

# Complete Genome Sequence Analysis of a Newcastle Disease Virus Isolated from a Wild Egret

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**We report here the complete genomic sequence of a novel Newcastle disease virus (NDV) strain, egret/China/Guangxi/2011, isolated from an egret in Guangxi Province, southern China. A phylogenetic analysis based on a fusion gene comparison with different NDV strains revealed that egret/China/Guangxi/2011 was phylogenetically close to genotype VIIa NDV, and the deduced amino acid sequence was <sup>112</sup>R-R-R-K-R-F<sup>117</sup> at the fusion protein cleavage site. The whole nucleotide sequence had the highest homology (93.3%) with the sequence of strain chicken/Sukorejo/019/10 (GenBank accession number [HQ697255](#)). This study will help us to understand the epidemiology and molecular characteristics of Newcastle disease virus in a migratory egret.**

Newcastle disease virus (NDV), synonymous with avian paramyxovirus-1, is the causative agent of Newcastle disease, which is a highly contagious and fatal viral disease that affects all species of birds (1, 3, 5).

NDV has a nonsegmented, negative-sense RNA genome consisting of six transcriptional units (3'-NP-P-M-F-HN-L-5') (4, 8). NDV strains have been classified into classes I (9 genotypes) and II (11 genotypes): class I strains are generally avirulent and have been isolated mainly from wild birds, whereas class II strains are virulent and avirulent and have been isolated from wild and domestic birds (2, 6).

In May 2011, NDV was isolated from a wild egret in Guangxi Province, southern China. The isolate's virus was named egret/China/Guangxi/2011. Nucleotide sequences of egret/China/Guangxi/2011 were amplified through reverse transcription-PCR (RT-PCR). The amplified products were purified and cloned into the pMD18-T vector (TaKaRa) and then sequenced (TaKaRa, Dalian, China). Sequences were assembled and manually edited to generate the final genome sequence.

Sequence analysis showed that the full genomic length of egret/China/Guangxi/2011 is 15,192 nucleotides (nt). A phylogenetic analysis classified this strain into class II, genotype VIIa. The whole nucleotide sequence had the highest homology (93.3%) with the sequence of strain chicken/Sukorejo/019/10 (GenBank accession number [HQ697255](#), class II, genotype VIIa). The amino acid sequence identities of the NP, P, M, F, HN, and L proteins between egret/China/Guangxi/2011 and Sukorejo01910 are 97.6%, 96.7%, 97.8%, 98%, 96%, and 97.3%, respectively. The amino acid sequence identities of the NP, P, M, F, HN, and L proteins between egret/China/Guangxi/2011 and strain La Sota (GenBank accession number [JF950510](#), class II, genotype II) are 84.2%, 81.8%, 83.7%, 84.2%, 81.9%, and 85.8%, respectively.

The homology of the 374-bp partial F gene (positions 4550 to 4923) of egret/China/Guangxi/2011 with the sequences of Que-66 (GenBank accession number [M24693](#), class II, genotype I), La Sota (GenBank accession number [JF950510](#), class II, genotype II), Aus-32 (GenBank accession number [M24700](#), class II, genotype III), Herts-33 (GenBank accession number [AY741404](#), class II, genotype IV), CA1085-71 (GenBank accession number [JQ247691](#), class II, genotype V), ISreal70-1 (GenBank accession number [AF001111](#), class II, genotype VI), chicken/Sukorejo/

019/10 (GenBank accession number [HQ697255](#), class II, genotype VIIa), QH-4-48 (GenBank accession number [AF378252](#), class II, genotype VIII), F48E9 (GenBank accession number [AY508514](#), class II, genotype IX), US(NJ) (GenBank accession number [EF565065](#), class I) were 79.7%, 75.4%, 80.2%, 81.0%, 81.8%, 84.8%, 96.3%, 82.6%, 78.6%, and 58.3%, respectively.

The sequence at the fusion protein cleavage site is a major determinant of NDV pathogenicity (7). The cleavage sites of virulent NDV strains contain multiple basic residues, whereas avirulent strains have few basic residues. The egret/China/Guangxi/2011 strain has a virulent fusion protein cleavage site sequence (<sup>112</sup>R-R-R-K-R-F<sup>117</sup>), and it accorded with the detection of an intracerebral pathogenicity index of 1.846.

To our knowledge, this is the first report of a phylogenetic analysis of the whole nucleotide sequence of NDV isolated from a wild egret. Thus, it will help us to understand the epidemiology and molecular characteristics of Newcastle disease virus in wild birds.

**Nucleotide sequence accession number.** The GenBank accession number of egret/China/Guangxi/2011 is [JX193074](#).

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