ABSTRACT

Human adenovirus type 3 (HAdV-3) is the causative agent of outbreaks of nosocomial as well as community acquired pneumonia with severe morbidity even with fatal outcome among the young children and neonates. It is also responsible for acute respiratory disease (ARD) among the military recruits. Studies revealed that in the last few years HAdV-3 has become most prevalent HAdV type worldwide. HAdV capsid protein hexon contains type specific epitopes in its hyper variable regions (HVRs) and is responsible for type-specific immunogenicity. In spite of increased prevalence of HAdV-3 as a respiratory pathogen, the overall diversity in hexon of globally circulating strains remains unexplored. This study was designed to find out the genetic variation in HVRs of hexon among the field strains reported globally and to speculate their possible association with increased prevalence. In this study, PCR and sequencing of hexon gene including 7 HVRs of HAdV-3 GB strain was done. The sequence data of worldwide circulating strain of HAdV-3 hexon gene with 7 HVR was collected from *Gen*Bank database. Out of 249 HAdV-3 strains with all HVRs of hexon, 38 representative HAdV-3 strains were selected for analysis on the basis of country of origin and homology of HVRs of hexon. Multiple sequence alignment (MSA), percentage of homology in their HVRs and phylogenetic analysis were done. The result showed that the HVRs of HAdV-3 are highly variable. A total of 25 genetically variable patterns were observed. The main variations of amino acid residues were found in HVR-6 and HVR-7. In phylogenetic analysis of hexon gene all the HAdV-3 strains were segregated into six clusters. As the epitopes of hexon are located in one or more HVRs, substitution of amino acid residue in HVRs might change the antigenic property and help the variant strain to circumvent the existing immunity of the host. This finding provides possible explanation why HAdV-3 has become most prevalent type of HAdVs worldwide and the reason for their frequent outbreak causing ability. Highly variable HVRs of HAdV-3 in this study also imply that development of vaccine that provides global protection might be challenging. The result of this study could be useful to understand molecular epidemiology HAdV-3.