at least weekly from quarterly or annually prior to 2016. CDC’s weekly updates of real-time surveillance data were successfully sent to states during the 2016 *Vibrio* season and the 2017 season thus far. Before 2016, data collection from state partners occurred at least annually. So far in 2017, states have provided preliminary data for 604 cases of *vibriosis* through the rapid notification mechanism of the weekly update, compared with 404 reported with the traditional case report form.

**Conclusions**: National *Vibrio* surveillance has successfully adapted to changes in diagnostic testing. Partnership between CDC, FDA, ISSC, and states has led to the sharing of timelier and more complete data, which aids prevention and response efforts. Future areas of work include improving seafood investigation data and continuing to streamline case reporting and data sharing.
Use of a Regional Poison Control Center to Track Human and Animal Illnesses Linked to a Harmful Algal Bloom

Authors: Cindy Burnett¹, Kaitlyn Brown², Heather Bennett², Barbara I. Crouch², Nathan LaCross¹

Affiliations: ¹Utah Department of Health, ²Utah Poison Control Center

Background: Exposure to harmful algal blooms (HABs) can cause a variety of health effects in humans and animals. The One Health Harmful Algal Bloom System (OHHABS) is a reporting system developed by CDC to better understand HAB-associated illness. In July 2016, a HAB occurred in Utah Lake, a popular body of water used for recreation and irrigation. We describe a coordinated effort between the Utah Department of Health (UDOH) and the Utah Poison Control Center (UPCC) to collect information about human and animal cases of HAB-associated illness using OHHABS.

Methods: The media reported the HAB on July 12, 2016 and the UPCC immediately responded to a surge of phone calls from concerned citizens who were exposed to the bloom, some of whom reported experiencing illness. UDOH granted UPCC personnel access to input cases of suspected HAB-associated human and animal illnesses directly into OHHABS. UPCC reports which met CDC criteria as suspect, probable or confirmed cases were entered into OHHABS.

Results: Between July 1 and August 31, 2016, a total of 199 human and 13 animal HAB-associated illnesses were identified and entered into OHHABS. The median age of human cases was 19 years (range: 1-80 years). Routes of exposure included: skin contact (n=163), ingestion (n=126), other/unknown (n=24), and inhalation (n=3). Illnesses in animals were reported in three species: dog (n=12), cat (n=1), and herd of horses (n=1). One HAB-associated death was reported in a cat.

Conclusions: Without the assistance of the UPCC, it would not have been possible to identify and document the large number of illnesses in humans and animals that were reported following the HAB at Utah Lake. Understanding the impact of the HAB on the community will help inform and provide guidance for future HAB response and resource allocation.
P-007

Genotyping Cryptosporidium informs risk factors and transmission patterns of cryptosporidiosis— Nebraska, 2015-2016

Authors: A. Carlson1, C. Pedati1, P.C. Iwen2, D. M. Roellig3, M. Hlavsa3, K. Fullerton3, T. Safranek1

Affiliations: 1 Division of Public Health, Nebraska Department of Health and Human Services, 2 Nebraska Public Health Laboratory, 3 Waterborne Disease Prevention Branch, Centers for Disease Control and Prevention

Background: Cryptosporidium is transmitted animal-to-person or person-to-person through contaminated water or food. Genotype characterization can enhance epidemiologic data and inform prevention and control. We evaluated the epidemiology and genetic diversity of Cryptosporidium in Nebraska.

Methods: Cryptosporidium-positive human stools sent to NPHL during September 2015–November 2016 were submitted to CDC for nested-PCR restriction-fragment-length-polymorphism analysis and subtyped by DNA sequencing. Epidemiologic data from case investigations were compiled. Descriptive analysis of demographic and clinical information, and logistic regressions evaluating risk factors were performed. GIS mapping was utilized for geographic trends.

Results: Ninety-one stools were positive for Cryptosporidium species including C. hominis (54), C. parvum (29), C. chipmunk genotype I (3), C. ubiquitum (2), C. canis (1), C. felis (1), and C. skunk genotype (1). Patient ages ranged from 0.6 to 79 years (median, 24 years) with 55 (60%) females. Seven hospitalizations and one death were reported. Reported risk factors included animal contact (n = 56), association with a childcare setting (n = 28), recreational water exposure (n = 27), and travel (n = 29). Animal exposures included ruminants (n = 12) and cattle (n = 10). Compared to other Cryptosporidium cases, C. parvum cases were 15.8 times as likely to have cattle exposure (P=0.0007; CI = 3.2–78.5), whereas C. hominis cases were 10.7 times as likely to have a childcare setting association (P=0.0005; CI = 2.8–40.4). GIS mapping showed C. hominis primarily exists in urban settings, while C. parvum was found in rural locations.

Conclusions: Cryptosporidium genotyping augmented epidemiological investigations by confirming known risk factors and distribution patterns. Unique cases of non-parvum or -hominis genotypes led to re-interviews, identifying dog, squirrel and skunk exposures previously unknown. A cluster of cases were identified as the same C. hominis subtype, but were associated with different childcare exposures. This suggested exclusion from one facility can lead to introduction in other facilities. Ongoing studies to increase sampling in rural and urban populations are necessary to more confidently demonstrate transmission dichotomies.
Author: Danyang Chen, MD, MPH

Background: Salmonellosis is one of the most common food-borne diseases, and a frequent cause of food-borne outbreaks. This report describes trends in incidence of Salmonella infection and hospitalizations in the sixth most populous state in the U.S., Pennsylvania.

Methods: Surveillance data on cases of salmonellosis reported from 2000-2015 were extracted from Pennsylvania’s National Electronic Disease Surveillance System (PA-NEDSS). Annual incidence rates (cases/100,000 population) were calculated using intercensal estimates. Age- and sex-specific incidence rates were also calculated. SAS software was used for data analyses.

Results: A total of 27,275 confirmed and probable salmonellosis cases were reported from 2000 to 2015. The average incidence of salmonellosis was 13.6 cases/100,000. The highest rate, 16.3/100,000, occurred in 2004, which was a year with three large tomato-related outbreaks. Salmonellosis incidence was significantly higher among children under 5 years of age (49.1/100,000) compared to persons 5 and older (7.2 cases/100,000, p<0.0001). Females had slightly higher incidence rates than males. A total of 1,838 cases (6.7% of all cases) were associated with recognized salmonella outbreaks. The proportion of outbreak-associated cases generally increased over time, roughly paralleling the proportion of isolates undergoing molecular typing using pulsed-field gel electrophoresis (PFGE).

Conclusions: Salmonellosis remains an important cause of food-borne disease and outbreaks every year, especially in children under 5 years of age. The proportion of cases associated with outbreaks has increased over the past decade. This is likely a reflection of improved outbreak identification due to the increased use of molecular techniques and multistate investigation efforts.
Progress towards an optimized *Salmonella* isolate recovery protocol

Authors: K. C. Dillon¹, J. R. Hensley¹, M. Patel¹, E. Trees², J. Besser², H. A. Carleton², A. D. Huang², A. J. Williams-Newkirk³

Affiliations: ¹Oak Ridge Institute for Science and Education, ²Enteric Diseases Laboratory Branch, CDC, ³IHRC, Inc.

Abstract: Nontyphoidal *Salmonella* is estimated to cause 1,000,000 infections each year in the US, with more than 19,000 hospitalizations and 380 deaths. Clinical laboratories in the US are adopting culture-independent diagnostic tests (CIDTs) to detect *Salmonella* and other pathogens in human stool in part because they provide clinically important information faster than traditional microbiological techniques. Despite multiple advantages, CIDTs jeopardize public health surveillance networks like PulseNet because they do not yield the isolates required for subtyping, virulence determination, and antibiotic resistance testing. The APHL Food Safety CIDT subcommittee identified the lack of an optimized standard protocol for the recovery of isolates from CIDT-positive stool specimens as a major barrier to isolate availability for surveillance. Initial studies at CDC and state public health labs tested the most commonly used enrichment and primary isolation methods for *Salmonella* and Shiga toxin-producing *E. coli*. This study uses a two-phase design to examine the most promising methods for *Salmonella* identified in the previous survey. Phase 1 identifies the optimal storage temperature (4°C and 22°C), plating media (Hektoen Enteric Agar and Xylose Lysine Deoxycholate Agar), and transport media (Cary-Blair Transport Medium and Gram-Negative broth) across different storage times (1, 4, and 7 days) using healthy stool spiked with two common *Salmonella* serotypes (*Salmonella enterica* ser. Newport and Oranienburg) at inoculum levels of $10^6$, $10^4$, and $10^2$ CFU/mL. Phase 2 determines the optimal enrichment media (Selenite Broth, Tetrathionate Broth Base, and Modified Semisolid Rappaport-Vassiliadis Medium) to use in combination with the media and temperature identified in Phase 1. Future work will test these protocols with clinical specimens at CDC and partner labs prior drafting final recommendations.
Evaluating Twitter for Foodborne Illness Outbreak Detection in New York City

Authors: K. Devinney¹, A. Bekbay¹, T. Effland², L. Gravano², D. Howell², D. Hsu², D. O’Hallorhan¹, C. Padhy¹, V. Reddy¹, F. Stavinsky¹, H. Waechter¹, S. Balter¹

Affiliations: ¹New York City Department of Health and Mental Hygiene, ²Columbia University

Background: Annually, the New York City (NYC) Department of Health and Mental Hygiene (DOHMH) manages over 4,000 foodborne illness (FI) reports received via the citywide complaint system (311) and identified on Yelp and detects about 30 outbreaks. With approximately 24,000 restaurants, 15,000 food retailers and >8.5 million residents in NYC, it is likely that many FI incidents remain unreported. DOHMH sought to evaluate an additional data source, Twitter, to enhance FI complaint and outbreak detection.

Methods: DOHMH and Columbia University developed a text mining algorithm to identify tweets indicating FI. Twitter data are received via a targeted API query using FI key words and selecting for tweets with a possible NYC location. Each tweet is assigned a sick score; those meeting a threshold value are manually reviewed, and a survey link is tweeted to users who have tweeted about FI, requesting more information regarding the FI event, as well as restaurant and contact information. Completed surveys are used to validate tweets as complaints and are incorporated in a daily analysis using all sources of complaint data to identify restaurants with multiple FI complaints within a 30-day period. The system was launched in November 2016.

Results: From November 28, 2016–July 12, 2017, 9,754 tweets were reviewed; 2,444 (25%) indicated FI in NYC, and 2,046 (21%) were tweeted a survey link. The tweets resulted in 75 likes, 55 replies, 333 survey link clicks and 23 submitted surveys (response rate 1%). All confirmed FI and were not reported via 311/Yelp; nine completed interviews. No outbreaks were identified.

Conclusions: The use of Twitter for FI outbreak detection continues to be evaluated; the identification of complaints not otherwise reported to 311/Yelp support its utility. Future plans include using feedback data to improve the sensitivity and specificity of the text mining algorithm. Also, we intend to share this system with other health departments so that they might incorporate Twitter in FI complaint and outbreak detection.

Authors: D Dewey-Mattia¹, K Manikonda¹, and S Crowe¹

Affiliation: ¹Division of Foodborne, Waterborne, and Environmental Diseases, CDC

Background: The Foodborne Disease Outbreak Surveillance System (FDOSS) collects reports from US state, local, and territorial health departments. Data describe the foods, pathogens, and settings of outbreaks and inform national food safety policies. We calculated national, regional, and state-specific reporting metrics, focusing on data completeness.

Methods: We determined the completeness of demographic and case outcome variables for outbreaks reported to FDOSS in 2015–2016, including the age and sex of patients and the number of reported illnesses, hospitalizations, and deaths. We also calculated the proportion of reports that included a confirmed etiology, implicated food, and how the food was implicated (e.g., epidemiologic or laboratory evidence).

Results: As of July 2017, 1,699 foodborne disease outbreak reports (914 in 2015 and 785 in 2016) from 49 states and Puerto Rico had been submitted. The mean state reporting rate (outbreaks per 1,000,000 persons per year) was 2.8 (range, 0.26 to 10.5). The rate varied by census region, from 1.6 in the Northeast and South to 3.2 in the West and 4.1 in the Midwest. Complete information on age and sex was reported for 1,671 (98%) outbreaks, and 1,677 (99%) had complete information on the number of laboratory-confirmed cases, hospitalizations, and deaths. Eight hundred and twenty-five (49%) outbreak reports included a confirmed etiology, 664 (39%) included an implicated food, and 422 (25%) had both. Among reports with an implicated food, 658 (99%) reported a reason the food was suspected.

Conclusion: The completeness of demographic and case outcome variables for outbreak reports was high. The rate of outbreak reporting varied among states and by region, however, and only a quarter of outbreaks reported both an implicated food and confirmed etiology. Strengthening the capacity of health departments to investigate and report outbreaks will improve foodborne disease outbreak surveillance data.
P-012

**A description of *Salmonella* zoonotic outbreak cases without exposure to the outbreak-associated animal, Georgia, 2010-2016**

Authors: Hope Dishman¹, MPH, Lana Jones¹, MPH, Amber Cochran², MPH, MLS, Melissa Tobin-D'Angelo¹, MD, MPH

Affiliations: ¹Georgia Department of Public Health Epidemiology, ²Georgia Department of Public Health Laboratory

**Background:** Of approximately 2500 *Salmonella* cases reported in Georgia annually, an average of 0.45% have been associated with zoonotic outbreaks during the past 7 years. CDC PulseNet (PN) analyzes all *Salmonella* pulsed-field gel electrophoresis (PFGE) and whole genome sequencing (WGS) data submitted from public health laboratories to detect increases among identical or closely related isolates. An identified increase may result in an epidemiologic investigation, which may identify an outbreak. However, outbreaks are often defined using laboratory data, not exposure data. We characterized the proportion of zoonotic outbreak-associated *Salmonella* cases epidemiologically associated with the animal of interest.

**Methods:** Georgia maintains databases of notifiable diseases and outbreak investigations. The notifiable disease and outbreak databases were queried for *Salmonella* cases and outbreaks associated with zoonotic transmission. Cases were cross-referenced to ensure uniformity across databases; exposure to the outbreak-associated animal was determined for each case.

**Results:** From 2010-2016, 81 Georgia residents were included in 26 PN-defined multi-state *Salmonella* outbreaks associated with zoonotic transmission. None of the outbreaks included epidemiologic data in the case definition. Animals associated with those 26 outbreaks included: live poultry (18), small turtles (6), frozen rodents (1), and lizards (1). Of all 81 outbreak cases, 48 (59%) reported exposure to the outbreak-associated animal, 16 (20%) reported no contact, and 17 (21%) were either unknown or lost to follow-up. Among cases with complete exposure information (64), 16 (25%) reported no contact with the implicated animal.

**Conclusions:** Outbreaks that include PFGE data without epidemiologic data in the case definition may include a substantial number of cases that are not truly part of the outbreak. This may be partially solved with the increased use of WGS in *Salmonella* outbreak investigations; however, epidemiologic data should be considered for outbreaks in which the exposure can be reliably recalled such as zoonotic outbreaks or outbreaks of uncommon food vehicles. Public health officials should evaluate this issue and consider the role of missing exposure data.
Norovirus outbreak caused by oysters, Canada, 2016-17

Authors: E. Galanis¹, R. McCormick², K. Hill³, P. Hasselback³, V. Mah⁵, L. Honish⁶, A. Fitzgerald-Husek⁷, Y. Whitfield⁷, L. McIntyre¹, C. Bateman⁴, N. Prystajecky⁸, Outbreak Teams

Affiliations: ¹British Columbia Centre for Disease Control (BCCDC), ²Public Health Agency of Canada, ³Island Health, ⁴Canadian Food Inspection Agency, ⁵Alberta Health, ⁶Alberta Health Services, ⁷Public Health Ontario, ⁸BCCDC Public Health Laboratory

Background: In 2016-17, Canada was affected by a multi-provincial outbreak of norovirus (NV) associated with the consumption of oysters from British Columbia (BC).

Methods: Cases were interviewed and associated premises were inspected. Shellfish tags were used to trace oysters to farms. Stool and oysters from retail locations and farms were tested using NAT.

Results: In Nov 2016, 118 diarrheal cases occurred in BC; the majority ate raw oysters at a festival. Six cases were confirmed NV GI. Oysters from 1 BC farm associated with 91% of cases were positive for NV GI. In Dec 2016-Mar 2017, 144 clusters (330 cases) occurred in BC, Alberta and Ontario; the majority consumed oysters from various farms in BC. Eighteen clusters were confirmed NV GI or GII. Oysters from 6 of 14 farms were positive for NV GI or GII. Twelve farms were closed.

Conclusions: No outbreak source was found. Human sewage and environmental factors may have led to marine contamination. Efforts are underway to improve detection, control and source identification.
Multistate Outbreak of *Salmonella* I 4,[5],12:i:- Infections Linked to Rotisserie Chicken Products, 2016–2017

Authors: L Gieraltowski, R Hassan, V Peralta, B Melius, J Anderberg, A Barnes, D Vugia, H Carleton, M Leeper, A Green, S Defibaugh-Chavez, D Noveroske, M Wise

**Background:** *Salmonella* causes 1.2 million infections and an estimated 450 deaths annually in the United States. On September 22, 2016, the California Department of Public Health reported two clusters of *Salmonella* I 4,[5],12:i:- infections to CDC. PulseNet was queried to identify other *Salmonella* I 4,[5],12:i:- infections with the same pulsed-field gel electrophoresis (PFGE) patterns. We investigated to identify the source and prevent additional illnesses.

**Methods:** A case was defined as infection with an outbreak strain of *Salmonella* I 4,[5],12:i:- by PFGE or whole-genome sequencing in a person with illness onset from July 5, 2016 – January 24, 2017. Patients were interviewed to identify common exposures. California, Washington, and US Department of Agriculture’s Food Safety and Inspection Service (USDA-FSIS) officials conducted traceback and environmental assessments at retail stores.

**Results:** We identified 63 illnesses from 13 states. Forty-five (88%) of 51 patients reported eating chicken before illness onset. Of these, 34 (76%) ate or purchased chicken from 11 Chain A locations, and 27 (60%) ate or purchased Chain A rotisserie chicken or rotisserie chicken products. On October 9, USDA-FSIS issued a public health alert due to a possible link between illnesses and rotisserie chicken salad prepared at a single Chain A location. Recordkeeping did not allow for traceback that could identify a single USDA-FSIS establishment linked to illnesses at all retail locations. After Chain A implemented procedural changes nationwide, including use of high-pressure pasteurized chicken in cold ready-to-eat (RTE) products, the number of illnesses reported nationally returned to baseline levels.

**Conclusion:** Outbreaks linked to RTE chicken products can result from many different breakdowns in food safety, including high pathogen burden in chicken, cross-contamination at retail, and inadequate cooking or improper handling practices by consumers. This outbreak demonstrates that corrective actions taken in any one of these areas can help prevent illnesses.
Arizona Food, Animal, and Water Exposure Survey

Authors: Bria Hamlet¹, BA, Mackenzie Tewell¹, MA, MPH, CPH, Joli Weiss¹, PhD, Marilee Kellis¹, BS, Brenna Garrett¹, BS

Affiliation: ¹Arizona Department of Health Services

Background: Arizona is unique in its geographic location, population, and availability of food items. Collecting exposure data from residents provides local epidemiologists with background rates to compare against significant items during enteric illness outbreaks. While national data from CDC’s Foodborne Diseases Active Surveillance Network (FoodNet) is available for reference, Arizona’s demography, geography, and food availability created a need to conduct an Arizona-specific survey. The Arizona Food, Animal, and Water Exposure Survey (AZFAWES) aimed to collect seven-day exposure histories of residents to generate background data for local epidemiologists.

Methods: The AZ FAWES was built using the Qualtrics© Insight Platform. Survey questions were formatted to mirror CDC’s FoodNet Population Survey. Quotas were established to ensure that participants were representative of Arizona’s demography. Participants were recruited online, and surveys were distributed by Qualtrics via email panels. Participants received a monetary award of $0.25 upon completion of the survey. The survey was launched in April 2016 and continued through April 2017.

Results: As of January 2017, 5,348 participants have reported their exposures. Initial data indicate a notable exposure difference in the number of participants reporting Mexican-style cheese consumption. Approximately 50% of Arizona residents reported consuming Mexican-style cheese, in comparison to just 6.4% of FoodNet’s survey participants. In July 2016, Maricopa County Department of Public Health investigated an outbreak of Salmonella Javiana. AZFAWES data were used in the development of a hypothesis about the source of the illness, comparing the number of cases reporting shrimp exposure to the number of survey participants reporting that exposure.

Conclusions: The survey results have been helpful in highlighting important risk factors for foodborne illness, as knowing differences in rates of exposure between national data and Arizona resident data has strengthened outbreak responses.
P-016

Multidrug Resistant *Shigella flexneri* infections in Tennessee, 2015-2016

Authors: Samir Hanna, MD, MSPH, Katie Garman, MPH, Steffany Cavallo, MPH, John Dunn, PhD, DVM, Tennessee Department of Health

**Background:** Shigellosis is the 3rd most common bacterial enteric infection in the US. Transmission is primarily person to person and *Shigella sonnei* outbreaks are common in daycare settings. *Shigella flexneri* is less commonly reported but multi-state outbreaks are increasingly recognized. We reviewed *S. flexneri* cases from 2015-2016 to assess involvement in multi-state clusters, and describe resistance profiles and risk factors.

**Methods:** Data was collected on cases including completion of standard case report forms, supplemental interviewing, and medical record review. Collaboration with the state HIV/STD program facilitated risk factor assessment including HIV status and sexual orientation. Isolates were subjected to antimicrobial susceptibility testing and PFGE. Analyses were performed using Epi Info 7.

**Results:** Twelve Tennessee cases were included in 5 multi-state clusters of antimicrobial resistant *S. flexneri*. Six PFGE patterns were identified. All cases were males; 11 (92%) resided in large metropolitan areas. Eight (67%) were African-American, 2 (17%) White, and 2 (17%) were unknown race. Median age was 33 years with a range of 17-51 years. Epidemiological data was available for 8 cases. Three cases were hospitalized. Duration of illness ranged from 5 to 7 days. Three were treated with antibiotics. Four (50%) self-identified as MSM, 6 (75%) were HIV/immune-compromised, and 2 (25%) reported a STD. One case (13%) reported drug use, and 2 (25%) reported recent domestic travel. All denied international travel. Antibiotic susceptibility results were available for 7 cases. All (100%) were resistant to ≥4 antimicrobial classes. One was a highly drug resistant, resistant to at least ampicillin, azithromycin, and TMP/SMX.

**Conclusions:** Emergence of domestically acquired antimicrobial resistant *S. flexneri* is a growing public health concern. We identified common features among Tennessee cases including male sex, MSM, HIV and other immunosuppressive conditions, and residing in metropolitan areas. Partnership with the HIV/STD staff facilitated data collection and education of cases and high-risk groups. Joint investigation and outreach between health department programs may assist in surveillance and prevention efforts for multidrug *S. flexneri*.
P-017


Authors: MC Hlavsa, DM Roellig, MH Seabolt, CryptoNet State Partners, KE Fullerton, L Xiao

Background: U.S. annual incidence of cryptosporidiosis has increased >3-fold since 2014. Fecal-oral transmission of Cryptosporidium can occur via ingestion of contaminated food or water (recreational or drinking) or following contact with infected persons or animals. Most Cryptosporidium species are morphologically indistinguishable by traditional diagnostic tests; only molecular methods can distinguish species and their subtypes. Thus, to optimize evidence-based prevention and control strategies, in 2015, CDC formally launched CryptoNet, a molecular-based surveillance system to elucidate Cryptosporidium chains of transmission and cryptosporidiosis epidemiology further.

Methods: CDC microbiologists and epidemiologists began closely working with state partners in AL, ME, MN, NE, NH, OH, TN, and WI in mid-2015. To date, the focus has been on increasing state public health laboratory capacity to perform Sanger-based amplicon typing and to collect corresponding diagnostic and epidemiologic data for each specimen submitted to CryptoNet for molecular typing.

