Whole-genome Sequencing Used to Investigate a Nationwide Outbreak of Listeriosis Caused by Ready-to-eat Delicatessen Meat, Denmark, 2014 - DTU Orbit (09/11/2017)

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Listeriosis is a serious foodborne infection. Outbreaks of listeriosis occur rarely, but have often proved difficult to solve. In June 2014, we detected and investigated a listeriosis outbreak in Denmark using patient interviews and whole-genome sequencing (WGS). We performed WGS on Listeria monocytogenes isolates from patients and available isolates from ready-to-eat foods and compared them using single-nucleotide polymorphism (SNP) analysis. Case patients had L. monocytogenes with ≤3 SNPs (the outbreak strain) isolated in September 2013-December 2014. Through interviews, we established case patients' food and clinical histories. Food production facilities were inspected and sampled, and we performed trace-back/trace-forward of food delivery chains. In total, 41 cases were identified; 17 deaths occurred (41%). An isolate from a delicatessen meat (spiced meat roll) from company A was identical to the outbreak strain. Half of the patients were infected while hospitalized/institutionalized; institutions were supplied food by company A. The outbreak strain was repeatedly isolated from further samples taken within this company and within companies in its distribution chain. Products from company A were traced and recalled from >6000 food establishments, after which the outbreak ended. Ready-to-eat spiced meat roll from a single production facility caused this outbreak. The product, served sliced and cold, is popular among the elderly; serving it at hospitals probably contributed to the high case-fatality rate. WGS used for patient isolates and isolates from food control inspections, coupled with routine epidemiological follow-up, was instrumental in swiftly locating the source of infections, preventing further illnesses and deaths.

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