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Corynebacterium pseudotuberculosis is a Gram-positive, facultative intracellular, pleomorphic, nonsporulating, noncapsulated, nonmotile bacterium that is the etiological agent of caseous lymphadenitis (CLA) in small ruminants and pyogranulomatous reactions, ulcerative lymphangitis, and mastitic, necrotic, and ulcerative dermatitis in cattle, all of which are diseases with medical and veterinary relevance. C. pseudotuberculosis affects several species, including sheep, goat, horse, cattle, llama, alpaca, buffalo, and human. This organism has various survival mechanisms and uses many strategies to adapt to its environment. After infection, the bacteria become encapsulated within walled-off lesions from which they evade immune system-mediated destruction, giving rise to a state of persistence (1–3). The molecular determinants of C. pseudotuberculosis virulence have been described and enable the search for potential targets for the development of new vaccine candidates by “omics” methodologies (4–7).

According to their capacity for nitrate reduction, the strains of C. pseudotuberculosis are divided into two biovars. The organisms that perform the reduction of nitrate are classified into biovar equi, most of which have been isolated from horses and cattle. Bacteria that cannot perform the reduction of nitrate belong to biovar ovis, frequently isolated from sheep and goat (8). However, in cattle there are reports of infection by both biovars (9).

Here, we report the genome sequencing of Corynebacterium pseudotuberculosis 262, the first strain belonging to biovar equi isolated from a bovine host. This strain has been deposited in a collection in Belgium.

C. pseudotuberculosis strain 262 was isolated from cow milk, and the genome sequencing was performed with an Ion Torrent PGM platform chip 318, with a fragment library. A total of 388,943,492 bp were produced, with 166× genomic coverage. Subsequently, the tool FastQC 0.11.4 (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) was used to evaluate the raw data, and FASTX-Toolkit (http://hannonlab.cshl.edu/fastx_toolkit/) was used to remove the reads with quality below Phred 20. The genome assembly was performed by Mira 4.0.2 (http://mira-assembler.sourceforge.net/), which produced 29 contigs with an N50 of 333,604 bp. The manual curation was performed through CLC Genomics Workbench 8 and Artemis 16.0.0 software (10). Automatic genome annotation was performed using Rapid Annotations using Subsystem Technology 2.0 (RAST) (11), and manual curation was performed with Artemis software and the nonredundant protein databases Uniprot (http://www.uniprot.org/) and the National Center for Biotechnology Information (NCBI) (http://www.ncbi.nlm.nih.gov/). tRNAs and rRNAs were predicted using the software tRNAscan-SE 1.21 (12) and RNAmer 1.2 (13), respectively. The plasticity of pathogenicity islands (PAIs) was assessed with the Pathogenicity Island Prediction Software 1.1 (PIPS) (14), using C. glutamicum strain ATCC 21831 (CP007722.1) as the reference genome, which identified 10 pathogenicity islands.

The C. pseudotuberculosis strain 262 genome contains 2,325,749 bp, a G+C content of 52.8%, 2,022 coding sequences (CDS), 50 pseudogenes, 48 tRNAs, and 12 rRNAs.

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