Results: For 2016, CryptoNet received 464 specimens, of which 292 (62.9%) were positive for Cryptosporidium by molecular methods. The following subtypes were identified in specimens of patients with outbreak-associated cases: C. hominis IdA19, C. hominis IfA12G1, C. parvum IlaA18G3R1, and C. parvum IlaA15G2R1. The following subtypes were most frequently identified in specimens of patients with sporadic cases: C. parvum IlaA15G2R1, C. hominis IfA12G1, and Cryptosporidium chipmunk genotype I. Identification of non-C. parvum and non-C. hominis species led to additional patient interviews and identification of distinct risk factors (e.g., squirrel contact).

Conclusions: CryptoNet is the first molecularly-based surveillance system for a parasitic disease. Early CryptoNet data indicate molecular typing can enhance detection of risk factors. Given this, reports of Cryptosporidium contamination of food, and the parasite’s extreme tolerance to chlorine (i.e., a barrier to infectious pathogen transmission), CryptoNet will likely increasingly detect foodborne transmission.
Characterization of *Salmonella* Typhimurium by Whole-Genome Sequencing Single Nucleotide Polymorphism-Based Analysis for Surveillance and Foodborne Outbreak Detection

Authors: M. Horn¹, S. Meyer¹, X. Wang¹, A. Jones Taylor¹, K. Smith¹, D. Boxrud¹

Affiliation: ¹MN Dept. of Health

**Background:** *Salmonella* Typhimurium is one of the most common *Salmonella* serotypes in the U.S.; however, current molecular subtyping methods such as pulsed-field gel electrophoresis (PFGE) lack adequate discriminatory power for isolates with common subtypes. In this retrospective analysis of outbreak and sporadic isolates, we identify how *S. Typhimurium* outbreaks cluster by WGS, preparing the criteria for prospective implementation of WGS-based outbreak detection for *S. Typhimurium*.

**Methods:** Forty-two clinical *S. Typhimurium* isolates from 13 epidemiologically confirmed foodborne outbreaks and 23 sporadic isolates were sequenced on the Illumina MiSeq and analyzed with reference strain LT2 (AE006468) using Lyve-SET. Smalt was used for mapping, and single nucleotide polymorphisms (SNPs) were called using Varscan.

**Results:** For 12 outbreaks, all isolates varied by <1 SNP from other isolates within the outbreak. Outbreak isolates differed by an average of 55 SNPs from the nearest nonrelated isolate, whereas sporadic isolates differed by an average of 24 SNPs from the nearest sporadic isolate. For 1 outbreak, associated with watermelon sold by different retailers, 2 isolates were within <2 SNPs of each other but 1 isolate differed by 16 SNPs. Three distinct outbreaks that shared the same PFGE pattern occurred in 2 separate years. Two of the outbreaks were 1-2 SNPs apart and were epidemiologically linked, with eggs from the same supplier as the likely source. The epidemiologically unrelated third outbreak had isolates that were 49-50 SNPs different from the others.

**Conclusions:** Our findings show that almost all outbreak isolates fall within <2 SNPs of each other. WGS provides greater resolution between outbreak and sporadic isolates than PFGE, supporting the use of WGS as an outbreak detection and characterization method for *S. Typhimurium*. This is particularly helpful when isolates have common PFGE patterns, as WGS results can support and enhance epidemiological information and exposure data.
**P-019**

**Epidemiology of Paratyphoid Fever, United States, 2010 – 2015**

Authors: Michael Hughes, Karen Wong, Kevin Chatham-Stephens

Affiliation: 1US Centers for Disease Control and Prevention

**Background:** Paratyphoid fever, an enteric fever caused by *Salmonella enterica* serotypes Paratyphi A, B, and rarely C, is rare in the United States. Most cases are associated with international travel, especially to south Asia. Typhoid and paratyphoid fever are clinically indistinguishable. Pertinent epidemiological data about paratyphoid fever are more similar to typhoid than nontyphoidal salmonellosis. However, in the National Notifiable Diseases Surveillance System (NNDSS), paratyphoid fever reports are not distinguishable from nontyphoidal salmonellosis. We review the epidemiology of paratyphoid fever cases in the National Typhoid and Paratyphoid Fever Surveillance (NTPFS) system to inform ongoing surveillance enhancements.

**Methods:** NTPFS receives demographic, epidemiological, and clinical information on culture-confirmed cases of typhoid and paratyphoid fever. Patients are interviewed using a detailed case report form, and health departments send completed forms to the CDC to supplement NNDSS. Travel-associated cases are defined as infections in persons who traveled outside of the United States within 30 days of illness onset. We describe trends in U.S. paratyphoid fever (serotype Paratyphi A only) cases during 2010–2015.

**Results:** There were 543 paratyphoid fever cases reported during 2010–2015; most (88%) were travel associated. Median age was 27 years (range 0–83 years); 32% occurred among children aged <18 years. Half were female. California (n=92; 17%), New York (n=69; 13%), and New Jersey (n=40; 9%) reported the most cases. The most frequent travel destinations were India (n=288; 66%), Pakistan (n=57; 13%), and Bangladesh (n=38; 9%). Three hundred sixty-four (64%) patients were hospitalized, and 1 (0.4%) died.

**Conclusions:** National paratyphoid surveillance data are useful for describing cases, characterizing illnesses, and assessing risk factors. Paratyphoid fever continues to cause illnesses and hospitalizations in the United States. This summary demonstrates the importance of being able to receive notifications for paratyphoid fever cases with epidemiologic information similar to that collected for typhoid fever.
Update on Shiga Toxin-Producing *E. coli* (STEC) National Surveillance

Authors: Jennifer C. Hunter, Michael Hughes, Karen Wong

Affiliation: 1US Centers for Disease Control and Prevention

**Background:** In 2013, the Council of State and Territorial Epidemiologists (CSTE) approved a position statement that identified a standard set of disease-specific data elements to be collected by all jurisdictions for all probable and confirmed Shiga toxin-producing *E. coli* (STEC) cases. The primary objective of defining standard data elements was to help investigators recognize shared exposures among cases across jurisdictions and to more quickly find the source of an outbreak. CSTE further recommended that CDC develop a data dictionary and a Message Mapping Guide (MMG) to receive these data through states’ routine data transmission mechanisms.

**Methods:** In 2016, the CDC Division of Foodborne, Waterborne, and Environmental Diseases (DFWED) began development of an MMG for national surveillance in collaboration with the CDC National Notifiable Diseases Surveillance System (NNDSS) and the Emerging Infections Program. Through this collaboration, we are developing a process to allow states to use their routine data transmission mechanisms for NNDSS while also delivering disease-specific data elements to the appropriate enteric diseases program within DFWED.

**Results:** CDC DFWED and the Emerging Infections Program have committed resources to drafting an MMG for several enteric conditions with defined disease-specific data elements, including STEC. FoodNet sites are currently piloting message transmission, validation, processing, and provisioning systems for Health Level 7 (HL7) case notifications. Additional testing with non-FoodNet sites is planned.

**Discussion:** Efforts to modernize STEC national surveillance and to fulfill the CSTE recommendations are underway. To fully implement these recommendations represents a substantial shift in national surveillance that will require epidemiology, informatics, and information technology support at state and federal levels. The potential impact of these surveillance improvements on outbreak response and virulence detection is enhanced through parallel investments in routine STEC isolate sequencing.
The Added Value of Next Generation Sequencing during Shigellosis Outbreak Investigations

Authors: Mateusz Karwowski¹, Elizabeth Adam¹, Valerie Morrill², Jasmine Huffman², Darlene Wagner², Heather Carleton², Kelley Hise², Eija Trees², state/local health department co-authors TBD

Affiliations: ¹Waterborne Disease Prevention Branch and ²Enteric Disease Laboratory Branch, Centers for Disease Control and Prevention

Background: Next generation sequencing has the potential to address limitations of pulsed-field gel electrophoresis (PFGE) in characterizing shigellosis outbreaks, particularly those with person-to-person spread. We used high-quality single nucleotide polymorphism (hqSNP) analysis to 1) determine isolate relatedness in a nine-state outbreak of an uncommon strain that included 14 PFGE patterns (Outbreak A); 2) assess isolate diversity in an outbreak in which a municipal water system was a suspected source (Outbreak B); and 3) evaluate risk factors in an outbreak spanning 37 states and territories (Outbreak C).

Methods: Isolates from each outbreak were sequenced on the Illumina MiSeq using NexteraXT (Illumina Inc.) library preparations and 2x250 bp sequencing chemistry. Reads were trimmed before mapping by SMALT. hqSNP analysis was conducted with Lyve-Set 1.1.4f (https://github.com/lskatz/lyve-SET) using closely related PacBio sequences as references with phage regions masked. SNPs were called using Varscan at >20x coverage, with >95% read support, and <5 bp apart. Phylogenetic trees were interpreted using epidemiologic data reported to the CDC by state and local health departments.

Results: Of 114 cases in Outbreak A, 69 case-isolates exhibiting 14 PFGE patterns were sequenced; 63 isolates exhibiting 10 PFGE patterns aligned into a single clade within 0-12 SNPs, suggesting they were part of the same outbreak. Of 158 cases in Outbreak B, 28 case-isolates were sequenced. These isolates clustered by source county into multiple subclades; the diversity of isolates from patients serviced by the water system (n=9, 0-25 SNPs) did not indicate a point source. Of 277 cases in Outbreak C, 77 case-isolates were sequenced; isolates from men who have sex with men clustered into a single clade within 0-29 SNPs and were distinct from clades associated with international travel.

Conclusion: hqSNP analysis added value to three recent shigellosis outbreak investigations by clarifying molecular relationships between isolates with unique PFGE patterns; linking cases over space and time; providing information to guide source attribution; and clarifying the role of specific risk factors in sustained transmission.
Arizona Enteric Disease Investigator Learning Collaborative

Authors: Marilee Kellis¹, BS, Mackenzie Tewell¹, MA, MPH, CPH, Joli Weiss¹, PhD, Alice White², MPH, Melisa Lindt², MPH

Affiliations: ¹Arizona Department of Health Services, ²Colorado Food Safety Center of Excellence

Background: In Arizona, local health agencies have jurisdiction for routine disease investigations. Enteric disease investigators represent a variety of educational backgrounds and perform multiple public health responsibilities in addition to enterics. The Arizona Department of Health Services (ADHS) identified a need for unifying this group to empower investigators and strengthen skills unique to enteric disease investigation.

Methods: Working with the Colorado Food Safety Center of Excellence (CoE), ADHS developed a six-session video series using Extension for Community Health Outcomes in Colorado (ECHO Colorado), titled Arizona Enteric Disease Investigator Learning Collaborative. ECHO is an education initiative for health professionals, allowing knowledge-sharing in real time via a video platform (Zoom) requiring only an internet connection. Sessions lasted one hour, consisting of three segments: didactic presentation by a subject matter expert; overview by a participant of a challenging case investigation; and open discussion by all participants. Topics covered in the series were: decoding enteric diseases, interview techniques, listening skills, questionnaire types, follow-up after an interview, and special case considerations.

Results: Between February and April 2017, 18 investigators of varying experience levels participated in the series. Ten of Arizona’s 15 county health departments and four tribal health organizations were represented. Ninety-three percent of participants attended four or more sessions. Fourteen participants completed a post-course survey. All respondents rated the quality of the series as good or excellent and would recommend this learning opportunity to a colleague. Ninety-three percent of respondents rated that the series was at the appropriate level based on their experience.

Conclusions: The ECHO model provided a useful platform for enteric disease investigators to interact and receive education. A second series is planned to begin in the fall of 2017 and the CoE plans to offer it nationwide.
P-023

2015 Indiana Food Safety and Defense Task Force and 2017 Midwest RRT Intentional Contamination Exercise

Author: Laurie Kidwell

Affiliation: Indiana State Department of Health (ISDH), Food Protection Program (FPP)

Abstract: In 2015, the Indiana Food Safety and Defense Task Force held a tabletop/drill exercise at the Ivy Tech Culinary School in Indianapolis that included a complex foodborne illness/intentional contamination scenario that affected a local community. The exercise brought together participants from local, state, and federal public health agencies; industry, healthcare, law enforcement, and consumer advocacy groups. The exercise’s purpose was to test current written state and local procedures, outbreak investigation actions, and recent Epi-Ready Trainings. In all, 63 players participated and several individuals in key leadership roles observed the exercise.

In 2017, the Midwest Regional Rapid Response Team (RRT) Meeting held an adapted version of the same tabletop/drill exercise in Madison, Wisconsin that was expanded to a multistate foodborne illness/intentional contamination scenario involving a distributed food item and impacted the Midwest region. The exercise brought together participants from several Midwest RRT states and their federal counterparts. The exercise’s purpose was to test current procedures, regional coordination and outbreak investigation actions. In all, approximately 40 players participated in the exercise.

Both exercise scenarios involved a disgruntled worker contaminating food with organophosphate chemicals resulting in multiple cases. The 2015 exercise involved a retail establishment resulting in mostly local cases and the 2017 exercise involving a multistate outbreak affecting the Midwest region. Initially, in both scenarios they looked like ordinary foodborne illness outbreaks which quickly evolved into a serious public health incident. The exercise began with tabletop discussions that included several small drills and then larger hands-on and actor drills.

Utilizing the same health hazard starting with a more localized event and then transitioning two years later to a multistate outbreak with a regional impact allowed the facilitators to compare and contrast appropriate investigation and mitigation actions, collaboration/communication between a localized versus a regional multistate event.
A Model Predicting Enteric Disease Outbreak Etiologies

Authors: HM Kisselburgh,1,2 SJ Crowe,1 KE Fullerton,1 AJ Hall,3 BB Bruce1

Affiliations: 1National Center for Emerging and Zoonotic Infectious Diseases, CDC, 2Atlanta Research and Education Foundation, 3National Center for Immunization and Respiratory Diseases, CDC

Background: Identifying the etiology of an enteric disease outbreak is an integral part of an outbreak investigation that usually requires laboratory confirmation using patients’ samples. Such samples are not always available, so we developed a model to predict outbreak etiology.

Methods: We analyzed outbreaks in the National Outbreak Reporting System during 2006–2015 with confirmed, single genus and some single species etiologies of Bacillus cereus, Campylobacter, Clostridium perfringens, Cryptosporidium, Escherichia coli, Giardia, norovirus, Salmonella, Shigella, Staphylococcus, and Vibrio (n = 10,795). Data were randomly divided into model training (n = 8,096) and test (n = 2,699) outbreaks. Multiple imputation of missing data was performed for all independent variables considered potentially useful for prediction in the model. A multinomial logistic regression model was developed based on the proportion of patients experiencing each of five symptoms or signs (cramps, bloody stools, fever, vomiting, and diarrhea), minimum incubation period, and the proportion who visited the emergency department. For each test outbreak, the model was applied and produced a ranked list of predicted etiologies. To evaluate the model, the percentage accuracy and Cohen’s kappa were calculated using the test data and compared with an intercept-only model (i.e., a prediction based on the frequency of each etiology without considering additional information).

Results: The top three model-predicted etiologies for each outbreak accurately included the laboratory-confirmed etiology 96% of the time (κ = 0.93) compared with 87% (κ = 0.76) for the frequency-based prediction. The model’s determination of the most likely etiology was accurate 74% (κ = 0.47) of the time vs. 65% (κ = 0.00) for the frequency-based prediction.

Conclusions: Our model outperformed a prediction based simply on frequency, and could be used as a tool to direct laboratory investigation of samples and to determine likely etiologies when samples are unavailable.
A Community Cluster of Restaurant-Associated Shigella Outbreaks

Authors: Stephen W. Klish, Matthew Zahn

Affiliation: County of Orange Health Care Agency, Epidemiology & Assessment

Background: Shigella sonnei is a common cause of gastrointestinal disease outbreaks, which classically occur in child care settings and situations with crowded living conditions. Under 10 restaurant-related Shigella outbreaks are reported nationally each year. (1) Three outbreaks of Shigella sonnei disease associated with restaurants were reported in Orange County, California in 2014.

Methods: California state statute mandates reporting of all Shigellosis cases to public health. Orange County Public Health (OCPH) attempts to interview all shigellosis cases to gather epidemiologic information. Once common restaurant exposure histories were identified in cases, OCPH conducted an investigation of each restaurant’s staff and facility to identify any possible source and mitigate any potential ongoing public health risk.

Results: Three restaurant-associated outbreaks were identified in Orange County in 2014, occurring in February, August, and September. Two of three restaurants emphasized serving organic vegetarian foods. Confirmed cases were persons who tested stool culture positive for S. sonnei and reported eating at the restaurant in the seven days prior to illness onset. The outbreaks caused a range of 5-9 cases, with 22 confirmed cases in total. Eight cases were hospitalized.

The August and September outbreaks occurred approximately four weeks apart, and were caused by a S. sonnei organism with an identical pulsed field gel electrophoresis (PFGE) pattern which was distinct from the February event. Each investigation led to restaurant closure for facility cleaning and food destruction while food handlers were cleared. In all events, case interviews revealed no common food exposure. 265 employees required clearance with stool testing. Three employees from two restaurants were found to be S. sonnei stool culture positive; it was unclear whether these illnesses precipitated the outbreaks or were caused by them. No social connections were identified between the different outbreaks.

Conclusion: A restaurant-associated shigellosis outbreak can cause significant illness burden, and the public health response is resource-intensive. Most restaurant associated events are thought to originate from food worker hand hygiene issues, but identifying outbreak sources can be challenging.

Illness Outbreaks Linked to Raw Milk—United States, 2015

Authors: Lia Koski¹,², Lauren Stevenson¹,², Megin Nichols¹

Affiliations: ¹Centers for Disease Control and Prevention, ²Oak Ridge Institute for Science and Education

Background: Consumption of raw milk has been associated with severe illness and death in the United States. The objectives of this analysis were: i) to describe the characteristics of 2015 illness outbreaks linked to raw milk; ii) to compare 2015 illness outbreaks linked to raw milk to outbreaks that occurred during 2010–2014; iii) to assess whether outbreaks linked to raw milk are more likely to occur in states where sale of raw milk is legal.

Methods: The Foodborne Disease Outbreak Surveillance System (FDOSS) collects data on disease outbreaks from local, state, and territorial health departments. Data for this analysis included 2010–2015 foodborne outbreaks, where the confirmed or suspected vehicle determined by states health officials was raw or unpasteurized milk. Legal status of raw milk sales in each state was determined through a literature review.

Results: The number of illness outbreaks linked to raw milk (n=11) in 2015 was not statistically significantly different from the median number of outbreaks during 2010–2014 (n=15.5; p=0.82). Between 2010–2015, 88 of 93 (95%) of outbreaks linked to raw milk occurred in states where the sale of raw milk is legal, either through herdshares, on-farm sales, or retail sales. In 2015, 53 people became ill during outbreaks linked to raw milk from several pathogens, including Campylobacter (41), Salmonella (6), Escherichia coli (4), and Cryptosporidium (2). In seven of the 11 (64%) 2015 illness outbreaks, severe outcomes were noted, including 11 hospitalizations and one person who developed Guillain-Barré syndrome.

Conclusions: Outbreaks linked to raw milk continue to occur and cause severe outcomes in the United States. Changes in rules that result in increased sale of raw milk may result in increased illnesses from this source.
P-027


Authors: J Latash¹,², V Reddy³, H Waechter¹, AM Fireteanu¹, R Fitzhenry¹, L Alleyne¹, E Amoroso¹, C Courtney², M Moy³, S Balter¹

Affiliations: ¹New York City Department of Health and Mental Hygiene, ²CDC/CSTE Applied Epidemiology Fellowship

Background: In 2014, NYC-area labs began to adopt multiplex PCR tests to detect enteric pathogens. We characterized multiplex PCR usage in NYC.

Methods: We determined number of reported infections in NYC residents diagnosed in 2014–2016 with positive lab tests for select routinely investigated (Cryptosporidium, Cyclospora, Salmonella, Shiga toxin-producing Escherichia coli, and non-cholera Vibrio) and non-routinely investigated (Campylobacter, Entamoeba, Giardia, Shigella, and Yersinia) infections. We calculated how many labs performed multiplex testing; frequencies of: multiplex vs. standard testing, reflex testing after multiplex testing, and multiplex test confirmation at public health labs; delay between specimen collection and result report; and used logistic regression to determine factors associated with multiplex receipt.

Results: Of 14,857 infections, 10% received a multiplex test, from <1% tested by 2 labs in 2014 to 19% by 12 in 2016. The percent of infections with a positive multiplex result receiving additional testing ranged from 12% for Giardia to 93% for Salmonella; the percent with a positive confirmatory test at a PHL ranged from 28% for STEC to 100% Cyclospora. For routinely investigated infections with specimens tested at labs using multiplex tests, multiplex receipt was associated with diagnosis in 2016, and patient hospitalization, Hispanic ethnicity, and residence in Bronx and Manhattan. Median time between specimen collection and first result notification was 2 days for multiplex tests, 5 for others.

Conclusions: Multiplex use increased over time, leading to timelier reporting but triggering further testing for public health action. The proportions of infections with reflex testing and positive confirmatory results varied by pathogen. Limitations include inability to determine whether negative confirmatory tests were due to false positive multiplex tests or poor specimen handling. As culture-independent tests pose challenges to public health practice, in 2016 the NYC Board of Health mandated reflex testing following positive non-culture results.
Whole-Genome Sequencing for Detecting Antimicrobial Resistance in Nontyphoidal Salmonella

Authors: McDermott PF1, Tyson GH1, Kabera C1, Chen Y1, Li C1, Folster JP2, Ayers SL1, Lam C1, Tate HP1, Zhao S1

Affiliations: 1Division of Animal and Food Microbiology, Office of Research, Center for Veterinary Medicine, U.S. Food and Drug Administration, Laurel, MD; 2Division of Foodborne, Waterborne, and Environmental Diseases, Centers for Disease Control and Prevention, Atlanta, GA

Background: We compared traditional phenotypic in vitro antimicrobial susceptibility testing for 14 drugs and whole genome sequencing (WGS) to assess correlations between resistance phenotypes and genotypes of Salmonella isolates.

Methods: Salmonella (n=640) representing 43 different serotypes were selected from among retail meat and human clinical isolates from the National Antimicrobial Resistance Monitoring System (NARMS). Clinical and Laboratory Standards Institute (CLSI) clinical breakpoints or NARMS consensus interpretive criteria were used to categorize MICs as susceptible or resistant. Resistance genotypes were determined using assembled WGS sequences through BLAST analysis with the cutoff set at 50% sequence length and 85% amino acid identity with known resistance proteins.

Results: We identified 65 unique resistance genes and mutations in two structural resistance loci. There were more unique resistance genes (n = 59) in the 104 human isolates than in the 536 retail meat isolates (n = 36). Overall, resistance genotypes and phenotypes correlated in 99.0% of cases. Correlations approached 100% for most classes of antibiotics but were lower for aminoglycosides and beta-lactams.

Conclusions: The results suggest that WGS has the potential to accurately predict resistance phenotypes for which genetic mechanisms have been defined.
P-029

Characterization of Shiga toxin-producing *Escherichia coli* (STEC) isolates from FSIS-regulated products using Whole Genome Sequencing

Authors: Jamie Wasilenko, Mustafa Simmons, Glenn Tillman

Affiliations: USDA–FSIS Eastern Laboratory Microbiology Characterization Branch, Athens, Georgia

**Background:** FSIS declared *Escherichia coli* O157:H7 as an adulterant in 1994 and the top-six Shiga toxin-producing *E. coli* (STEC) of clinical relevance were declared as adulterants in 2011. In 2015, FSIS began using whole genome sequencing of STEC isolates in support of outbreak analyses as well as characterization of stx, eae, serotype and Multi-Locus Sequence types (MLST).

**Methods:** From 2015-2017 the Top Six STEC and O157:H7 isolates from FSIS-regulated commodities were sequenced using Illumina MiSeq (v2 chemistry). FASTA files were created from the MiSeq FASTQ files using CLC Genomics v8. Nucleotide BLAST databases were created for MLST (University of Warwick), stx subtypes (CGE Virulence Finder), eae subtypes (publicly available eae sequences on NCBI), and serotypes (wzx, wzy, wzt, wzm, fliC, flkA, fltA, fliA genes).

