TITLE: COMPARATIVE GENOMIC STUDY OF *Corynebacterium pseudotuberculosis* STRAIN 226 (BIOVAR *ovis*)

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ABSTRACT: *Corynebacterium pseudotuberculosis* is a gram-positive, facultative intracellular, non-sporulating and non-encapsulated bacterium, it is non-motile although it has fimbriae, and can assume coccoid or filamentous forms (pleomorphic). This pathogen has two biovars: *ovis*, which usually affects small ruminants and causes caseous lymphadenitis, and biovar *equi*, more common in equines, bovines, camelids and bubalines, causing ulcerative lymphangitis. Their infection can lead to carcass condemnation, for example, and consequently, economic losses to the agricultural industry around the world. Currently, there is no vaccine effective against these diseases. To obtain a better understanding of these species biologically, the main objective of this work is to analyze, using comparative genomics, the strain *C. pseudotuberculosis* 226 biovar *ovis*, isolated from a caprine in California, comparing it to other strains from biovars *ovis*, such as C231, 1002, I19, PAT10, 42/02-A, 3/99-5, FRC41, 267, P54B96, 48252, CS_10, Ft_219367 and VD57 and *equi* such as CIP 52.97, 1/06-A, 316, 31, 258, Cp162. The synteny analysis revealed highly conserved gene order between strain 226 and other biovar *ovis* strains. Phylogenomic analyses showed that the strains I19 and 267 are, respectively, the closest and the more distant phylogenetically from strain 226. Among biovar *equi* strains, the one with the greater phylogenomic proximity to strain 226 was strain 1/06-A. Eight pathogenicity islands were predicted, with *C. pseudotuberculosis* best characterized virulence genes in literature being present in island 1. No new regions related to virulence genes could be found compared to other strains, 248 orthologous genes could be found between strains I19, 267 and 226, while 282 orthologous genes could be found between strains 258, 1/06-A and 226. Based in this study it is possible to assume that strains from biovar *ovis* have a little varied gene repertory and strains from biovar *equi* have less genes shared with strain 226, reinforcing the genetic diversity between these biovars.

Keywords: *C. pseudotuberculosis*, goat, pathogenic, biovar *ovis* and *equi*.

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