Food-Borne Illness Research Identifies Outbreak Source with DNA

American Society for Microbiology

Research from the University of Melbourne, Australia, could make it easier for public health investigators to determine if a case of food poisoning is an isolated incident or part of a larger outbreak. The findings are published ahead of print in the Journal of Bacteriology.

The study focuses on a test called multi-locus variable number tandem repeats variable analysis (MLVA). The test, which is increasingly used in the detection and investigation of foodborne outbreaks, analyzes specific sequences of DNA (called loci) that change rapidly enough over time to distinguish outbreak strains from other circulating strains of the bacteria but not so rapidly that connections could be masked by changes arising during the course of an outbreak.

However, the rates at which MLVA profiles change have not been directly investigated for Salmonella, and thus it is sometimes unclear how these profiles should be interpreted in the context of outbreak detection and investigation.

In the study, the investigators grew an isolate of Salmonella Typhimurium from an Australian food poisoning outbreak, and observed changes in its MLVA profile during more than 28,000 generations of growth in the laboratory. Then, using the same bacterial lineage, they observed changes in MLVA profile during 500 days of growth in mice.

They estimated the rates of copy number change at each of the five loci that are commonly used for S. Typhimurium MLVA. Three of the loci saw changes in the DNA, but two did not. Based on these results, the researchers are recommending that isolates with zero or one variation in the three rapidly changing loci but no differences in the other two should be considered part of the same cluster.

They also noted that the relative rates of change among the loci were the same in the Petri dish studies and in the mouse study.

"This tells us we don't need to worry about where the bacteria were isolated from—humans or food," says Kathryn Holt, an author on the study.

MLVA is used for investigations of food-borne illnesses besides Salmonella, including Listeria, and E. coli. It is the primary method for investigations of Salmonella outbreaks in Europe, the UK, Australia, and elsewhere, says Holt.

"In the U.S., the Centers for Disease Control and Prevention uses another technique called PFGE for initial investigations and follows that with MLVA," she says.

Journal of Bacteriology is a publication of the American Society for Microbiology (ASM). The ASM is the largest single life science society, composed of over 39,000 scientists and health professionals. Its mission is to advance the microbiological sciences as a vehicle for understanding life processes and to apply and communicate this knowledge for the improvement of health and environmental and economic well-being worldwide.

Source URL (retrieved on *09/15/2014 - 12:12am*):
http://www.foodmanufacturing.com/news/2014/06/food-borne-illness-research-identifies-outbreak-source-dna