

TITLE: COMPLETE SEQUENCING OF *sodA* AND *sodC* GENES IN *Corynebacterium pseudotuberculosis* ISOLATES OF GOAT AND SHEEP FROM THE SEMI-ARID REGION OF PERNAMBUCO

AUTHORS: ROSA, D. S.; GONÇALVES, Y. S.; NERI, A. O.; AMANSO E. S.; MEIRA, M. L.; NOGUEIRA, J. F.; FRANÇA, C. A.; GOUVEIA, G. V.; FELIX, W. P.; COSTA, M. M.

INSTITUTION: UNIVERSIDADE FEDERAL DO VALE DO SÃO FRANCISCO, CAMPUS CIÊNCIAS AGRÁRIAS, PETROLINA, PE (RODOVIA BR-407, KM 12 LOTE 543, S/N – PROJETO DE IRRIGAÇÃO NILO COELHO, CEP 56300-000, PETROLINA – PE, BRAZIL)

ABSTRACT:

Corynebacterium pseudotuberculosis is the etiologic agent of caseous lymphadenitis, which affects mainly goats and sheep. One of the main survival factors of the bacteria is a superoxide dismutase (SOD, EC 1.15.1.1), a multimeric metalloenzyme that is part of the defense system against the free radicals of various intracellular pathogens. The SOD can be classified into four groups according to its cofactor: Fe⁺⁺ (*sodB*), Mn⁺⁺ (*sodA*), Ni⁺⁺ (*sodD*), Cu⁺⁺/Zn⁺⁺ (*sodC*). In the complete sequence of the genome of *C. pseudotuberculosis*, it is observed a presence of genes encoding two isoforms of the enzyme superoxide dismutase (*sodA* and *sodC*), which suggests new studies these genes. Despite the existence of several types of vaccines available, efficacy in the prevention of this disease is still low. However, recent researches have shown that recombinant vaccines confer greater safety and efficacy on other types of vaccines, especially for intracellular microorganisms. The present work aimed at the complete sequencing of *sodA* and *sodC* genes in clinical isolates of *C. pseudotuberculosis*. For that, three positive isolates were used for the target genes, which were identified in previous work, from different properties of the state of Pernambuco. Using PCR, the complete amplification of the genes in each sample was obtained, and the amplification products were sent to the private company for sequencing. The electropherograms were obtained by bidirectional Sanger method, analyzed by Phred program to verify their quality, the sequence assembled by the CAP3 tool through BioEdit, and the Basic Local Alignment Search Tool (BLAST) was used to identify similarities with sequences in databases. Then, the sequence obtained of the genes was analyzed in the programs Sequence Manipulation Suite (SMS): Color Align Conservation and Color Align Properties, ORF finder, SMARTBLAST, Conserved Domains and PROVEAN. Thus, complete sequencing of the *sodA* and *sodC* genes was obtained from the three samples analyzed, with 642 nt and 213 aa, 621 nt and 206 aa, respectively. No mutations were found that could affect protein functionality generated by each gene. Therefore, this study obtained the first complete sequencing of *sodA* and *sodC* genes in *C. pseudotuberculosis* species.

Keywords: *Corynebacterium pseudotuberculosis*, *sodA*, *sodC*, complete sequencing

Development Agency: Fundação de Amparo à Ciência e Tecnologia de Pernambuco (FACEPE) and Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq)