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Whole genome sequencing as a tool to investigate a cluster of seven cases of listeriosis in Austria and Germany, 2011 – 2013

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Whole genome sequencing in Listeria cluster investigation

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ABSTRACT

A cluster of 7 human cases of listeriosis occurred in Austria and in Germany between April 2011 and July 2013. The *L. monocytogenes* SV 1/2b isolates shared PFGE and fAFLP patterns indistinguishable from those from 5 food producers. The 7 human isolates, a control strain with a different PFGE/fAFLP profile, and 10 food isolates were subjected to whole genome sequencing (WGS) in a blinded fashion. A gene-by-gene comparison (MLST+) was performed and the resulting whole genome allelic profiles were compared using SeqSphere software version 1.0 (Ridom GmbH, Muenster, Germany). Analyzing 2298 genes, the 4 human outbreak isolates from 2012 and 2013 had different alleles at ≤ 6 genes, i.e. differed by ≤ 6 genes from each other; the dendrogram placed these isolates in between 5 Austrian unaged soft cheese isolates from producer A (≤ 19 genes difference to human cluster) and 2 Austrian ready-to-eat-meat isolates from producer B (≤ 8 genes to human cluster). Both food products appeared on grocery bills prospectively collected by these outbreak cases after hospital discharge. Epidemiological results on food consumption and MLST+ clearly separated the 3 cases in 2011 from the 4 2012/2013- outbreak cases (>48 differing genes). We showed that WGS is capable of discriminating *L. monocytogenes* SV 1/2b clones not distinguishable by

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