Template of abstract for Poster Presentation

Pathway based therapeutic targets identification and development of an interactive database CampyNIBase of *campylobacter jejuni* RM1221 through non-redundant protein dataset

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Abstract

The bacterial species *Campylobacter jejuni RM1221*(*CjR*) causes campylobacteriosis posing global threat for human health. Antibiotic treatment might be ineffective due to the development of multiple resistances. Therefore, new medicine and drug targets on demand which can be obtained by targeting essential protein(s) of *CjR*. We conducted this *in silico* study to identify therapeutic targets by subtractive *CjR* proteome analysis. The most important proteins of *CjR* proteome including chokepoint enzymes, plasmid, virulence and antibiotic resistant proteins were annotated and subjected to subtractive analyses to filter out the *CjR* essential proteins from duplicate or human homologous proteins. Through the subtractive and characterization analysis we have identified 38 eligible therapeutic targets including 1 potential vaccine target. Also, 12 potential targets were found in interactive network, 5 targets to be dealt with FDA approved drugs and one pathway as potential pathway based drug target. In addition, a comprehensive database 'CampyNIBase' has also been developed. Besides the results of this study, the database is enriched with other information such as 3D model of the identified targets, experimental structures and Expressed sequence tag (EST) sequences. This study including the database might be exploited for future research and identifying better therapeutics against campylobacteriosis. URL: http://nib.portal.gov.bd/site/page/4516e965-8935-4129-8c3f-df95e754c562#Banner.

Keywords: *Campylobacter jejuni RM1221*, Proteome, therapeutic targets, Database.