Identification of New Target and Drug against *Salmonella typhi*using Homology and Docking Studies

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ABSTRACT

Typhoid feveris caused by *Salmonellaenteric* subspecies *enteric serovar Typhi* (*Salmonellatyphi*). It is transmitted by the fecal-oral route, mainly via contaminated food and water in the developing world. The proteome of this bacterium was analyzed. All known protein sequences were collected from Genpept database. From these seuqnences, 99 annotated protein sequences were retrieved from Genpept database. From the annotated protein, genes with targets filtered. From the retrieved targets, based on similarity between filtered genes and targets, three targets selected. Drugs for these targets derived from drugbank. Tertiary structure for the filtered genes predicted and structure for the drugs derived from drugbank. Docking was carried out between targets and drugs. Molecular properties for the drugs were predicted through molinspiration tool. In the current study the consolidation of subtractive proteomics methodology, structural prediction and docking has been performed to discover possible drug targets in *Salmonellatyphi*to enhance the future treatment administration. From the docking scores and Lipinski's Rule of Five, best drug Cidofovir was selected. However, wetlab studies have to be performed to confirm the role of Cidofovir in control of *Salmonella typhi*.

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