



Genomic sequence of infectious bursal disease virus from Zambia suggests evidence for genome re-assortment in nature

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Infectious bursal disease virus (IBDV) is a bi-segmented RNA virus, which belongs to the genus *Avibirnavirus* of the family *Birnaviridae*. Two serotypes, 1 and 2, exist in IBDV. The serotype 1 IBDVs are the causative agents of infectious bursal disease (IBD) in chickens worldwide and lead to immunosuppression in young birds. Genome re-assortment has been speculated to occur and contribute to the emergence of new IBDV strains. However, evidence was lacking until recently when two re-assortant viruses were detected in China. In this study, we determined the complete nucleotide sequence of an IBDV, designated KZC-104, from a confirmed natural IBD outbreak in Lusaka, Zambia in 2004. The genome consisted of 3074 and 2651 nucleotides in the coding regions of segments A and B, respectively. Alignment of both nucleotide and deduced amino acid sequences, and phylogenetic analysis revealed that the genome segment A of KZC-104 was derived from a very virulent strain, whereas its segment B was derived from a classical attenuated strain. On BLAST search, the full-length segments A and B sequences showed 98% closest nucleotide homology to the very virulent strain D6948 and 99.8% closest nucleotide homology to the classical attenuated strain D78, respectively. This is a unique IBDV reassortant strain, which has emerged in nature involving segment B of a live attenuated vaccine. This observation provides direct evidence for the involvement of vaccine strains in the emergence of reassortant IBDV in the field. Taken together, these findings suggest an additional risk of using live IBDV vaccines, which may act as genetic donors for genome re-assortment. Further studies are required to investigate the epidemiology and biological characteristics of reassortant strains so that the appropriate and safe IBDV vaccines can be recommended.