

**Complete genome sequence of the animal pathogen
Listeria ivanovii, which provides insights into host
specificities and evolution of the genus *Listeria*.**

C. Buchrieser, C. Rusniok, P Garrido, T Hain, M Scotti, R Lampidis, U.
Karst, T Chakraborty, P Cossart, J Kreft, et al.

► **To cite this version:**

C. Buchrieser, C. Rusniok, P Garrido, T Hain, M Scotti, et al.. Complete genome sequence of the animal pathogen *Listeria ivanovii*, which provides insights into host specificities and evolution of the genus *Listeria*.. *Journal of Bacteriology*, American Society for Microbiology, 2011, 193 (23), pp.6787-6788. <10.1128/JB.06120-11>. <pasteur-01423120>

HAL Id: pasteur-01423120

<https://hal-pasteur.archives-ouvertes.fr/pasteur-01423120>

Submitted on 28 Dec 2016

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



GENOME ANNOUNCEMENTS

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

C. Buchrieser,^{1*} C. Rusniok,¹ P. Garrido,^{1,2,3} T. Hain,⁴ M. Scotti,^{3,5} R. Lampidis,⁶ U. Kärst,⁷ T. Chakraborty,⁴ P. Cossart,⁸ J. Kreft,⁶ J. A. Vazquez-Boland,^{3,5} W. Goebel,^{6,9} and P. Glaser^{2*}

Institut Pasteur, Biologie des Bactéries Intracellulaires and CNRS URA 2171, 75724 Paris, France¹; Institut Pasteur, Laboratoire Evolution et Génomique Bactériennes and CNRS URA 2171, 75724 Paris, France²; Grupo de Patogénesis Molecular Bacteriana, Facultad de Veterinaria, Universidad Complutense de Madrid, 28040 Madrid, and Universidad de León, 24071 León, Spain³; Institute of Medical Microbiology, Justus-Liebig-University, Frankfurter Strasse 107, 35392 Giessen, Germany⁴; Microbial Pathogenesis Unit, Centres for Infectious Diseases and Immunity, Infection & Evolution, School of Biomedical Sciences, University of Edinburgh, Edinburgh EH9 3JT, United Kingdom⁵; Biocenter-Microbiology, University of Würzburg, Am Hubland, 97074 Würzburg, Germany⁶; Department of Cell Biology/Cellular Proteomics, Helmholtz-Centre for Infection Research, Inhoffenstrasse 7, 38124 Braunschweig, Germany⁷; Institut Pasteur, Unité des Interactions Bactéries-Cellules, F-75015 Paris, Inserm U604, F-75015 Paris, INRA USC2020, Paris, France⁸; and Max von Pettenkofer Institute for Hygiene and Medical Microbiology, Ludwig-Maximilians-University München, Pettenkoferstrasse 9a, 80336 München, Germany⁹

Received 2 September 2011/Accepted 19 September 2011

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 meningoen- cephalitis, 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). Finish-

ing 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 non-pathogenic 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

* Corresponding author. Mailing address: Institut Pasteur, CNRS URA 2171, 28 Rue du Dr. Roux, 75724 Paris Cedex 15, France. Phone for C. Buchrieser: (33-1)-45-68-83-72. Fax: (33-1)-45-68-84-06. E-mail: cbuch@pasteur.fr. Phone for P. Glaser: (33-1)-45-68-89-96. Fax: (33-1)-45-68-84-06. E-mail: pglaser@pasteur.fr.

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.

We are grateful to Louis Jones for setting up the interactive genome browser LivaList.

This work was supported by the Institut Pasteur, the Centre National de Recherche Scientifique (CNRS), the German Federal Ministry for Education and Research (BMBF) through the Competence Network PathoGenoMik (031U213B), the European Union (FP6), and the Spanish Ministry for Science and Innovation (GEN2006-27774). Work in the laboratory of J.A.V.-B. is supported by The Wellcome Trust.

REFERENCES

1. Aureli, P., et al. 2000. An outbreak of febrile gastroenteritis associated with corn contaminated by *Listeria monocytogenes*. *N. Engl. J. Med.* **342**:1236–1241.
2. Cazalet, C., et al. 2004. Evidence in the *Legionella pneumophila* genome for exploitation of host cell functions and high genome plasticity. *Nat. Genet.* **36**:1165–1173.
3. Cummins, A. J., A. K. Fielding, and J. McLauchlin. 1994. *Listeria ivanovii* infection in a patient with AIDS. *J. Infect.* **28**:89–91.
4. Dalton, C. B., et al. 1997. An outbreak of gastroenteritis and fever due to *Listeria monocytogenes* in milk. *N. Engl. J. Med.* **336**:100–105.
5. Dominguez-Bernal, G., et al. 2006. A spontaneous genomic deletion in *Listeria ivanovii* identifies LIPI-2, a species-specific pathogenicity island encoding sphingomyelinase and numerous internalins. *Mol. Microbiol.* **59**:415–432.
6. Frangeul, L., et al. 2004. CAAT-Box, Contigs-Assembly and Annotation tool-box for genome sequencing projects. *Bioinformatics* **20**:790–797.
7. Glaser, P., et al. 2001. Comparative genomics of *Listeria* species. *Science* **294**:849–852.
8. Guillet, C., et al. 2010. Human listeriosis caused by *Listeria ivanovii*. *Emerg. Infect. Dis.* **16**:136–138.
9. Hof, H., and P. Hefner. 1988. Pathogenicity of *Listeria monocytogenes* in comparison to other *Listeria* species. *Infection* **16**(Suppl. 2):S141–S144.
10. Ivanov, I. 1962. Untersuchungen über die Listeriose der Schafe in Bulgarien. *Monatsh. Veterinarmed.* **17**:729–736.
11. Rocourt, J. 1988. Taxonomy of the genus *Listeria*. *Infection* **16**:89–91.
12. Schmid, M. W., et al. 2005. Evolutionary history of the genus *Listeria* and its virulence genes. *Syst. Appl. Microbiol.* **28**:1–18.
13. Seeliger, H. P. R. 1984. Modern taxonomy of the *Listeria* group—relationship to its pathogenicity. *Clin. Invest. Med.* **30**:217–221.
14. Vazquez-Boland, J. A., et al. 2001. *Listeria* pathogenesis and molecular virulence determinants. *Clin. Microbiol. Rev.* **14**:584–640.