POSTER - DNA AND GENOMICS

# PANGENOME ANALYSIS OF CLOSTRIDIUM SCINDENS

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Commensal bacteria of the human intestinal microbiota are important for the regulation of the growth of pathogenic species. Recent studies propose that the metabolic activity of host bile acids by C. scindens protects against C. difficile infection. Proliferation and infection of C. difficile occur under conditions of dysbiosis and it has been proposed that a type of primary bile acid induces germination of its spores, in contrast, the conversion of primary bile acids into secondary ones such as deoxycholic acid (DCA ) produced by C. scindens, prevents spore germination and the growth of vegetative cells. The mechanism of DCA formation and C. difficile inhibition has not yet been fully studied at the genetic and genomic level in C. scindens. The main objective of this work was to perform comparative genomics and determine the pangenome and core genome of C. scindens, the analysis included complete genomes of 9 newly isolated strains, 8 complete genomes obtained from NCBI, 17 partially complete genomes from NCBI, and additionally another set of ~200 metagenome-assembled genomes (MAGs). Preliminary results obtained from the Roary program and analyzing a set of 34 strains indicate that C. scindens has an open pangenome with a total of 12.720 gene clusters, a core genome with 1.630 gene family, a soft-core genome with 130 gene family, in addition, 3.979 and 6.981 gene family in its “shell” and “cloud” genome respectively, also 4.039 unique genes were found. The core genome contains 39% of proteins with metabolic function, while in the accessory and unique genome, storage and

information processing function predominates with 41% and 50% of proteins respectively. It was also observed clustering of genomes into two groups, which was supported by phylogenomics. This study represents a contribution of the structure and function of the C. scindens pangenome, providing a genetic basis of importance for many aspects of research on the gut microbiota.