**Results:** 408 stx-positive isolates were characterized for stx, eae and MLST type from the WGS data. The STEC isolates in the FSIS sample set included 17 different MLST types. Of 147 serotype O157:H7 strains sequenced, 98.0% were ST-11. A single serotype was identified for each serogroup with the exception of O103 which had 3 serotypes. Seven stx combinations were identified along with 5 different eae subtypes. A single eae subtype was identified for each serotype with the exception of O45:H2 which had 2 eae subtypes identified. 78% of the isolates had stx1a alone (59%) or in combination with additional stx genes.

**Conclusion:** WGS data from the FSIS STEC isolates from 2015-2017 had a narrow range of serotypes identified within each serogroup. The diversity of eae was limited within a serotype.
Molecular characterization cefotaxime-resistant *Salmonella* Typhimurium and 4,[5],12:i:- clinical isolates between 2009 and 2016 in Korea.

Authors: Jungsun Park*, Jin Seok Kim, Eunkyung Shin, Soojin Kim, Hyun Ju Jeong, Byung-Hak Kang, Hyo-Sun Kwak and Junyoung Kim

Affiliations: Division of Bacterial Diseases, Center for Laboratory Control of Infectious Diseases, Korea Centers for Disease Control and Prevention, Chungcheongbuk-do, Republic of Korea

**Background:** Non-typhoidal *Salmonella* infection is an important public health problem, which has caused food-borne illnesses worldwide. In recent years, antimicrobial resistance is increasing in non-typhoidal *Salmonella* isolates, with the emergence of resistance to third-generation cephalosporins. In this study, we described to characterize cefotaxime-resistant *Salmonella* Typhimurium and 4,[5],12:i:- isolates from humans and their plasmids carrying extended-spectrum beta-lactamase (ESBL) genes.

**Methods:** As a part of the national surveillance system and outbreak cases, we collected clinical samples of *S*. Typhimurium and 4,[5],12:i:- from humans with diarrhea. These isolates were tested for the resistance of cephalosporins by broth microdilution methods. All the cefotaxime resistant isolates were analyzed using PCR assay for the presence of ESBL genes and plasmid replicon typing.

**Results:** During 2009-2016, we identified a total of thirty-two cefotaxime-resistant *S*. Typhimurium (n=20) and 4,[5],12:i:- isolates (n=12). All resistant-isolates were found to harbor the *blaCTX-M*-types of ESBL genes: CTX-M-1 (n=6), CTX-M-14 (n=4), CTX-M-15 (n=3), CTX-M-55 (n=9), CTX-M-65 (n=4) and CTX-M-90 (n=1) with the combination of beta-lactamase genes such as *blaTEM*, *blaCMY-II* and *blaDHA*. Most plasmids harboring the *blaCTX-M* belonged to incompatibility group IncI1 (n=9), followed by IncA/C (n=5), IncHI2 (n=4), IncF (n=3), IncZ (n=2), IncK (n=1) and two were non-typeable.
P-031

Single-nucleotide polymorphism (SNPs) for the introduction of next-generation molecular epidemiology testing of Shigella sonnei

Authors: Soojin Kim, Jin Seok Kim, Jungsun Park, Eunkyung Shin, Hyun Ju Jeong, Byung-Hak Kang, Hyo-Sun Kwak and Junyoung Kim

Affiliation: Division of Bacterial Diseases, Center for Laboratory Control of Infectious Diseases, Korea Centers for Disease Control and Prevention, Chungcheongbuk-do, Republic of Korea

Background: Molecular typing methods are effective tool for detection of infectious diseases. In recent times, Pulsed-field gel electrophoresis (PFGE) is used routinely as genetic diversity analysis. However some species showed indistinguishable PFGE patterns in outbreak. Whole-genome sequencing (WGS) based typing is alternative method to outbreak detection and source trace back. In this study, we analysis of single-nucleotide polymorphism (SNPs) for the introduction of next-generation molecular epidemiology testing of Shigella sonnei

Methods: The 20 strains were selected for WGS in this study. Isolates were characterized to 'domestic', 'imported', 'outbreak' and 'sporadic' cases based on the epidemiological information of the case patient and the isolates' PFGE profiles. The WGS was performed on the Illumina Miseq, PacBio RS II single-molecule real-time (SMRT) sequencing and BAC-end sequencing platforms.

Results: Pairwise comparison of all S. sonnei genomes to the reference genome yielded a total of 94,235 SNPs with average reference genome coverage of 92.35% and sequence identity of 99.8%. Subsequent filtering procedures led to the identification of 466 SNPs and 421 genes. A minimum spanning tree based on analysis of SNPs showed three major clusters with isolated time point: Group 1, representative strain of large outbreaks in Korea; Group 2, antimicrobial resistant strains during 2001-2003; Group 3, recently emerging strains since 2006.

Conclusion: We selected 466 SNPs corresponding to the epidemiology of Shigella infections in humans, providing the evidence for the introduction of SNP-based molecular typing of S. sonnei strains.
Comparison of the Antibiotic Resistance Phenotype with the Genotype in *Salmonella* isolates from the cecal contents of food animals

Authors: Glenn Tillman, Mustafa Simmons, Jamie Wasilenko, Jovita Haro and Cesar Morales

Affiliation: USDA–FSIS Eastern Laboratory Microbiology Characterization Branch, Athens, Georgia

**Background:** With the implementation of Whole Genome Sequencing (WGS) of foodborne bacterial pathogens, most laboratories are intending to move to a singular workflow to capture characterization of pathogens. This includes prediction of antimicrobial resistance (AMR) based on the AMR gene identification from WGS data, including short-read MiSeq data.

**Methods:** The phenotypic AST profile of 1,130 *Salmonella* isolates collected in 2016 from the cecal contents of cattle, swine, chicken and turkey was generated using NARMS protocols and panels. All 1,130 were concurrently sequenced using the MiSeq Version 2 chemistry. Assemblies (FASTA format) were generated using CLC Genomics Workbench Version 8. A command-line version of BLAST+ was used to create a database using a local version of ResFinder to identify AMR genes. All of the assemblies (n=1,130) were used as query sequences against the ResFinder Database.

**Results:** The overall concordance between the resistance phenotype and the predicted phenotype from the genotype was 95.00%. For pan-susceptible isolates (n=769), there was 99.1% concordance. The following concordances for several of the major antibiotic classes were: Beta-lactam class, 99.1%; tetracycline class, 99.1%; phenicols, 97.6%; folate pathway inhibitors (sulfisoxazole), 98.1% and 72.7% for trimethoprim. In the aminoglycoside class, there was 98.8% concordance for streptomycin. However, for GenR phenotypes, there were resistance genes in 76.2% of isolates (n=21), while 70.97% of GenS isolates (n=31) had resistance genes identified.

**Conclusions:** Identification of horizontally acquired antibiotic resistance genes through ResFinder can be accomplished through utilization of a local BLAST database. Overall, a high concordance was observed between actual resistance phenotype and the predicted genotype.
P-033

The Utilization of hqSNP Analysis in the Investigation of *Salmonella Saintpaul*

Authors: Andrew Classon, Jasmine Huffman, Beth Tolar, Taylor Griswold, Heather Carleton

**Background:** PulseNet is a national laboratory network that uses molecular subtyping to identify clusters of foodborne diseases. In September 2016, PulseNet identified a multistate cluster of *Salmonella Saintpaul* isolates with indistinguishable Pulsed Field Gel Electrophoresis (PFGE) patterns. Whole genome sequencing (WGS) was performed on 72/111 isolates from the cluster and high quality single nucleotide polymorphism (hqSNP) analysis was performed to determine the genetic relatedness among isolates.

**Methods:** WGS was performed using the Illumina MiSeq. Reads were trimmed based on quality then mapped by SMALT. SNPs were called with LyveSET 1.1.4f using a closed reference genome (2009K-0668) with prophage regions masked, and informative SNPS filtered and used to construct a phylogenetic tree with RAxML. The hqSNP phylogenetic tree was annotated using TINSEL.

**Results:** The hqSNP analysis showed the isolate genomes separating into two distinct clades. Clade A consisted of isolates that were geographically located in Northeastern states. These isolates differed by 0 – 14 SNPs with a median difference of 5.5 SNPs. Clade B consisted of isolates geographically located in Western states. These isolates were highly related differing by 0 – 4 SNPs. Clades A and B were unrelated to each other by WGS, differing by 98 – 156 SNPs.

**Conclusion:** WGS analysis was able to separate isolate genomes into two distinct clades that were indistinguishable by PFGE. This aided in the epidemiologic investigation to demonstrate that these clusters of isolates were likely from different sources.
Applying Next Generation Sequencing To Subtype Listeria monocytogenes Isolates From Fish-Processing Facilities

Authors: Xia Xu, Division of Microbiology Assessment, Center for Drug Evaluation and Research, US Food & Drug Administration, Silver Spring, MD; Paul M. Morin, Northeast Food & Feed Laboratory, Office of Regulatory Affairs, Jamaica, NY

Background: Listeriosis is the third leading cause of death from infections caused by foodborne pathogens. Listerial infection occurs through ingestion of foods contaminated with Listeria monocytogenes. This pathogen has a wide distribution in different environments and a strong capability to survive under various stressful conditions. Long-term presence of L. monocytogenes in food processing environments poses a difficult challenge for public health and food safety. This study was to evaluate next generation sequencing technology as an applicable subtyping tool for L. monocytogenes contamination for smoked fish-processing facilities.

Methods: Sequencing genomic libraries of L. monocytogenes isolates derived from five smoked fish-processing facilities over ten years were prepared using the Illumina Nextera XT kit and subsequently applied for 2×250bp paired-end sequencing runs on the Illumina MiSeq sequencer. The raw data of fastq files were imported as paired reads into the Qiagen CLC Genomics Workbench for further data analysis and SNP-based phylogenetic tree construction.

Results: We have successfully sequenced 71 L. monocytogenes genomes from those fish-processing facilities using the Illumina MiSeq sequencer. By using K-mer based spectra, 7 best matched references derived from NCBI genome database were yielded for those 71 genomes, among which 35% (25/71), 25% (18/71) and 30% (21/71) of L. monocytogenes genomes matched to 3 core references. K-mer based phylogenetic analysis revealed NZ_HG813249 as the common reference for further analysis. We were able to yield average coverages of 120±34 for sequencing depth, (95.3%±2.4) of mapped reads and 64,832±56,355 high quality variants (range 198-254,281) when mapping reads to the common reference. SNP-based phylogenetic analysis revealed 14 clades resulting in 3 large ones containing 20, 16 and 18 genomes, respectively.

Conclusions: Our data indicate that next generation sequencing is a valuable subtyping tool for analyzing L. monocytogenes isolates from smoked fish firms.
Whole Genome Sequence and Pulsed Field Gel Electrophoresis Analysis of Environmental *Listeria monocytogenes* Isolates from an Ice Cream Processing Facility

Authors: Laura Howard and Paul M. Morin

Affiliation: FDA Northeast Food & Feed Laboratory, Office of Regulatory Affairs, US Food & Drug Administration, Jamaica, NY

**Background:** *Listeria monocytogenes* (causative agent of listeriosis) is the 3rd leading cause of foodborne illnesses and has recently been shown to be associated with human outbreaks due to ice cream contamination. Approximately 16% of people who contract listeriosis will die each year. The most recent *Listeria* outbreak in ice cream resulted in 10 hospitalizations and 3 deaths across 4 states. The presence of *L. mono* in ice cream processing facilities poses a difficult challenge for public health and food safety.

**Methods:** PFGE was performed on 18 *Listeria monocytogenes* environmental strains using the PulseNet protocol PNL04. FastDigest enzymes were used to restrict the agarose plugs; AscI (SgsI) and Apal. Gels were run using the Bio-Rad CHEF-MAPPER and CHEF DR-III units, stained with ethidium bromide and DNA patterns analyzed using the BioNumerics software. Whole Genome Sequencing was additionally performed on these isolates using the GenomeTrakr protocol. Genomic DNA was extracted using the QIAcube instrument, genomic libraries were prepared using the Nextera XT kit, and the sequencing was performed using the MiSeq instrument. WGS was analyzed using the CLC Genomics Workbench and the NCBI pathogen database.

**Results:** The 18 isolates yielded 5 different PFGE patterns with the primary enzyme AscI and 3 different patterns with the secondary enzyme Apal. WGS analysis showed that all 18 isolates were closely related with a serovar of 1/2b, wgMLST 5 and a best match to a *Listeria monocytogenes* strain NC_021824. Furthermore, the 18 isolates were found to be associated with 3 different SNP clusters.

**Conclusions:** Our data demonstrated that environmental strains of *Listeria monocytogenes* from an ice cream processing facility were closely related to each other but not closely related to any other food, environmental, or clinical isolate in the NCBI or PulseNet database.
Distribution of porA genotypes in *Campylobacter jejuni* isolated from FSIS collected samples

Authors: Mustafa Simmons, Jamie Wasilenko, Glenn Tillman

Affiliation: USDA–FSIS Eastern Laboratory Microbiology Characterization Branch, Athens, Georgia

**Background:** *Campylobacter jejuni* is one of the leading causes of bacterial foodborne illness in the United States. Bacterial subtyping methods and their nomenclature schemes are important in the investigation of foodborne illness outbreaks. In *Campylobacter*, porA encodes for the major outer membrane protein (MOMP) which has been shown to be involved in adherence to host cells and antibiotic resistance. Molecular typing using porA has been demonstrated to be a useful subtyping scheme that can be easily determined from WGS results.

**Methods:** *Campylobacter jejuni* isolates from food samples collected by USDA-FSIS were sequenced using the Illumina MiSeq. FASTQ files were assembled using CLC genomics version 8. A nucleotide BLAST database was created using the allele sequences hosted on the Pasteur Institute website. The porA genotype was determined by using assemblies as the query sequence and aligning to porA sequences using BLAST.

**Results:** 1336 *Campylobacter jejuni* isolates were analyzed from various sample types including chicken products as well bovine, porcine, and poultry cecal samples. In total 158 porA genotypes were identified. When considering sample types with at least 100 representative isolates (dairy cow cecal, heifer cecal, steer cecal, poultry rinse, and intact poultry) the predominant porA genotypes were more commonly identified with one animal species over the other. porA types 1265, 39 and 292, which represent 27.9% (277/992) of the porA genotypes identified in bovine isolates, were identified in only 2.45% (8/326) of the poultry isolates; with genotype 1265 not being identified in any poultry derived isolates. Similarly porA types 749 and 6, which represent 12.88% (42/326) of the porA genotypes identified in poultry, were identified in only 0.4% (4/992) of the bovine isolates.

**Conclusions:** Based on the distribution of porA types amongst sample types, porA typing may be useful in predicting the likelihood a given *Campylobacter* was associated with a particular commodity. Also, porA typing can be used in conjunction with traditional 7-gene MLST to find related reference genomes for analyses as well as serve as a succinct and static nomenclature.
P-037

Use of WGS for Salmonella Serotype Determination

Authors: Mustafa Simmons, Jamie Wasilenko, Joseph Minicozzi, Glenn Tillman

Affiliation: USDA–FSIS Eastern Laboratory Microbiology Characterization Branch, Athens, Georgia

Background: Salmonella serotype is traditionally determined by using antisera specific to O-antigens and H-antigens. This method is laborious, expensive, and subjective. Currently there are also genetic methods to determine serotype such as molecular serology. Molecular serology relies on the detection of serotype determinants such as rfb and wzx for O antigens and flIC and flijB for H antigens. With whole genome sequencing (WGS) now being performed on all Salmonella isolates and the drive to streamline the number of analyses performed, serotypes can potentially be determined using only WGS and NVSL when factors are not detected.

Methods: Salmonella isolates were sequenced using the Illumina MiSeq. Sequences are assembled and the resulting FASTAs are processed using a bash script. The script uses a python program that performs exact matching of FASTA file subsequences and short sequences based on probe sequences from Fitzgerald et al. and McQuiston et al. The next step is to perform BLAST with each isolate’s assembly as the query and a database based on the sequences used by Seqsero (Zhang et al.). Factors from the python script and BLAST are combined for each isolate, and any redundant factors removed. These factors are then checked against a dictionary, based on the Kauffman-White scheme to determine serotype.

Results: 4205 Salmonella isolates with Salmonella serotypes and WGS sequences were compared. For 96.2% (4045/4205) of the isolates the WGS determined serotype matched the molecular serology or NVSL determined serotype. For 3.8% (160/4205) of the isolates the WGS determined serotype did not match the molecular serology or NVSL determined isolate. A total of 77 serotypes were successfully identified using WGS. The most common reason for non-matching results (123/160) was missing factors.

Conclusions: Using WGS data to determine serotype is largely successful (96.2%). The small portion (3.8%) of non-matching serotypes could be lowered if raw read mapping was used or if MLST type was used in combination as a predictor. WGS serotype determination is a step towards a single streamlined characterization method which can lead to both cost and time savings.

P-038

Poster withdrawn
P-039

Progress towards an optimized Salmonella isolate recovery protocol

Authors: K. C. Dillon¹, J. R. Hensley¹, M. Patel¹, E. Trees², J. Besser², H. A. Carleton², A. D. Huang², A. J. Williams-Newkirk³

Affiliations: ¹ Oak Ridge Institute for Science and Education, ² Enteric Diseases Laboratory Branch, CDC, ³ IHRC, Inc.

Nontyphoidal Salmonella is estimated to cause 1,000,000 infections each year in the US, with more than 19,000 hospitalizations and 380 deaths. Clinical laboratories in the US are adopting culture-independent diagnostic tests (CIDTs) to detect Salmonella and other pathogens in human stool in part because they provide clinically important information faster than traditional microbiological techniques. Despite multiple advantages, CIDTs jeopardize public health surveillance networks like PulseNet because they do not yield the isolates required for subtyping, virulence determination, and antibiotic resistance testing. The APHL Food Safety CIDT subcommittee identified the lack of an optimized standard protocol for the recovery of isolates from CIDT-positive stool specimens as a major barrier to isolate availability for surveillance. Initial studies at CDC and state public health labs tested the most commonly used enrichment and primary isolation methods for Salmonella and Shiga toxin-producing E. coli. This study uses a two-phase design to examine the most promising methods for Salmonella identified in the previous survey. Phase 1 identifies the optimal storage temperature (4°C and 22°C), plating media (Hektoen Enteric Agar and Xylose Lysine Deoxycholate Agar), and transport media (Cary-Blair Transport Medium and Gram-Negative broth) across different storage times (1, 4, and 7 days) using healthy stool spiked with two common Salmonella serotypes (Salmonella enterica ser. Newport and Oranienburg) at inoculum levels of 106, 104, and 102 CFU/mL. Phase 2 determines the optimal enrichment media (Selenite Broth, Tetrathionate Broth Base, and Modified Semisolid Rappaport-Vassiliadis Medium) to use in combination with the media and temperature identified in Phase 1. Future work will test these protocols with clinical specimens at CDC and partner labs prior drafting final recommendations.
Increasing the Percentage of Isolates from *Salmonella* Cases Characterized at the State Public Health Laboratory Improves Epidemiological Investigation

Authors: Marie-Claire Rowlinson¹, Jason Blanton¹, Matthew Schimenti¹, Nicole Kikuchi², Jamie DeMent²

Affiliations: Bureau of Public Health Laboratories (BPHL)¹, Bureau of Epidemiology (BOE)², Florida Department of Health (FDOH), Tallahassee, FL

**Background:** The Florida BPHL has been a part of PulseNet since its inception, performing sero-grouping, -typing and pulsed-field gel electrophoresis (PFGE) on *Salmonella* isolates. Prior to 2012, BPHL received isolates on less than 20% of reported cases, and isolate submission was not mandated. FDOH has implemented several changes to improve submission and characterization of *Salmonella*.

**Method:** Since 2012, BPHL hired two additional staff and performed outreach to commercial laboratories for isolate submission. BPHL implemented molecular serotyping, improved PFGE capacity and implemented whole genome sequencing (WGS). In October 2016, FDOH successfully changed a Florida Rule, mandating that clinical laboratories submit *Salmonella* positive specimens or isolates to BPHL.

**Results:** BPHL increased the percentage of isolates received to 56% of all reported *Salmonella* cases in 2016. The predominant *Salmonella* serotype is Javiana. In 2012, IV 50:z4,z23:- (Flint) was the second most predominant but was only the fifth in 2016.

<table>
<thead>
<tr>
<th>Year</th>
<th>Total # <em>Salmonella</em> received (%)</th>
<th>Total # reported cases</th>
<th>Predominant serotypes</th>
</tr>
</thead>
<tbody>
<tr>
<td>CY2012</td>
<td>1,320 (20%)</td>
<td>6,523</td>
<td>Javiana, IV 50:z4,z23:-, Newport</td>
</tr>
<tr>
<td>CY2013</td>
<td>1,835 (30%)</td>
<td>6,133</td>
<td>Javiana, Newport, IV 50:z4,z23:-</td>
</tr>
<tr>
<td>CY2014</td>
<td>1,866 (31%)</td>
<td>6,019</td>
<td>Javiana, Newport, IV 50:z4,z23:-</td>
</tr>
<tr>
<td>CY2015</td>
<td>2,401 (41%)</td>
<td>5,924</td>
<td>Javiana, Newport, IV 50:z4,z23:-</td>
</tr>
<tr>
<td>CY2016</td>
<td>3,173 (56%)</td>
<td>5,621</td>
<td>Javiana, Newport, Enteritidis</td>
</tr>
</tbody>
</table>

**Conclusions:** In light of the Rule change and advancing technologies, improvements must continue. The Rule ensures submission of more *Salmonella* isolates and positive specimens, but it is unknown how this potential increase in volume and submission of culture-independent diagnostic test (CIDT)-positive samples will impact BPHL. Nevertheless, increasing the number of *Salmonella* isolates that are characterized for cases provides a more accurate reflection of *Salmonella* epidemiology in the state and allows for improved detection and prevention of outbreaks.
**P-041**

**Iowa’s rapid response to a *Salmonella* Braenderup outbreak in the age of culture-independent diagnostic testing and whole-genome sequencing.**

Authors: ²Von Stein D, ¹Kline GM, ¹Trannel AM, ²Oni KO, ¹Hall N, ¹Moet G, ¹Aldous WK, ¹Jepson RT

Affiliations: ¹State Hygienic Laboratory at the University of Iowa Coralville, IA; ²Iowa Department of Public Health Des Moines, IA

**Presenter:** Ryan Jepson

**Background:** In July 2016, a multi-county *Salmonella* Braenderup outbreak from potato salad was identified in Iowa. The first increase in cases was noted on July 18, 2016. The product was removed on July 22, 2016 and a consumer advisory issued on July 25, 2016.

**Methods:** 31 *Salmonella* Braenderup isolates and positive culture-independent diagnostic (CIDT) stool specimens were sent to the State Hygienic Laboratory at the University of Iowa (SHL) from eight different hospitals and healthcare centers. The Iowa Department of Public Health (IDPH) interviewed cases using Iowa’s hypothesis generating questionnaire. The confirmed case was a person with *Salmonella* Braenderup infection and illness onset between June 26, 2016 and July 23, 2016 with an isolate matching PFGE XbaI pattern JBPX01.0039. The person had consumed grocery store x traditional or zesty potato salad in the 12-72 hours before becoming ill.

**Results:** 55 total cases (31 confirmed/24 probable) were reported with 100% of respondents reporting eating grocery store x potato salad. 4 of the 55 cases (7.3%) required hospitalization, and zero deaths were recorded. CIDT stool samples took an average of 6.7 days from collection to PulseNet receipt versus 5.6 days for cultured isolates. The contaminated potato salad was confirmed as the source of the outbreak on July 27, 2016 by pulsed-field gel electrophoresis and whole-genome sequencing using Bionumerics and hqSNP analysis at the Centers for Disease Control and Prevention.

