Joint Conference

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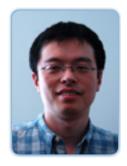
6th Annual Conference on

MICROBIOLOGY

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Yi Chen

Center for Food Safety and Applied Nutrition, USA

Whole genome and core genome analyses of Listeria monocytogenes associated with recent outbreaks

A number of listeriosis outbreaks have been reported recently, in which next generation sequencing was used to complement epidemiologic investigations. In this presentation, I discuss multiple whole genome sequencing and core genome sequencing approaches using these outbreaks as case studies. The analyses provide insights to the selection of appropriate approaches to define the scope of an outbreak, to differentiate epidemiologically unrelated isolates, and to study the persistence and microevolution of isolates in a single outbreak

Biography

Dr. Yi Chen joined FDA in 2008 and has been working on the method development and validation for the detection, enumeration and whole genome sequencing analysis of *L. monocytogenes*. As a subject matter expert on *L. monocytogenes*, he has provided scientific advice for various FDA assignments, outbreak investigations and laboratory analyses. He currently serves as a General Referee for AOAC International and editorial board member for Applied and Environmental Microbiology.

Notes: