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Complete Genome Sequence of *Mycoplasma putrefaciens* Strain 9231, One of the Agents of Contagious Agalactia in Goats

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***Mycoplasma putrefaciens* is one of the etiologic agents of contagious agalactia in goats. We report herein the complete genome sequence of *Mycoplasma putrefaciens* strain 9231.**

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Mycoplasma putrefaciens is one of the etiologic agents of contagious agalactia in goats, a syndrome listed by the World Organisation for Animal Health (OIE) (1) and characterized by mastitis, arthritis, keratoconjunctivitis, pneumonia, and septicemia (“MAKePS”) (2). It can also be found as a commensal organism in the ear canal (3). This mycoplasma is phylogenetically related to the *Mycoplasma mycoides* cluster, which comprises five major ruminant pathogens: *M. mycoides* subsp. *mycoides*, *M. mycoides* subsp. *capri*, *M. capricolum* subsp. *capricolum*, *M. capricolum* subsp. *capripneumoniae*, and *M. leachii* (4, 5). *M. putrefaciens* was characterized only in 1976 (6). This species is not as frequently isolated as some members of the *Mycoplasma mycoides* cluster (7), although it has a worldwide distribution (3, 8, 9). Since the whole annotated genome of the type strain KS1^T has been recently published (10), an additional *M. putrefaciens* genome will allow comparative analyses to gain insight into the pan genome of the species as well as the intra-species polymorphism.

The genome sequence was determined by the Sanger method (GATC, Constanz, Germany) and resulted in 8.4× average depth. *De novo* assembly was performed using SeqMan (version 7.0; DNASTAR Lasergene, Madison, WI) and resulted in 3 scaffolds. Gap closure was completed by PCR amplification and Sanger sequencing. Annotation was conducted using a customized version of the CAAT-BOX platform (PMID, 14752000) with automatic preannotation for coding sequences (CDS), followed by expert validation as previously described (11).

The complete genome consisted of an 859,996-bp sequence with a global G+C content of 26.96%. It is composed of a single circular chromosome that contains 749 genes, of which 667 cor-

respond to CDS, 44 to pseudogenes, and 38 to structural RNAs. Unlike the genome of strain KS1^T, in which no functional mobile elements were found, a 23.9-kb-long integrative conjugative element (ICE) and a single copy of an IS3 family insertion sequence were identified in 9231, which mainly explains their difference in size. The ICE comprises 16 CDS, including the *traG* and *traE* genes. The last two ICE genes are duplicated in the genome and may represent a vestige of a previous ICE integration.

The availability of high-quality genome sequences, as for *M. putrefaciens* 9231, and comparative analyses with related species will improve our understanding of the pathogenomic evolution of ruminant pathogens.

Nucleotide sequence accession number. The annotated genome sequence was deposited in GenBank under accession no. CP004357 and in the MolliGen database.

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