

Comparative genomic analysis of *Corynebacterium pseudotuberculosis*: A quest for biofilm biosynthesis genes.

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Abstract

Corynebacterium pseudotuberculosis is the etiological agent of Caseous Lymphadenitis (CLA) in sheep and goats (*C. pseudotuberculosis* biovar ovis), and present some cases of infections in large ruminants as well. Our laboratory studies *C. pseudotuberculosis* as a model organism and, in 2013, Soares et al. performed a pan-genomic study of *C. pseudo-tuberculosis* using fifteen strains. After that, a hundred and eight strains were sequenced and deposited in the National Center for Biotechnology Information (NCBI), and several studies such as Exoproteome, Transcriptome, and Proteome were done. Now, we want to associate these studies and explore other areas of pan-omics analyses. In this work, we propose to research evidence of genes belonging to the biosynthesis of biofilm in *C. pseudotuberculosis* genomes. For this, thirty *C. pseudotuberculosis* samples from lymph nodes of abscesses of goats and sheep from Pernambuco-Brazil were isolated. All strains belonged to the biovar ovis group, proven by the nitrate reductase biochemistry test and multiplex PCR. These strains were sequenced by the Illumina Hiseq paired-end platform with 450bp insert, and 151bp per reads length. All strains have an average genome size of 2,34Mb, the genomes were de novo assembled using SPAdes v. 3.9.1 software with 121 k-mers, and we got five or six contigs per genome with coverage of 971.40 fold. After, all the thirty genomes were deposited in the GenBank database in NCBI. For comparative genomic analyses, we used the programs Gegenees v. 3.1, BRIG v. 0.95, MAUVE using progressiveMauve and ACT: the Artemis Comparison Tool. Previous results described that among the thirty *C. pseudotuberculosis* samples, CpCap3W and CpOVI03 strains showed characteristics of biofilm formation, different from CpOvi2C and CpCAPJ4 strains. From the results of comparative genomics, the strains are 99.5% similar and very clonal. We could not find a concise difference about the presence or absence of genes belonging to biofilm biosynthesis among the studied strains. However, in the Cp38MAT strain, a unique region with a cluster of eight genes was found. Among these genes, we identified the dps gene (DNA starvation/stationary phase protection protein) involved in iron homeostasis, in addition to 5 proteins involved in the process of transport and plas-matic membrane structure, and VanZ gene (Glycopeptide antibiotics resistance protein). Probably, this metabolic process of biofilm biosynthesis may be better clarified through specific transcriptome and proteome studies.

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