## Characterization of phage sequences on Corynebacterium pseudotuberculosis genomes

Flavia Figueira Aburjaile, Amália Raiana F. Lobato, Luís Carlos Guimarães, Ana Lídia Queiroz Cavalcante, Kenny da Costa Pinheiro, Adonney Allan de Oliveira Veras, Rafael Azevedo Baraúna, Artur Silva, Rommel Thiago Jucá Ramos

Institute of Biological Sciences, Federal University Pará, Belém, Pará, Brazil

The phage infection in bacterial genomes is a process that can lead to expression atypical characteristics, such as, virulence or resistance to antimicrobials. The detection of phage on pathogenic bacteria, such as, Corynebacterium pseudotuberculosis, may explain the virulence phenotype expression and the adaptation mechanisms used to survive in different hosts. C. pseudotuberculosis is a pathogenic bacterium that affects cattle and it is classified on biovars equi (positive nitrate reductase) and *ovis* (negative nitrate reductase) which cause expressive losses in the livestock. 17 sequences of phage were found in *C. pseudotuberculosis* genomes. The *ndrF2* gene was conserved in all 35 strains analyzed, the ychF gene is conserved in all strains of biovar ovis and some strains of biovar equi. In addition, hypothetical protein (405 nc) is present in some strains of biovar equi and 8 sequences were conserved in all strains of biovar ovis. These sequences presented synteny, and some of them are differentially expressed under conditions of abiotic stresses. The nrdF2 gene present in all the strains and related to phages is a precise marker to differentiate the biovars of bacteria by phylogeny performed. This study showed that the phage sequences were highly conserved among strains of C. pseudotuberculosis and, one being possible to be phylogenetic marker to differentiate the biovars. The differential expression of these sequences in response to abiotic stress and characterization of products in silico indicates the importance of the role of those sequences in the survival of the bacteria. However, many of these sequences still need to be annotated through functional prediction to products or homologous domains in databases, the hypothetical protein with 228 pair bases was induced in all the stresses applied in vitro and is conserved in all strains of biovar *ovis*, it is a potential target to be investigated in further studies.

Funding: CNPq, CAPES and PROPESP.