Pan-Genome Analysis of Human Gastric Pathogen H. pylori: Comparative Genomics and Pathogenomics Approaches to Identify Regions Associated with Pathogenicity and Prediction of Potential Core Therapeutic Targets - DTU Orbit (11/01/2019)

Helicobacter pylori is a human gastric pathogen implicated as the major cause of peptic ulcer and second leading cause of gastric cancer (similar to 70%) around the world. Conversely, an increased resistance to antibiotics and hindrances in the development of vaccines against H. pylori are observed. Pan-genome analyses of the global representative H. pylori isolates consisting of 39 complete genomes are presented in this paper. Phylogenetic analyses have revealed close relationships among geographically diverse strains of H. pylori. The conservation among these genomes was further analyzed by pan-genome approach; the predicted conserved gene families (1,193) constitute similar to 77% of the average H. pylori genome and 45% of the global gene repertoire of the species. Reverse vaccinology strategies have been adopted to identify and narrow down the potential core-immunogenic candidates. Total of 28 nonhost homolog proteins were characterized as universal therapeutic targets against H. pylori based on their functional annotation and protein-protein interaction. Finally, pathogenomics and genome plasticity analysis revealed 3 highly conserved and 2 highly variable putative pathogenicity islands in all of the H. pylori genomes been analyzed.