

Comparison between *Listeria sensu stricto* and *Listeria sensu lato* strains identifies novel determinants involved in infection.

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Abstract

The human pathogen *L. monocytogenes* and the animal pathogen *L. ivanovii*, together with four other species isolated from symptom-free animals, form the "*Listeria sensu stricto*" clade. The members of the second clade, "*Listeria sensu lato*", are believed to be solely environmental bacteria without the ability to colonize mammalian hosts. To identify novel determinants that contribute to infection by *L. monocytogenes*, the causative agent of the foodborne disease listeriosis, we performed a genome comparison of the two clades and found 151 candidate genes that are conserved in the *Listeria sensu stricto* species. Two factors were investigated further *in vitro* and *in vivo*. A mutant lacking an ATP-binding cassette transporter exhibited defective adhesion and invasion of human Caco-2 cells. Using a mouse model of foodborne *L. monocytogenes* infection, a reduced number of the mutant strain compared to the parental strain was observed in the small intestine and the liver. Another mutant with a defective 1,2-propanediol degradation pathway showed reduced persistence in the stool of infected mice, suggesting a role of 1,2-propanediol as a carbon and energy source of listeriae during infection. These findings reveal the relevance of novel factors for the colonization process of *L. monocytogenes*.

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