

TITLE: *IN SILICO* CHARACTERIZATION OF PROPHAGE SEQUENCES IN *Corynebacterium pseudotuberculosis* GENOMES

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ABSTRACT:

Corynebacterium pseudotuberculosis is a pathogenic bacterium that affects meat animals, classified into the biovars *equi* (nitrate reductase-positive) or *ovis* (nitrate reductase-negative) and causes significant harm in the livestock sector. This bacterium can be influenced by external genetic material, like horizontal gene transfer, as phage infection that can lead bacterial genomes to express atypical characteristics. However, the infection of phages on *C. pseudotuberculosis* genomes was not explored on the light of bioinformatics, so the aim of this study was to relate the presence of phages in *C. pseudotuberculosis* genomes and deduce the possible biological information of these phage-related sequences. 35 genomes of *C. pseudotuberculosis* had been analysed and seventeen phage-related sequences were found in those genomes. The *ndrF2* gene was conserved in all strains and had a better bootstrap differentiating between biovars of this species than the *rpoB* gene. Eight genes were conserved in all strains of the biovar *ovis* as a remnant prophage region of 5.976 Kb. The *ychF* gene was present in the biovar *ovis* and some strains of the biovar *equi*, while a hypothetical protein of 134 aminoacids was present in some strains of the biovar *equi*. The synteny analysis showed a high conservation of the phage remnant region in the genomes of *C. pseudotuberculosis*. The RNA-Seq data results showed that some prophage-related sequences were differentially expressed under abiotic stress. Yet, some sequences did not have products or homologous domains in protein databases, such as a hypothetical protein with 75 amino acids that is conserved in all strains of biovar *ovis* and was induced by all applied stresses *in vitro*, indicating that it is an important target for investigation in future studies.

Keywords: Prophage decay, comparative genomics, genome synteny, phylogenetic.

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