Yashoda Mittal et al., J Proteomics Bioinform 2013, 6:7
http://dx.doi.org/10.4172/0974-276X.S1.069

OMICS Group Conferences
Accelerating Scientific Discovery

3rd International Conference on
Proteomics & Bioinformatics
July 15-17, 2013 Courtyard by Marriott Philadelphia Downtown, USA

Analysis of some common pathogenic bacteria using "Bacterial Lectindb"

Yashoda Mittal[1] **and Dharmendra Kumar**[2]
[1]KLDAV(PG) College,Roorkee, India
[2]Pt. LMS Govt. P G College, India

Common pathogenic bacteria like E. coli, V. cholera and S. typhimurium display surface lectins that could be potentially involved in pathogenesis. Due to the importance of these strains in causing the infectious disease, especially in developing countries we performed an extensive analysis of the lectins displayed on pathogenic bacterial surfaces using "BacterialLectinDb". Lectins from E. coli, V. cholera and S. typhimurium were compared to gain insights into the possibilities of common motifs that could be responsible for contributing to host pathogen interaction. The various information about these lectins such as amino acid sequence, gene name, PDB code etc. were obtained using Swiss-prot, SOPMA, Prodom, ClustalW etc. from "BacterialLectinDb". Multiple sequence alignment using ClustalW was used to compare the protein sequences of the E. coli lectins F17a-G fimbrial adhesion, Gafd (F17C-Type) fimbrial adhesion and and S. typhimurium lectin sialidase. Multiple sequence alignment of F17a-G fimbrial adhesin and Gafd (F17C-Type) fimbrial adhesin both from E. coli show positive similarity with high score of 95. Comparison of E.coli, F17a-G fimbrial adhesion and Gafd (F17C-Type) fimbrial adhesion lectin sequences to that of sialidase from S. typhimurium generated a very low similarity score of only 1. These results thus point out to the role of these lectins in host pathogen interactions.

Biography

Yashoda Mittal did Ph.D. from University of Roorkee (now IIT-Roorkee), India. They have authored several research papers, published a book and developed 4 biological/lectins databases jointly.

research.bioinformatics@gmail.com