**Conclusion:** The rapid increase in the number of *Salmonella* detected through CIDT and electronic reporting was a direct result of the increased sensitivity and specificity of syndromic testing. Routine surveillance only recorded four *Salmonella* Braenderup isolates received between June 29, 2016 and July 1, 2016. Between July 19, 2016 and July 22, 2016 that number increased to 10 *Salmonella* Braenderups (5 CIDT/5 isolates) with the addition of CIDT testing.
P-042

Not this child again! A shift in PFGE pattern observed following a 13 week exclusion of daycare attendee

Authors: Jamie Yeadon-Fagbohun and Madhura Sundararajan

**Background:** Indiana requires 2 negative stool cultures following a diagnosis of Shiga-toxin producing *E. coli* (STEC) for a child to return to daycare. In the fall of 2016, Indiana received 13 specimens from one patient over a 13 week period of time, in the parents attempt for two negatives. The child was STEC positive and ultimately out of daycare for 2 months.

**Methods:** Standard *E. coli* protocol is when specimens are received they are processed and plated on *E. coli* selective media and gram-negative (GN) broth. After 24 hours, plates are checked for *E. coli* growth and the GN broth is tested for STEC by PCR. Colonies demonstrating agglutination with an *E. coli* antisera are then tested again by PCR to verify that the colony is STEC positive. Specimens that confirm are evaluated by Pulse-field Gel Electrophoresis (PFGE) and Whole Genome Sequencing (WGS) to complete further testing for outbreak surveillance.

**Results:** 10 specimens were positive for *E. coli* O26 and Stx 1 & 2. PFGE and WGS were completed, and results were uploaded to PulseNet for the initial specimen received. At the 60-day mark from the initial specimen, PFGE was again completed. To our surprise, the patterns were slightly different. With this discovery, PFGE was completed for all the positive specimens from this child. The patterns were not identical, and WGS also showed a difference in the isolates.

**Conclusions:** The different PFGE patterns and difference in WGS for this patient over this time period were not only interesting but warranted further investigation. The local health department spoke with the child’s family regarding sources of contamination and possible sources of re-infection. The child had identified exposures for the initial onset of symptoms, but no sources of re-infection were determined and no other family members were ill. The patient was asymptomatic after the first specimens were submitted for testing. This case was well outside the standard range of bacterial shedding and continued to shed viable bacteria for 13 weeks. We were unable to find a reason for the varying patterns. In general, further investigation into the effect of variable PFGE patterns on prolonged shedding remains needed.
Enterotoxigenic *Escherichia coli* (ETEC) are an important cause of diarrhea in children under the age of five in developing countries. ETEC strains secrete heat-labile (LT) and/or heat-stable (ST) enterotoxins that induce diarrhea by water and electrolyte imbalance. In this study, we characterized 40 ETEC serogroup O6 strains from 1975 to 2016 by whole genome sequencing (WGS) and present the findings on whole genome high-quality single nucleotide polymorphisms (WG-hqSNPs), core genome (CG) SNPs and antimicrobial resistance (AR). The closed genome of ETEC O6 strain 2011EL-1370-2 (USA) was the reference strain. DNA libraries prepared with the Nextera XT kit (Illumina Inc.) were sequenced on the MiSeq (Illumina Inc.) 2 x 250-bp chemistry. Raw reads that passed quality control using PRINSEQ were assembled with SPAdes. WG-hqSNP analysis was performed with Lyve-SET 1.1.4f with the following options: 20x minimum coverage, 95% read support, phage-masking and clustered SNPs within 5 base pairs of each other were filtered. CG SNP analysis was performed using Parsnp. All strains were tested for antibiotic susceptibility to a panel of 14 antibiotics. ResFinder tool in the Center for Genomic Epidemiology (CGE) website and quinolone resistance determining regions (QRDR) workflow identified mutations associated with AR. ETEC O6 strains clustered into three major clades namely clade I, clade II and clade III by WG-hqSNP and CG analyses. 0-840 hqSNPs, 2-206 hqSNPs and 0-444 hqSNPs were present in the genomes of clades I, II and III respectively in WG-hqSNP phylogeny. 201-960 SNPs, 377-542 SNPs and 309-929 SNPs were detected in the genomes of clades I, II and III respectively in CG phylogeny. Median number of WG-hqSNPs in monoclonal ETEC O6 outbreaks were <10. Phenotypic AR correlated with resistance determinants for streptomycin, ampicillin, tetracycline, sulfonamides, trimethoprim in 11/37 strains and for nalidixic acid in 10/37 strains. No ciprofloxacin resistant strains were identified. In summary, WG-hqSNP and CG SNP analyses have revealed similar evolutionary relationships and an overall diversity of ETEC O6 strains independent of time and geographical location. In future, WG multilocus sequence typing (wgMLST) may be pursued for routine surveillance of ETEC.
P-044

Evaluation of Whole Genome Sequencing for Campylobacter jejuni Surveillance and Outbreak Detection

Authors: Lavin A. Joseph¹, Heather A. Carleton¹, Darlene Wagner¹, Michael Hughes², Eija Trees¹, Janet Pruckler¹, Grant Williams¹, Kelley B. Hise¹, Hannes Pouseele³, and Collette Fitzgerald¹

Affiliations: Enteric Diseases Laboratory Branch¹, Enteric Diseases Epidemiology Branch², Centers for Disease Control and Prevention, Atlanta, GA, Applied Maths NV, Belgium³

Background: Pulsed-field gel electrophoresis (PFGE) is currently used within PulseNet for Campylobacter surveillance and outbreak investigations. However, PulseNet is moving towards whole genome multi-locus sequence typing (wgMLST) for WGS-based cluster detection. We examined the ability of wgMLST to cluster or differentiate outbreak-associated and sporadic C. jejuni isolates indistinguishable by PFGE.

Methods: Smal/KpnI PFGE patterns for 140 C. jejuni isolates (83 isolates from nine outbreaks and 57 sporadic isolates) were generated using the PulseNet Campylobacter protocol and analyzed in BioNumerics v.6.6.10. These isolates were sequenced using the Illumina MiSeq or HiSeq and the sequences were analyzed using the Campylobacter wgMLST allele database (BioNumerics v.7.6) developed in collaboration with domestic and international partners. In addition, the PFGE and wgMLST results from the outbreak-associated isolates were compared with high quality single nucleotide polymorphism (hqSNP) analysis results generated using the LYVE-SET pipeline (github.com/lskatz/lyve-SET).

Results and Conclusions: On average, 1561 (1347-1800) wgMLST loci were identified per genome among the C. jejuni sequences in this analysis. Outbreak-associated C. jejuni isolates indistinguishable by Smal/KpnI PFGE were differentiated from epidemiologically unrelated isolates by wgMLST analysis. These results were concordant with hqSNP analysis of the sequences. Our study shows that both wgMLST and hqSNP analysis provide greater resolution and epidemiological concordance compared to PFGE for Campylobacter surveillance and outbreak detection. Additionally, hqSNP analysis is dependent on a priori knowledge of isolates to select the correct reference genome before an analysis is run. However, selection of a reference genome is not required for wgMLST analysis making this method more user-friendly and requiring less specialized knowledge to perform.
P-045

FSIS Category 3 Establishments Salmonella Isolates Monitoring Action Plan


Background: FSIS samples poultry establishments producing young chicken and turkey carcasses, and raw chicken parts to test Salmonella and Campylobacter. FSIS uses the sampling results to assess establishment performance based on a 3-category system. The establishments that fail the standard are placed in Category 3. FSIS also uses serotypes/PFGE patterns of the salmonella isolates recovered from Category 3 establishments to track temporal matched clinical isolates and collect food histories from those patients to detect foodborne illnesses possibly associated with consumption of FSIS regulated products.

Methods: If the FSIS salmonella isolates are included in the CDC PulseNet active surveillance clusters, FSIS will review epidemiologic information from CDC SharePoint and SEDRC. If case-patients’ food histories suggest linkage to FSIS products, FSIS will monitor or investigate those clusters per FSIS Directive 8080.3. If the salmonella isolates are not included in those clusters, FSIS will use T-cube to track sporadic clinical isolates that match FSIS isolates by serotypes/PFGE patterns. If the serotypes are common both in poultry products and human infections (Enteritidis, Newport, Infantis, Typhimurium, Heidelberg, and I 4,[5],12:i:-) and the clinical isolates show a potential geographic or demographic clustering, FSIS will request those case-patients’ food histories. If the food histories suggest a possible linkage to FSIS products, FSFSIS will monitor or investigate those potential clusters.

Results: in 2017, 38 FSIS salmonella isolates from category 3 establishments have been included in 11 CDC PulseNet active clusters. In addition, through T-cube tracking, 3 single state salmonella clusters that match temporal FSIS salmonella isolates have been identified. FSIS have followed up the 14 clusters and 5 clusters have suggested possible linkages to FSIS products.

Conclusions: FSIS product testing results are not only used to closely monitor establishments’ process control performance, but also a useful tool to early detect foodborne illnesses possibly associated with consumption of FSIS regulated products.
Background: A goal of the Microbiology Characterization Branch is to determine pulsed-field gel electrophoresis (PFGE) patterns of *Salmonella* isolates that originated from USDA-FSIS inspected commodities (meat, poultry, egg, and Siluriforme products), for comparison with clinical PulseNet PFGE patterns, and to use the data for surveillance of food-borne illness outbreaks.

Methods: The FSIS MLG was followed for the isolation of *Salmonella* from foods and the molecular serotyping of isolates. The CDC-PulseNet methods were followed for characterization. National Antimicrobial Monitoring System (NARMS) methods were used to determine antimicrobial resistance (AMR) profiles.

Results: From 2010 through 2016, MCB used PFGE to characterize 15,985 *Salmonella* isolates from food. The five most common serotypes were: Dublin, Enteritidis, Heidelberg, Kentucky and Typhimurium. The top five patterns detected were: JDX01.0004, JQG01.0004, JF6001.0022, JGP01.0027, and JM601.0346; accounting for 59%, 50%, 25%, 21%, and 8% of the isolates per serotype, respectively. MCB has twice as many *Salmonella* isolates from poultry as from a bovine source and nine times as many from poultry as from porcine sources. Fifty percent of *Salmonella* from foods were pan-susceptible for the compounds on the NARMS AMR panels. In 2014, FSIS began including whole genome sequencing (WGS) on *Salmonella* isolates.

Conclusion: The number of isolates, serotypes, and PFGE pattern types are driven by the type and quantity of active FSIS sampling programs. Changes in sampling programs make year to year comparisons of the data difficult. *Salmonella* serotypes exhibit a wide spectrum of PFGE pattern type diversity. We expect WGS to provide more accurate cluster identification, particularly amongst serotypes with extremely low or high PFGE pattern type diversity. When included, FSIS isolates make up a small portion of a PulseNet cluster. As PulseNet incorporates the more discriminating WGS analysis for *Salmonella* cluster detection, the number of FSIS isolates per cluster is decreasing.
P-047
Symptoms and Exposures of New York City Vibriosis Patients Diagnosed by Culture Versus Culture-Independent Diagnostic Tests, 2015–2017

Authors: L.Li1, H.Waechter1, K.Devinney, D.Osuagwu1, L.Chicaiza1, V.Reddy1

Affiliation: 1New York City Department of Health and Mental Hygiene

Background: Vibriosis is often associated with consumption of raw seafood or exposure to seawater and can cause gastrointestinal (GI) illness, wound infection, and septicemia. Since 2015, many clinical laboratories in New York City (NYC) have implemented culture-independent diagnostic testing (CIDT) and started testing stool with GI panels, leading to an increase of vibriosis cases diagnosed by CIDT. It is unknown if vibriosis patients diagnosed by CIDT are systematically different from the culture-confirmed patients traditionally reported to health departments.

Methods: All Vibrio cases in NYC are required to be reported to the NYC Department of Health and Mental Hygiene (DOHMH) and isolates sent to the Public Health Laboratory (PHL). We analyzed Vibrio non-cholera cases diagnosed from stool collected during January 2015–June 2017 and described the symptoms, duration of illness, and exposures of patients with culture-confirmed vibriosis and of those diagnosed by CIDT-only.

Results: Of 58 vibriosis cases, 33 (57%) were diagnosed from stool specimens. Of those, 25 (76%) were culture-confirmed among which 7 (28%) were also CIDT-positive, and 8 (24%) were diagnosed by CIDT-only; of the 8 CIDT-only cases, 7 were culture-negative, and 1 was not tested by culture. Among interviewed patients, 92% (22/24) of those with culture-confirmed illness and 67% (4/6) of those diagnosed by CIDT-only reported diarrhea; the median duration of illness was 6 days (range: 1–32) and 3 days (range: 0–7), respectively. Eighty-eight percent (21/24) of patients with culture-confirmed illness and 60% (3/5) of patients diagnosed by CIDT-only reported any exposure to seafood/seawater, and only patients with culture-confirmed illness reported oyster (8/8) or clam (7/7) consumption. None of these differences were statistically significant.

Conclusion: Preliminary data suggest that a lower percentage of patients diagnosed by CIDT-only reported diarrhea and seafood/seawater exposure than patients with culture-confirmed vibriosis. Additional data are needed to evaluate whether these differences are statistically significant, reflect testing bias (providers may be more likely to request Vibrio culture for patients who report seafood exposures), and/or could be falsely positive.
Discrepancies in Testing; Utility of Gastrointestinal PCR Panel During a Foodborne Outbreak of *Salmonella* Enteritidis — Nebraska, 2017

Authors: B. Loeck¹, J. Rother², D. Ortbahn³, N. Hill³, T. Safranek¹, A. Carlson¹

Affiliations: ¹ Division of Public Health, Nebraska Department of Health and Human Services, ² Northeast Nebraska Public Health Department, ³ South Dakota Department of Health

**Background:** In June 2017, the Nebraska Department of Health and Human Services (NDHHS) was notified of an outbreak of gastroenteritis at a wedding reception. Soon after the event, several attendees reported developing diarrhea and abdominal pain consistent with gastrointestinal illness. Four cases sought care and had positive *Salmonella* culture results from facilities in South Dakota; one was a South Dakota resident, three lived in two Nebraska communities in different health department jurisdictions. Four additional cases from three different Nebraska health department jurisdictions sought care and were tested in Nebraska; only one of these tested positive for *Salmonella* by culture, three were negative for stool culture.

**Methods:** An investigation was initiated to identify cases, establish etiology, and prevent further illnesses. A standardized questionnaire was developed to collect information, including clinical history. Attendees who reported seeking medical care and submitting a stool sample, but did not have a positive result, were contacted. NDHHS requested they resubmit a stool, or the laboratory send the initially negative stool on to the Nebraska Public Health Laboratory (NPHL) for subsequent testing with the GI PCR Panel (GIP).

**Results:** The GIP identified 3 positive cases of *Salmonella* in samples that were originally negative by culture. These samples were reflex cultured at NPHL with successful isolation for serotyping and pulsed-field gel electrophoresis (PFGE). *Salmonella* Enteritidis was ultimately confirmed by stool culture from all 8 individuals (5 were initially culture positive, 3 were positive only after GIP detection).

**Conclusions:** Due to the 4 initial positive cultures residing in 2 states and 3 different jurisdictions, this cluster would likely not have been detected until much later when serotype/PFGE was reported by South Dakota. Overall, this outbreak demonstrated increased sensitivity of GIP (8/8) for *Salmonella* versus culture (5/8), the utility of the GIP as a first-line test in cluster detection, and suggests that targeted use of the GIP in outbreak settings appears to be beneficial.
Do sporadic and cluster-associated *Salmonella enterica* serotype Javiana infections have different epidemiologic characteristics?

Authors and Affiliations: Sarah V. Luna, PhD NCEZID/DFWED/EDEB, Thai-An Nguyen, MPH NCEZID/DFWED/ORPB/OAU, Andrew Classon NCEZID/DFWED/EDLB, Jennifer C. Hunter, DrPH, MPH NCEZID/DFWED/EDEB/NST

**Background:** Incidence of *Salmonella enterica* serotype Javiana infections has been increasing in the United States over the past decade, even as overall *Salmonella* rates have remained stable. Javiana infections occur most frequently in young children, southern states, and warmer months. We hypothesize that cases associated with PFGE-defined clusters have a distinct epidemiologic profile compared with sporadic cases, which may reflect different underlying sources of infection between these two types of cases.

**Methods:** Javiana isolates in PulseNet from US residents during 2007–2016 were included if state and county of residence were known. We considered an isolate “cluster-associated” if it was submitted during a period when the number of isolates of that PFGE pattern exceeded the expected average 5-day case count compared to the 5-year historical baseline by two standard deviations. All other isolates were classified as “sporadic.” We described the frequency of cluster-associated and sporadic isolates by state and year and assessed age and seasonality distributions using the Kruskal-Wallis test.

**Results:** 20,982 of 26,921 Javiana isolates (78%) had complete state and county data and were included in the analysis. Ten percent (2,046) of isolates were cluster-associated, representing 104 clusters (range: 1–312 isolates per cluster, median: 11). The proportion of isolates that were cluster-associated differed by year (2–18%) and state (0–100%). Compared with sporadic isolates, cluster-associated isolates were more likely to come from adults 18–64 years old (47% versus 34%) and less likely to come from children 0–4 years old (26% versus 36%, p<0.01). We observed increased incidence during warmer months only for sporadic isolates; cluster-associated isolates had no distinct pattern.

**Conclusion:** Cluster-associated Javiana infections have a demographic and temporal profile that is distinct from sporadic infections, and these differences may provide insights into the sources of these infections.
Foodborne Disease Outbreaks in Nursing Homes — United States, 1998–2015

Authors: K Manikonda¹ and SJ Crowe¹

Affiliations: ¹ Center for Emerging and Zoonotic Infectious Diseases, CDC

Background: Residents of nursing homes are often immunocompromised and at risk for serious complications if they contract an infectious disease. Morbidity and mortality of foodborne disease outbreaks in these facilities can be high, as can the number of cases, due to the communal-style meals often prepared and served in these settings. We describe the epidemiology of foodborne outbreaks in nursing homes.

Methods: Data from 1998–2015 were obtained from CDC’s Foodborne Disease Outbreak Surveillance System. Outbreaks were included if they occurred in a nursing home, assisted living facility, or similar long-term care institution. An outbreak was defined as ≥2 illnesses resulting from ingestion of a common food.

Results: During 1998–2015, 247 outbreaks were reported in 42 states, resulting in 7,816 illnesses, 431 hospitalizations, and 56 deaths. Median outbreak size was 22 illnesses (range: 2–190). A confirmed etiology was reported for 166 outbreaks (67%); the remaining were mainly due to Salmonella (32%), Clostridium perfringens (3%), and Escherichia coli (3%). A food was implicated in 27% of norovirus and 65% of bacterial outbreaks; eggs (9, 16%), fruit (8, 15%), and chicken (5, 9%) were the most commonly reported foods. Among the 51 deaths with a confirmed etiology, most were caused by bacteria (36, 70%), including Salmonella (19), Listeria (10), and Escherichia coli (5). The pathogen-food pairs associated with the most deaths were Listeria and turkey (8) and Salmonella and seeded vegetables (3). An implicated food was prepared in the nursing home in 195 outbreaks. Among outbreaks with a contributing factor indicated, handling of food by an infected person was the most commonly reported food safety issue in norovirus outbreaks (30/34, 88%); contaminated raw food was the most commonly reported issue in bacterial outbreaks (13/27, 48%).

Conclusion: Foodborne outbreaks in nursing homes remain an important public health problem. Interventions should address both viral and bacterial causes, and should in part focus on ensuring that proper food preparation practices are followed in these facilities and that ill food handlers do not report for work.
P-051

Are Culture-Independent Diagnostic Tests Changing Outbreak Detection?

Authors: Marder E1, Sundararaman P1, Burzlaff K2, Cahoon J3, Cieslak P4, Cronquist A5, Dunn J6, Eikmeier D7, Hurd S8, Jones L9, Lathrop S10, Libby T11, Geissler A1

Affiliations: ¹Centers for Disease Control and Prevention, ²New York State Department of Health, ³Maryland Department of Health and Mental Hygiene, ⁴Oregon Health Authority, ⁵Colorado Department of Public Health and Environment, ⁶Tennessee Department of Health, ⁷Minnesota Department of Health, ⁸Connecticut Emerging Infections Program, ⁹Georgia Department of Public Health, ¹⁰University of New Mexico, ¹¹California Emerging Infections Program

Background: Identification of outbreaks (OB) and OB-associated cases is reliant on molecular subtyping. However, use of culture-independent diagnostic tests (CIDTs) is increasing, and they do not provide subtype information. Without this information, OB detection and surveillance of OB-associated cases is impaired.

Methods: We analyzed data from the Foodborne Diseases Active Surveillance Network (FoodNet) and the National Outbreak Reporting System (NORS) to describe changes in OB-associated cases and OBs of Shiga toxin-producing E. coli (STEC), Salmonella, and Campylobacter as CIDT use has increased. We defined a CIDT-only case as a positive CIDT result without culture confirmation.

Results: During 2012–2013, 8% (n=191) of STEC, 1% (n=193) of Salmonella, and 13% (n=1958) of Campylobacter cases were CIDT-only and 10% (n=238) of STEC, 6% (n=908) of Salmonella, and 0.5% (n=72) of Campylobacter were OB-associated. During 2014–2015, the percentage of CIDT-only cases increased to 14% (n=383) of STEC, 3% (n=545) of Salmonella, and 21% (n=3403) of Campylobacter. The percentage of OB-associated cases significantly decreased to 8% (n=226; p=0.03) for STEC, and did not change significantly for Salmonella (n=974, 6%) or Campylobacter (n=57, 0.4%). The average number of single etiology OBs, including multistate, reported to NORS in FoodNet states, decreased from 28.5 to 26 for STEC, 79.5 to 76 for Salmonella, and 17.5 to 15 for Campylobacter.

Conclusions: While the proportion of CIDT-only cases increased, the proportion of OB-associated STEC cases and number of OBs reported for all three pathogens decreased slightly. Other changes, such as differences in food contamination or states’ capacity to perform subtyping, may influence the occurrence and recognition of outbreaks. Continued monitoring of outbreak reports is needed to determine whether the uptake of CIDTs is affecting outbreak detection. Reflex culture (culturing of a specimen with a positive CIDT result), commonly used for Salmonella, is essential for obtaining isolates for molecular subtyping needed to identify OBs and link OB-associated cases.
Multistate Outbreak of *Listeria monocytogenes* Infections Linked to Raw Milk Soft Cheese

Authors: Marus J, Conrad A, Stroika S, Waechter H, Tompkins B, Nicholas D, Applewhite C, Pereira E, Fields A, Beal J, and Gieraltowski L

**Background:** In January 2016, CDC PulseNet identified a cluster of *Listeria monocytogenes* (Lm) clinical isolates with an indistinguishable pulsed-field gel electrophoresis (PFGE) pattern combination that were highly related to one another by whole genome sequencing (WGS). CDC, FDA, and state and local public health officials investigated to determine the outbreak source and prevent additional illnesses.

**Methods:** We defined a case as illness in a person infected with the outbreak strain of Lm isolated between September 1, 2016 and March 13, 2017. All ill people were interviewed with the Listeria Initiative questionnaire; a supplemental questionnaire was used to assess common exposures. Regulatory agencies conducted traceback, and state and federal regulatory partners performed retail sampling of reported products.

**Results:** We identified eight ill people from Connecticut (1), Florida (1), New York (5), and Vermont (1). All eight people were hospitalized, and two died. All patients reported consuming soft cheese, a proportion significantly higher than expected based on case-case analysis (p=0.014). An open sample of cheese collected from one patient’s home yielded the outbreak strain, which was identified as a raw milk cheese from Creamery A. Seven ill people reported purchasing cheese at stores where Creamery A products were sold. Testing of intact wheels of this same cheese collected at Creamery A during inspection and at retail yielded the outbreak strain. On March 10, 2017, Creamery A voluntarily recalled all varieties of its cheese.

