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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 meningoencephalitis, sepsis, abortion, and gastroenteritis (1, 4, 9, 14), *L. ivanovii* predominantly infects small ruminants and cattle, causing septicemic 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 8× coverage was done by capillary sequencing using the 3730xl DNA Analyzer (Applied Biosystems). Finishing to obtain a single contig, definition of coding sequences, and annotation were done as described previously (7) by using CAAT-box software (6). All predicted coding sequences were examined visually.

L. ivanovii subsp. *ivanovii* PAM 55 contains one circular chromosome of 2,928,879 bp (average G+C content, 37.1%, similar to the other *Listeria* genomes). Like all other sequenced listerial genomes, that of *L. ivanovii* contains six complete rRNA operons. Predicted genes included 2,782 protein-coding genes and 67 tRNA genes. Furthermore, genome-wide synteny among the different finished listerial genomes sequenced to date is very high, and no large inversions, deletions, or rearrangements were identified.

Genes encoding functions essential for intracellular multiplication of *L. monocytogenes* and under the control of PrfA are all present in *L. ivanovii* and are missing in nonpathogenic species, except for *Listeria seeligeri* (12). As in other *Listeria* sp., surface proteins are a prominent class; however, *L. ivanovii* encodes 17 soluble internalins, compared to 5 in *L. monocytogenes*. It encodes two paralogs of InlA and three paralogs of InlB. The most surprising finding was the presence of genes encoding a capsule. This capsule, together with the family of soluble internalins and the previously described *L. ivanovii*-specific sphingomyelinase (5), might be one reason for its particular host specificity for ruminants. A specific feature of the *L. ivanovii* genome is that it contains 86 pseudogenes, of which 37 are truncated and 53 (106 open reading frames [ORFs]) are interrupted by

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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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