

Biovar equi versus ovis: What genetically differentiate them?

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Abstract

Corynebacterium pseudotuberculosis is a pathogenic bacteria that causes significant economic losses in global livestock. This organism is classified into biovars ovis and equi. Strains from biovar ovis are more clonal and infect small ruminants, such as goats and sheep, and eventually humans. Strains from biovar equi infect bigger animals such as bovines, buffaloes and horses causing different diseases. This study aims to extend a previous work in which genes that could differentiate the biovars equi and ovis were identified in six *C. pseudotuberculosis* genomes isolated in Mexico. All the 53 complete and non-redundant genomes available from NCBI were used. The Bacterial Pan Genome Analysis (BPGA) pipeline was used to estimate the pangenome and find specific genes of genome subgroups. Groups of orthologs were defined with a similarity cutoff of 70%, using USERACH tool. The results show a pangenome of 2,290 and a core genome of 1,277 genes. The core genome can be used to identify new targets for vaccine and diagnosis methods. The total number of biovars exclusive genes is 265, 65 of them from biovar ovis (15 with known function) and 200 from biovar equi (54 with known function). As expected, we identified genes known to differentiate the biovars, such as the nitrate reductase operon narGHIJ. In addition, the results corroborate the previous study with Mexican strains that pointed CRISP-Cas genes and a restriction endonuclease type III (Restriction Modification System) as exclusive from biovars equi and ovis, respectively. The remaining genes will be further studied.

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