**Conclusions:** Outbreaks linked to cheese can be challenging to solve because they often involve patients who consume a variety of cheese types and brands and might not recall brand information. Cheeses that are cut and repackaged at a retail cheese counter are also subject to potential cross-contamination or mislabeling. This investigation demonstrates that laboratory testing of consumer samples and retail products can be especially important for outbreaks associated with products like cheese that are sold in multiple forms and often repackaged at retail sites.
Analysis of Vibriosis Cases Reported in Florida Using Culture-Independent Diagnostic Tests
Laura Matthias, MPH and Jamie DeMent, MNS, CPM
Florida Department of Health

Background: The use of culture-independent diagnostic tests (CIDT) to detect pathogens is increasing. The number of vibriosis cases reported in Florida via CIDT has increased from four reports in 2015 to 21 reports as of June 1, 2017, representing a 5-fold increase. The Florida Department of Health (FDOH) evaluated vibriosis cases reported with CIDT results and reviewed reported exposures that could lead to infection to see if CIDT results were consistent with culture-based testing.

Methods: Reported cases of vibriosis from January 4, 2015 – June 1, 2017 were extracted from Florida’s electronic disease reporting system, Merlin. Cases were analyzed based on lab testing methodology and those with CIDT were reviewed for exposures to seawater or consumption of seafood, health outcomes and co-infections.

Results: There were 489 cases of vibriosis reported between January 4, 2015 – June 1, 2017. Of those cases, 34 (7%) were first reported using CIDT. Of the 34 CIDT cases, 20 (59%) were reflex culture negative, 3 (9%) were reflex culture positive, and 11 (32%) did not have a reflex culture performed. Seventeen cases reported an exposure and 15 (88%) of those were related to consumption of seafood. Sixteen (47%) reported no exposures to seawater or consumption of seafood and one (3%) had unknown exposures. Ten (29%) cases had one or more additional pathogens detected. Nineteen cases reported being hospitalized. However, it was noted two of the cases were hospitalized for illnesses other than vibriosis.

Conclusions: The use of CIDT and detection of vibriosis through this method is increasing. Case investigations in Florida have revealed that 50% of cases reported an exposure that could lead to a Vibrio infection. Of those with reflex culture testing, few were validated by traditional culture methods. Lack of identified exposures and negative culture results in CIDT positive patients could be of concern for traditional vibriosis surveillance efforts potentially leading to an artificial inflation of reported cases.
P-054

GastroBusters: Evaluation of an Online Reporting System for Foodborne Illness in Toronto, Canada

Authors: Sylvia Ota MHSc, Anne Arthur MSc, and Effie Gournis MSc, MPH

Affiliation: Communicable Disease Control, Toronto Public Health, Toronto Canada

Background: Foodborne illness (FBI) is under-reported to public health. In the summer of 2015, Toronto Public Health (TPH) launched a six-month pilot of GastroBusters, an online FBI reporting tool for the public, to complement traditional surveillance methods such as reporting by phone or through TPH’s food premise complaint system. An evaluation was conducted to: (1) assess the added value of GastroBusters to existing FBI surveillance, (2) assess system design and identify areas for improvement, and (3) make recommendations for future use.

Methods: The CDC’s Framework for Evaluating Public Health Surveillance Systems for Early Detection of Outbreaks guided the evaluation. A mixed methods approach combined qualitative and quantitative data from GastroBusters, internal TPH focus groups, food premise inspection results, and other surveillance data. Data were collated in MS Access and analyzed with SAS version 9.3.

Results: From August 1, 2015 to January 31, 2016, TPH received 752 FBI reports from all reporting methods. Of these, 238 (32%) were received through GastroBusters, including 44 (18%) that were also reported via another method. Most (60%) provided enough information to initiate a public health investigation. Those 39 years and younger reported more frequently through GastroBusters than other methods. Of those reported only via GastroBusters, 50/194 (25.8%) resulted in a food safety inspection; six identified critical infractions and one premise was closed. No community outbreaks were detected by any method during the pilot period. Issues raised included duplication with other reporting methods, and collection of information that was not useful for the investigation.

Conclusion: GastroBusters provided added value to existing FBI surveillance by representing a younger population and identifying food premises with food safety infractions that may not have otherwise been reported. Continued use of an online FBI tool after integration with the existing food premise complaint system was recommended to ensure a seamless customer experience and reduce reporting redundancies.
P-055

Changing Epidemiology of Yersinia Infections — Foodborne Diseases Active Surveillance Network (FoodNet), 2010–2016

Authors: Ray, LC¹; Barrett, K²; Burzlaff, K³; Cahoon, J⁴; Garman, K⁵; Rounds, J⁶; Shiferaw, B⁷; Wilson, E⁸; Wilson, S⁹; Griffin, P²; Geissler, A²

Affiliations: ¹Oak Ridge Institute for Science and Education, Oak Ridge, TN; ²Division of Foodborne, Waterborne, and Environmental Diseases, National Center for Emerging & Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, Atlanta, GA; ³New York State Department of Health, Albany, NY; ⁴Maryland Department of Health, Baltimore, MD; ⁵Tennessee Department of Health, Nashville, TN; ⁶Minnesota Department of Health, Saint Paul, MN; ⁷Oregon Public Health Division, Portland, OR; ⁸Colorado Department of Public Health and Environment, Denver, CO; ⁹Georgia Department of Public Health, Atlanta, GA

Background: Yersinia enterocolitica (YE) causes an estimated 116,716 illnesses annually in the United States. In 2009, FoodNet reported decreases in YE incidence, possibly due to targeted educational efforts, particularly among the historically highest incidence group, young black children. In 2012, FoodNet began including reports of positive culture-independent diagnostic tests (CIDTs) in addition to culture (cx). During 2016, many clinical laboratories adopted syndromic panel CIDTs that include Yersinia, a pathogen not typically detected by routine stool cultures.

Methods: We summarized data on laboratory-confirmed Yersinia enterocolitica (YE) infections reported to FoodNet during 2010–2016. We calculated annual incidence rates (IRs) per 100,000 persons.

Results: During 2010–2016, sites reported 935 YE infections, resulting in 295 (32%) hospitalizations and 12 (1%) deaths. Among 199 CIDT-positive infections, 62 (31%) were cx-confirmed YE; 173 (87%) were reported in 2016 alone. Average IR of cx-confirmed YE during 2010–2015 was 0.27 and varied little by year (range 0.22 to 0.30); however, it increased in 2016 to 0.33. When cx-confirmed or CIDT-positive-only infections were combined, the IR for 2016 was 0.55. Seasonality overall was highest in colder months (55% Nov-Apr). Among the 838 (90%) YE cases with race data, Asians had the highest average IRs (0.4) during 2010-2016, followed by blacks (0.3), and whites (0.2). Among infants (children <1 year old), the IR decreased from 4.2 in 2010–2012 to 2.2 in 2014–2016. This was driven by marked decreases among black (12.6 to 4.4) and Asian infants (11.0 to 5.2).

Conclusions: In 2016, the overall IR of YE infections increased. The rise in overall IR is likely due to increased use of CIDTs and confirmation of YE by cx. Marked demographic differences underscore the need for focused prevention efforts, particularly among Asians and blacks. These findings emphasize the importance of sentinel site surveillance of Yersinia, because it is not nationally notifiable, to inform comparisons of incidence and guide control measures.
Pacific Pearls: Norovirus Outbreaks Associated with Oysters

Authors: Roshan Reporter, Marifi Pulido, Michelle Chan

Affiliations: Los Angeles County Department of Public Health, Los Angeles, CA

Background: Los Angeles County Department of Public Health (LAC DPH) noted trend of norovirus outbreaks for 3 successive years, 2015-2017, where source was determined to be from oysters.

Methods: Each outbreak was investigated by case control study using an outbreak specific interview; EH restaurant inspections and traceback; testing of human cases (RT-PCR performed in LAC PHL, sequence analysis by CDC); and testing of oysters (RT-PCR and sequence analysis at FDA Gulf Coast Seafood Laboratory).

Results: OB2015 was at an All You Can Eat (AYCE) sushi restaurant where 3 separate parties reported illness after dining 2/24-3/1/2015. Case control study implicated oysters and salmon; p<0.0001 for both. Patrons(4/4) and employees(2/31) tested positive for norovirus. Owner stated they had recently changed the supplier for oysters served.

OB2016 was also an AYCE sushi restaurant where 4 separate parties reported illness after dining 3/12-4/9/2016. Oysters were only item close to significant (p=0.282). Patrons(3/3) and employees(0/13) tested positive for norovirus.

OB2017 was an AYCE Mother’s Day brunch buffet on 5/14/17; 2 parties reporting illness afterwards. The 3 of 4 patrons who ate oysters met a clinical case definition for norovirus; 1/3 patrons tested positive for norovirus. Case control numbers were too small to see statistical significance.

Oysters in all 3 restaurants were frozen, from the same origin (Korea), packed by the same company. Oysters were tested in 2015 and 2016; oysters from 2017 results are pending. Genotypes GI and GII were found both years. Control actions: removed oysters from restaurants, state DPH notified, restaurant violations corrected per EH.

Conclusions: Oyster consumption caused illness in all 3 outbreaks. Imported frozen farmed oysters may carry pathogens from sewage effluent that can cause enteric illness. Restaurants may not be aware that frozen imported oysters are meant to be cooked or treated prior to serving; thus better labeling of such products is recommended.
P-057

What’s that Pathogen? A Foodborne Atypical Enteropathogenic E. coli (aEPEC) Outbreak at a Minnesota Restaurant, 2015

Authors: A. Saupe¹, E. Cebelinski¹, V. Lappi¹, J. Fischer¹, K. Swenson², J. Harmon², K. Smith¹

Affiliations: ¹MN Dept of Health, ²Brown-Nicollet Environmental Health

Background: Typical Enteropathogenic E. coli (tEPEC) are characterized by two virulence genes (eae, bfp); atypical EPEC (aEPEC) carry only eae. Whereas tEPEC is an important cause of pediatric diarrhea in developing countries, less is known about aEPEC. To our knowledge, this is the first aEPEC outbreak reported in the U.S.

On October 20, 2015, the Minnesota Department of Health (MDH) was notified of a complaint regarding gastrointestinal illness among attendees of a catered lunch.

Methods: Local environmental health specialists performed an environmental assessment at the restaurant, interviewed employees, and implemented general interventions. A case-control study was conducted – a case was defined as a patron who developed vomiting or diarrhea (≥3 loose stools in 24 hours). Stool samples were tested at MDH.

Results: Thirty cases were identified, with onsets during October 14–19. All reported diarrhea, 22 (79%) cramps, 7 (30%) fever, 5 (17%) vomiting, and 1 (3%) bloody stool. Five (17%) cases sought medical care. The median incubation period was 20 hours (range, 3.5 to 106 hours), and the median duration of illness was 67 hours (range, 4 to 196 hours).

No major environmental health issues were identified. One food worker reported illness onset on October 19. Eleven (patrons and the employee) of 12 stools were positive for aEPEC (eae); seven isolates were recovered and had indistinguishable PFGE patterns. Serotype O167:H9 was determined by WGS analysis. Testing for conventional pathogens was negative.

Conclusions: This was a foodborne aEPEC outbreak associated with a restaurant. The vehicle was not confirmed; however, the outbreak was likely caused by a contaminated ingredient received by the restaurant, or possibly transmission from an infected food handler. Expanded laboratory testing was vital in identifying and confirming aEPEC as the causative agent. Investigators should consider novel pathogens like aEPEC as a potential etiology for foodborne outbreaks.
P-058


Authors: C. Schwensohn¹, K. Gambino-Shirley¹, ², A. Tesfai³, B. Tolar¹, C. Burnett⁴, D. Eikmeier⁵, J. Stone⁶, J. Hines⁷², S. Viazis³, M. Wise¹, K. Neil¹

Affiliations: ¹Division of Foodborne, Waterborne, and Environmental Diseases, National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, Atlanta GA; ²Epidemic Intelligence Service Program; ³Coordinated Outbreak Response and Evaluation Network, Food and Drug Administration, College Park, MD; ⁴Utah Department of Health, Salt Lake City; ⁵Minnesota Department of Health, St. Paul; ⁶Oklahoma State Department of Health, Oklahoma City; ⁷Oregon Public Health Division, Portland, OR.

Background: *Salmonella* causes an estimated 1 million foodborne illnesses and 400 deaths in the United States annually. In January 2016, PulseNet, the national laboratory network for foodborne disease surveillance, detected a multistate outbreak by a novel strain of *Salmonella* Virchow. We investigated to identify the source and prevent additional illnesses.

Methods: A case was defined as infection with the pulsed-field gel electrophoresis outbreak pattern of *Salmonella* Virchow occurring between 12/5/2015 and 4/12/2016. Patients were interviewed to identify common exposures, and results were compared with healthy people in the 2006–2007 FoodNet Population Survey. We investigated product and supplier information to identify a common source of ingredients and inspected production facilities. Samples of the suspected product and its ingredients were cultured for *Salmonella*.

Results: Thirty-five cases from 24 states were identified; 6 hospitalizations and no deaths were reported. Thirty-one (94%) of 33 patients reported consuming powdered supplements in the week before becoming ill, which is significantly higher than the 4% of healthy people in the FoodNet Survey (P<.001); 30 of 31 patients reported consuming Brand A, a raw organic powdered shake product consumed as a meal replacement. Laboratory testing identified the *Salmonella* Virchow outbreak strain from leftover Brand A products collected from three patients’ homes and from moringa leaf, an ingredient in Brand A imported from South Africa.

Conclusions: This is the first reported salmonellosis outbreak linked to a raw meal replacement powder. Company A issued a voluntary recall and reformulated the product to exclude moringa leaf. As this product has a long shelf-life, the recall likely prevented additional illnesses. This investigation identified a novel outbreak-related food and highlighted a potential risk with similar ready-to-eat products.
Outbreaks of norovirus genotype GII.4 are associated with severe health outcomes – United States, 2009–2016

Authors: Minesh P. Shah, Mary E. Wikswo, Leslie Barclay, Anita Kambhampati, Jennifer Cannon, Umesh D. Parashar, Jan Vinjé, Aron J. Hall

Affiliation: Division of Viral Diseases, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA

Background: Norovirus is the leading cause of acute gastroenteritis outbreaks in the United States. Over the last decade, GII.4 genotypes emerged every 2–4 years, often leading to more severe health outcomes, although it is unclear if these are due to viral, host, or setting factors.

Methods: Acute gastroenteritis outbreaks that occurred during 2009 – 2016 with norovirus reported as the single confirmed etiology to the National Outbreak Reporting System (NORS) were matched with laboratory-confirmed norovirus outbreaks reported to CaliciNet. GII.4 and non-GII.4 outbreaks were analyzed for epidemiologic characteristics including setting, transmission mode, age, gender, clinical symptoms, and health outcomes. Univariate analyses were performed for hospitalization and mortality rates, and multivariable models were fitted to estimate the independent effect of each factor.

Results: Of 14,982 confirmed norovirus outbreaks reported to NORS and 7,509 outbreaks reported to CaliciNet, 3,748 outbreaks were matched. Over the 7-year time-span, the most common genotypes reported were GII.4 Sydney (41%), GII.4 New Orleans (20%), GII.6 (6%) and GI.3 (6%). Compared to non-GII.4 outbreaks, GII.4 outbreaks were more likely to be spread by person-to-person transmission (75% vs. 62%), and to occur in long-term care facilities (68% vs. 39%). GII.4 outbreaks resulted in higher rates of hospitalization (24.2 vs. 10.0 per 1,000 cases, p<.0001) and mortality (24.7 vs. 12.4 per 10,000 cases, p<.0001) than non-GII.4 outbreaks. In multivariable models, age ≥ 75 years (adjusted incidence rate ratio [aIRR] 1.1-2.7) and presence of fever (aIRR 1.0-2.3) were significantly associated with higher hospitalization rates. GII.4 viruses (aIRR 2.2-18.4) and healthcare settings (aIRR 10.8-90) were significantly associated with higher mortality rates.

Conclusions: While the severity of norovirus outbreaks are multifactorial, GII.4 viruses are independently associated with higher mortality rates. These results support further investigation into mechanisms of increased severity by norovirus genotype and validate the inclusion of GII.4 in candidate norovirus vaccines.
Community Size and Retail Risk Factors in Iowa Retail Food Establishments

Author: Sherri Sigwarth

Affiliation: Investigative Division: Food & Consumer Safety Bureau

Iowa Department of Inspections and Appeals (DIA), International Food Protection Training Institute (IFPTI), 2017 Fellow in Applied Science, Law, and Policy: Fellowship in Food Protection; This research was conducted as part of the International Food Protection Training Institute’s Fellowship in Food Protection, Cohort VI.

Abstract: This study evaluated the perception that rural retail food establishments pose a higher food safety risk than urban establishments; a perception shared by the author and other food safety inspectors employed by the Iowa Department of Inspections and Appeals (DIA), Food and Consumer Safety Bureau. The study analyzed food safety risk violations found in urban, urban cluster, and rural establishment inspections in Iowa as well as risk factor patterns associated with the type of ownership, length of ownership, and presence of a Certified Food Protection Manager (CFPM). The U.S. Census Bureau categorizes communities based on population: urban > 50,000, urban cluster > 2,500 and < 50,000, and rural < 2,500. The study found that there were some slight differences in the type or rate of specific CDC risk factor violations among retail food establishments based on the size of the community. This study found a slight difference in the rate of food safety risk violations related to ownership type, with sole proprietorship showing a relatively higher violation rate in risk factors than franchise and corporate ownership. This study also found that retail food establishments with a CFPM on staff had a lower occurrence of all risk factor violations than retail food establishments that did not have a CFPM on staff. The study concluded that increased reliance on statistical analysis by food safety inspectors would tend to offset erroneous impressions regarding rural food establishments. The study recommended that an annual food safety risk factor statistical report be prepared and made available to all food safety regulators in Iowa.
The Global Importance of a Publically Available, Genomic Database for Environmental and Food Isolates

Authors: Eric Stevens, Ruth Timme, Maria Sanchez Leon, Marc Allard, Maria Hoffmann, Sabina Lindley, George Kastanis, Tim Muruvanda, Errol Strain, Justin Payne, Arthur Pightling, Hugh Rand, James Pettengill, Yan Luo, Narjol Gonzalez-Escalona, David Melka, Eric Brown

Affiliation: US Food and Drug Administration, College Park, MD

Background: In 2012 the United States Food and Drug Administration (FDA) launched GenomeTrakr, a pilot project that aimed to use whole-genome sequence (WGS) technology to respond to foodborne disease outbreaks. This freely available repository is currently supported by a network of about 60 federal, state, international, and public health laboratories, which collect and share WGS data in real time.

Methods: The GenomeTrakr network continued to expand in 2016 and early 2017 by adding new labs and over 80,000 foodborne isolates. The data analysis pipeline implemented within GenomeTrakr, and our partners at NCBI, allowed us to compare and cluster pathogens across four public surveillance efforts: Salmonella enterica, Listeria monocytogenes, E. coli, and Campylobacter. The network also provides daily phylogenetic updates that are both freely and publically available to allow greater transparency between public health agencies, our industry partners, academia, and international partners.

Results: WGS has fundamentally altered the way we approach and respond to foodborne diseases by combining multiple microbiological tests into one (e.g. organism identification, antimicrobial resistance, subtyping). Here we provide two examples for how WGS can provide critical insight into resolving both domestic and global foodborne outbreaks.

Significance: The GenomeTrakr project provides an example for how public health agencies can use genomic data (with its associated metadata) alongside traditional epidemiologic methods to resolve foodborne outbreaks. As the cost of WGS decreases, its emerging rollout among foodborne disease surveillance systems emphasizes its increasing importance as a public health tool. GenomeTrakr serves as a resource for generating possible matches to inform outbreak investigations within the United States and this function only becomes more pronounced as the database grows. These genomic sequences – and the associated metadata (e.g. year of collection, geographic location, food source) – need to be made available for its successful use as a global public health resource to make food safer globally.
Salmonella Illness Outbreaks Linked to Live Poultry — United States, 2017

Authors: Lauren Stevenson, Lia Koski, Valerie Morrill, Megin Nichols

**Background:** Annual outbreaks of Salmonella illnesses linked to live poultry have increased in the United States (US) since 2008. By June 2017, the number of Salmonella infections linked to live poultry had surpassed the number reported during the same time period in previous years. In the US, most Salmonella infections from live poultry contact are due to contact in backyard flocks. Twenty major hatcheries supply live poultry to feedstores for use in US backyard flocks. Investigating behaviors among ill people and conducting traceback on purchased poultry are important to understand risk factors for these outbreaks and identify prevention measures.

**Methods:** Outbreak strains were identified through PulseNet. Ill people were interviewed with state specific enteric and live poultry supplemental questionnaires. Feedstore and hatchery staff were interviewed to ascertain origin of poultry. Data were collected in SEDRIC and Epi Info 7, and descriptive statistics were calculated using SAS 9.4.

**Results:** As of July 7, 2017, 790 people in 48 states were infected with one of 20 Salmonella outbreak strains. Seventy-four percent (409/553) of ill people reported contact with live poultry prior to illness onset. Among ill people the following behaviors were reported: touching poultry (72%), snuggling or kissing poultry (24%), touching cages (66%), and keeping poultry indoors (34%). Eighty-one percent (211/261) reported owning poultry and traceback identified forty different feedstores and 15 different hatcheries. Nine ill people reported occupational contact with live poultry. Thirty-seven percent of ill people did not know about the connection between Salmonella and live poultry.

**Conclusions:** Salmonella illness outbreaks linked to US backyard flocks have continued to increase. In 2017, ill people engaged in behaviors that might have led to Salmonella transmission. Education of poultry owners and feedstore employees on the link between Salmonella and live poultry might prevent behaviors that lead to illness. Encouraging identified hatcheries to reduce human disease-causing Salmonella strains in the hatchery environment might help further reduce the number of illness outbreaks.
Outbreaks Attributed to Shellfish — United States, 1998–2015
Sundararaman P1,2, Crowe SJ1

Affiliations: 1National Center for Emerging and Zoonotic Infectious Diseases, CDC, 2Atlanta Research and Education Foundation

Background: Shellfish are responsible for nearly 9% of foodborne disease outbreaks that occur in the United States each year. We describe the features of these outbreaks and propose interventions that might prevent them.

Methods: We reviewed outbreaks reported to CDC’s Foodborne Disease Outbreak Surveillance System (FDOSS) during 1998–2015. A foodborne outbreak is defined as ≥2 similar illnesses due to ingestion of a common food. Outbreaks were included in the analysis if the implicated food was a crustacean (e.g., crabs, lobsters, and shrimp), mollusk (e.g., clams, oysters, and mussels), or unspecified shellfish.

Results: During 1998–2015, 393 outbreaks were attributed to consumption of shellfish, resulting in 4,239 illnesses, 156 hospitalizations, and 2 deaths. The median outbreak size was 4 illnesses (range 2–400). The average number of outbreaks declined from 29 per year during 1998–2006 to 15 per year during 2007–2015. Florida (114 outbreaks, 30%), Washington (53, 14%), and California (40, 11%) reported the most single-state outbreaks. There were 14 outbreaks in which ill persons were exposed in more than one state. Of the 267 single-etiology outbreaks, Vibrio (119 outbreaks, 45%), and norovirus (81, 30%) were the most common causes. Of 363 outbreaks with a single food reported, more than half (214, 59%) were due to oysters, followed by shrimp (44, 12%) and crab (34, 9%). Vibrio in oysters (83 outbreaks), norovirus in oysters (75), and Vibrio in crab (11) were the most frequent etiology-shellfish pairs. Raw shellfish was reported in 52% (205) of outbreaks; oysters (180, 84%) and clams (8, 40%) were the types most often consumed raw. Contamination likely occurred before preparation in 91% of 88 outbreaks with a point of contamination specified.

