Infectious bursal disease virus (IBDV) belongs to the genus Avi-
birnavirus within the family Birnaviridae. This nonenveloped
icosahedral virus has a double-stranded RNA genome consisting
of two segments named A and B (1).

IBDV is a highly contagious avian pathogen affecting com-
mercial poultry production worldwide (2). All pathogenic IBDVs (se-
rotype 1) can be divided into classic, variant, and very virulent
strains according to antigenic and pathogenic criteria (3). Phylo-
genetic analyses have consistently recovered the clades or lineages
corresponding to these strains, including a clade composed of
vaccine-like strains and a recently described distinct global lineage
(4). This distinct lineage (dIBDV) is widely distributed in South
America (4, 5).

The IBDV strain was collected in 2014 from a 27-day-old com-
mercial broiler flock suffering from respiratory problems and in-
creased mortality. Viral RNA was isolated from bursae tissue using
TRIzol reagent (Invitrogen). First-strand cDNA was synthesized
using random hexamers (Thermo Scientific). The IBDV was di-
agnosed as a non-virulent virus by real-time PCR (6). The complete
genome sequence of this isolate was obtained by reverse
transcription PCR, using overlapped consensus primers and di-
rect sequencing. Purified products were sequenced in both direc-
tions by Macrogen Inc. (Seoul, Republic of Korea). Sequences
were compiled and edited using the SeqMan program (Laser-
gene). Multisequence alignments were performed with MEGA5
(7), and phylogenetic trees were constructed using PhyML.

The coding region of segment A (3,073 nucleotides) contains
two open reading frames that encode VP5 (145 aa) and a VP2-
VP4-VP3 polyprotein (1,012 aa); segment B encodes VP1
(879 aa), the viral RNA polymerase.

The phylogenetic analysis of the VP2 hypervariable region in-
dicates that the virus belongs to the dIBDV lineage. This was con-
firmed by the presence of a unique and conserved molecular sig-
nature (272T, 289P, 290I, and 296F) that is a diagnostic charac-
ter for the classification of dIBDVs (4). Segment B also associates with
strains of the dIBDV lineage and shows the 243P diagnostic
marker. Consequently, the strain was denoted as dIBDV/UY/
2014/2202. This is the first full-length sequence of the coding ge-
nome of a strain belonging to the dIBDV lineage.

Comparative analysis of the complete segment A shows higher
nucleotide similarity (96%) with classical strains (e.g., Edgar and
HPR-2). In the case of VP1 (segment B), the highest similarity
(96.4%) was found with strains that are not very virulent (e.g., JD1
and Irwin Moulthrop).

The comparison of the VP2 hypervariable region of dIBDV/
UY/2014/2202 with most vaccine strains commonly used in South
America showed an amino acid similarity ranging from 88.9 to
92.1%; D78 (Nobilis D78) and Winterfield 2512 (Cevac IBD L)
were the most similar strains.

A comprehensive study of more genomic sequences of these
dIBDVs is needed to understand the virus’s epidemiology and to
contribute to the effective control of IBDV infection.

Nucleotide sequence accession numbers. The full-length cod-
ing sequence of strain dIBDV/UY/2014/2202 has been deposited
in GenBank under the accession numbers KT336459 (segment A)
and KT336458 (segment B).

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