Prioritization of Vaccine Target by Resistance Pathway Analysis in *Shigella flexneri*

Vishnu Vinayak S,[1] Ravindranath B S,[1]

[1]Manipal Institute of Technology, Manipal Academy of Higher Education, Manipal. India

Abstract

Introduction: *Shigella flexneri* is a gram-negative enteric pathogen resistant to multiple antibiotics. *S.flexneri*, is the causative agent of diarrhoea and shigellosis, it is the major cause of morbidity and mortality of children < 5 years of age globally. It has been ranked as the significant global human health concern, owing to the susceptibility to multiple antibiotics. Identification of novel therapeutic targets to design vaccine is crucial to combat the *S.flexneri* pathogenicity.

Objective Methods: The current study is designed to identify and prioritize vaccine targets in multiple drug resistant (MDR) *S. flexneri*. A total of five resistance pathways (KEGG) namely Beta-lactam resistance, Cationic antimicrobial peptide (CAMP) resistance, Peptidoglycan biosynthesis, Carbapenem resistance, Vancomycin resistance were searched for crucial proteins and the same were analysed to identify potential vaccine targets. Various computational tools were employed to filter the proteins based on essential, human non-homologous and virulence factors which are required for pathogenicity and survival. The protein sequences were retrieved from UniProtKB for further analysis of qualitative characterization which is directional in prediction and prioritization of vaccine targets.

 Results: Subtractive pathway analysis predicted a list of 31 proteins from *S. flexneri* as essential, human non-homologous metabolic proteins. Further, we prioritized 1 protein acriflavine resistance protein B (acrB) involved in beta-lactam resistance and CAMP resistance pathway as potential vaccine target. acrB is localized to the cytoplasmic membrane, it can be used as broad-spectrum vaccine target as it possesses 26 specific epitopes and it has a potential to interact with other related proteins to form an AcrAB-TolC complex which exhibits druggable properties.

Conclusion: Our findings mentioned above suggests that the strategy applied to search for resistance pathways to identify and analyse physicochemical properties of specific crucial proteins is promising in prioritization of one vaccine target.

Keywords: *Shigella*, shigellossis, diarrhea, MDR, vaccine target