Conclusions: Outbreaks attributed to shellfish have declined, but remain an important public health problem. Implicated shellfish were often consumed raw, so postharvest interventions should be considered to prevent illnesses caused by shellfish.
P-064

Physician knowledge, attitudes, and practices surrounding antibiotic prescribing to patients diagnosed with Shigellosis in Indiana

Authors: Madhura Sundararajan, MPH, Allison Miller, MPH, Betsy Schroeder, DVM, MPH, Jamie Yeadon-Fagbohun

Background: In 2014, the Indiana State Department of Health (ISDH) responded to a widespread outbreak of Shigella sonnei with 862 laboratory-confirmed cases. The majority of cases showed resistance to trimethoprim-sulfamethoxazole, an antibiotic frequently prescribed by physicians. The ISDH revised the communicable disease reporting rule to ease the recommendation for antimicrobial therapy before returning to school or daycare in patients diagnosed with Shigellosis by allowing return after 24-48 hours of being asymptomatic. Our study evaluated physician knowledge, attitudes, and practices (KAP) surrounding diagnosis and antibiotic prescribing for Shigella species infections.

Methods: A web-based, 17-question KAP survey was developed using SurveyMonkey and targeted to Indiana physicians likely to evaluate and treat patients with enteric illness. The instrument was disseminated through the State Health Commissioner’s physician e-mail list. This list did not target Indiana physicians by sub-specialty.

Results: Responses were received from 101 physicians, with a response rate of 3.5%. Antimicrobial resistance in Shigella species was perceived to be a significant problem in practice for 10 (10%) respondents. Barriers to consulting antibiotic susceptibility test results prior to prescribing included lag time (n=24; 24%), limited follow-up capacity (n=4; 4%), and restricted laboratory capability (n=6; 6%). Providers also stated that hospital antibiograms may be out of date (n=2; 2%) or do not include Shigella species. The most common barrier to discharging patients without prescribing antibiotics was patient and family expectation of needs (n=23; 23%).

Conclusion: Systemic barriers, including limited follow-up in emergency department settings, patient demand, timeliness of testing, and inability to identify Shigella species based on clinical presentation alone inhibit appropriate treatment. Additionally, use of point-of-care culture-independent testing methods restrict susceptibility testing. Timely, region-specific guidance around observed susceptibility patterns might help providers be informed and increase awareness. Hospital outreach to update and promote the use of antibiograms may also be useful, inform hospitals and increase awareness.
Enhanced Communication: Continual Improvement to Indiana’s Rapid Response Team

Author: Megan Teachout

Background: The effectiveness of a Rapid Response Team (RRT) relies on communication and collaboration among environmental investigators, laboratorians, and epidemiologists. In 2016, Indiana State Department of Health Laboratories (ISDHL) initiated a project to give local health departments access to resources to alleviate food sampling issues. RRT members have also taken this time to explore avenues to improve outbreak response through enhanced communication.

Methods: Increasing the frequency of meetings does not always improve communication; key is to enhance its effectiveness. ISDHL, ISDH Food Protection Program (FPP), and ISDH Epidemiology Resource Center (ERC) have implemented changes that include new meetings, periodic reviews, and templates that better disseminate important information to the appropriate people.

Results: For years, ISDHL and ERC have held biweekly meetings to discuss viral and bacterial outbreaks. Unfortunately, detailed discussions cannot fit into a one hour meeting with such a broad scope. Staff from ISDHL, FPP, and ERC agreed that a separate foodborne illness outbreak meeting could allow us to have discussions that would normally get lost in emails.

ISDHL Environmental Microbiology Division Director created an outbreak notification email template that is used within the division. Critical information regarding the event, samples and reporting is monitored via email to keep everyone apprised of ongoing outbreaks.

After-action reviews are conducted if issues arise during outbreak investigations. This allows ISDH to work with all levels of management and staff to make immediate improvements for future investigations.

A quarterly meeting between the RRT main players has allowed points of contact to be established between state agencies that rarely interact with each other.

Conclusion: Avenues created to improve communication are still a work in progress. Although quarterly RRT meetings have been in place for 3 years, the process still needs restructuring to eliminate redundancy with other meetings. The new email template and foodborne illness outbreak meeting have strengthened partnerships at ISDH. However, the improved collaboration has not eliminated the need to have after-action reviews following some outbreaks.
Washington Rapid Response Team (RRT): PFOS/PFOA Contamination of Municipal Well Water Supply Impacting Manufactured Food Processors

Author: Randy Treadwell, MPH

Affiliation: Washington State Department of Agriculture

Background: In May 2017, levels of Perfluorooctane sulfonate (PFOS) and Perfluorooctanoic acid (PFOA) well above the established EPA lifetime health advisory levels were discovered in municipal wells providing potable processing water to large food-manufacturing facilities in eastern Washington State. The compounds were historically used in the region as fire suppressants. Health advisory levels for exposure to these chemicals through food ingestion pathways have not been established; however, studies have indicated that exposure to PFOS and PFOA over certain levels may be associated with adverse developmental, liver, immune, and thyroid effects as well as cancer.

Methods: The Washington Rapid Response Team (RRT) was activated to coordinate multi-agency investigation activities, assist with recalls, share information with public health partners, and provide impacted firms with food safety-related technical assistance. Primary response partners included the Washington State Department of Agriculture (WSDA) and the U.S. Food and Drug Administration Seattle District Office (FDA SEA-DO). The Incident Command System (ICS) was used to coordinate field activities and share information with approximately 16 agencies/programs. The RRT remained activated until the identified public health threat was controlled.

Results: A voluntary recall of approximately 319,000 pounds of meat, frozen meals, and bakery products was conducted. Environmental assessments were performed at the recalling facility to identify and mitigate possible areas of cross-contamination between contaminated and potable water. Product-specific exposure guidance was provided by Federal subject matter experts in a timely manner in order to guide recall decision-making by regulated industry. Additionally, visits to other impacted facilities were coordinated by the RRT and executed by joint WSDA/FDA investigation teams.

Conclusions: The Washington RRT proved to be an effective coordinating system for activities and information during a complex water and food emergency response with multiple stakeholders.
Challenges of Two Simultaneous Outbreaks (Norovirus and Influenza A)

Authors: Varsha Vakil, MPH; Edward Davila, MPH; Stephen Long, MD, MPH; Kirstin Short, MPH

Affiliation: Houston Health Department

Background: Epidemiologists at Houston Health Department (HHD), Bureau of Epidemiology (BOE) are well-versed with the management of gastrointestinal (GI) outbreaks like Norovirus. In January 2017, the BOE was notified of an outbreak at a senior center. Upon investigation, it was learned that two simultaneous outbreaks of GI and respiratory illnesses were prevailing; both residents and staffs were affected. This outbreak demanded coordinated preventative measures on two different public health aspects.

Methods: Diseases reported through phone/fax, Electronic Lab Reporting, Bureau of Consumer Health are routinely investigated. Epidemiologists conducted site visits and interviewed key personnel at the facility. Specimens were collected from ill individuals to determine the outbreak etiology. Data was compiled and analyzed. Customized preventative measures were applied to contain the outbreaks.

Results: Total number of residents at the facility was 69 and staff 85. Positive lab test results identified the outbreaks as Norovirus and Influenza A.

Norovirus outbreak: BOE recommended use of disposable mop heads and hand sanitizers, and post hand-wash signs. Residents’ attack rate was 28% (19/69); among staff it was 8% (7/85). Females were 74% among residents, and 86% among staff. Sixty-eight percent residents and 86% staff had diarrhea. Seventy-nine percent residents were of age group 71+; 43% staff were of age group 31-40. Resident stools tested at a commercial lab were positive for Norovirus; no specimens were obtained from staff.

Influenza A outbreak: BOE recommended droplet precautions, use of disposable masks and cleaning of air filters. Residents’ attack rate was 36% (25/69); among staff it was 9% (8/85). Ninety-six percent residents and 100% of staff were females. Ninety-six percent residents affected were 71+; among staff age groups 41-50 (25%) and 61-70 (25%) were tied. Symptoms of cough were experienced by 80% residents and 38% staff. Resident specimens tested at a commercial lab were positive for Influenza A; no specimens were obtained from staff.

Conclusions: With recommended preventative measures and effective collaboration both the outbreaks were contained within five days of reporting.
Salmonella Typhimurium Outbreak Associated with a Daycare in Kentucky, 2016

Authors: Tracy L. Vaughn, RN, Rudrani Ghosh, MBBS, MPH, Carrell Rush, MPH, and Robert L. Brawley, MD, MPH

Background: In September 2016, the Kentucky Department for Public Health (KDPH) and a local health department began an investigation of a Salmonella Typhimurium outbreak in central Kentucky. The cases reported association with the same daycare facility (daycare A) prior to becoming ill.

Methods. A case was defined as: Any child, visitor or staff member working or attending the daycare facility, who had (including ongoing) at least 2 or more episodes of vomiting and/or diarrhea in a 72 hour period between 09/05/2016-09/14/2016. Each lab confirmed case was interviewed using the Kentucky Foodborne Waterborne Illness Investigation form, and entered into the National Electronic Disease Surveillance System (NEDSS). A full kitchen inspection was performed by the local environmental team, and the kitchen was closed until re-inspection. The Kentucky Division of Laboratory Services (DLS) serotyped and performed pulsed-field gel electrophoresis (PFGE) analysis on each clinical isolate. Five clinical isolates were sent to the Michigan Regional State Public Health Lab (SPHL) for Whole Genome Sequencing (WGS).

Results: Four cases (culture confirmed) were identified as part of the outbreak: three attendees (separated by classrooms) and one daycare employee. Laboratory testing of the daycare attendees’ clinical isolates identified Salmonella Typhimurium, patterns JPXX01.0167 and JPXX01.0442. The daycare employee was responsible for preparing meals in a shared kitchen and delivering them to the daycare classrooms. Laboratory testing of the daycare employee’s clinical isolates identified Salmonella Typhimurium, patterns JPXX01.4917 and JPXX01.0442. Isolates with other PFGE patterns were confirmed to be part of the outbreak by WGS.

Conclusion: The source of this outbreak was not identified. However, through epidemiologic, laboratory, and environmental assessments KDPH was successfully able to associate the outbreak to the daycare facility. The daycare employee continued to test positive for Salmonella Typhimurium for three months and was not cleared to return to work until December 12, 2016. It was not possible to determine in this outbreak investigation if the daycare employee was the source of the outbreak strain or a secondary case.
An unsolved multistate cluster investigation of listeriosis among patients of Eastern European background, 2015–2016

Authors: H. Waechter¹, M. Boyle², E. Harvey³, Y. Khachadourian⁴, A. Conrad⁵

Affiliations: ¹New York City Department of Health and Mental Hygiene, ²Maryland Department of Health, ³Massachusetts Department of Public Health, ⁴Philadelphia Department of Public Health Division of Disease Control, ⁵Centers for Disease Control and Prevention

Background: Whole genome sequencing (WGS) is a powerful tool for solving foodborne outbreaks of listeriosis; however, detailed exposure data remain critical in these investigations. We describe challenges of a large multistate investigation of listeriosis predominantly affecting patients of Eastern European background.

Methods: Cases, identified by PulseNet, were interviewed with the standard Listeria Initiative (LI) questionnaire and Eastern European-specific (EES) food questionnaires. Menus from nursing homes and meal delivery services were reviewed to identify common items. Home and retail store visits were conducted; food was collected for testing and environmental swabs were taken. WGS was completed for all isolates.

Results: Thirty-eight cases with diagnosis dates 11/24/2015–11/3/2016 were identified from 10 states. WGS identified 3 different strains of Listeria monocytogenes among clinical isolates. In total, 34 cases were interviewed with the LI questionnaire and 20 with an EES questionnaire; 33 patients, including patients with each Listeria strain, reported shopping at Russian or Eastern European grocery stores. Patients consumed a variety of store-bought ready-to-eat (RTE) foods including herring, deli meat, and cheeses. Most food items of interest were RTE and store-prepared or store-handled products; thus, brand information was unknown. Three environmental swabs and 1 leftover product yielded 2 of the outbreak strains but could not be traced back to a single source.

Conclusion: While not all cases were closely related by WGS, epidemiologic data suggested a common culturally-specific exposure. However, lack of background consumption rates of culturally-specific foods and possible cross-contamination at retail locations hindered our ability to identify a suspect food vehicle. This investigation highlights how challenging Listeria outbreaks can be and demonstrates that sometimes outbreaks can remain unsolved despite comprehensive WGS data, especially when detailed case exposure information is unavailable.
P-070

Environmental Assessment Challenges – State Perspectives on Eastern European Foods and an Unsolved Multi-State Listeriosis Cluster

Authors: D’Ann Williams¹, Brandi Hopkins², David Nicholas³

Affiliations: ¹Maryland Department of Health, ²Massachusetts Department of Public Health, ³New York State Department of Health

Background: In a 2016 ten state cluster of LM (38 cases), epidemiological evidence obtained from case interviews suggested various Eastern European Food products as the source. Eleven separate environmental assessment (EA) investigations were conducted at case patient homes or retail firms, two in Massachusetts (MA), six in New York (NY) and three in Maryland (MD).

Methods: During these state investigations, samples were collected comprising various retail product samples, retail deli meats, sausage, smoked/salted fish, caviar, store produced salads, butter and cheese (n=94); home food remnant samples (n=15); and retail environmental swab (ES) samples (n=98).

Results: A specific vehicle was not identified as the cause of the outbreak. Environmental samples positive for LM (n=14) and Listeria spp. (n=10) were found on tables, slicers, cutting boards, handles and knobs, drains, condensation pans and refrigerator seams. Multiple Listeria species were identified however only one home meal remnant sample (MD) and three ES sample isolates (MA) were related to the LM outbreak strain.

Conclusion: Listeria spp. exist in community structures and LM is often outcompeted. Listeria spp. survive in a wide-range of environments, biofilms and niches. Susceptibility varies based on virulence and resistance factors complicate the isolation, collection and laboratory enrichment of LM. To address gaps in our knowledge about survival in environmental reservoirs, methods must be developed to improve our understanding of product vulnerability, collection efficiency, and sample analysis. Also additional guidance on remediation and clearance is needed for regulatory response at retail establishments with samples positive for LM and Listeria species. To address these needs, it is necessary to identify and document home and retail practices associated with the antecedents, contamination, survival, and proliferation of Listeria species. Surveillance, EA, interagency collaborations and targeted multi-lingual Listeria education, food safety and remediation strategies are critical to prevent future outbreaks and the morbidity and mortality caused by LM.
Expanded Outbreak Surveillance through the National Outbreak Reporting System (NORS), 2009-2015

Authors: Mary E. Wikswo, MPH, Caroline Pilewski, MPH, Virginia A. Roberts, MSPH, Kathleen E. Fullerton, MPH, Samuel J. Crowe, PhD, Aron J. Hall, DVM

Affiliation: Centers for Disease Control and Prevention, Atlanta, GA

**Background:** The National Outbreak Reporting System (NORS) collects data on all reported foodborne, waterborne, and AGE outbreaks transmitted by person-to-person contact, animal contact, environmental contamination, and unknown modes of transmission.

**Methods:** Finalized data reported to NORS on outbreaks occurring during 2009–2015 were extracted for descriptive analysis. Waterborne outbreak data for 2015 were not available for analysis; waterborne data for 2013 and 2014 are preliminary. Reports with fewer than two persons ill were excluded.

**Results:** A total of 22,720 outbreaks were reported to NORS by all 50 US states, Washington, D.C., and Puerto Rico. Annual reports increased from 2,176 in 2009 to 3,634 in 2015. Forty-two reporting sites reported one or more outbreaks per million population in 2009; this increased to 48 states in 2015.

The most commonly reported mode of transmission was person-to-person (n=13,822, 61%), followed by foodborne (n=5,761, 25%). In total, 635,677 illnesses were reported. Person-to-person outbreaks had the greatest number of illnesses per outbreak (median 24, range 2–2,500).

At least one suspected or confirmed etiology was reported in 16,323 (72%) outbreaks. Norovirus was the most common, reported in 11,411 (70%) outbreaks as the sole outbreak etiology, followed by *Salmonella* (n=1,520, 9%) and *Shigella* (n=665, 4%).

Among the three most common etiologies, the case fatality rates were highest in salmonellosis and norovirus outbreaks (0.2%, each) and lowest in shigellosis outbreaks (0.02%). The hospitalization rate was highest in salmonellosis outbreaks (19%). In shigellosis and norovirus outbreaks, the hospitalization rates were 6% and 2%, respectively.

**Conclusion:** Reporting to NORS has increased since its inception, with more sites reporting more outbreaks. The expanded surveillance through NORS provides a more comprehensive picture of the relative contribution of each mode of transmission, which can help guide appropriately targeted interventions.
P-072
Integration of the National Outbreak Reporting System (NORS) and CaliciNet
Authors: Mary Wikswo, Leslie Barclay, Jan Vinjé, Aron Hall
Affiliation: Division of Viral Diseases, Centers for Disease Control and Prevention, Atlanta, GA

Background: The National Outbreak Reporting System (NORS) is used by local and state health departments to report waterborne, foodborne, and enteric disease outbreaks to CDC. CaliciNet is a national outbreak surveillance network of federal, state, and local public health laboratories who submit laboratory data from norovirus outbreaks. In March 2017, the databases were connected to allow data sharing to provide more complete information on norovirus outbreaks. This abstract summarizes the NORS-CaliciNet integration feature and describe its usage since release.

Methods: NORS outbreak reports are matched to CaliciNet norovirus outbreak reports using reporting site, NORS report ID, and first illness date (+/- 90 days) NORS users are notified of matches and may choose one of two actions: import or ignore (hide) the CaliciNet data. Reports were downloaded from both systems for Jan 2009 – Jun 2017 and compared to see how many reports have been matched and whether data was imported.

Results: A total of 7,519 CaliciNet reports and 31,017 NORS reports (16,400 suspected or confirmed norovirus) were available for analysis. Of 3,700 reports from 45 states that could be matched, NORS users from 19 (42%) states have added 297 (8%) matched reports to NORS and ignored 27 (1%). State users took action on 26% of matched reports from 2016 and 2017, but on only 5% of reports from 2009–2015. A total of 3,863 (54%) of 7,145 confirmed norovirus outbreaks reported in NORS and 3,819 (51%) in CaliciNet could not be matched. No NORS report ID was provided in 2,096 unmatched CaliciNet reports. Other reasons for unmatched reports may include incomplete use of the two systems by state or local agencies or errors inputting the fields used to match reports.

Conclusions: The NORS-CaliciNet integration combines laboratory and epidemiologic data from norovirus outbreaks into a single database. During the 4 months since implementation, 19 states have used this new feature. Further outreach with states may be necessary to increase use of the NORS-CaliciNet integration and thereby provide a more complete picture of epidemic norovirus in the U.S.
P-073

Culture-independent diagnostic testing of enteric pathogens: Managing the impact in Colorado

Authors: Elisha Wilson, Emily Travanty, Alicia Cronquist

Affiliation: Colorado Department of Public Health and Environment, Denver, CO

Background: The use of culture-independent diagnostic tests (CIDTs), specifically multiplex PCR gastrointestinal panels for stool specimens is increasing rapidly. We summarize Colorado’s experience with the changing testing practices and the impact on surveillance for enteric pathogens.

Methods: Colorado regularly surveys clinical laboratories on the use of CIDTs and collects information about the type and brands of tests performed. Colorado encourages clinical laboratories to perform reflex culture for all bacterial enteric pathogens, and requires submission of isolates or clinical material for Salmonella, Shigella, Shiga toxin-producing E. coli (STEC), Vibrio and Yersinia. Two data sources were examined: a survey of clinical laboratories conducted during spring 2016 and surveillance data from 2014–2016.

Results: By spring 2016, 15 (of 50) clinical laboratories adopted multiplex PCR panels. Eight clinical laboratories perform reflex culture for Salmonella and Shigella, 2 for Campylobacter and STEC, 1 for Vibrio, and 0 for Yersinia. During 2014-2015, 16% (568/3623) of Campylobacter, Salmonella, Shigella, STEC, Vibrio, and Yersinia cases reported were tested using PCR. In 2016, the percent of cases tested using PCR for those same pathogens increased to 42% (1027/2454). Among cases detected by CIDTs in 2016, a reflex culture was attempted on approximately 74%. Only 20% of CIDT-positive Campylobacter had a reflex culture at a clinical laboratory, while over 90% of CIDT-positive Salmonella, Shigella, STEC and Vibrio had a reflex culture at either a clinical laboratory or the state public health laboratory. Among cases detected by CIDTs where a reflex culture was performed, isolate recovery ranged from 92% for Salmonella to 34% for Yersinia.

Conclusions: The percent of bacterial enteric infections detected by CIDTs is increasing. Although we encourage labs to perform reflex culture, a large burden falls to the SPHL. Outreach with hospitals, laboratories, and local public health partners has been key in addressing many of the challenges posed by the rapid adoption of CIDTs in Colorado.
P-074

Norovirus Outbreaks Leads to New Investigation Tools for Long Term Care Facilities

Authors: Amy Winchester, Donna Allen, Charles Clark, Christina Wheeler

Affiliation: Indiana State Department of Health

Background: Norovirus is a highly contagious gastrointestinal (GI) illness with the ability to cause outbreaks. In Indiana, outbreaks are commonly reported in institutional settings such as long term care facilities (LTCF). During the 2015-2016 norovirus season (August through July), 17 LTCs GI outbreaks were reported to Indiana State Department of Health (ISDH); during the 2016-2017 norovirus season, 81 LTCF GI illness outbreaks were reported. Additionally, a new strain of norovirus GII.4 was introduced in Indiana during the 2016-2017 norovirus season.

Methods: Outbreak incidents in LTCFs are reported to the ISDH Long Term Care Division to meet regulatory requirements and forwarded to the ISDH Infectious Disease Epidemiology (IDE) program for investigation. The LTCF outbreak investigation tools prioritized three tasks: communication of sanitizing precautions to the facility, collection and timely submission of three to five stool specimens for testing at the state laboratory, and submission of a line list to the IDE program. IDE field epidemiologists communicated the recommendations to LTCF staff and answered questions throughout the outbreak.

Results: During the 2016-2017 norovirus season, 81 LTCF GI illness outbreaks were reported to the ISDH and 28 (34.6%) had an etiology identified through laboratory testing. Eight specimens (9.8%) were rejected because they were received more than 5 days after collection or had insufficient patient information. Of the 81 outbreaks reported, 60 (74%) LTCFs submitted an outbreak line list. Of the 16 facilities that tested positive for the new GII.4 strain, 13 (81%) submitted an outbreak line list.

Conclusions: The new GII.4 norovirus strain is likely the reason for an increase in outbreaks throughout the state. The increase in outbreaks allowed the IDE program to identify areas of improvement within our outbreak response process. Based on feedback from the past norovirus season, a checklist of steps to take during a GI outbreak will be provided to LTCFs, including procedures to notify public health officials, collecting and submitting specimens for testing, and tracking symptoms of ill patients or staff. Instructions on submitting specimens might reduce the number of rejected specimens and can ease the transition to other LTCF staff during shifts change. With widespread use of the checklist, the IDE program seeks to increase the number of LTCFs that submit specimens for testing and increase the percentage of outbreaks that have confirmed etiology.
The Secrets to Improving Foodborne Outbreak Investigations at Local Health Jurisdictions: Public Health — Seattle and King County’s Experience

Author: Phil Wyman

Affiliation: Public Health — Seattle and King County, WA

Like many local health jurisdictions, Public Health – Seattle and King County’s (PHSKC) foodborne outbreak investigation efforts suffered from inadequately trained health investigators who were ready and competent able to respond to requests for foodborne illness investigations. An inadequate level of resources were dedicated for trainings and there were other misplaced competing priorities limiting our capacity to respond to outbreaks. Over the last four years in response to several high-profile outbreaks and increased scrutiny by the media, PHSKC developed a multi-disciplinary Foodborne Illness Investigation Team (FIIT). The FIIT is composed of Public Health Nurses, Epidemiologists, Environmental Health Investigators, and Public Information Officers. Having the team has significantly transformed how foodborne illnesses are investigated, documented and shared as necessary with the public. Focus has been put on providing a strong connection between all disciplines, especially during field investigations. We will describe how the FIIT functions and share the materials that have been developed to foster our collaborative team efforts and ways it has boosted confidence among our Environmental Health Investigators, improving the quality and consistency of our foodborne outbreak investigations.
The Clone Wars: WGS analysis of clonal Salmonella Newport PFGE patterns, Tennessee, 2015-2016

Authors: Jane Yackley¹, Lisha Constantine-Renna², Katie Garman², John Dunn²

Affiliations: ¹CSTE Applied Epidemiology Fellowship, ²Tennessee Department of Health

Background: Whole genome sequencing (WGS) has increased the ability to detect clusters of cases within clonal pulse field gel electrophoresis (PFGE) patterns. Salmonella Newport patterns JJPX01.0030 and JJPX01.0041 occur annually in Tennessee, however, common exposures are rarely identified. We used WGS to assess genetic relatedness within these clonal patterns and determine if subclusters for investigation could be retrospectively identified.

