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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Corynebacterium pseudotuberculosis* Strain 1/06-A, Isolated from a Horse in North America

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***Corynebacterium pseudotuberculosis* causes disease in several animal species, although distinct biovars exist that appear to be restricted to specific hosts. In order to facilitate a better understanding of the differences between biovars, we report here the complete genome sequence of the equine pathogen *Corynebacterium pseudotuberculosis* strain 1/06-A.**

Corynebacterium pseudotuberculosis is a cause of disease in several host species. Two distinct biovars have been described (1); *C. pseudotuberculosis* bv. ovis, which predominantly affects small ruminant species (primarily sheep and goats), and *C. pseudotuberculosis* bv. equi, which predominantly affects horses. Significantly, strains belonging to *C. pseudotuberculosis* bv. equi are unable to cause infection in small ruminants. Previous studies have revealed that *C. pseudotuberculosis* represents a largely clonal population (2). Clearly, however, each biovar has adapted to a particular host, although the nature of these adaptations is currently unclear.

Most previously sequenced strains of *C. pseudotuberculosis* belong to biovar ovis, and here we report the genome sequence of *C. pseudotuberculosis* 1/06-A, an equine isolate originating from North America.

The *C. pseudotuberculosis* 1/06-A genome was sequenced using 454 GS-FLX and Solexa 50-bp paired-end sequencing. Reads were assembled using Velvet (8) and CABOG (Celera assembler with the best overlap graph) (5), and gaps were closed using unmapped 454 and Illumina reads.

Structural annotation was achieved using the following software: FgenesB (a gene predictor); RNAmmer (an rRNA predictor) (3); tRNA-scan-SE (a tRNA predictor) (4); Tandem Repeat Finder (to predict repeat DNA regions; http://tandem.bu.edu/trf/trf.html). Functional annotation was performed using InterProScan (7) analysis and homology analyses using public databases. Manual annotation was then completed using Artemis software (6).

The presence of pseudogenes within the genome was determined using CLCBio Workbench 4.02 software. Manual analysis was also conducted based on the Phred quality of each base, and with analysis of coverage depth at the frameshift region allowed identification of false-positive pseudogene results.

The *C. pseudotuberculosis* 1/06-A genome consists of a single 2,279,118-bp circular chromosome with an average G+C content of 52.20%. The genome was predicted to contain 1,963 coding sequences (CDSs), four rRNA operons, and 49 tRNAs. In addition, 103 pseudogenes were identified.

The sequencing of this isolate will allow comparison of genomes derived from the two distinct biovars and should offer insights into the organism's host specificity.

Nucleotide sequence accession number. The genome sequence described in this study has been deposited in the GenBank database under the accession number CP003082.

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