CONCLUSION & FUTURE PROSPECTS

Keeping in view the disease and economic burden associated with the diarrheal diseases, it becomes imperative to study the epidemiological and etiological features of this disease in the different regions of the country. This study indicates the predominance of rotavirus in the region and a significant disease burden can be attributed to this virus among all age groups. Enterovirus is also detected in considerable fraction and thus imposing a need to consider it as a potential pathogen accountable for human diarrhea. However, a very important diarrheagenic virus, norovirus was detected in a very low frequency. This study not only throws light on the relative prevalence of the important diarrheagenic viruses but also furnish preliminary data which would be helpful in formulating the preventive strategies against them. In particular, the high infection rate of rotavirus in children and its year round prevalence warrants immediate attention in order to reduce the morbidity and suspected mortality due to this pathogen.

G1P[6] was observed as the predominant cause of rotavirus diarrhea in the region. However, G9P[6] and G12P[6] were also detected in significant proportion. As a whole, this study provides crucial data on rotavirus epidemiology and strain diversity in children and adult population of the region. We anticipate that this data will be helpful in implementing the preventive strategies accordingly which would be helpful in reducing rotavirus associated disease burden in the otherwise unexplored state of Himachal Pradesh. Further molecular analysis of G10 isolates is required to study their evolutionary characteristics which could probably ascertain interspecies transmission mechanism.

The phylogenetic and molecular analysis of VP7 gene reveals the belonging of isolates to a novel sublineage within lineage 1. The isolates under investigation have considerable amino acid differences as compared to the vaccine strains in the epitope region and thus might have an adverse effect on the vaccine efficacy. Although, \textit{in silico} analysis revealed no adverse effect on the binding of antibody to the antigen. But this cannot be ascertained without further serological analysis and extensive genetic and molecular studies including larger proportion of circulating strains at different time intervals (pre- and post-vaccination). However, this molecular analysis gives preliminary information on the genetic diversity of the circulating strains and can navigate the further approaches to study the diversity of G1 rotaviruses circulating in Himachal Pradesh, India.
In a nutshell, this study paves way for more extensive molecular and serological studies in future involving larger spectrum of viral and bacterial pathogens.