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Whole-Genome Sequence of *Corynebacterium pseudotuberculosis* PAT10 Strain Isolated from Sheep in Patagonia, Argentina

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In this work, we report the complete genome sequence of a *Corynebacterium pseudotuberculosis* PAT10 isolate, collected from a lung abscess in an Argentine sheep in Patagonia, whose pathogen also required an investigation of its pathogenesis. Thus, the analysis of the genome sequence offers a means to better understanding of the molecular and genetic basis of virulence of this bacterium.

The incidence of caseous lymphadenitis (CLA) is high in many regions of the world, resulting in huge and significant economic losses in agribusinesses, as it is responsible for a decrease in wool production and carcass quality (3). The disease is endemic in flocks in the provinces of Chubut and Santa Cruz in the Southern Patagonia region of Argentina, thereby leading to an outrageous prevalence rate of about 70% within individual flocks in Patagonia (4). Diseases caused by *Corynebacterium pseudotuberculosis* present in various clinical forms, and sheep and goats are affected by CLA (1). Analysis of the genome sequence improves our understanding of the molecular and genetic basis of the virulence of the bacterium. We hereby report the whole-genome sequence of *C. pseudotuberculosis* PAT10 as determined using the SOLiD platform. In total, we generated 27,858,221 mate-paired short reads (25 bp) of usable sequences (296-fold coverage). Furthermore, a hybrid *de novo* assembly approach was applied using 16,885,903 short (25-bp) mate-paired SOLiD filtered reads; that strategy allowed close gaps without a bench work time cost (2). The automatic and manual annotations were done using several algorithms in a multistep process.

For structural annotation, the following software was used: FgenesB (gene predictor); RNAmmer (rRNA predictor) (5); tRNA-scan-SE (tRNA predictor) (6); and Tandem Repeat Finder (repetitive DNA predictor) (http://tandem.bu.edu/trf/trf.html). Functional annotation was performed using similarity analyses and public databases and by InterProScan analysis (8). Manual annotation was performed using Artemis software (7). Identification and confirmation of pseudogenes in the genome were carried out using CLCBio Workbench 4.0.2 software. Manual analysis was performed based on the Phred quality of each base combined with analysis of the depth of coverage of the frameshift region. That analysis allowed the identification of false-positive pseudogene results. The genome of the PAT10 strain consists of a 2,335,323-bp circular chromosome, and the average G+C content of the chromosome is 52.19%. The genome was predicted to contain 2,079 coding sequences (CDS), four rRNA operons, 49 tRNAs, and 61 pseudogenes.

The characterization of the PAT10 genome should identify and unravel the mechanisms of virulence of this pathogen through comparative analyses performed with other sequenced genomes of the genus and the same species, thereby allowing the development of new diagnostics kits and vaccines.

Nucleotide sequence accession number. The genome sequence obtained in this study has been deposited in the GenBank database under accession number CP002924 (chromosome).

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