ABSTRACT

Acute respiratory tract infections (ARI) are one of the major causes of morbidity and mortality among young children in developing countries. Information on the incidence of human metapneumovirus (hMPV) and human bocavirus (HBoV) infections in developing countries especially among rural children is very limited. The study was done to identify if these viruses were associated with ARI among children less than 5 years of age in rural and peri-urban population of South India.

The study is cross-sectional with prospective nature of sample collection. Oropharyngeal swabs were collected from children less than 5 years of age presenting ARI. The two viruses, hMPV and HBoV were identified using semi-nested (N gene) and non-nested (NP gene) polymerase chain reaction assays respectively.

Lower limit of detection of hMPV and HBoV were $6.69 \times 10^5$ plasmid copy and $5.77 \times 10^3$ plasmid copies per 5µl PCR reaction input respectively. The frequency of hMPV infections was higher in children compared to HBoV. The different detection rates of hMPV in patients of various age groups with URI and LRI were compared and found the variance to be insignificant. In the 38 children who were hMPV positive, the majority (73.7%) were from rural community. The overall hMPV positive rate was higher in the rural population and the difference from the peri-urban population was however found to be statistically insignificant. The genetic variability of partial nucleoprotein (N) gene sequences of hMPV strains identified were compared with reported sequences available in the GenBank repository.

In the study, the majority of the strains belonged to genetic lineage B2 (71.1%), followed by A2b (18.4%), A2a (7.9%), and B1 (2.6%), demonstrating the presence of 4 of the 5 known genotypes of hMPV. Global alignment of the nucleotide sequences showed that the strains are closely related to sequences from Canada, The Netherlands, and Australasia. When investigated for selective pressure, the sequences showed 1 positively selected site and 19 negatively selected sites.