

Molecular characterization of two Bangladeshi infectious bursal disease virus isolates using the hypervariable sequence of VP2 as a genetic marker

Abstract

Two Bangladeshi infectious bursal disease virus (IBDV) isolates collected in 2007, termed GB1 and GB3, were subjected to comparative sequencing and phylogenetic analyses. Sequence analysis of a 474-bp hypervariable region in the VP2 gene revealed that among four major amino acid substitutions observed in the strains, two were unique to GB1 and GB3 (Ser217Leu and Ala270Thr) while one substitution was only found in GB1 (Asn299Ser). Among IBDVs from Bangladesh including GB1 and GB3, the rate of identity and homology was around 97~99%. The amino acid sequences of GB1 and GB3 differ from those of previous Bangladeshi IBDV isolates and contain amino acid substitutions Pro222Ala and Asn299Ser (in GB3 only). Phylogenetic analysis revealed that GB1 and GB3 are grouped with other very virulent IBDVs of European and American origin in contrast to two previously isolated Bangladeshi IBDV strains (GenBank accession Nos. AF362776 and AF260317), which belong to the Asian group. It was concluded that GB1 and GB3 belong to a very virulent group of IBDVs. However, amino acid sequences of GB1 and GB3 differ from those of the other Bangladeshi IBDVs by one or two amino acids encoded in the hypervariable region of the VP2 gene.