

**TITLE: IDENTIFICATION AND CHARACTERIZATION IN SILICO CLUSTER OF THE *tox* GENE IN *Corynebacterium pseudotuberculosis***

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**ABSTRACT:**

*Corynebacterium pseudotuberculosis* is pathogenic specie of veterinary interest, relevance and potentially diphtheria toxin producer. *C. pseudotuberculosis* has two biovars, *equi* (positive nitrate), which mainly infects large ruminants and horses, causing ulcerative lymphangitis and edematous disease of the skin; and *ovis* (negative nitrate), that affects small ruminants causing caseous lymphadenitis, also causing chronic subacute lymphadenitis in humans. Recently, the *tox* gene in *C. pseudotuberculosis* lineage 31 was identified suggesting its potentially toxigenicity. The objective was to characterize the grouping of the *tox* gene present in *C. pseudotuberculosis* lineage 31. For initial characterization of the *tox* gene cluster, strains of *C. pseudotuberculosis*, *C. diphtheriae* and *C. ulcerans* were recovered from GenBank. Gegenes was used for comparison of *C. pseudotuberculosis equi* using *C. pseudotuberculosis* 31 as a reference. The PHAST software was used for identification of phage sequences within the genome of the target strain. To compare the *tox* gene cluster among the different species, the Artemis Comparison Tool was used. Once the reference analysis of the genome of *C. pseudotuberculosis* 31 comparing with other *equi* genomes was finished, except strains isolated in Egypt, it was possible to identify a region of 115961 bp exclusive in the genome of *C. pseudotuberculosis* 31 and absent in the other *equi* evaluated, which contains the *tox* gene. Analyzing the conservation of the genomic order of *Corynebacterium* genomes, the *tox* gene region present in the *C. pseudotuberculosis* 31 chromosome is highly conserved in relation to *C. diphtheriae* and *C. ulcerans*, carriers of this gene, and is absent on the chromosome of *C. pseudotuberculosis* 1002, biovar *ovis*. When investigating the genome of *C. pseudotuberculosis* 31 for putative prophages using the PHAST web tool, only an intact prophage was found, a region that coincides with the exclusive region in *C. pseudotuberculosis* 31. In the majority of the prophage region, there is a significant similarity to FAGO\_Coryne\_BKF\_NC\_0097991, where most were identified as hypothetical proteins or phages, also containing integrase and terminase, and coinciding with the region identified by the Gegenes software in the genome of *C. pseudotuberculosis* 31. The presence of phages in the proximity of the *tox* gene indicates that this gene, extremely important for virulence of the species, was probably acquired by horizontal transfer.

**Keywords:** *Corynebacterium pseudotuberculosis*, *tox* gene, ruminants, biovar *ovis* and *equi*.

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