

# Partnering to Solve Foodborne Outbreak in Massachusetts

[Announcer] This program is presented by the Centers for Disease Control and Prevention.

[Sarah Gregory] Hello, I'm Sarah Gregory, and today I'm talking with Quynh Vo, an epidemiologist at the Massachusetts Department of Public Health. We'll be discussing how cross-discipline collaboration among state and local health departments improved surveillance for an outbreak of *Salmonella* in Massachusetts.

Welcome, Quynh.

[Quynh Vo] Hi, thank you for having me.

[Sarah Gregory] *Salmonella*'s a big problem with our food worldwide. Tell us what it is and how it affects a person?

[Quynh Vo] Yeah. *Salmonella* is a bacteria that causes diarrheal disease in humans. Symptoms like, you know, fever, diarrhea, stomach ache are usually associated with it. They usually begin about 12 to 96 hours after you've become infected with the bacteria. It's also one of the most common pathogens causing foodborne illness.

[Sarah Gregory] Can it be deadly?

[Quynh Vo] Yeah, the CDC estimates *Salmonella* infections cause about 420 deaths every year in the United States.

[Sarah Gregory] Is it easily transmitted?

[Quynh Vo] Yes. There are 3 main ways to get *Salmonella*. In no particular order, the first is from contaminated food such as eggs, poultry, milk—unpasteurized milk, specifically—in juice, cheese, raw fruits, and vegetables. Second, it can be transmitted to humans from animals, particularly reptiles, amphibians, and birds. And third, it can be spread from person to person when an infected person doesn't wash their hands after using the bathroom.

[Sarah Gregory] How many people does it infect each year worldwide and in Massachusetts, in particular?

[Quynh Vo] So, the CDC estimates that *Salmonella* causes about 1.2 million illnesses every year. On average, Massachusetts reports about 1,200 cases per year.

[Sarah Gregory] And how does it get into our food supply?

[Quynh Vo] So you can get *Salmonella* from a variety of foods, but food animals, such as chickens) often serve as the reservoirs for the pathogen. In fruits and vegetables, *Salmonella* is considered a contaminant that may be, you know, introduced from contact with human or animal feces.

[Sarah Gregory] So, these huge outbreaks of food are due to basically somebody's poo touching the food somewhere along the line in the vegetable chain? Is that what you're saying?

[Quynh Vo] We consider it a contaminant. So, we don't think that fruits and vegetables naturally harvest *Salmonella*. We know it's sort of prevalent in...in animals, like chickens. But anywhere from farm to table can be an introduction of what we consider contaminants. It's like, we don't

consider *Salmonella* to be naturally a part of fruits and vegetables, whereas we sort of expect it to be in chickens, just historically.

[Sarah Gregory] There are outbreaks going on right now in onions and in peaches. People tend to think of *Salmonella* as more associated with meat and poultry—as you just mentioned poultry—but actually vegetables seem to be more...the more likely culprit in recent years. Is that right?

[Quynh Vo] So, among the outbreaks linked to food, in particular, the two big ones in 2020 have been linked to produce. But in past years, it's been sort of a mix of both. So according to the CDC, we had 7 foodborne outbreaks related to produce in 2019, and then most *Salmonella* foodborne clusters in 2018 were linked to poultry. And I'm emphasizing the foodborne aspect here because there have been recent outbreaks associated with backyard chickens and live poultry as well, as I mentioned above.

[Sarah Gregory] Are there any treatments if a person does get infected?

[Quynh Vo] The good news is that most *Salmonella* infections resolve without any treatment. Antibiotics are typically only used for severe illness.

[Sarah Gregory] And what would be considered a severe illness?

[Quynh Vo] So, there are people that become hospitalized or, you know, go to the doctor often. If you have a weaker immune system and, you know, the diarrhea could be extreme or, you know, someone who's...who has comorbidities and gets a fever, then they would be probably...and this is...I'm not a clinician, but, you know, subjectively a clinician would maybe in that case treat them with antibiotics. But for most healthy individuals, *Salmonella* resolves without treatment.

