Complete Genomic Sequence of Chinese Virulent Duck Enteritis Virus

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The Chinese virulent (CHv) strain of duck enteritis virus (DEV) has a genome of approximately 162,175 nucleotides with a GC content of 44.89%. Here we report the complete genomic sequence and annotation of DEV CHv, which offer an effective platform for providing authentic research experiences to novice scientists. In addition, knowledge of this virus will extend our general knowledge of DEV and will be useful for further studies of the mechanisms of virus replication and pathogenesis.

Duck viral enteritis (DVE) is an acute, septic, contagious, and lethal disease that attacks ducks, geese, swans, and other members of the family Anatidae, order Anseriformes (6). The first known occurrence of DVE in the world was a major outbreak in the Netherlands in 1923 (1), and the first instance of DVE in China was reported in 1957. Nowadays, it is one of the most widespread and devastating diseases of waterfowl in the Anatidae family and has severely affected the waterfowl industry because of its relatively high mortality and wide host range.

Duck enteritis virus (DEV) is the causative agent of DVE and was alternatively known as anatis herpesvirus 1 (AnHV-1) and duck plague virus (DPV). It has been clustered in the *Alphaherpesvirinae* subfamily, according to the eighth report of the International Committee on Taxonomy of Viruses (ICTV) (3). DEV may be closely related to mardiviruses, but it has not yet been classified in any genus. Lack of a genome sequence and genomic organization information is a factor that limits DEV taxonomy. Here we report the complete genomic sequence of the DEV Chinese virulent strain (CHv), which was isolated from infected ducks that showed a characteristic hemorrhagic button or band-like lesions on the mucosal surface of the intestines.

Construction of the library and sequencing of the DEV genome were performed as previously described (2). Considering the tandem duplication pattern of the DEV genome (5), we amplified the 5' and 3' ends of the DEV genome using a pair of primers. The shotgun library was sequenced and assembled.

The DEV genome is linear, double-stranded DNA which consists of two covalently linked components, designated unique long (UL) and unique short (US), with each component consisting of unique sequences bracketed by the internal and terminal inverted repeat sequences (IRS and TRS, respectively): UL-IRS-US-TRS. The 5'-untranslated region (UTR) is 5,686 bp in length and contains 25 TATA boxes, 8 CAAT boxes, 8 poly(A)s, and 1 GC box, while the corresponding component of 3' UTR has 3, 13, 4, and 7, respectively. All of them are regarded as potential transcriptional regulatory elements. Also, the 3' UTR possesses seven tandem repeats which can be defined as minisatellites, since the length of the repeat unit reaches up to 40 nt (4).

A total of 78 ORFs were predicted to code the potential functional protein. Of these ORFs, 65 and 11 ORFs are located in the UL and US regions, respectively, whereas the remaining two (ICP4/IE180) are located completely in the IRS and TRS regions. It is worth noting that the UL15 gene is likely to be divided into

two exons by UL16 and UL17. The functional products of DEV genes are divided into two main groups: structural proteins, which are packaged into mature virions to become parts of the particle-like capsid, tegument, and envelope proteins, and replication-associated proteins, or zymoproteins.

Our findings show that the overall genome organization of DEV follows that of the alphaherpesviruses. It is hoped that these data will not only facilitate future investigations of the molecular pathogenesis of DEV but also contribute to the elucidation of the structure and function of DEV gene-derived products.

Nucleotide sequence accession number. The complete genome sequence of DEV CHv is available in GenBank under accession number [JQ647509](https://www.ncbi.nlm.nih.gov/nuclot/JQ647509).

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