Conclusion

Conclusion

V. parahaemolyticus is quite prevalent in the environmental samples. However, the major pathogenic strain of *V. parahaemolyticus* is quite less in the in environmental samples. The genes under T3SSI of *V. parahaemolyticus* are well distributed in both pathogenic and non-pathogenic strain of *V. parahaemolyticus* and could be used as a molecular marker to identify the *V. parahaemolyticus*. The virulent genes under T3SSII are restricted only in the pathogenic strain of *V. parahaemolyticus.* The *tdh* and *trh* positive strains of *V. parahaemolyticus* hemolyzed human RBCs quite faster in comparison to *tlh* positive strain. Both the *tdh* and *trh* positive isolates showed high cytotoxicity in HEK cell line in comparison to *tlh* positive strain. The genetic diversity of *V. parahaemolyticus* is very high and lack of genetic structure. The MLST analysis also revealed high genetic diversity of isolated strains of *V. parahaemolyticus* in India. Furthermore, five "moonlighting proteins" were identified by secretomic analysis of *V. parahaemolyticus* which normally present in the cell and play a major role in the metabolic pathway and also act as a virulent factor when they were secreted out from the cell. The pathogenicity study reveled that, interperitonial and oral administration of the bacteria are the most effective route of infection. The histopathological changes confirm the tissue-specific infection of *V. parahaemolyticus*. The gene expression study showed that, after experimental challenge the expression of toll-like receptor, proinflammatory cytokines like IL-β, IL-6, TNFα, complement factor 3 and *Hsp 70* was upregulated during infection provide insights on immune gene regulation. The 3D model of the Trh protein was predicted using comparative homology modeling approach and further validated using Ramachandran plot analysis and ProSA analysis. 19 drugable pockets were identified out

of which one pocket (pocket 2) is most important for drug targeted site. The present study revealed the genetic diversity in India and pathogenicity of *V. parahaemolyticus*. Furthermore, the identification of druggable pockets in Tdh andTrh protein, open a new vistas for drug designing and development of medical therapeutics against *V. parahaemolyticus* infections which would help in the monitoring and control of disease in near future.