

## Diversity of Genome Segment B from Infectious Bursal Disease Viruses in the United States

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### Important Findings

Several phylogenetic lineages of the infectious bursal disease virus (IBDV) genome segment B have been identified. Although this genome segment has been shown to contribute to virulence, little is known about the genetic lineages that exist in the United States. The nucleotide genome segment B sequences of 67 IBDV strains collected from 2002 to 2011 in the United States were examined. Although they were from nine different states, a majority (47) of these viruses were from California. The study results included:

- Phylogenetic analysis of the 67 nucleotide sequences revealed four significant genome segment B lineages among the U.S. viruses.
- When the available sequences in GenBank were added to the analysis, two additional lineages were observed that did not contain U.S. viruses; one included viruses from China and the other contained viruses from the Ivory Coast.
- Although the samples tested do not represent all poultry producing regions in the United States, serotype 1 viruses from states outside California all belonged to one genome segment B lineage.
- The other three lineages observed in the United States were populated with viruses exclusively found in California, except the serotype 2 lineage, where the type strain was a serotype 2 virus from Ohio.

The data provide further evidence for the importance of genome segment B identification during routine molecular diagnosis of all IBDV strains.

### Significance of Findings

Although examining additional IBDV may reveal other genome segment B lineages, the data indicate that at least four significant lineages of this genome segment can be found in the United States. Overall, it was interesting that all four genome segment B lineages were represented by the IBDV from California, and two of these (Australia and serotype 2) contained exclusively reassorted very virulent infectious bursal disease virus (vvIBDV). This raises the possibility and concern for additional vvIBDV reassorted viruses and confirms the need to examine the sequence of genome segment B routinely when conducting a molecular diagnosis of these viruses.

### Additional Information

The IBDV is a member of the genus *Avibirnavirus*, family *Birnaviridae*. These viruses have a genome that consists of two segments of double-stranded RNA designated A and B. Genome segment B encodes VP1, the RNA-directed RNA-polymerase. It has been shown that VP1 is incorporated into virions through an interaction with VP3 in the cytoplasm of infected cells.

Nucleotide sequencing and phylogenetic analysis has identified more than one lineage of genome segment B. Hon and coworkers showed that vvIBDV emerged after a reassorting of genome segment A with an undocumented segment B. Further studies indicated that the genome segment B of vvIBDV was highly conserved and distinct from non-vvIBDV. In one study that examined 23 viruses, the eight vvIBDV had similar genome segment B sequences that clustered in one phylogenetic group and a second phylogenetic group contained classic, variant, and vaccine non-vvIBDV strains. Three genetic lineages of genome segment B were reported in another study that examined 32 IBDV strains. One lineage exclusively contained the vvIBDV and the other two included a variety of non-vvIBDV strains. In a study that used the parsimony method for phylogenetic analysis of 50 viruses, the vvIBDV were again exclusively found in one genome segment B lineage, and non-vvIBDV could be significantly divided into at least four additional genetic lineages.

The virulence of IBDV appears to be linked to certain sequence patterns in VP1. An IBDV reassortant containing a vvIBDV genome segment A and a non-vvIBDV genome segment B was less pathogenic in specific-pathogen-free (SPF) chickens. Reduced pathogenicity of a vvIBDV genome segment A and non-vvIBDV genome segment B reassortant virus was also reported in China.

The 2009 identification of vvIBDV in the United States included analysis of both genome segments A and B, and SPF chick challenge was used to confirm the diagnosis of vvIBDV from suspect field cases in California. The potential for reassorted viruses necessitates the identification of both vvIBDV genome segments. Recently, we identified several reassorted IBDV in California that contained vvIBDV genome segment A sequences, but their genome segment B sequences were unrelated to the vv viruses. Phylogenetic studies on the nucleotide sequence of genome segment B indicated that results obtained on the 5' two-thirds of this molecule were comparable to results observed for the entire segment B sequence and, therefore, most GenBank sequences of the IBDV genome segment B include only this 5' region. The objective of this study was to sequence a 5' region of genome segment B from IBDV found in the United States and to compare the phylogenetic lineages of these viruses with previously published data that included the 5' nucleotide sequences found in GenBank.