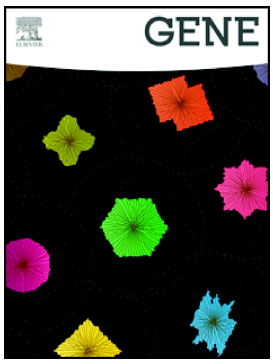

Genomics driven approach for identification of novel therapeutic targets in Salmonella enterica

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Genomics driven approach for identification of novel therapeutic targets in *Salmonella enterica*

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ABSTRACT

Salmonella enterica is a causative agent of enteric and systemic salmonellosis that affects human and many other animal species. Due to the emergence of drug-resistant strains, available drugs against *S. enterica* infection are no more effective as before. Thus, there is an urgent need to develop new therapeutic strategies. The current study aims at prioritizing therapeutic targets by an *in-silico* genomics driven method. The method involves searching proteins of each *Salmonella* strain for essentiality, virulence and antibiotic-resistance and host-pathogen protein-protein interactions. Using subtractive genomics approach, we further confirmed that none of the selected protein shares sequence homology with any human (host) protein and also with protein from the microbes of human symbiotic gut flora. Pathway analysis of these screened proteins revealed associated biological processes. Presence of proteins in pathogen-specific pathways was used as one of the assessment property in the subsequent scoring scheme. Simultaneously proteins are screened based on parameters like druggability (sequence similarity with existing drug targets), sub-cellular localization and presence of transmembrane domain. The implemented scoring scheme depicted a final list of 14 potential therapeutic targets out of which 6 could be identified as 'high-confidence' targets based on extensive literature curation. Identified therapeutic targets can aid in the design and development of effective antibacterial agents against *S. enterica*. The genomics driven strategy adopted in this study can also be applied to screen therapeutic targets for other pathogens.

Keywords:

Salmonella enterica; Subtractive genomics approach; Target prioritization; Druggability; Therapeutic targets