National Enteric Disease Surveillance: The *Listeria* Initiative

Surveillance System Overview: The *Listeria* Initiative

Listeria monocytogenes is estimated to cause about 1,600 illnesses each year in the United States with more than 1,500 related hospitalizations and 260 related deaths (1). *Listeria* infections (listeriosis) are nationally notifiable. Nearly all cases in persons who are not infants result from eating food contaminated with *L. monocytogenes*; newborn infants can develop listeriosis if their mothers ate contaminated food during pregnancy.

The *Listeria* Initiative is an enhanced surveillance system that collects reports of laboratory-confirmed cases of human listeriosis in the United States. Demographic, clinical, laboratory, and epidemiologic data are collected using a standardized, extended questionnaire. The *Listeria* Initiative was piloted in the Foodborne Diseases Active Surveillance Network (FoodNet) in 2004 and implemented nationwide in 2005. The number of states participating increased to 47 states and the District of Columbia by 2014. The proportion of all listeriosis cases reported to the *Listeria* Initiative continues to increase.

A main objective of the *Listeria* Initiative is to aid in the investigation of listeriosis clusters and outbreaks by decreasing the time from outbreak detection to public health intervention. Patient interviews are conducted as cases are reported, rather than after clusters are identified, to minimize the effect of recall bias on food consumption history. In addition, clinical, food, and environmental isolates of *L. monocytogenes* are subtyped. Pulsed-field gel electrophoresis (PFGE, a type of DNA fingerprinting) subtyping results are submitted to PulseNet, the National Molecular Subtyping Network for Foodborne Disease Surveillance, to identify clusters of possibly related cases. Since September 2013, state laboratories, CDC, the Food and Drug Administration (FDA), and the US Department of Agriculture's Food Safety and Inspection Service also perform whole genome sequencing on clinical, food, and environmental *L. monocytogenes* isolates. This method provides high-resolution genetic information. Whole genome sequencing can identify related illnesses that are not evident using PFGE alone. Genetically related bacteria may have different PFGE patterns, and distantly related bacteria can have the same pattern. When clusters are identified, *Listeria* Initiative data are used to rapidly conduct epidemiological analyses. The food consumption histories of patients with cluster-associated illnesses are compared with those of patients with sporadic illnesses to identify foods possibly associated with the cluster. Without the *Listeria* Initiative database, appropriate comparison data ("controls") for listeriosis investigations would be difficult to obtain through traditional methods; the population at risk for invasive listeriosis—older adults, immunocompromised persons, and pregnant women—is a small segment of the general population.

National Center for Emerging and Zoonotic Infectious Diseases

Division of Foodborne, Waterborne, and Environmental Diseases

Local, state, and territorial public health professionals are encouraged to complete the *Listeria* Initiative questionnaire for all cases of laboratory-confirmed listeriosis. English and Spanish versions of the questionnaire are available at http://www.cdc.gov/listeria/surveillance.html. All *Listeria* isolates should be forwarded promptly to state or national laboratories for subtyping.

Overview of Listeria

The genus *Listeria* contains seven species (*monocytogenes, ivanovii, seeligeri, innocua, welshimeri, martii,* and *grayi*), two of which are pathogenic. *L. monocytogenes* is pathogenic to humans and animals; *L. ivanovii* (previously *L. monocytogenes* serotype 5) primarily infects animals and very rarely causes disease in humans.

Serotyping differentiates isolates of *Listeria* below the species level. Serotypes are designated based on the immunoreactivity of two cell surface structures, the O and H antigens. Twelve serotypes of *L. monocytogenes* (1/2a, 1/2b, 1/2c, 3a, 3b, 3c, 4a, 4b, 4c, 4d, 4e, and 7) are recognized, three of which (1/2a, 1/2b, and 4b) cause most (95%) human illness; serotype 4b is most commonly associated with outbreaks.

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Suggested Readings

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