

CDC *Vital Signs* Town Hall Teleconference

When Food Bites Back: Act Locally, Control Nationally  
Q&A

June 11, 2013  
2:00–3:00 pm EDT

Richard Schieber: Thank you, all, for these excellent presentations. For the question and answer period, I'd like to remind everyone that you can get in the queue to ask a question by pressing star 1. Record your name when prompted and you'll be announced into the conference by Jane our operator when it's your turn to ask the question.

I encourage you to take advantage of this opportunity to share the strategies you've used and the lessons you've learned, challenges that remain, and your success stories.

Jane, I'm not seeing any questions in the queue at this point. I'd like to start out then by asking the participants if they could think of a local or even state-based outbreak, and things they did in particular that kept it from being more of a national or regional outbreak.

Coordinator: We do have one question from the phone lines at this time if you'd like to take it.

Richard Schieber: I don't hear any responses to my question, so let's take that on.

Coordinator: Ed Labuza, your line is open.

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Ed Labuza: I have a question about the future of pulsed gel. Do we know what percentage would be false positives or false negatives? And recently there has been a number of papers which people are predicting that we'll be getting rid of pulsed gel and switching over to a complete genome typing, which sounds like a very expensive process, but I'd like your comments on that.

Richard Schieber: Ben, do you have any thoughts on that?

Benjamin Silk: Sure. I'd love to hear from Dr. Maguire, too. So let's see the first part of the question was about false positives or false negatives with Pulsed Field Gel Electrophoresis or PFGE. If you're talking about PFGE results themselves for any given isolate, I don't understand that to be a major issue. I'm not a microbiologist but I do know that part of the appeal of PFGE is that it's fairly straightforward and easy to do in most laboratories, and that is what makes it appealing as a method for molecular sub-typing. You could almost think of it as a common denominator in what most referenced labs can do.

It is true that we sometimes get small differences in PFGE results during an outbreak investigation and that those differences might manifest as different outbreak subtypes when in fact they're part of the same strain. And that has been confirmed with other molecular typing methods. So maybe that was the nature of the question.

And so often we look to use PFGE as a sort of a first line of molecular characterization to initially detect clusters and outbreaks. And then we typically confirm those results with some other laboratory methods. Some states like Colorado can do MLVA for example, and we've done that here as well to confirm that outbreak subtypes or one subtype are part of the same strain.

In PulseNet, PFGE cluster detection is not perfect and as Melissa showed the 60-day window that we often use for defining a set of isolates with the same PFGE subtype that might be related it, that 60-day window is somewhat arbitrary. Melissa showed that they had to use a wider window.

I suppose that could be thought of as a false negative as well although it's also true that often we just use the 60-day window really as a starting place to detect clusters and then if we think there's a problem with a particular subtype then we might widen that window, again as Melissa demonstrated.

The other part of the question was about newer methods. It is true that the future is in whole genome sequencing. I don't think we're there yet but there are more resources and interest in doing full characterization of genomes of *Listeria* that might be related to outbreaks or even sporadic disease. And I expect that that holds a lot of promise for outbreak investigation and even understanding the virulence of different strains of *Listeria* as well.

Hugh, did you want to comment more on the question from a true microbiology standpoint?

Hugh Maguire: I don't know about that last part but absolutely, I'd like to comment. We cannot undersell PulseNet. For well over a decade, that has been the premiere method of cluster identification and detection for the nation. And that it is now standard practice almost in every state public health lab in the country.

But it didn't happen overnight, it took a lot of funding, a lot of dedication—primarily by people at CDC and then later by each individual public health lab to implement all of the processes that go into supporting PulseNet.

But one of the key things that is becoming the challenge now and that many of us are on the bandwagon about, you know, getting the word out is that all of

this activity in PulseNet is dependent on obtaining a pure culture isolate from either a food matrix or from a patient sample. Without that the whole system starts to slowly erode to where we will not be able to make the kinds of responses to the outbreaks that we are seeing. Certainly would not have been possible with the cantaloupe outbreak since we're talking about *Listeria* here. And I'm certain that as Melissa clearly described it would not have happened in Massachusetts.

As far as what we do next you're right; whole genome sequencing is probably the future for all of us. But there is going to be that transitional period from where we are right now to where we will need to in the future if we're going to improve upon the basic foundation that PulseNet has provided outbreak investigations for a very long time.

The issue is still going to be the ability to obtain culture isolates and many of us in the public health laboratories have done a lot of work behind the scenes to retain the relationships that I was kind of alluding to earlier; in this case especially our clinical partners, so that they see the importance of their work as a contribution to the work that public health laboratories and public health epidemiologists do.

Ultimately as we move to the next technology that is going to take a while. It's not going to happen that we can all go out and purchase the correct instrument to coordinate our actions and activities in the public health lab. We're going to have to be able to gradually phase in the clearly vetted and appropriate technology that will last equally as long as PFGE has had. And PFGE will not go away but say five, eight years from now it will not be the premiere or the primary tool that we use to identify clusters.

In order to get there, state laboratories can't just wish really hard and have some sort of new instrumentation appear. There's going to have to be a

commitment made by some entity, most likely a federal entity, to support the implementation of that new technology.

Ed Labuza: That's great. Thank you.

Benjamin Silk: Rich, one correction. I misspoke, for the record the window that CDC uses for *Listeria* cluster detection is 120 days, not 60 days.

Ed Labuza: Okay, thank you.

Richard Schieber: Operator, we have another question? We have a couple of minutes left.

Coordinator: Yes, we have a question from David Byrd. Your line is open.

David Byrd: Hi. I'm from Missouri. This is for Melissa—we were wondering, of the 18 other *Listeria* patterns that you had, did anyone investigate if those matched any of the other patterns that were found in the dairy that didn't match the outbreak strain?

Melissa Cumming: So your question is were any of the other clinical isolates we received matches to the other pattern seen in the dairy? And if that's the question the answer is no they were not.

David Byrd: Okay. That was my question. Thank you.

Melissa Cumming: Yes. Okay.

Coordinator: We have no further questions.

Richard Schieber: Please let us know how we can improve these teleconferences to be beneficial to you by emailing your suggestions to OSTLTS, O-S-T-L-T-S feedback, all

one word, [ostltsfeedback@cdc.gov](mailto:ostltsfeedback@cdc.gov). We hope you'll be able to join us for next month's call. It will be on prescription narcotic overdose on July 9.

Look for new Public Health Practice Stories from the Field from Colorado and Massachusetts on the [STLT Gateway](#).

I would like to end by saying thank you to our presenters and thanks to everyone who attended the call. That ends today's call. Goodbye.

Coordinator: That does conclude today's conference. Thank you for participating. You may disconnect at this time.