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Comparative study of data generated by structural annotation of the genome for identifying the unique parameter responsible forpathogenic property of *Helicobacter pylori*

Megha Vaidya

Sardar Patel University, India

Abstract

Helicobacter pylori are the most common bacterial infection worldwide. They are generally acquired during childhood and the infection can persist in gastric ecosystem throughout the life span of the host, if untreated. There are similarities and the variations in the size of genomes of several strains. The disease causing factor Cag Pathogenic Island is present in almost all the strains but yet the different strains cause different diseases. In present studies, detailed comparative studies of each genomes is carried out to check possibility of prediction of the type of disease it would cause and suggest some target for treatment on the bases of structural annotation. It is found that comparative studies of structural features of genomes give important outcomes but, cannot give detailed idea about the type of disease the strains would cause. Functional analysis of genome or study of gene order and rearrangement of genome may solve the mystery of disease specific genes and give some better target for treatment.

Biograpgy

Megha vaidya graduated with Bioinformatics subject form 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.Phill) in Bioinformatics from Saurashtra University and she was university first for the M.Phill program. Currently she is persuing PhD 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 have 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.Phill –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.