Complete Genome Sequence of *Corynebacterium pseudotuberculosis* Strain E19, Isolated from a Horse in Chile


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*Corynebacterium pseudotuberculosis* is related to several diseases infecting horses and small ruminants, causing economic losses to agribusiness. Here, we present the genome sequence of *C. pseudotuberculosis* strain E19. The genome includes one circular chromosome 2,367,956 bp (52.1% G+C content), with 2,112 genes predicted, 12 rRNAs, and 48 tRNAs.

The genome was automatically annotated using Rapid Annotations using Subsystem Technology (RAST) (10). The manual curation of the annotation was performed using Artemis software (9) and the nonredundant (nr) protein database of the National Center for Biotechnology Information (NCBI) and UniProt (http://www.uniprot.org). CLC Genomics Workbench 8 software was used to control indel errors in homopolymer regions. rRNAs and tRNAs were predicted using RNAmmer (11) and tRNAScan-SE (12) software, respectively.

The genome includes one circular chromosome of 2,367,956 bp (52.1% G+C content), and 2,112 genes were predicted, of which 565 (26.7%) were classified as hypothetical proteins, with 12 rRNAs and 48 tRNAs; 10 pseudogenes were also identified.

**Nucleotide sequence accession number.** The genome project has been deposited in GenBank under the accession number CP012136.

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**REFERENCES**