[Sarah Gregory] I see, okay. Massachusetts has mandatory reporting to the health department if a person is sick with *Salmonella*. Is this important?

[Quynh Vo] Yeah. As our report highlights, *Salmonella* isolates are required to come to lab for sequencing and then the reporting of *Salmonella* can help to identify clusters of outbreaks with the public author...the public health authorities in an act to prevent further illness in the community.

[Sarah Gregory] Well, what systems does Massachusetts use to track infectious diseases?

[Quynh Vo] So, we use an integrated web-based surveillance and case management system called MAVEN—that stands for the Massachusetts Virtual Epidemiologic Network—to track over 90 reportable infectious diseases. Electronic laboratory reports for these...for, you know, these 90 reportable infectious diseases come into MAVEN automatically.

[Sarah Gregory] Your study was about the collaboration between epidemiologists and laboratories using whole-genome sequencing in Massachusetts. First off, how does epidemiology work in tracking down an outbreak?

[Quynh Vo] All commercial and clinical laboratories in Massachusetts report *Salmonella* infection to MAVEN. Once a case appears in MAVEN, the local board of health are notified for case investigation. This is where those classic epidemiological variables, such as person, place, and time, are collected, as well as an extensive food and animal exposure history. Then, epidemiologists, like myself, at the state health department review these case reports for commonalities.

[Sarah Gregory] And how does whole-genome sequencing work?

[Quynh Vo] In Massachusetts, isolates are sent from commercial and clinical laboratories to the state laboratory for confirmation. Until 2015, the Massachusetts Department of Public Health used a DNA fingerprint method called pulsed-field gel electrophoresis, or PFGE, to identify local clusters, and then we report these isolate patterns to CDC's PulseNet. So, both PFGE and whole-genome sequencing are molecular genetic approaches for pathogenetic identification. But whole-genome sequencing allows for more precise detection with a strain typing tool. The higher resolution you can see with whole-genome sequencing allows for a more concrete understanding of relatedness between strains associated with an outbreak.

[Sarah Gregory] And how were they used together to find an answer to this outbreak?

[Quynh Vo] So, when we used PFGE data only, a total of 84 isolates were included in this cluster. Epidemiological case investigation identified a venue associated with several case patients in a geographic area. And then whole-genome sequencing data narrowed the scope of the investigation to a clade within the larger cluster of the PFGE phylogenetic tree.

[Sarah Gregory] Was this an unusual approach?

[Quynh Vo] It was a fairly novel approach at the time of the outbreak investigation, when PFGE was the primary method of DNA fingerprinting and analysis of sequence data was performed at the CDC. But now, in 2020, all state laboratories have transitioned from PFGE to whole-genome sequencing for fingerprinting. And then sequencing of these data can now be performed in house.

[Sarah Gregory] Oh, but I mean the collaboration of epidemiology and whole-genome sequencing—is that unusual to partner those two?

[Quynh Vo] Yeah, I think so. You know, one thing that is unique about Massachusetts...you know, oftentimes the laboratory and the epidemiology staff are, you know, work in silos. But in Massachusetts, we work very closely together. They meet monthly to go over cluster outbreaks. And that collaborative work between the laboratory staff and the epidemiology staff really, I thought, you know, expedited the investigation.

[Sarah Gregory] So, is this an approach you think all health departments should be using?

[Quynh Vo] Yeah. It...it really helps to streamline the investigation. And I think, you know, our cluster demonstrates how important that is.

[Sarah Gregory] Why do you think the EID journal chose to publish your study out of the thousands we receive every year?

[Quynh Vo] So, it's a brief report just sort of detailing one of, you know, many common food investigations we do. But, you know, when public health works well, it often goes unnoticed because we're preventing additional disease. An incredible amount of work takes place to reduce additional exposures after someone sees a clinician for an infection that may not be obvious to the public. So, our report highlights both the importance of public health and the importance of collaboration among jurisdictions to combat foodborne infectious disease. It also, as mentioned previously, underscores the importance of collaboration between the laboratory and epidemiology staff to get the work done quickly. You know, too often they are siloed, but in Massachusetts we work closely together.

