



Complete Genome Sequence of Genotype Psittacine Beak and Feather Disease Virus, a Strain Identified from Budgerigars in China

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ABSTRACT Psittacine beak and feather disease virus (PBFVD) has been reported in many countries, such as Australia, Poland, the United States, South Africa, etc. In this study, the complete genome of a PBFVD isolate was determined and characterized from budgerigars in China.

Psittacine beak and feather disease virus (PBFVD) is a nonenveloped virus with a diameter of 14 to 16 nm and belongs to the genus *Circovirus* in the family *Circoviridae*. The genome of PBFVD is a 2-kb circular single-stranded DNA molecule possessing two major open reading frames (ORFs) encoding a replication-associated protein (Rep) and the capsid protein (Cap) (1, 2). Psittacine beak and feather disease (Pbfd) is characterized by immune suppression, loss of feathers, weight loss, and the development of morphologically abnormal feathers, and it sometimes leads to sudden death in young birds (3, 4).

PBFVD is distributed worldwide with a wide range of hosts, including more than 60 species of psittacine birds (5). PBFVD has been reported in many countries, such as Australia, Poland, the United States, South Africa, etc. (6–8). In this study, the full-genome sequence of PBFVD isolated from budgerigars in Shandong Province, China, was determined and analyzed. Clinical signs of feather loss were observed in budgerigars at a breeding facility. The feather samples were collected and homogenized, and total DNA was extracted from the feather samples using a QIAamp minikit (Qiagen, Hilden, Germany). A primer pair (forward, 1,368 bp-TTGGGTCCTCCTATCGGGATC-1,392 bp; reverse, 1,868 bp-AGACACCGTTTTACAACCAATAG-1,843 bp) targeting 500 bp of the capsid gene was designed using Primer Premier version 5.0 (Canada). The DNA samples were screened using PCR, and the PCR products were sequenced using Sanger sequencing by the TsingKe Biological Technology Company (Beijing, China). All of the clinical samples were positive for the identical sequence; this indicated that these birds were infected with PBFVD. To further characterize the pathogen, the full genome of one psittacine beak and feather disease virus isolate in the positive samples (named PBFVD-GD) was sequenced and analyzed. DNA isolated from the samples was directly amplified using a second pair of primers to cover the full genome (forward, 1 bp-GTT ATGTAGTCAGAATTCCAAATTA-25 bp; reverse, 2,000 bp-GTTAGCTAAAATGGAAATGAGG CCCAC-1,973 bp). The resulting PCR product (2 kb) was sequenced using Sanger sequencing in both directions and walking primers. The final genome was assembled and analyzed with the Lasergene software version 7.0 (DNASTar, USA) (9).

The genome of the PBFVD-GD isolate was found to be 2,000 bp long, with 52% GC content, and contains two ORFs which encode Rep (289 amino acids [aa]) and Cap

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(237 aa). Our data showed that PBFVDV-GD shares about 77% to 90% similarity with the PBFVDV genomes deposited in GenBank from Australia, South Africa, and New Zealand, suggesting that the PBFVDV circulating in China is different from those PBFVDV strains found in Australia, South Africa, and New Zealand.

Given the extensive international bird trade, PBFVDV has spread worldwide and poses a threat to psittacine birds. The PBFVDV strain identified in the diseased budgerigars indicates that a different lineage of PBFVDV is circulating in China. Although PBFVDV was identified in the diseased budgerigars, it remains to be confirmed whether PBFVDV was the sole cause of the observed disease. Further active surveillance is needed to determine the prevalence of PBFVDV in China.

Data availability. The complete genome sequence reported here was submitted to GenBank under the accession number [MK120438](https://www.ncbi.nlm.nih.gov/nuclseq/MK120438).

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