

# Genomic analysis of *Corynebacterium pseudotuberculosis* strain 262

Raquel Enma Hurtado Castillo<sup>1</sup>, Marcus Vinicius Canário Viana<sup>1</sup>, Anne Cybelle Pinto Gomide<sup>1</sup>, Vasco A. de C. Azevedo<sup>1</sup>, Rommel Thiago Jucá Ramos<sup>2</sup>, Artur Silva<sup>3</sup>

*1 UFMG*

*2 UNIVERSIDADE FEDERAL DO PARA*

*3 UFPA*

## Abstract

*Corynebacterium pseudotuberculosis* is a Gram-positive and facultative intracellular pathogen, causing important economic losses mainly in the ruminant production. The biovar ovis is nitrate negative and causes caseous lymphadenitis in sheep and goats, while biovar equi is nitrate positive and causes ulcerative lymphangitis, mastitis, and oedematous skin disease in a wide range of hosts. *C. pseudotuberculosis* 262 is an equi biovar strain isolated from cow milk. Genomic and phylogenomic analysis of *C. pseudotuberculosis* strains have been shown this strain as the most external of equi genomes and the closest one to ovis. In order to better characterize its genomic features, we present here a comparative genomic analysis between strain 262 and other 52 strains of *C. pseudotuberculosis*. A phylogenetic analysis based on a gene presence-absence matrix among strains of *C. pseudotuberculosis* does not cluster strain 262 in any of the two different clusters (biovars equi and ovis). Accessory genes shared between strain 262 and equi strains were predicted, such as a toxin and antirepressor, immunity-specific protein, CAAX protease self-immunity, serine hydrolase and superoxide dismutase. Accessory genes among 262 and ovis strains are genes related to ABC transporter protein, spermidine synthase, secreted protein and surface-anchored membrane protein. Sixteen genomic islands were predicted. Part of an island PiCp1 is a region of 10 Kb shared only with biovar equi, which presents CRISPR-associated protein. We also identified regions shared only with biovar ovis strains. In addition, strain 262 presented unique regions, containing 49 genes, such as MFS transporter, secreted protein, and hypothetical proteins, that could carry genes potentially associated with virulence. Finally, the pan-genomic analysis report accessory and unique genes that allow characterization of the strain 262. These findings enable us to better characterize the unique genomic features of strain 262 and generate new hypothesis to understand the differentiation of the *C. pseudotuberculosis*.

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