Abstract

Shigellosis is an endemic disease prevalent in developing and poor countries due to fecal-oral transmission resulting a significant morbidity and mortality rate. Emergence of multi-drug resistant (MDR) in Shigella sp. reveals the ineffectiveness towards the first line antibiotics like quinolones, co-trimoxazole and ampicillin against it. There is continuous need to monitor the characteristics and antibiotic resistance patterns of this pathogen regarding the identification of new potential therapeutic drug targets. Availability of complete protein of different Shigella species viz flexneri, body, dysentery and son has made it possible to carry out the In-silico analysis of its protein for the identification of potential vaccine and drug targets. Subtractive
proteomics approach is being used to mine the list of proteins present in different Shigella species which are non-homologous to human and essential for the survival of the pathogen. The metabolic chokepoint analysis also enriches the list of essential protein and adds those proteins in the list which are uniquely found in pathogenic pathway, catalyzed by single enzyme and involved in multi pathways. Screening of essential proteins against human gut flora and approved drug targets revealed the targets which are non-homologous to human gut flora and homologous to the approved drug targets. Broad spectrum drug targets screening revealed a list of highly conserved proteins of various pathogens including different Shigella species. Probably the drug developed against these targets may be useful in treating multiple diseases or diseases which results due to co-infection of different pathogens. Subcellular localization prediction revealed a list protein, which could be potential vaccine targets in different Shigella species. Virtual screening against these identified targets might be useful in the discovery of novel Drug against MDR Shigella species.

Refer
ences

- Gasteiger E., A. Gattiker, C. Hoogland, I. Ivanyi, R. D. Appel, A. Bairoch,
Choke Point Analysis with Subtractive Proteomic Approach for Insilico Identification of Potential Drug Targets in Shigella Dysenteriae


**Index Terms**

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**Keywords**

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