

**TITLE:** Expression of DNA repair genes in *Corynebacterium pseudotuberculosis* in response to threats of abiotic stress

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**ABSTRACT:**

*Corynebacterium pseudotuberculosis* is the pathogen that causes infectocontacting diseases, which bring losses to the world agribusiness. Pathogenic bacteria, such as *C. pseudotuberculosis*, are exposed to a host infection like changes in temperature, media molarity and pH. These conditions can generate DNA damage to the bacterial genome. In this study, 40 genomes of *Corynebacterium pseudotuberculosis* obtained through NCBI were used. We sought to identify genes related to DNA repair in the annotated genomes. After identification of the genes, an expression of genes was evaluated with the TopHat pipeline and Cufflinks, in some lineages: 258 and 1002, under the conditions of thermal stress, osmotic, acid, and a control condition. Analysis of gene expression was done using the foldchange of 2. The UvrABCD complex genes that participate in conserved excision repair in the lineages. In the expression analysis only the *uvrC* and *uvrD* genes were differentially expressed, and in some studies show that mutations in this gene cause an increase in hypersensitivity to DNA-damaging agents. The BER system in most cases has enzymes that overlap functions, meaning that the substrate can recognize more than one enzyme. This fact is observed with the *nfo* gene and the *xth* gene, the *nfo* gene is absent at all lines. It was observed that the Cpt-UNG gene is hyperexpressed under pH and osmotic conditions, this gene preventing mutations, increases the resistance to intrinsic nitrogen (RNI). The genes that act in the MMR system are absent in *Corynebacterium pseudotuberculosis*. The interface of DNA repair systems and the declaration of these genes in *C. pseudotuberculosis* can allow identification of the essential components for the growth and visibility of organisms.

**Keywords:** RNA-seq, *Corynebacterium pseudotuberculosis*, DNA repair.

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