

# Complete Genome Sequence of a Duck Astrovirus Discovered in Eastern China

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**We report here the complete genome sequence of a duck astrovirus (DAsV) isolated from a dead duckling in eastern China. Sequence analyses indicated that the genome of the astrovirus possessed a typical astrovirus organization. Comparison of the partial polymerase gene sequences of DAsV-1 and DAsV-2 showed that the astrovirus shared 94.4% and 64.2% nucleotide identity, respectively. The whole nucleotide sequence of the astrovirus had the highest homology with the sequence of DAsV-1 strain C-NGB (98.7%). Therefore, the strain we describe here is a DAsV-1 isolate.**

Astroviruses in ducks have been associated with a fatal hepatitis and were historically known as duck hepatitis virus type 2 (DHV-2), which occurred in the United Kingdom (1, 3, 4), and a later described serotype 3 (DHV-3) which was isolated in the United States (5). According to the ninth report of the International Committee on Taxonomy of Viruses (ICTV) (1a), DHV-2 and DHV-3 are classified as duck astrovirus type 1 (DAsV-1) and duck astrovirus type 2 (DAsV-2), respectively. In China, a severe outbreak of duck viral hepatitis caused by DAsV-1 was first reported in 2008 (2). Here we report a new DAsV-1 strain isolated from a 2-day-old dead duckling.

In January 2012, DAsV-1 strain WF1201 was isolated from a commercial duck farm with an outbreak of an infectious disease displaying the typical symptoms of duck viral hepatitis in Shandong Province in eastern China. To determine the complete genome sequence of the isolate, 16 pairs of primers were designed based on DAsV-1 strain C-NGB to generate overlapping amplicons by reverse transcription-PCR (RT-PCR). The amplified products were purified, cloned into the pMD18-T vector (TaKaRa), and sequenced by Sangon Biotech Co., Ltd. (China). DNASTar version 7.0 and ClustalW were applied to the genomic analysis.

The complete genome of WF1201 revealed a length of 7,752 nucleotides (nt) with a 30-nt poly(A) tail, a 7,483-nt coding region, a 22-nt short 5' untranslated region (UTR), and a 247-nt 3' UTR. Comparison of the partial polymerase sequences showed that WF1201 shared 94.4% nucleotide similarity with DAsV-1 isolate M52 and 64.2% nucleotide similarity with DAsV-2 isolate X1222A (8), which indicated that WF1201 is a DAsV-1 isolate. DAsV-1 strain WF1201 had 92.2% to 98.7% genomic nucleotide sequence identity to the other five DAsV-1 strains (C-NGB, DA06, DA07, DA08, and DA93) and had the highest homology with strain C-NGB.

The coding region of strain WF1201 included three overlapping open reading frames (ORFs): ORF1a contained 3,723 nt (positions 23 to 3745), ORF1b contained 1,551 nt (positions 3736 to 5286), and ORF2 contained 2,196 nt (positions 5310 to 7505). The three ORFs encoded polypeptides of 1,240, 516, and 731 amino acids, respectively. Like other astroviruses, a ribosomal frameshift signal was found in the overlap region between ORF1a and ORF1b of WF1201, consisting of the heptameric sequence AAAAAAC

from nt 3736 to 3742, followed by a stem-loop sequence, GGG GCCTGAAACATCATGGCCCC, from nt 3750 to 3772 (2, 6, 7). The ORF2 of WF1201 was not in the same reading frame as either ORF1b or ORF1a. This feature was the same as in all other DAsV-1 strains (C-NGB, DA06, DA07, DA08, and DA93) but different from other astroviruses.

WF1201 is the first DAsV-1 strain whose poly(A) tail has been sequenced. The genome data for this new DAsV-1 strain isolated from a dead duckling in eastern China will be helpful for understanding the epidemiology and evolution of DAsV-1.

**Nucleotide sequence accession number.** The complete genome sequence of DAsV-1 WF1201 strain was submitted to GenBank under the accession number [JX439643](https://www.ncbi.nlm.nih.gov/nuccore/JX439643).

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