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GENOME ANNOUNCEMENTS

Complete Genome Sequence of the Animal Pathogen Listeria ivanovii, Which Provides Insights into Host Specificities and Evolution of the Genus Listeria

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We report the complete and annotated genome sequence of the animal pathogen Listeria ivanovii subsp. ivanovii strain PAM 55 (serotype 5), isolated in 1997 in Spain from an outbreak of abortion in sheep. The sequence and its analysis are available at an interactive genome browser at the Institut Pasteur (http://genolist.pasteur.fr/LivaList/).

Listeria ivanovii, a Gram-positive, facultative intracellular pathogen, belongs to the genus Listeria, which comprises eight species that are phylogenetically closely related (12). Listeria monocytogenes and L. ivanovii are the etiological agents of listeriosis, a food-borne infection (11, 13); the other six species are harmless environmental saprophytes. Whereas L. monocytogenes infects both humans and animals, causing meningococcal sepsis and meningitis (1, 4, 9, 14), L. ivanovii predominantly infects small ruminants and cattle, causing septicaemic disease with enteritis, neonatal sepsis, and abortion but no infection of the brain (10). Human cases of L. ivanovii infections are extremely rare, as only seven cases have been reported in the literature since its first isolation in 1955 (3, 8).

Genome sequencing of strain PAM55 was done as previously described (7). Briefly, two libraries (1 to 3 kb) were generated by random mechanical shearing of genomic DNA, followed by cloning of the fragments into pcDNA-2.1 (Invitrogen). A scaffold was obtained by end sequencing clones from a BAC library that was constructed as described previously (2). Sequencing to 8x coverage was done by capillary sequencing following synthesis of BAC library DNA fragments

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The sequence and its analysis are available at an interactive genome browser at the Institut Pasteur (http://genolist.pasteur.fr/LivaList/).

Listeria monocytogenes and L. ivanovii are the etiological agents of listeriosis, a food-borne infection. The other six species are harmless environmental saprophytes. These species differ in their ability to infect different mammal species.

The complete genome sequence of L. ivanovii provides insights into its host specificity and evolution within the genus Listeria.
frameshift mutations (143 ORFs all together). This suggests that L. ivanovii has undergone a recent bottleneck in its evolution, possibly leading to the better adaptation to ruminants. The sequence analysis uncovered features related to host range and virulence, and comparative analysis with the other Listeria species allows the proposal of a refined model for the evolution of virulence in the genus, suggesting a dynamic transition between adaptation to intracellular parasitism and environmental saprophytism.

**Nucleotide sequence accession number.** The L. ivanovii subsp. ivanovii serovar 5 (PAM55/ATCC BAA-678/CIP 107777) genome sequence has been deposited in the EMBL database under accession no. FR687253.

The Listeria consortium dedicates this work to Juergen Wehland, who passed away prematurely.

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