## Genome sequencing speeds foodborne illness investigations

## The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion and analysis.

In August 2015, whole-genome sequencing connected 24 Listeria cases reaching back to 2010. But good old-fashioned epidemiology is what tracked down the source - soft cheeses produced by Karoun Dairies of San Fernando, CA.

Eighteen victims said they ate Middle Eastern, Eastern European, Mediterranean or Mexican-style cheeses, and Ani, Bulgarian feta, Middle Eastern-style string cheese and nabulsi were some of the cheeses not specifically on the radar before.

CDC began investigating four of the cases now involved in the outbreak back in 2013.
"We saw there was a Middle East connection back then, but there was just too little information," says medical epidemiologist Brendan Jackson.

Then, in August 2015, PulseNet — the national network of public health and food regulatory agency laboratories that tracks foodborne illnesses - flagged some Listeria cases.
"Suddenly, we went from just a few cases ... to upwards of 20," Jackson says. "Once we had those numbers, it was fairly easy to see that there was a signal for soft cheese."

Thanks to the Listeria Initiative, which began in 2004, all Listeria patients were interviewed using a standardized questionnaire that asks about the same foods.

There's no doubt that the Listeria Whole Genome Sequencing Project has had an impact on illness investigations.

But don't forget about the epidemiology. It's still important to interpreting the sequencing results and to cracking outbreak investigations, as the soft cheese-linked outbreak shows.
"There is a perception among some people out there that whole-genome sequencing will make epidemiology obsolete," Jackson says. "Investigation after investigation shows that's just not the case. They have to be used together to be the most effective."

Read full, original post: Don't Forget the Epidemiology: Unraveling a Five-Year Listeria Outbreak

