Abstract title

Molecular epidemiology and genetic characterization of human respiratory syncytial virus detected in inpatient and outpatient children in Tehran

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Background

Human respiratory syncytial virus (HRSV) is the leading cause of acute lower respiratory tract infection in infants and young children. While no treatment is yet available, recent clinical trials on RSV vaccines are promising. Therefore RSV genotyping data before vaccine introduction are necessary. Limited information exists regarding HRSV genotypes in Iran.

Methods

In order to better understand HRSV strain diversity; we evaluated in-depth the genetic variability to the HRSV G and F protein detected in inpatient and outpatient children less than two years old with acute respiratory symptoms during 2015-2016 in a local area of Iran (Tehran). A total of 180 nasopharyngeal swabs specimens were evaluated. HRSV positive samples were genotyped based on G and F gene sequences using RT-PCR and sequencing methods. Genetic and antigenic characteristics of G and F genes were investigated in all selected sequences.

Results

Fifty-five out of 83 HRSV positive samples were sequenced in our survey. All of them were classified as subgroup A and belonged to the ON1 genotype. This study is the first report regarding the emergence of ON1 in Iran. The phylogenetic tree showed that ON-1 Iranian sequences clustered in 4 different lineages according to G and F genes. Fusion gene sequence analysis showed that all genetic changes in the Iranian isolates were base substitutions and no deletion, insertions, or frame-shift mutations were identified.

Conclusions

This study provided the first genetic analysis of HRSV F protein in Iran. The results of the present study highlight that standard molecular surveillance programs for early detection of circulating genotypes are necessary to improve the development of targeted therapies .

Keywords

Molecular epidemiology Genetic characterization Human respiratory syncytial virus

Tehran