Methods: WGS of 2015 and 2016 Salmonella Newport patterns JJPX01.0030 and JJPX01.0041 was conducted using the Illumina MiSeq. High quality single nucleotide polymorphism (hqSNP) analysis was performed by CDC. WGS clusters were identified using SNP thresholds: <5, <10, and <25. The number, size, demographic commonalities, and reported exposures within clusters were compared, using temporal PFGE clusters as the reference.

Results: Pattern JJPX01.0030 (n=39) and JJPX01.0041 (n=24) isolates separated into two distinct clades. WGS identified up to 5 clusters of pattern JJPX01.0030 isolates depending on the SNP threshold, compared to 3 temporal clusters identified by PFGE. The largest pattern JJPX01.0030 cluster was identified using the <25 SNP threshold (27 cases), followed by PFGE (18 cases), and the <10 SNP threshold (5 cases). WGS identified up to 4 clusters of JJPX01.0041 isolates, compared to 2 by PFGE. The largest pattern JJPX01.0041 clusters identified by PFGE and WGS were 17 cases. For both patterns, only clusters of 2 were identified at the <5 SNP threshold. Some WGS clusters spanned both years.

Conclusions: This is the first analysis assessing genetic relatedness of Salmonella Newport cases from Tennessee using WGS. PFGE patterns JJPX01.0030 and JJPX01.0041 were distinct by WGS. The size of clusters identified decreased as the SNP threshold decreased. Analyses suggested that outbreaks were not undetected using PFGE, however, S. Newport strains persisted over multiple years supporting the environmental reservoir hypothesis. Determination of optimal SNP thresholds for S. Newport cluster identification will continue prospectively to detect and investigate outbreaks.
P-077

**Enterohemorrhagic *Escherichia Coli* O157 outbreak among residents of a high school dormitory and community acquired sporadic case of multi-prefecture in August–September 2013, in Japan**

Authors: Yuichiro Yahata¹, Fumie Ando², Kunio Kawabata¹,³, Masami Nagira⁴, Tomimasa Sunagawa¹, Tamano Matsui¹, Hidemasa Izumiya¹, Makoto Ohnishi³, Kazunori Oishi³

Affiliations: ¹National Institute of Infectious Diseases, Japan, ²Naha City Public Health Center, ³Hiroshima Prefectural Government Office, ⁴Shimane Prefectural Institute of Public Health

**Background:** On August 26 2015, six students developed at least one gastrointestinal illness such as diarrhea, bloody stool or abdominal cramps in a high school. All cases lived in a high school dormitory. A local public health center and FETP conducted the outbreak investigation.

**Methods:** The investigation conducted retrospective cohort study, trace-back investigation and environmental study. We collected the information for consumed foods, visited place, participated event, and behavioral information of the dormitory from student and sporadic case of O157 in the city level which included outside of the prefecture.

**Results:** Total number of residents of student was 117 in the dormitory (male: 105; female: 12). Confirmed case was 35 cases (30%), suspected case was 27 cases (23%) and asymptomatic case was 35 cases (30%) among 117 students. Some cases complained that Okonomi-yaki (Japanese food; thin and flat pancake cooked on a hot plate with bits of meat, seafood and cabbages) was partially-cooked. Okonomi-yaki was baked by steam convection oven. Meat loaf was also cooked by steam convection oven during August 20–24.

A lot of meal time at the dormitory was significantly associated with O157 infection among suspected exposed period in August 20–24. The risk of O157 infection was significantly associated with consumed meat loaf (relative risk [RR]=4.16, p=0.020) and Okonomi-yaki (RR=4.1, p=0.001).

Community acquired sporadic O157 case was six cases who was from three prefectures. Of six cases, five cases consumed beef. According to trace-back investigation, the beef was distributed by same meat processing company.

Both student cases and community acquired cases were same type of multiple-locus variable tandem repeat analysis.

**Conclusion:** We concluded that the O157 outbreak was caused by contaminated partially-cooked meat loaf.
Salmonella Serotype Prediction from Whole Genome Sequencing Data in California Using SeqSero Pipeline

Authors: Varvara Kozyreva¹, Shaokang Zhang², John Crandall¹, Adam Smith¹, Fengfeng Xu¹, Xiangyu Deng², Vishnu Chaturvedi²

Affiliations: ¹Microbial Diseases Laboratory, California Dept. of Public Health, Richmond, CA; ²Center for Food Safety, University of Georgia, Athens, GA

Background: Serotyping has been a gold standard for the Salmonella classification and outbreaks tracking for over a half century. Whole Genome Sequencing (WGS) is being widely introduced for Salmonella genotyping and it is an attractive option to use the same genomic data for in silico serotype prediction.

Methods: Total of 213 clinical Salmonella enterica isolates from California isolated between 2014-2015 were selected. Serotyping was performed using standard technique with in-house Salmonella monoclonal and polyclonal antisera. The WGS was performed using Nextera XT library preparation with 2x300 bp sequencing chemistry on the Illumina MiSeq sequencer. SeqSero pipeline v.1.0 (http://denglab.info/SeqSero) was used for the serotype prediction from raw reads. For phylogenetic analysis, genomes were firstly assembled using SPAdes, and the draft genomes were aligned using Parsnp. Core genome SNPs were then identified to build a Maximum Likelihood tree.

Results: In the dataset, 147 serotypes were identified by traditional serotyping. Average coverage of generated genomes was 41x (9x-101x). Isolates in 63% of the cases had complete antigenic formula unambiguously identifying a single serotype which matched the traditional serotyping results. In other 28% of the cases the serotype prediction was correct but due to the shared antigenic formula resulted in two alternative serotypes. Six percent of the isolates possessed genes of the antigenic determinants which did not express; in the majority of those instances the fidelity of the SeqSero prediction was confirmed by phylogenetic clustering with the genomes of the corresponding serotypes. In total, 97% of the serotypes were successfully predicted from WGS data using SeqSero tool. In the remaining 3% of the isolates disagreement in conventional and in silico serotypes was caused by missing antigenic determinants in the predicted formula.

Conclusions: Salmonella serotypes were predicted with high confidence from WGS data. This approach presents great potential for an integrated work flow in the public health laboratories.
Implementation of the enhanced laboratory capacity for foodborne outbreak investigations at the California Department of Public Health Microbial Diseases Laboratory

Authors: Danya Alvarez; Francine Arroyo; Hillary Berman-Watson; Anthony Bermudez; Sherry Chou; John Crandall; Christine Hatch; Beverly Kaneko; Chun Kim; Zhirong Li; Rituparna Mukhopadhyay; Robert Nakamura; Marice Shiozaki; Matthew Sylvester; Jennifer Tanka; Kelly Trinh; Linda Troung; Yueqing Zhao; Gregory Inami; Varvara Kozyreva; Stephanie Abromaitis; Vishnu Chaturvedi

Background: The California Department of Public Health Microbial Diseases Laboratory (MDL) provides enteric bacteria testing to support Local Public Health Laboratories throughout California and is an active member of the PulseNet Network. MDL performs PFGE on Salmonella, Listeria, STEC, and Shigella. In the last two years, MDL faced the challenge of incorporating whole genome sequencing (WGS) into the laboratory’s routine workflow for disease surveillance and outbreak investigation. MDL developed unique strategies and a tiered goal setting approach to implement WGS and meet the demand for better surveillance through advanced molecular detection (AMD).

Methods: MDL isolates and identifies enteric bacteria using traditional biochemical techniques, proteomic analysis, and molecular typing. As a PulseNet laboratory, MDL performs molecular typing of bacteria using PFGE, MLVA, and WGS. MDL developed a structure for isolate transfer between laboratories and rapid communication with epidemiologist and external partners. A systematic approach was taken for the laboratory implementation of WGS including training for laboratorians and epidemiologists, CLIA-compliant validation, and testing prioritization.

Results: In 2016, MDL received over 6,800 specimens and isolates for identification and characterization. PFGE was performed on 3,838 bacterial isolates and MLVA was completed for 365. MDL also validated WGS for bacterial pathogens as a CLIA-compliant LDT. So far, MDL sequenced over 1,300 isolates, implemented L. monocytogenes universal WGS for 116 isolates, and uploaded all sequenced genomes to the national databases. A combination of PFGE, WGS and epidemiological data were successfully used to inform testing choices and workflow.

Conclusion: MDL has advanced the implementation of CDC recommended AMD approaches for foodborne diseases while maintaining standard laboratory services. The new multiphasic testing methodology with expanded genotyping, has contributed to improved outbreak investigations and collaborations among key stakeholders.
Summary of National Botulism and Enteric Toxins Team Sequencing Activities and Future Direction

Authors: Jessica Halpin, Janet Dykes, Carolina Luquez

Affiliation: Enteric Diseases Laboratory Branch, Centers for Disease Control and Prevention

Background: The National Botulism and Enteric Toxins Team at CDC has been using short read shotgun sequencing of Clostridium botulinum regularly for surveillance and research since the acquisition of an Ion Torrent PGM instrument in late 2014. Whole genome sequence data has provided a comprehensive and rapid method of analysis of these strains, including toxin gene type and subtype as well as phylogenetic relationships between C. botulinum strains isolated from implicated foods and clinical specimens.

Methods: Standard microbiological methods were employed to identify isolates and a combination of PCR and ELISA or the mouse bioassay determined toxin type prior to each isolate entering the historical inventory. We extracted genomic DNA from a fresh TPGY culture using a method based on the Epicentre MasterPure Complete DNA and RNA Purification Kit and 200 bp (prior to Dec 2016) or 400bp libraries were constructed with Kapa Biosciences fragmentation and library kits. The Ion Chef automated system templated and enriched libraries and loaded chips for sequencing on the Ion Torrent system. Sequence data was subjected to quality control (FastQC v.0.11.5), assembled using SPAdes v3.1.0 (-k 21,33,55,77,99), and assemblies evaluated with Quast v4.3. CLC Genomic Workbench v.9.5.2 “Map reads to reference” feature identified the toxin genes within each sequence and determined their subtype.

Results: Over the course of the last three years, we improved sequence and assembly quality and increased the number of isolates sequenced per year. Two or more isolates per specimen are usually sequenced, resulting in an internal quality control check as well as providing data on the diversity of strains found within single specimens. We have used whole genome sequence data and high quality single nucleotide polymorphism analysis in the course of several outbreak investigations to strengthen the epidemiological hypothesis.

Conclusions: Here we present an overview of isolates sequenced, projects completed, challenges faced, and future directions for the technology both within our group and with our external partners. Among other future endeavors, we are developing a wgMLST database for C. botulinum in partnership with PulseNet and Applied Maths.
High quality SNP-typing (hqSNPs): Quality assurance and troubleshooting of analyses

Authors: Gladney, L.M.1,2, Katz, L.S.1,3, Griswold, T.1, Wagner, D.1,2, Schroeder, M.1, Carleton, H.A.1

Affiliations: 1Enteric Diseases Laboratory Branch, Centers for Disease Control and Prevention, Atlanta, GA, 2IHRC, Inc., Atlanta, GA, 3Center for Food Safety, University of Georgia, Griffin, GA

Background: PulseNet conducts surveillance of potential outbreak clusters that occur in the states using a variety of subtyping approaches, including whole genome sequencing (WGS). To link cases that are likely to have shared a common exposure, such as a contaminated food product, high-level resolution using WGS is often needed. One way to achieve this is using a high quality single nucleotide polymorphism (hqSNP) typing pipeline such as Lyve-SET. Lyve-SET ties together multiple tools for read processing, read mapping, variant calling and tree-building. We identified and evaluated quality metrics that can be interpreted for quality assurance and troubleshooting of SNP analyses.

Methods: We focused on a single outbreak containing 14 isolates of Escherichia coli serotype O157:H7 to better understand SNP results in scenarios where WGS quality is compromised. Samples that were contaminated or incorrectly identified were also included as part of the study. Read-processing and SNP analyses were performed with Lyve-SET version 1.1.4f. Read mapping metrics were calculated with Samtools version 1.4.1 and CLCBio Genomics Workbench version 10. Mega version 5 was used to visualize the alignments and trees.

Results: Metrics identified that could alert potential problems in the analyses included genome coverage (43-165x, average 77x), insert size (60-969 bp, average 353 bp), percent reads mapped (89-92%, average 91%) and percent reads properly paired (74-80%, average 76%); these examine the quality of the mapping step. The number of ambiguous bases (N’s) or sites masked for each isolate in the analysis is reported by Lyve-SET and also addresses the mapping quality as a whole. Even with passing coverage and quality (Q) scores, the bases are masked at a high percent for most samples (12-57%). This results in more N’s in the alignment which leads to fewer informative bases and less resolution in the tree.

Conclusion: The metrics we identified will help ensure quality SNP data is used for surveillance analysis and may even improve concordance with other data types such as epidemiological data. These quality metrics identified issues with the WGS data that were not detected by using coverage or read quality cutoffs alone.
Development of a BioNumerics Database for Whole Genome Sequence (WGS) Quality Assessment and Identification of Enteric Bacteria with Average Nucleotide Identity using MUMmer

Authors: R. L. Lindsey¹, G. Williams², T. Griswold¹, A.C. Lauer¹, A. Huang¹, J. Pruckler², L. S. Katz¹, M. Santovenia¹, Z. Kucerova¹, H. Pouseele², C. Tarr¹, P. Gerner-Smidt¹, H. Carleton¹

Affiliations: Enteric Diseases Laboratory Branch, Centers for Disease Control and Prevention (EDLB), Atlanta, GA¹, Applied Maths, Inc., Belgium²

Conventional phenotypic and genotypic methods used to identify enteric bacteria, including *Campylobacter*, *Escherichia*, *Listeria*, *Salmonella* and *Vibrio*, are labor-intensive, expensive, and require multiple workflows. We are developing an Enteric Reference Identification (RefID) database using the PulseNet BioNumerics infrastructure to check WGS quality and to identify these enteric bacterial species in a single workflow.

The workflow for the RefID database is basic quality assessment, assembly, and bacterial identification through Average Nucleotide Identity using MUMmer (ANIm). Sequence coverage, average read quality, and contamination status (with Kraken) will be assessed. Quality metric thresholds, including expected genome size, must be met for each sequence before further analysis is initiated. Reference identification is performed by determining the percent coverage and percent identity of genomic regions shared by two bacterial strains. ANIm in RefID compares query sequences to reference sequences from a custom database, comprised of six *Campylobacter* spp., three *Escherichia* spp., six *Listeria* spp., two *Salmonella* spp. and six *Vibrio* spp. genomes.

A total of 564 validation strains, selected based on the taxonomic diversity of our target organisms and the frequency of receipt in EDLB, were used to assess the ANIm-based identification. ANIm showed identities of ≥95% for *Escherichia/Shigella* and *Vibrio* species, ≥93% for *Salmonella* species, and ≥92% for *Campylobacter* and *Listeria* species.

This RefID database will provide a single, unified approach for initial quality assessment and accurate species identification. Through continued collaboration with domestic and international partners, we will continue to test and expand identification to additional species within the next year.
A Whole Genome Multi-Locus Sequence Typing (wgMLST) workflow for Reference Characterization, Surveillance, and Outbreak Detection of Shiga Toxin-Producing *Escherichia coli* (STEC) in the United States using BioNumerics

Authors: R. Wirth¹, M. Schroeder¹, H. Pouseele², E. Trees¹, N. Strockbine¹, E. M. Ribot¹, P. Gerner-Smidt¹, H. Carleton¹

Affiliations: Enteric Diseases Laboratory Branch, Centers for Disease Control and Prevention, Atlanta, GA³, Applied Maths NV, Belgium²

**Shiga toxin-producing *Escherichia coli* (STEC)** is an important foodborne pathogen capable of causing mild to severe disease in humans. The Enteric Diseases Laboratory Branch is working to replace traditional characterization methods with those using whole genome sequence (WGS) data in BioNumerics (Applied Maths, Austin, TX). This will allow outbreak detection and reference characterization of STEC in a single workflow using whole genome multi-locus sequence typing (wgMLST), *in silico* PCR, and BLAST based gene identification.

A set of 325 reference and 152 outbreak sequences were analyzed. The STEC outbreak sequences were also characterized with high quality single nucleotide polymorphism (hqSNP) analysis using the LYVE-SET pipeline v1.1.4f (github.com/lskatz/lyve-SET). Results were compared to validate the ability of the BioNumerics-based approach to correctly cluster outbreak isolates by wgMLST. The *E. coli* genotyping plugin detects genes encoding virulence factors, antimicrobial resistance and O and H antigens from databases at the Center for Genomic Epidemiology (http://genomicepidemiology.org). The genotyping plugin contains *in silico* PCR capabilities to confirm virulence prediction results and to assist in pathotype prediction from WGS data.

Whole genome MLST using the BioNumerics clustered surveillance isolates by the outbreak and in concordance with hqSNP data. Of the 325 reference isolates, the genotyper plugin was in 100% concordance with conventional typing methods for virulence, serotype and pathotype.

The BioNumerics-based WGS approach provides a single, cost effective strategy to identify and characterize isolates for outbreak detection and surveillance. The tool is expected to be made available to the PulseNet participants early in 2018.
Evaluation of Illumina’s MiniSeq Sequencing Platform

Authors: Angela Poates, Ashley Sabol, Eija Trees

Affiliation: PulseNet USA, CDC, Atlanta, GA

**Background:** PulseNet Central supports implementation of whole genome sequencing (WGS) for foodborne disease surveillance and outbreak detection by providing validated and standardized protocols to a vast array of laboratories with different needs and testing throughputs. New technologies and chemistries that may meet the needs of these laboratories are continuously evaluated. Currently, the Illumina MiSeq is the most widely used WGS platform within the network. Recently Illumina released the MiniSeq, which utilizes a two-channel chemistry, and has a lower price point and shorter run times than the MiSeq. Here we present the preliminary results for the validation of the MiniSeq and data comparison against the MiSeq.

**Methods:** For the initial validation phase, 25 *Escherichia coli* isolates (6 serogroups) previously sequenced on the MiSeq, were sequenced on the MiniSeq. A second subset of 7 *E. coli* isolates (2 serogroups) whose genetic relationships belong to the “gray zone” (10-20 SNPs) was also sequenced. CG-Pipeline was used for read quality checks and cleaning (github.com/lskatz/CG-Pipeline). High quality single nucleotide polymorphism (hqSNP) analysis was performed using the Lyve-SET pipeline version 1.1.4f (github.com/lskatz/lyve-SET) with appropriate external reference genomes. Phylogenetic trees and hqSNP matrices were created to evaluate the correlation of the data generated by the two platforms.

**Results:** Preliminary results indicate that the data generated by the MiniSeq is of comparable quality to that generated by the MiSeq. HqSNP analysis reveals no greater than a 1 SNP difference between MiSeq and MiniSeq sequences. Phylogenetic trees and matrices generated from MiniSeq data appear to be concordant with those generated using data acquired on the MiSeq.

**Conclusions:** The MiniSeq would be advantageous to laboratories with a smaller budget, and ideal for laboratories with either a low or a medium throughput. However, there is some concern that shorter read length chemistry will lead to missing allele calls in whole genome multi-locus sequence typing (wgMLST) analysis particularly in complex genomes such as *E. coli*. Future goals include sequencing additional isolates of other PulseNet organisms and performing wgMLST analysis.
Sequencing all *Salmonella* on a NextSeq: Cost, Turn-Around Time, and Additional Quality Assurance

Authors: S.E. Wirth, D.J. Baker, N. Boucher, A.E. Cukrovany, M.C. Dickinson, E. Lasek-Nesselquist, P. Lapierre, M. Palumbo, M. Shudt, L. Thompson, J. Williams, P. VanRoey, N. Dumas, K.A. Musser, L. Mingle, and W.J. Wolfgang

Affiliation: Wadsworth Center, NYSDOH, Albany, NY USA

**Background:** CDC provided funding for PulseNet labs to sequence all *Salmonella*. The Wadsworth Center implemented Illumina NextSeq sequencing as a way to increase capacity (80 samples per run) and decrease sequencing costs ($60 savings per sample) for sequencing the approximate 1600 *Salmonella* isolates per year.

**Methods:** All *Salmonella* isolates are first analyzed by PFGE and a serotype determination is made based on PFGE pattern, or if necessary, conventional serotyping. Weekly, WGS IDs are requested and DNA is extracted using a QIAcube and quantified with a Qubit. Once 80 samples have been collected, they are diluted into 96-well plates, transferred to our core sequencing facility where libraries are prepared and the samples are sequenced. The Q30 score of the run and the depth per sample are determined. Samples that fail QC are re-sequenced on a MiSeq. The sequence files are downloaded from BaseSpace to a local server where they are processed through the SeqSero pipeline. The SeqSero-inferred serotype is then compared to the previously ascertained serotype as a verification step. Once all quality assurance is complete, sequence files are shared with CDC.

**Results:** Depending on seasonal volume, the Wadsworth Center completes 1-3 NextSeq runs per month. At 1,600 samples/year, sequencing using the NextSeq is projected to save $96,000 annually. Batching has resulted in an increased median turn-around time (TAT) for the NextSeq compared to MiSeq, 14-43 and 9 days respectively. To date, only 2% of samples failed sequencing quality metrics.

**Conclusion:** The NextSeq enables higher sequencing throughput for *Salmonella* at a 33% decreased cost without sacrificing sequence quality, however, TAT is increased. The NextSeq is a valuable resource that can enable public health labs to economically sequence large numbers of bacterial samples.
Using SeqSero to infer Salmonella serotypes during routine PulseNet surveillance in New York

Authors: Samantha Wirth1,3, Oneida Shushe2,3, Michelle Dickinson1, Deborah Baker1, Lisa Thompson1 Ashley Cukrovany1, Michael Palumbo1, Patrick VanRoey1, Nellie Dumas1, Kimberlee Musser1, Pascal Lapierre1, Erica Lasek-Nesselquist1, William J. Wolfgang1, Lisa Mingle1

Affiliations: 1Wadsworth Center NYSDOH Albany, NY; 2Colgate University Hamilton, NY; 3These authors contributed equally to this work.

Background: The Wadsworth Center is in the process of transitioning Salmonella surveillance from Pulsed Field Gel Electrophoresis (PFGE) determined serotype to whole-genome sequencing (WGS) determined serotype. Serotype result will continue to be an important characteristic to transmit to our partners once other typing technologies have been supplanted by WGS. The SeqSero software offers a means to infer serotype from raw reads. To determine the utility of this approach we have performed a prospective study comparing SeqSero analysis with our standard serotyping methods.

Methods: SeqSero was used to infer the serotype from 720 Salmonella samples collected since January of 2017 during our routine PulseNet activities. The raw reads were analyzed in house through the command line version 1 of SeqSero. The output was then compared to our standard methods for serotyping, a combination of PFGE determined serotype and conventional serotyping.

