

Story 1: Using Bioinformatics to Track Foodborne Illnesses in Texas

In 2022, the Texas Department of State Health Services (DSHS) Laboratory's Genetic Sequencing Branch expanded its whole genome sequencing (WGS) capacity to collect, analyze, and compare "DNA fingerprint" data of foodborne pathogens taken from specimens submitted to the Laboratory. Whole genome sequencing data from these specimens are critical to the DSHS Epidemiology team in investigating outbreaks and in helping industry and food regulatory agencies improve food and water supply chain systems in Texas and across the U.S.

With funding from the Laboratory Flexible Funding Model (LFFM) cooperative agreement, the DSHS Laboratory in cooperation with the U.S. Food & Drug Administration (FDA) enabled the Genetic Sequencing Branch to purchase their first Illumina® MiSeq sequencers in 2014 to initiate WGS activities. Since then, the branch's Advanced Molecular Detection (AMD) Team has performed WGS of *Salmonella enterica*, *Listeria monocytogenes*, *Shigella* spp., *Campylobacter* spp., *Vibrio* spp., and Shiga toxin-producing *E. coli* (STEC) obtained from clinical, food, and environmental specimens. The pathogens' sequenced data—including species identification, subtype, and allele code information—are then uploaded to the National Center for Biotechnology Information (NCBI) database. Run by the National Library of Medicine, the NCBI database is open access and allows researchers in the U.S. and across the world to compare submitted sequences from food and environmental samples to analyze the data for indications of disease clusters (outbreaks of foodborne illnesses caused by the same bacteria).

The AMD Team analyzes their uploaded sequences on the NCBI database weekly and sometimes more frequently during outbreak investigations. Evidence of clusters is immediately shared with DSHS epidemiologists to initiate an outbreak response. Since 2015, the Laboratory has generated over 2,450 sequences from food or environmentally sourced enteric pathogens that are now available in the NCBI database for collaborative use. Sequencing data from clinical specimens that are received for the purpose of patient care are also accessible to the Centers for Disease Control and Prevention's PulseNet national laboratory network. Sharing data with other public health and food regulatory laboratories via databases such as PulseNet allows for easier tracking and identification of foodborne disease clusters that represent unrecognized outbreaks across the U.S.

On the Trail of an Elusive Bug

Each day the DSHS Laboratory receives clinical specimens, food, and environmental samples as well as organism isolates for serotyping. Many of these will be sequenced by the AMD group.

Maliha Rahman, the AMD Team Lead working on the LFFM-funded project, recalls how through WGS analyses a specific strain of *Listeria monocytogenes* was linked to contaminated semisoft cheese (queso fresca) and to persistent outbreaks of listeriosis in the U.S. over the past 18 years.

WGS data uploaded to the NCBI database were utilized by the GenomeTrakr and PulseNet networks to determine the majority of listeriosis cases caused by strain REPGX602 occurred in Texas, and the majority of cases in Texas occurred in just three southern border counties. *L. monocytogenes* isolates related to the REPGX602 strain are being investigated by DSHS epidemiologists as part of local outbreak clusters. A specific manufacturer of the semisoft cheeses at the center of the investigations has not yet been identified and the case remains open.

Rice and Beans, and More

In March 2022, the DSHS Laboratory was alerted that a community dinner event in North Texas had been linked to a Salmonella outbreak. Salmonella isolates from the rice and beans served at the event were prioritized and sequenced using WGS. These actions helped quickly identify Salmonella enterica serotype I4:i:- as the culprit. The sequence data were uploaded to the NCBI database. Through communication with participants in the GenomeTrakr and PulseNet networks, by April 21, 2022, 44 clinical isolates (from patients) and isolates from the rice and beans from the dinner clustered as highly related.

Since the cluster analysis indicated the rice and beans at the community dinner as the source of the *Salmonella enterica* serotype I4:i:- outbreak, the Texas DSHS Epidemiology team was able to close this case as an isolated outbreak event.

Through these investigations and several more, and with the support from the LFFM, GenomeTrakr and PulseNet, DSHS Laboratory continues its focus on monitoring the safety of Texans' food by closely tracking and responding quickly to sporadic cases or outbreaks of foodborne illnesses.

Norovirus Outbreak Investigations at DSHS

Norovirus is the most common cause of acute gastroenteritis and foodborne disease outbreaks in the United States, with 19 to 21 million cases each year costing about \$2 billion. This price tag is mostly due to lost productivity and healthcare costs.

This hardy and highly contagious virus is most commonly spread directly from person-to-person and indirectly through fecally contaminated food and water. However, norovirus outbreaks tend to be underreported to public health officials, so the true incidence of the illness is likely higher.

A norovirus infection is usually self-limiting and typically includes nausea, vomiting, and diarrhea that lasts 1–3 days, but immunocompromised individuals may develop more serious long-term infections. Since the symptoms of a norovirus infection are similar to other gastrointestinal (GI) illnesses, testing patients for unknown GI illnesses helps detect cases and community outbreaks of the illness. Submitting specimens for testing also contributes to the national norovirus outbreak surveillance network CaliciNet, a program in which the DSHS Laboratory participates.

Information: Submitting Norovirus Surveillance Specimens to DSHS Austin Laboratory

During norovirus outbreak investigations, local or regional health departments may request healthcare providers to forward clinical specimens to the DSHS Laboratory for molecular analysis. It is important for providers to submit these specimens to the Laboratory. Doing so helps DSHS and the CaliciNet surveillance network link individual cases during outbreak investigations.

Existing submitters may submit specimens for the surveillance program without changing their regular submission process. If a provider has not submitted to the DSHS Laboratory before, they must first set up a submitter account with the DSHS by:

1. downloading a Submitter ID Number Request Form, available at [Submitter-Request-Form-Sept--2017.pdf \(texas.gov\)](#),
2. completing all applicable fields in the form, and
3. emailing the form to labinfo@dshs.texas.gov or faxing to (512) 776-7533.

A Lab Reporting team member will create a submitter account, provide a G2-B submission form and Security Right forms to request DSHS Web Portal access to allow the submitter to view, download or print results.

Submitter Guidance is Available

An important factor in successful specimen testing at the DSHS Laboratory is receiving correctly labeled specimens with the correct submission form. To help providers navigate these specimen submission requirements, the DSHS created norovirus surveillance specimen submission guidance flyers that can be printed out for reference. Alternatively, you may download from Norovirus Specimen Submission Guidance.

Norovirus Surveillance Testing is Free!

The DSHS Laboratory does not charge for testing clinical specimens that are requested for norovirus outbreak investigation.

Sources:

1. LFFM Objectives <https://www.fda.gov/federal-state-local-tribal-and-territorial-officials/grants-and-cooperative-agreements/laboratory-flexible-funding-model-cooperative-agreement-program>

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