Genome Sequencing Identifies Two Nearly Unchanged Strains of Persistent Listeria monocytogenes Isolated at Two Different Fish Processing Plants Sampled 6 Years Apart - DTU Orbit (07/04/2019)

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Listeria monocytogenes is a food-borne human-pathogenic bacterium that can cause infections with a high mortality rate. It has a remarkable ability to persist in food processing facilities. Here we report the genome sequences for two L. monocytogenes strains (N53-1 and La111) that were isolated 6 years apart from two different Danish fish processors. Both strains are of serotype 1/2a and belong to a highly persistent DNA subtype (random amplified polymorphic DNA [RAPD] type 9). We demonstrate using in silico analyses that both strains belong to the multilocus sequence typing (MLST) type ST121 that has been isolated as a persistent subtype in several European countries. The purpose of this study was to use genome analyses to identify genes or proteins that could contribute to persistence. In a genome comparison, the two persistent strains were extremely similar and collectively differed from the reference lineage I strain, EGD-e. Also, they differed markedly from a lineage I strain (F2365). On the proteome level, the two strains were almost identical, with a predicted protein homology of 99.94%, differing at only 2 proteins. No single-nucleotide polymorphism (SNP) differences were seen between the two strains; in contrast, N53-1 and La111 differed from the EGD-e reference strain by 3,942 and 3,471 SNPs, respectively. We included a persistent L. monocytogenes strain from the United States (F6854) in our comparisons. Compared to nonpersistent strains, all three persistent strains were distinguished by two genome deletions: one, of 2,472 bp, typically contains the gene for inlF, and the other, of 3,017 bp, includes three genes potentially related to bacteriocin production and transport (lmo2774, lmo2775, and the 3′-terminal part of lmo2776). Further studies of highly persistent strains are required to determine if the absence of these genes promotes persistence. While the genome comparison did not point to a clear physiological explanation of the persistent phenotype, the remarkable similarity between the two strains indicates that subtypes with specific traits are selected for in the food processing environment and that particular genetic and physiological factors are responsible for the persistent phenotype.

General information
Publication status: Published
Organisations: National Food Institute, Department of Systems Biology, Center for Biological Sequence Analysis, Allegheny College, United States Department of Agriculture
Pages: 2944-2951
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: Applied and Environmental Microbiology
Volume: 79
Issue number: 9
ISSN (Print): 0099-2240
Ratings:
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.25 SJR 1.899 SNIP 1.414
Web of Science (2013): Impact factor 3.952
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Original language: English
DOIs:
10.1128/AEM.03715-12
Source: dtu
Source-ID: n:oat:DTIC-ART:highwire/385192783::27883
Research output: Contribution to journal › Journal article – Annual report year: 2013 › Research › peer-review