Two listeria outbreaks caused by smoked fish consumption-using whole-genome sequencing for outbreak investigations - DTU Orbit (18/01/2019)

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Listeria monocytogenes may contaminate and persist in food production facilities and cause repeated, seemingly sporadic, illnesses over extended periods of time. We report on the investigation of two such concurrent outbreaks. We compared patient isolates and available isolates from foods and food production facilities by use of whole-genome sequencing and subsequent multilocus sequence type and single nucleotide polymorphism analysis. Outbreak cases shared outbreak strains, defined as Listeria monocytogenes isolates belonging to the same sequence type with fewer than five single nucleotide polymorphism differences. We performed routine food consumption interviews of L. monocytogenes patients and compared outbreak cases with sporadic cases. Two outbreaks were defined, each consisting of ten outbreak cases in the period 2013-15. Seven outbreak cases and a fetus in gestational week 38 died. Listeria monocytogenes isolates from cold smoked or gravad fish products or their two respective production environments were repeatedly found to belong to the outbreak strains. Outbreak cases more often than sporadic cases stated that they consumed the relevant fish products, odds ratio 10.7. Routine collection and typing of food isolates was key to solving the outbreaks. Furthermore, these outbreaks illustrate the value of whole-genome sequencing for outbreak definition and investigation. Whole-genome sequencing combined with epidemiological investigations provided the discriminatory power to recognize low-intensity, extended time-period outbreaks and link them to food products from two different contaminated production facilities with sufficient strength for food authorities to intervene on. Cold smoked and gravad fish constitute risk products and may be responsible for more listeriosis cases than previously recognized.

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