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GENOME ANNOUNCEMENT

Whole-Genome Sequence of *Corynebacterium pseudotuberculosis* Strain Cp162, Isolated from Camel

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***Corynebacterium pseudotuberculosis* is a pathogen of great veterinary and economic importance, since it affects livestock, mainly sheep and goats, worldwide, together with reports of its presence in camels in several Arabic, Asiatic, and East and West African countries, as well as Australia. In this article, we report the genome sequence of *Corynebacterium pseudotuberculosis* strain Cp162, collected from the external neck abscess of a camel in the United Kingdom.**

Corynebacterium pseudotuberculosis is a facultative intracellular pathogen which causes caseous lymphadenitis (CLA) in sheep and goats, ulcerative lymphangitis in horses, and diseases in cattle and in humans (11). In camels, *C. pseudotuberculosis* affects almost 10% of the population in a herd (1). Arthritis, periarthritis, and pleuritis in camels have been found in Gran Canaria island, Spain (13).

CLA causes the formation of abscesses in large superficial lymph nodes and occasionally in the lymph nodes of internal organs in small ruminants and mammals other than humans, yet it has a different lesion nature in camels (5). Early reports of CLA in sheep from Saudi Arabia (8) and nearby Middle East countries describe the disease prevalence in camel herds. The most prevalent biovar in camelids has long been described as biovar ovis (15), but further studies have indicated the susceptibility of dromedary camels to biovar equi in a close environment with CLA-affected horses or cattle (14).

CLA was first reported for United Kingdom goat and sheep flocks in 1990 and 1991, respectively (4, 10). The *C. pseudotuberculosis* strain Cp162 was obtained from an external neck abscess of a camel in 1999 and was originally designated W00644. The biochemical characteristics were determined using the API Coryne test (bioMérieux, Marcy-l'Etoile, France), according to the manufacturer's instructions. Cp162 is nitrate positive and was typed using a multilocus sequence typing (MLST) technique by the Moredun Research Institute whose sequence type (ST) was 3 (2).

We sequenced the genome of Cp162 using a fragment library of the SOLiD v3 Plus sequencing platform (Applied Biosystems), generating 75,659,346 reads of 50 bp in length. After quality filtering (9), reads representing an average Phred quality of less than 20 were removed, followed by the correction of sequencing errors with the SAET software program. In total, 31,568,756 reads with a high quality score were selected, with 686-fold coverage, considering the size of the reference genome used (2.3 Mb), that of *C. pseudotuberculosis* strain FRC41 (NC_014329). The reads were mapped against the reference genome of *C. pseudotuberculosis* 316 (CP003077) through the CLC Genomics Workbench, generating a genome scaffold containing gaps, which were resolved by recursive alignments of short reads (3) and manual curation.

The functional annotation of the genome for open reading frame (ORF) prediction was performed using the software program FgenesB (Softberry). The software program RNAmmer (6) was used for the prediction of rRNA using hidden Markov models (HMM); to identify transfer RNAs (tRNAs), the tRNAscan-SE program was used (7).

Identification of protein domains and families was performed with InterProScan software (16), which integrates several related databases. The nonredundant protein database of NCBI (nr) was used to characterize the coding sequences (CDS) with the help of the Artemis software tool (12). Thus, the genome of Cp162, having a size of 2,293,464 bp, 52.17% GC content, 2,002 coding sequences, 4 rRNA operons, 49 tRNA genes, and 87 pseudogenes, was deposited in the NCBI database.

Further genome analysis will provide deep insight into the virulence of this pathogen at the molecular and genetic levels and will aid in detecting effective vaccine and drug targets in postgenomic studies.

Nucleotide sequence accession number. The genome sequence obtained in this study has been deposited in the GenBank database under accession number CP003652.

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