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Draft Genome Sequence of *Corynebacterium pseudotuberculosis* Strain PA07 Biovar *ovis*, Isolated from a Sheep Udder in Amazonia

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ABSTRACT In this work, we present the draft genome sequence of *Corynebacterium pseudotuberculosis* strain PA07 biovar *ovis*, isolated from a caseous secretion from a sheep udder in Pará, Brazil. The genome contains 2,320,235 bp, 52.2% G+C content, 2,191 coding sequences (CDSs), five pseudogenes, 48 tRNAs, and three rRNAs.

*C*orynebacterium pseudotuberculosis is a Gram-positive, facultative intracellular, pleomorphic, nonsporulating, noncapsulated, nonmotile bacterium that, together with *Mycobacterium*, *Nocardia*, and *Rhodococcus*, forms the CMNR group which shares specifics characteristics, such as (i) high G+C content and (ii) specific cell wall organization, characterized by the presence of peptidoglycan, arabinogalactan, and mycolic acids (1, 2).

C. pseudotuberculosis is the etiological agent of caseous lymphadenitis (CLA), ulcerative lymphangitis, mastitis (clinical and subclinical), and ulcerative dermatitis. CLA is characterized by the formation of abscesses in the superficial lymph nodes and subcutaneous tissues (3, 4). CLA is a widespread disease that has been reported all over the world (5). This disease is associated with direct economic losses due to the progressive reduction in weight gain, depreciated wool and skin, reduced milk production, and eventually death caused by toxemia of the infected animals. Moreover, this bacterium presents significant zoonotic potential (5).

C. pseudotuberculosis presents some variable tools for persistence and escape from the immune system of the host (3). Thus, the molecular study of the genome of this pathogen and the search for new target genes is an important step for vaccine development (6, 7).

Herein, we present the draft genome of *C. pseudotuberculosis* strain PA07 biovar *ovis*, isolated from a Santa Inês sheep udder in Pará, Brazil. To the best of our knowledge, we report the first recovery of *C. pseudotuberculosis* from an abscess located in sheep udder in the state of Pará. This strain is part of the collection of Laboratory of Genomics and System Biology located at the Federal University of Pará, Belém, Pará, Brazil.

The genome sequencing was performed using an Ion Torrent personal genome machine (PGM) (Thermo, Fisher) with a fragment library. The *de novo* assembly strategy was performed using SPAdes genome assembler software version 3.9.0 (8). The assembly generated seven contigs with 2,320,235 bp. The contigs were automatically annotated using Rapid Annotations using Subsystems Technology (RAST) (9). The genome has 2,191 coding sequences (CDSs), five pseudogenes, 48 tRNAs, three rRNAs, and a G+C content of 52.2%.

Accession number(s). The *C. pseudotuberculosis* whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. MQVG00000000. The version described in this paper is MQVG01000000.

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