

***In silico* analysis of different *Helicobacter pylori* strains and its proteins responsible for gastro-intestinal tract diseases in human**

Megha Vaidya and Hetalkumar Panchal
Sardar Patel University, India

Helicobacter pylori (*H. pylori*) are a Gram-negative microaerophilic, spiral bacteria that specially colonize the gastric mucosa, and it is the most common bacterial infection worldwide. Due to presence of its pathogenic-island (Cag-PAI) *H. pylori* causes chronic persistent and atrophic gastritis in adults and children that often culminate in development of gastric and duodenal ulcers. The complete genome sequences have provided a plethora of potential drug targets. Subtractive study holds the promise of providing a conceptual framework for identification of potential drug targets from the information contained in genomics. The comparative structural studies of each genome were carried out to predict correlation between structural feature and type of disease it would cause and suggest some diseases specific marker. The proteins of Cag-PAI encodes cag-Type IV Secretion System (T4SS) consisting of inner- and outer membrane-spanning Cag protein complexes and a surface-located pillus. T4SS mediates translocation of the *H. pylori* cyto-toxin associated gene A (CagA) effector protein in host. The cyto-toxic factors of Cag Pathogenic Island are present in almost all the strains but yet the different strains cause various diseases. There are many unknown and unidentified proteins in the Island which were identified by *in silico* analysis to have better idea of their structures and functions, which in turn will help to deduce the structure and interaction between the PAI proteins so that the formation of T4ss can be blocked or hindered to prevent translocation of CagA and help in reducing pathogenicity.

Biography

Megha vaidya graduated with Bioinformatics subject from N.V.Patel college of Pure and Applied Sciences and Post Graduated with Bioinformatics subject from Dept. of computer science both affiliated to Sardar Patel University (SPU). She did Masters in Philosophy (M.Phil) in Bioinformatics from Saurashtra University and she Was university first for the M.Phil program. Currently she is persuing Ph.D. in Bioinformatics from Dept. of Computer science, Sardar Patel University, Vallabh Vidyanagar-Gujarat (India). Additionally she has appointed as junior research fellow (JRF) at DST Purse Program at SPU and has also published many papers in National and International Journals and also in many conferences & Seminars. Megha serve as a visiting trainee for Boot-camps in M.Phil –Bioinformatics program at Gujarat State Biotechnology Mission (GSBTM), gandhinagar. Recently she have scripted a book entitled "Annotation of data generated from next generation sequencer, processing data to knowledge" as lead author published by Lambert publishing.

mbv26887@gmail.com