# Molecular Epidemiology of Group A Rotaviruses (RVA) in Children of the State of Imphal, Manipur, India

**A thesis submitted in partial fulfilment of the requirements for award of the degree of**

**Doctor of Philosophy**

**By**

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**July, 2022**

# CHAPTER 7

# OVERALL SUMMARY AND FUTURE PROSPECTS

## 7.1. Overall summary

The occurrence of diarrhoea was observed mainly in the winter months during the study period. Rotavirus prevalence was found high (68.56%) during the study period from December 2015 to March 2019 and children in the age group of 6-23 months were found more susceptible to rotavirus infection. G3, G1 and G2 were the prevalent G-genotypes strains. While, P[4], P[6], P[8] and P[11] were the most prevalent P-genotypes. The VP7 and VP4 sequences identified in this study were genetically closely related with human strains. Seasonal pattern of norovirus, astrovirus and adenovirus was similar to rotavirus. Co-infection of RVA with other enteric viruses was observed in 23.99% (124/517) of children of Imphal, Manipur, India.RVAs circulating in northeast India are diverse and found mutations in the antigenic epitopes of VP7 and VP4 that were reported for association with escape from neutralizing mAbs. Genome sequence of RM251122016 isolated from 12-month infected male child was G3P[8] strain with a human Wa-like I1-R1-C1-M1-A1-N1-T1-E1-H1genotype backbone. Phylogenetic analysis of each gene segment of RM251122016 revealed two genes (VP1 and VP7) having close similarity with porcine and equine rotavirus strains. Multi-epitope constructs have been designed and they are predicted to be safe, immunogenic and may provide heterotypic protection against rotavirus. Four recombinant proteins were over-expressed and affinity chromatography for purification of the recombinant protein has been standardized and the antigens can be used as prototype for further experimental validations in the laboratory.

## 7.2. Future prospects

There is need for monitoring of rotavirus surveillance post-introduction of indigenous rotavirus vaccines to understand the rotavirus disease burden and impact of vaccination. Whole genome analysis can be done for remaining unusual strains identified in the present study. Cell culture adaptation of whole genome sequenced rotavirus isolate identified in this study may be carried out to study biology of RVA isolate using various experimental systems. B-cell epitopes predicted in this study may be further validated and use for peptide-based ELISA detection of rotavirus antigen in stool specimens.