

Analysis of genetic diversity and molecular evolution of human group B rotaviruses based on whole genome segments

Abstract

Group B rotavirus (GBR) is a rare enteric pathogen that causes severe diarrhoea, primarily in adults. Nearly full-length sequences of all 11 RNA segments were determined for human GBRs detected recently in India (IDH-084 in 2007, IC-008 in 2008), Bangladesh (Bang117 in 2003) and Myanmar (MMR-B1 in 2007), and analysed phylogenetically with the sequence data of GBRs reported previously. All RNA segments of GBR strains from India, Bangladesh and Myanmar showed >95 % nucleotide sequence identities. Among the 11 RNA segments, the VP6 and NSP2 genes showed the highest identities (>98 %), whilst the lowest identities were observed in the NSP4 gene (96.1 %), NSP5 gene (95.6 %) and VP8*-encoding region of the VP4 gene (95.9 %). Divergent or conserved regions in the deduced amino acid sequences of GBR VP1-VP4 and NSP1-NSP5 were similar to those in group A rotaviruses (GARs), and the functionally important motifs and structural characteristics in viral proteins known for GAR were conserved in all of the human GBRs. These findings suggest that, whilst the degree of genetic evolution may be dependent on each RNA segment, human GBR may have been evolving in a similar manner to GAR, associated with the similar functional roles of individual viral proteins.