

**Title: TRANSFER RNA AND SMALL RNA DIFFERENTIAL EXPRESSION IN *Corynebacterium pseudotuberculosis* STRAIN 258 UNDER ABIOTIC STRESSES**

**Authors** Silva, Y.R.O.<sup>1</sup>, Sá, P.C.G.<sup>1</sup>, Barreto, D.F.<sup>1</sup>, Alves, J.T.C.<sup>1</sup>, Dias, L.M.<sup>1</sup>, Cavalcante, A.L.Q.<sup>1</sup>, Veras, A. A. O.<sup>1</sup>, Pinto, A.C.<sup>2</sup>, Ramos, R.T.J.<sup>1</sup>, Silva, A.<sup>1</sup>, Azevedo, V.<sup>2</sup>, Carneiro, A.R.<sup>1</sup>

**Institution** <sup>1</sup> UFPA – Federal University of Para (Rua Augusto Corrêa, 1 - Guamá, Belém - PA, 66.075-110), <sup>2</sup> UFMG – Federal University of Minas Gerais (Av. Antônio Carlos, 6627 – Pampulha, Belo Horizonte - MG, 31.270-901)

**Abstract:**

*Corynebacterium pseudotuberculosis* is the causative agent of caseous lymphadenitis in ovines and caprines. This disease is widely distributed over the world and causes many economic losses due to carcass condemnation, devaluation of skin and reduction in production of milk, wool and meat. During infection process, bacteria are engulfed by macrophages and exposed to stressful conditions, including low pH, heat-shock and high saline concentrations. To survive under these conditions, bacteria may use their small RNAs (sRNA) to regulate gene expression by base-pairing with messenger RNAs (mRNA) to control their availability or by changing sRNA conformation itself to control the availability of translation start sites of downstream genes. There are also two other well-characterized classes of non-coding RNA: ribosomal RNA (rRNA) and transfer RNA (tRNA), that act in the process of translation. The objective of the present study was to predict and to annotate sRNAs and tRNAs of *C. pseudotuberculosis* strain 258 and analyze changes in their expression profile between three stress conditions (acidic, thermal and osmotic) and a control. INFERNAL was used to predict the RNAs, using covariance models from Rfam database under the taxonomic suborder "*Corynebacterineae*". In CLC Genomics Workbench, the reads from the RNA-Seq experiments were aligned with the complete genome and expression values were generated and analyzed. Using the default parameters, INFERNAL has predicted 107 RNAs from 19 different families. Only 12 sRNAs could be annotated after filtering out the results referring to rRNAs and tRNAs already annotated in the genome and only *trans*-encoded sRNAs were used in differential expression analysis. 6C RNAs had higher expression on osmotic stress, tmRNA had no significant differential expression and RNase P gene was down regulated on osmotic stress. Most tRNA genes were upregulated in at least two conditions, and only aspartic acid was down regulated on low pH. 6C RNAs might have a role in stress response and tRNAs that were upregulated may reveal the amino acid content of stress response genes. Differential expression of both types of RNA may be related to the expression of genes involved in virulence.

**Keywords:** *Corynebacterium pseudotuberculosis*, non-coding RNA, RNA-Seq, small RNA, transfer RNA.

**Financial support:** CAPES, CNPq, UFPA, FAPESPA