Chapter 6

Summary and Conclusion

This is the first study reporting the frequency of hMPV and HBoV from South India and that too among rural children. To date, there is only limited data available from India. The four top clinical features found in our study are dry cough, cough with secretions, coryza and rhinitis, but there are no significant association with hMPV positive status. The frequency of hMPV positives and negatives were compared during different months. The positive rate of hMPV was higher during the cooler and wet months (July to January) of the year. Detection rate of hMPV in patients at different age groups with URI and LRI were compared and found insignificant. The overall hMPV positive rate between rural and peri-urban population was also found to be insignificant. The frequency of hMPV infections is higher in children compared to HBoV. The frequency of hMPV in our study is consistent with other studies reported from other parts of the world. We investigated the genetic variability of partial nucleoprotein (N) gene sequences of hMPV strains identified among young children in India (South). The sequences of the N gene were compared with the previously reported sequences available in the GenBank repository. The results showed strain localization in a geographically circumscribed area (topotype). The frequency of hMPV positives and negatives were compared during different months. The positive rate of hMPV was higher during the cooler and wet months (July to January) of the year. In our study, majority of the strains belonged to genetic lineage B2 (71.1%) followed by A2b (18.4%), A2a (7.9%) and B1 (2.6%) showing the presence of 4 of 5 known genotypes of hMPV. Global alignment of nucleotide sequences showed the strains to be closely related to sequences from Canada, The Netherlands and Australasia region. Changes both at nucleotide level and amino acid level were compared. The results provide evidence for the diversity of N gene of hMPV in samples collected from India (South) compared with global strains. The sequences when investigated for selective pressure showed one positively selected site and 19 negatively selected sites. These data could be a prerequisite to investigate further the evolutionary dynamics of hMPV infection.