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FSL J1-208, a virulent uncommon phylogenetic lineage IV Listeria monocytogenes strain with a small chromosome size and a putative virulence plasmid carrying internalin-like genes. [1]

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[2]

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Abstract The bacterial genus Listeria contains both saprotrophic and facultative pathogenic species. A genome size has been suggested to be associated with the loss of pathogenic potential of *L. virens* and *L. seeligeri*. In this paper we present data on the genome of *L. monocytogenes* strain FSL J1-208, representative of phylogenetic lineage IV. Although this strain was isolated from a clinical case of bovine mastitis, it can grow on a caprine host and has no decreased invasiveness in human intestinal epithelial cells, our analysis shows that this strain has one of the smallest *Listeria* chromosomes reported to date (2.78 Mb). The chromosome contains 2,772 protein-coding genes, including well-characterized virulence-associated genes, such as *inlA*, *inlB*, and *inlC* and the full *prfA* gene cluster. The small genome size is mainly explained by the absence of prophages in the genome of *L. monocytogenes* FSL J1-208, and further analysis showed that the total size of prophage-related regions is highly correlated to chromosome size in all *Listeria* species in the genus *Listeria*. *L. monocytogenes* FSL J1-208 carries a unique type of plasmid of approximately 1.2 Mb that does not carry genes annotated as being involved in resistance to antibiotics or heavy metals. All accessory genes in this plasmid belong to the internalin family, a family of virulence-associated genes, and therefore this is the first report of a potential virulence plasmid in the genus *Listeria*.

URL <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1900329/> [29]

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