Results: In general, we observed 78% concordance between SeqSero and our standard methods. The following discrepant results were observed. In 13% of samples SeqSero was unable to infer a single serotype, and two serotypes were called. In most of these cases, but not all, one of the two was concordant with the serotype called by our standard methods. For 4% of our samples, our standard method yielded an I 4,[5],12:i:- serotype formula, while SeqSero called the serotype Tumodi. Interestingly, when these reads were run through the SeqSero web based portal instead of the command line version 1 of SeqSero, a concordant serotype call was achieved. We also observed in 1% of cases that SeqSero produced no typing information. In rare circumstances, SeqSero analysis inferred a single discordant serotype. Finally, SeqSero called a serotype for some samples when our standard methods failed.

Conclusion: SeqSero produces a WGS determined serotype that for the most part is concordant with serotyping results produced by our standard methods. Nonetheless discrepancies are observed in this dataset. The basis and frequency of these differences will need further examination in order to understand the limitations of SeqSero-based serotype determination as we move into the genomic age.
Using a SharePoint Site to Communicate Laboratory and Epidemiologic Information on Whole Genome Sequencing of Enteric Pathogens: The New York State Department of Health Experience


Affiliation: New York Department of Health, Albany, NY

Background: Results from whole genome sequencing (WGS) have been communicated between laboratorians and epidemiologists over the past four years within the New York State Department of Health (NYSDOH).

Methods: Information communicated is specific to surveillance and cluster detection for enteric organisms. Results of WGS cluster analysis were initially shared via email and in word documents, but have evolved to uploading surveillance and cluster information into a SharePoint site that is accessible to both laboratorians and epidemiologists. Data, text descriptions, and images (i.e phylogenetic trees) are included on the site. In addition to patient metadata associated with each isolate of interest, the site shows the epidemiological rationale for the sequencing request, the laboratory analysis and interpretation of the WGS data, and the epidemiological outcome.

Results and Discussion: The SharePoint site has become an efficient and flexible conduit for communicating between laboratorians and epidemiologists resulting in a simpler workflow, which may serve as a best practice by other agencies.
Application of Whole Genome Sequencing to an Outbreak of \textit{E. coli} O157:H7 in a Rural Community in Utah and Arizona

Authors: Kelly F. Oakeson, Jennifer Marie Wagner, Erik Poole, Lori Smith and Robyn Atkinson-Dunn

Affiliation: Utah Public Health Laboratory

\textbf{Background}: Shiga toxin producing \textit{Escherichia coli} subtypes, including \textit{Escherichia coli} O157:H7 are responsible for an estimated 265,000 infections and 30 deaths annually in the United States according to the Centers for Disease Control and Prevention. In July of 2017, the Utah Department of Health and Utah Public Health Laboratory (UPHL) identified a cluster of \textit{E. coli} O157:H7. During the course of the investigation, UPHL applied whole genome sequencing and molecular phylogenetic analysis to patient and environmental samples to aid in the investigation, to help identify the source of the outbreak, and to help prevent further illness.

\textbf{Methods}: The Utah Public Health Laboratory performed whole genome sequencing, bioinformatic analysis, and molecular phylogenetics on 15 confirmed \textit{E. coli} O157:H7 isolates linked to the outbreak, including 11 patient isolates and 4 environmental isolates (horse and bull manure). Bioinformatic and phylogenetic analyses were all performed using an analysis pipeline developed by UPHL (reference).

\textbf{Results}: All 15 of the patient and environmental isolates form a single monophyletic clade with short branch lengths and high statistical support. This indicates all the isolates are highly related and share a common molecular evolutionary history lending evidence to the conclusion that exposure to animal manure may have been a potential source of infection.

\textbf{Conclusions}: The methods used during this outbreak provided the phylogenetic relationships of isolates as well as provided near complete genotypic information for each isolate in near real time. Additionally, the information generated by WGS could be further exploited to gain insights into virulence factors that may present in the outbreak associated isolates. This work demonstrates how WGS can be applied in near real time to an ongoing outbreak and highlights the benefits of WGS and advanced bioinformatic analyses for outbreak investigations.
P-089

Whole Genome Sequencing and Bioinformatic Analysis of Two Foodborne Illness Outbreaks: Campylobacter jejuni and Salmonella enterica

Authors: Kelly F. Oakeson, Jennifer Marie Wagner, Andreas Rohrwasser and Robyn Atkinson-Dunn

Affiliation: Utah Public Health Laboratory

Background: Whole genome sequencing (WGS) is rapidly becoming a powerful tool for determining the relatedness of bacterial isolates in foodborne illness detection and outbreak investigation. WGS has been applied to large national outbreaks and surveillance, however, WGS has rarely been used in smaller local outbreaks. This work describes the retrospective application of reference free whole genome sequencing and bioinformatic analysis to a local outbreak of Campylobacter jejuni associated with raw milk.

Methods: UPHL performed retrospective whole genome sequencing and bioinformatic analysis, including phylogenetic analysis, on 61 isolates from confirmed cases with an additional 18 isolates obtained from bulk raw milk storage tanks and packaged raw milk from the suspect dairy display case.

Results: Sixty-one of the patient isolates and 14 of the raw milk isolates form a single clade with extremely short branch lengths with high statistical support, 100% bootstrap support, indicating close phylogenetic relatedness. The analysis shows that all of the isolates involved in the outbreak are phylogenetically related indicated by short branch lengths.

Conclusions: The genomic approaches of the current study can provide true phylogenetic relationships of isolates as well as provide near complete genotypic information for each isolate. A significant benefit of the bioinformatic analysis developed is that a reference genome sequence is not needed. The genotypic information generated by WGS could be further exploited to gain insights into virulence factors that may present in the outbreak associated isolates or to determine antibiotic resistance in these isolates. The bioinformatic analysis workflow described in this work has the ability to provide near complete information of the genotype of the isolates analyze.
P-090

Specialized Workflow for Whole Genome Sequencing Analysis at the Virginia Division of Consolidated Laboratory Services

Authors: Tannor, F.; Levesque, S.; Dela Cruz, S.; Turner, L.

Affiliation: Virginia Division of Consolidated Laboratory Services

Background: The Virginia Division of Consolidated Laboratory Services (DCLS) is the PulseNet Area Laboratory for the Mid-Atlantic Region and performs Whole Genome Sequencing (WGS) analysis on Virginia clinical, environmental and food isolates and isolates from Mid-Atlantic State labs upon request. DCLS is a pilot site for the BioNumerics 7.6 wgMLST analysis software for Listeria monocytogenes and earned PulseNet Certification for Listeria monocytogenes wgMLST Analysis in 2016. The addition of WGS testing required the development of a specialized workflow to ensure continuity of existing laboratory testing with existing personnel resources.

Methods: An analysis was conducted of the processes necessary for WGS at DCLS and the WGS workflow was divided into five procedural components including (i) isolate tracking, (ii) extraction, (iii) sequencing, (iv) quality assurance, and (v) analysis. Process management solutions were identified to support these components including shared spreadsheets, distribution lists and controlled documents guiding the implementation of each functional step. Listeria monocytogenes testing and analysis were used as a model to assess the timeliness of each procedural component in the WGS workflow because PFGE and WGS are performed concurrently at DCLS for this organism.

Results: Through a process review, it was determined that the real-time testing turnaround time for Listeria monocytogenes WGS averaged eight days, from isolate receipt to uploading of the wgMLST profile to the Listeria National Database. The workflow analysis showed the turnaround time may be reduced to five days for an optimal sample.

Conclusions: DCLS’ implementation of WGS in real-time required the identification of new procedural controls and well defined procedural components. These strategies have allowed for effective use of existing personnel resources and provided a framework for the future implementation of WGS real-time testing for additional organisms as analysis databases are made available.
Seq_ID: A Bioinformatics Pipeline for Taxonomic Label Verification of WGS Data

Authors: Libuit, K.G.¹, Turner, S.², Nassiri, A.¹, Turner, L.¹

Affiliations: ¹Division of Consolidated Laboratory Services, Richmond, VA, ²University of Virginia, Charlottesville, VA

Background: The Division of Consolidated Laboratory Services (DCLS), Virginia’s Public Health Laboratory, submits whole genome sequencing (WGS) data to public health partners and National data repositories. These data contribute to the surveillance of infectious diseases on a national scale. Critical to these initiatives is the assurance that sample identifiers, metadata, and taxonomic labels (i.e. species and serotypes) are associated with the appropriate read files. For quality control purposes, DCLS developed Seq_ID, a bioinformatics pipeline that incorporates well established, peer-reviewed bioinformatics tools to perform in silico taxonomic label verification of WGS data.

Methods: Seq_ID was written in a combination of BASH and Makefile. The pipeline can be executed on any LINUX OS distribution (development and validation was performed on Ubuntu 14.04).

An anonymized dataset of 314 isolates (110 Shiga toxin-producing Escherichia coli (STEC), 53 Listeria spp., 121 Salmonella spp., and 30 Shigella spp.) was analyzed using the Seq_ID pipeline. Results were compared to reference taxonomic identifications previously determined through conventional biochemical, serology and/or molecular serotyping results. The performance of Seq_ID was gauged on accuracy with respect to references and reproducibility amongst technical replicates. Time of analysis (run time) was also tracked for determination of practicality in implementation.

Results: Seq_ID results aligned with molecular subtyping results for 310 of the 314 isolates analyzed (98% accuracy). Zero variance was observed in Seq_ID output amongst all technical replicates. On an Amazon Web Services EC2 m4.4xlarge image (16vCPU, 53.5 ECU, 64GiB memory), the runtime of Seq_ID averaged 12 min/sample.

Conclusions: These results suggest that Seq_ID is an accurate, reliable, and efficient quality assurance tool that can be used to verify taxonomic labels associated with WGS data. Routine use of Seq_ID will strengthen the confidence of DCLS results shared with national partners and published in data repositories.
P-092

Use of wgMLST Schemes for Typing and Clustering Foodborne Bacterial Pathogens in the NCBI Pathogen Detection Pipeline

Authors: William Klimke, Richa Agarwala, Mike DiCuccio, Lewis Geer, Lianyi Han, Avi Kimchi, Michael Kimelman, Valerii Lashmanov, Eyal Mozes, Oleg Shutov, Alexandre Souvorov, Eugene Yaschenko, Alex Zasypkin, Jim Ostell

Affiliation: NIH/NLM/NCBI

Background: The NCBI Pathogen Detection (PD) system was built to aid the analysis of foodborne (Campylobacter, E. coli/Shigella, Listeria, Salmonella) pathogen genome sequences for outbreak and traceback investigation. A total of 132,343 genomes have been processed in the first four years that the pipeline has been operational, with the number of sequences expected to increase. NCBI has made improvements to the processing time by using whole genome multi locus sequence typing (wgMLST).

Methods: NCBI has developed a new and fast de-novo assembler (SKESA). After assembly with SKESA, wgMLST schemes were generated: genes were called using Prodigal and reference allele propagation and alignment to each other, and loci selected. For Salmonella and Listeria, 60,840 and 12,771 genomes were used, resulting in 13,362 and 4,992 loci, respectively, in the scheme. For new incoming isolates, wgMLST allele differences are used for a nearest neighbor analysis, as well as for clustering of isolates prior to SNP processing.

Results: A pilot phase project with FDA-CFSAN Salmonella and Listeria sequences was initiated with the aim to have a table of nearest neighbors produced within one hour of submission. The project has been running for one month, with 162 submissions of Listeria and 772 of Salmonella: 442 were reported in less than one hour of submission, 83 were not reported due to technical reasons, and the rest took longer than an hour. Use of wgMLST distances as input to the SNP pipeline during preliminary testing have showed that at least an order of magnitude decrease in processing time.

Conclusions: Development of wgMLST schemes aids analytical processing of foodborne bacterial pathogens by SNP analysis, and results in rapid reports to get at the fundamental answers that are needed for outbreak and traceback investigations: is this newly sequenced isolate clonally related to any other isolate in the database, is there a point source for clinical illnesses?
P-093

The Rapid Response Team’s Role in the 2015 *Salmonella Oranienburg* Outbreak in Missouri

Author: Mark Buxton

Affiliation: Missouri Department of Health and Senior Services

**Background:** A sporadic outbreak of *Salmonella Oranienburg* began in April, 2015 and stretched into November, 2015. The investigation presented challenges due to the temporal distribution of cases and the lack of common exposures. Although cases were linked to a few restaurants in the same chain, other cases were linked to groceries and different restaurants from different franchises. Jurisdictional issues also added complexity.

**Methods:** State and federal agencies activated the Missouri Rapid Response Team for food and feed (MRRT) to enhance communications, commit resources, bridge jurisdictional issues and prioritize resolution of the outbreak. Multiple agencies, epidemiologists, environmental public health and laboratory partners combined their expertise into a single team. Environmental health specialists and epidemiologists traced products, sampled and tested potential sources.

**Results:** Epidemiologists and environmental public health specialists found the vehicle causing the outbreak and traced the product back to the firm where the organism originated. Pulsed-field gel electrophoresis (PFGE) and Whole Genome Sequencing (WGS) further supported links between cases, the food vehicle and the firm at the source of the outbreak. Products were embargoed from sale. The firm and investigative partners collaborated to address production concerns and end the outbreak.

**Conclusion:** The MRRT enhanced communications, helped resolve jurisdictional issues and committed multiple resources to solve a complex outbreak.
P-094
The impact of whole genome sequencing on the epidemiological investigation of national foodborne illness outbreaks due to *Salmonella* and *Listeria*: the changing landscape in Canada

Authors: Jennifer Cutler, Joyce Cheng, Mihaela Gheorghe, Elizabeth Hillyer, Rima Kandar, Ashley Kerr, M. Kate Thomas

**Background:** In 2017, Canada began prospective whole genome sequencing (WGS) for *Salmonella* and *Listeria monocytogenes* (LM). Prior to this, clusters were assessed based on serotype and/or pulsed field gel electrophoresis (PFGE) pattern. The change in laboratory methodology has impacted the investigation of foodborne illness outbreaks by public health epidemiologists in Canada.

**Methods:** WGS clusters are identified by the national laboratory and reviewed with federal epidemiologists. Clusters are then prioritized for investigation to determine the source of the illnesses.

**Results:** The number of multijurisdictional *Salmonella* clusters has increased, with 82 identified in the first four months. This has increased the time spent by federal epidemiologists assessing and prioritizing clusters, and increased the number of requests for epidemiological information to provincial and territorial partners. Exposure information highlighted the burden of infections associated with travel and with chicken. Thirty-two percent of cluster isolates are likely associated with travel to Mexico and the Caribbean. A further 41% of cluster isolates are likely associated with chicken. The increased discriminatory power of WGS has been beneficial for LM. Only three multijurisdictional LM clusters were identified in eight months of implementation, sparing resources spent investigating what would otherwise be common (often unrelated) PFGE patterns.

**Conclusions:** Implementation of WGS has changed the landscape of foodborne illness outbreaks in Canada, decreasing the number of national LM investigations, and increasing the number of *Salmonella* investigations, most notable in common serotypes. It has demonstrated the disproportionate burden of travel and chicken on reported salmonellosis in Canada. The experience during the first few months has challenged epidemiologists to consider new investigative approaches, enhancing collaboration among federal and provincial/territorial epidemiologists and laboratory colleagues to improve the detection and response to foodborne illness outbreaks in Canada.
On-site Detection and Characterization of *Salmonella* from Environmental Samples

Authors: Tamar Dickerson\(^1\), Joseph Russell\(^1\), Elizabeth Reed\(^2\), Christina Ferreira\(^2\), Joseph Baugher\(^2\), Guojie Cao\(^2\), Rachel Pfuntner\(^3\), Laura Truitt\(^3\), Laura K. Strawn\(^3\), Steven L. Rideout\(^3\), Rebecca Bell\(^2\), Marc Allard\(^2\), Eric Brown\(^2\), Jonathan Jacobs\(^1\)

Affiliations: \(^1\)MRIGlobal, Division of Global Health Surveillance & Diagnostics, Gaithersburg, MD; \(^2\)Office of Regulatory Science, Center for Food Safety & Applied Nutrition, US Food & Drug Administration, College Park, MD; \(^3\)Food Science and Technology Department, Virginia Tech — Eastern Shore Agricultural Research & Extension Center, Painter, VA

Abstract: Field-ready methods for on-site, rapid detection and characterization of *Salmonella* directly from food and/or environmental samples could have a significant impact on both the economic impact of food borne illnesses and reduce the sample-to-answer turn-around times typical for current surveillance efforts. To address this challenge, we demonstrated the use of field-based protocols and systems such as the Biomeme two3 qPCR system and Oxford Nanopore Technologies MinION sequencing platform for on-site detection and sequence-based characterization of *Salmonella* in soil, water and sediment. The goals of this study were to assess the ability to rapidly test field samples and strain-type *Salmonella* in under 24 hours. Field collected samples originating from the Delaware State Aquatic Resources Education (ARE) Center and the Virginia Tech Eastern Shore Agriculture Research and Extension Center (AREC) will be analyzed for the presence of *Salmonella* by modified FDA-BAM methods and tested for *Salmonella* by real-time qPCR assay on the hand-held Biomeme two3 system. Positive samples will be subjected to metagenomic sequencing using the portable MinION platform for rapid sample characterization on site. We will present the results of our field study, outcomes, and lessons learned. The successful demonstration of these methods is an important step towards developing and validating field-ready methods aimed at shortening the sample to answer timelines for routine foodborne pathogen surveillance and outbreak investigations.
Produce-Related Outbreaks in Canada: A Summary of Epidemiological Findings and Investigative Strategies, 2000–2015

Authors: Mihaela Gheorghe¹, Alexander Todd¹±², Philippe Belanger¹, April Hexemer¹ for the Produce-Related Outbreak Team¹

Affiliations: ¹Public Health Agency of Canada, Centre for Food-borne, Environmental and Zoonotic Infectious Diseases, Outbreak Management Division, Ottawa, ON; ²Canadian Food Inspection Agency, Inspection Support Directorate, Office of Food Safety and Recall, Ottawa, ON

Background: Many recent Canadian foodborne illness outbreaks have been linked to fresh produce. Due to multiple documented challenges in investigating outbreaks associated with produce, identifying strategies for successfully investigating these outbreaks is essential. The objective of this project was to describe the public health significance of produce-related outbreaks in Canada, and identify investigative strategies that could be used to reduce the public health impact of these outbreaks.

Methods: Federal government foodborne outbreak data sets were analyzed to identify Canadian produce-related outbreaks between 2000 and 2015. A selection of recently published Canadian and international manuscripts about produce-related outbreaks were reviewed to identify investigative challenges and potential strategies. Canadian and international publications about produce-related outbreaks between 2009 and 2015 were reviewed to identify investigative challenges and potential strategies. Informal discussions to explore how to address these issues were held with public health investigators.

Results: In total, there were 57 Canadian produce-related outbreaks reported between 2000 and 2015, with an estimated 2,261 cases of foodborne illness. The number of reported outbreaks per year ranged between one and seven, with a median of 3.5. The largest proportion of reported outbreaks was attributed to Salmonella spp. (38.2%) and to Escherichia coli (25.5%). The most commonly reported food vehicles included leafy greens (41.2%) and sprouts (20.1%). Commonly identified challenges in Canadian investigations, as well as in the literature, included timely investigation due to short product shelf life, complex traceback investigations, and the lack of sub-typing methods for certain pathogens. Strategies identified in solving produce-related outbreaks included: improving data quality, developing adequate laboratory methodology, and creating communication platforms for information sharing.

Conclusions: The number of produce-related outbreaks reported in Canada has remained relatively consistent between 2000 and 2015; similarly, the number of illnesses continues to be high. This work will inform the implementation of investigative strategies to support timely source identification in produce-related outbreaks. This could in turn result in the ability to take public health action sooner, thus minimizing the impact on the health of Canadians.
P-097
Poster withdrawn

P-098

**Molecular Epidemiology and Antimicrobial Susceptibility Profiles of *Salmonella* spp. From Food Samples and Clinical Specimens in Lebanon Between 2011 and 2016**

Authors: Bassam El-Hafi¹,², Sari Rasheed¹,², Sukayna M. Faddallah¹,², Majd Saleh³, Zeina Naser³, Nada Ghosn³, Walid Ammar³, Rima El-Hajj⁴, Ghassan M. Matar¹,²

Affiliations: ¹Department of Experimental Pathology, Immunology, and Microbiology, Faculty of Medicine, American University of Beirut (AUB), Lebanon; ²Center for Infectious Diseases Research, American University of Beirut Medical Center, Lebanon; ³Epidemiological Surveillance Unit, Ministry of Public Health (ESUMOH), Lebanon; ⁴Lebanese Agriculture Research Institute (LARI), Lebanon

**Introduction:** Foodborne illnesses are among the most common human infections that can be attributed to a wide range of bacterial pathogens, including *Salmonella* spp. To investigate and monitor the sources of foodborne infection outbreaks, PulseNet International was implemented in Lebanon (AUB-ESUMOH). The network aimed at identifying circulating pathogens at the phenotypic and molecular levels, and linking pathogens from clinical specimens to food sources during outbreaks.

**Methods:** Between 2011 and 2016, clinical and food *Salmonella* isolates referred from the ESUMOH and LARI, were identified to the species level using API 20E, serotyped using the Kauffman–White classification scheme, tested for their resistance to a panel of antimicrobials using the Kirby–Bauer procedure, and had their DNA fingerprint patterns determined using Pulsed-Field Gel Electrophoresis (PFGE) according to PulseNet protocols (CDC, USA), followed by BioNumerics analysis.

**Results:** A total of 779 *Salmonella* isolates were identified; n=646 from clinical and n=133 from food samples. Serotyping revealed the presence of 10 serotypes distributed among the isolates, with S. Typhimurium and S. Enteritidis having the highest prevalence. Antimicrobial susceptibility testing showed that resistance to Ciprofloxacin and Ampicillin in isolates from clinical and food sources was common. PFGE analysis showed a diversity of pulsotypes among bacterial serotypes, with JEGX01.0001 being the most prevalent in S. Enteritidis.

**Conclusion:** The study provided necessary information required for food safety management, infection control policies, and outbreak containment. The importance of foodborne pathogen surveillance is also implicated.
Building a pan-genome allele database for whole genome sequence-based genotyping of *Salmonella* isolates of all serovars

Authors: Chien-Shun Chiou, Yueh-Hua Tu, Yen-Yi Liu, Bo-Han Chen

Affiliation: Central Regional Laboratory, Center for Diagnostics and Vaccine Development, Centers for Disease Control, Taichung City, TAIWAN

**Background:** Whole genome sequencing (WGS) has been a promising method for genotyping of bacterial isolates for epidemiological investigation of disease outbreaks and active disease surveillance. WGS-based genotypic data can be comparable among laboratories when the genetic profiles are generated by using a common pan-genome allele database (PGAdb). A PGAdb is needed for genotyping of *Salmonella* isolates of all serovars.

**Methods:** A total of 5,175 genomes from the NCBI database were used to construct a *Salmonella* PGAdb using a previously developed PGAdb-builder pipeline. The usefulness of the PGAdb in generating wgMLST profiles of isolates for identifying epidemiologically-related clusters was assessed using isolates of 3 set of isolates with different serovars.

**Results:** A *Salmonella* PGAdb was constructed using 5,175 genomes from more than 133 serovars, including S. Typhi (38.5%), S. Typhimurium (15.2%), S. Enteritidis (7.9%), S. Heidelberg (3.7%), and other serovars (34.6%). The database contained 101,090 loci (genes) of which 1,906 loci were shared by ≥80% of the genomes (core genes), 42,771 loci by 80% of the genomes to 2 genomes (dispensable genes), and 56,413 loci by one genome (unique genes). The distribution of dispensable genes among the genomes is associated with serovars. Because the database was not constructed with genomes of all *Salmonella* serovars, the database could not be applicable to all serovars. In spite of this, the database were evaluated by generating wgMLST fingerprints of 3 sets of isolates of different serovars and the genetic profiles were applied to successfully discriminate epidemiologically-related strains from unrelated strains.

**Conclusions:** The *Salmonella* PGAdb built with a large number of genomes from diverse serovars can be a useful tool for generating genetic profiles from WGS data of isolates. Whether the database can be applied to all *Salmonella* serovars, further assessment has to be conducted using isolate sets of various serovars.