[Sarah Gregory] Why don't you give us a brief summary of your study—the years it covered, and how you conducted it?

[Quynh Vo] The investigation took place from October 2018 through December 2018. So, really just 2 months. Our study report illustrates that classic epidemiological case follow-up integrated with molecular approaches to cluster detection expanded the scope of a restaurant-associated outbreak. Open communication between epidemiologists and laboratory personnel about epidemiologic and whole-genome sequencing data narrowed the scope of the investigation to a clade within a larger PFGE cluster's phylogenetic tree. This allowed us to focus investigative activity from 18 cases and improve the timeliness of the control measure implementation. We have identified an infected food handler, who was probably...probably shedding *Salmonella* and then, if hygiene practices were inadequate, could have contaminated ready-to-eat food, such as lettuce and tomatoes. Alternatively, a ready-to-eat food could have been the common source for all 18 cases in this cluster.

[Sarah Gregory] In previous *E. coli* outbreaks, such as the one in spinach about 13 years ago, people were advised to not eat it raw but to boil it for at least a few minutes. But with all these recent *Salmonella* outbreaks, people are advised to just throw out the food. Why is cooking it not advised with *Salmonella*?

[Quynh Vo] The new advisory is probably more comprehensive to cover food handling practices. Food handling can be an important source of transmission for *Salmonella*—for example, cross-contamination on a cutting board or undercooking can result in food poisoning from *Salmonella*.

[Sarah Gregory] So it's not really any intrinsic difference between cooking and not cooking with *E. coli* and *Salmonella*. It's more just caution about people not actually being able to take the care that would be needed to keep the food safe, is that right?

[Quynh Vo] Yeah, I think so. I think, you know, as outbreaks have highlighted that, potentially, you know, it's the food handler who may be implicated, it was the handling process that may have caused the transmission. You know, the other thing is when you're eating fresh food, there's no "kill" step. So, I think in an abundance of caution that's probably why the advice has changed.

[Sarah Gregory] I see, okay. Well, tell us about your job—what you do and what you like most about it?

[Quynh Vo] Epidemiologists at the Bureau of Infectious Disease and Laboratory Science, we have to answer the five steps that we used—who, what, where, when, and why—often at breakneck speed in situations involving over 70 immediately reportable conditions in Massachusetts. I think it's exciting and it has given me the opportunity to work with a range of different people, such as clinicians, laboratorians, animal control officers, local boards of health, federal regulators, supervised care settings, and the public on a wide range of infectious diseases. I've seen the, you know, firsthand the importance of data collection and basic epidemiology in public health, and I've also learned to communicate more effectively with a wide range of audiences regarding health risk and disease prevention and control.

[Sarah Gregory] What do you do for fun and relaxation in these mask-wearing, social-distancing times?

[Quynh Vo] I spend a lot of time outdoors.

[Sarah Gregory] Hiking? Swimming? Bicycling?

[Quynh Vo] We...you know, we have a small yard, and we usually just work or, you know, go out. But this, you know, this past six months, we've spent so much more time in our backyard. And I've used my backyard more than any other year I've lived in this house. And, you know, hiking is a great activity. You know, when we are wanting to see relatives, we host them usually in our backyard—six feet apart, of course, with masks on. So, I guess outdoors for us has...has been in my backyard.

[Sarah Gregory] Okay. Well thank you so much for taking the time to talk with me today, Quynh.

[Quynh Vo] Well thank you for having me, Sarah. It was my pleasure.

[Sarah Gregory] And thanks for joining me out there. You can read the July 2020 article, *Linking Epidemiology and Whole-Genome Sequencing to Investigate Salmonella Outbreak, Massachusetts, USA, 2018*, online at [cdc.gov/eid](https://www.cdc.gov/eid).

I'm Sarah Gregory for *Emerging Infectious Diseases*.

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