

Complete Genome Sequence of a Newcastle Disease Virus Isolate from an Outbreak in Central India

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The complete genome sequence of a Newcastle disease virus (NDV) strain NDV/Chicken/Nagpur/01/12 was isolated from vaccinated chicken farms in India during outbreaks in 2012. The genome is 15,192 nucleotides in length and is classified as genotype VII in class II.

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Newcastle disease virus (NDV) causes a highly pathogenic viral disease known as Newcastle disease (ND) in avian species. It is classified under avian paramyxovirus serotype 1 (APMV-1). NDV is a single-stranded, nonsegmented, negative sense RNA virus belonging to the genus *Avulavirus*, in the family *Paramyxoviridae* (1). The genome sizes of NDV strains isolated from different parts of the world are categorized into three different groups: the isolates before 1960 are 15,186 nucleotides (nt) long, the isolates reported from China are 15,192 nt long, and the isolates discovered in Germany are 15,198 nt long (2). Based on genetic analysis, strains of NDV are classified into classes I and II. Avirulent strains isolated from wild birds are classified under class I genotype, whereas both virulent and avirulent strains isolated from wild and domestic birds are classified under class II (3).

In India, there have been continuous reports of ND outbreaks which have affected the economy of domestic poultry industries significantly despite various drives of vaccination programs (4, 5). For effective control of NDV, a greater understanding of NDV's genetic diversity is necessary. In the year 2012, ND outbreaks were reported from chicken farms located in the Nagpur district of the state Maharashtra in India. The affected commercial chickens were vaccinated with NDV strain LaSota. The outbreak has caused nearly 100% mortality. The various pathognomonic signs and symptoms observed in the diseased chickens were pinpoint hemorrhages at the tips of the proventricular glands and cecal tonsil and button ulcers in the duodenum and large intestine. In addition, mild congestion of brain, liver, and in the bursa was also observed. The virus was isolated and propagated in 9-day-old embryonated chicken eggs. One of the isolates, namely, NDV/Chicken/Nagpur/01/12, was plaque purified in chicken embryo fibroblast and the complete genome sequence was determined by reverse transcription (RT)-PCR using overlapped consensus primers and direct sequencing (6). To determine the 3' and 5' ends of the viral genome, rapid amplification of cDNA ends (RACE) was used (7). The complete genome of NDV/Chicken/Nagpur/01/12 is 15,192 in length. The sequence identities of

amino acids of fusion (F) and hemagglutinin-neuraminidase (HN) proteins between NDV strain NDV/Chicken/Nagpur/01/12 and the lentogenic vaccine strain LaSota are 88.4% and 85.3%, respectively. From the sequence analysis it has been found that the circulating strains of the outbreak are distinctly different from the vaccine strain.

The sequence of the F protein cleavage site is the major determinant of the NDV pathogenicity. The strain NDV/Chicken/Nagpur/01/12 has a virulent pathotype, with ¹¹²RRQKR¹¹⁶ at the C terminus of the F2 protein and F at residue 117 (8). The phylogenetic analysis by MEGA 5.2 of the F gene suggests that the present isolate belongs to genotype VII of class II (9).

Nucleotide sequence accession number. The complete genome sequence of NDV/Chicken/Nagpur/01/12 is deposited in GenBank under the accession no. [KP089979](https://www.ncbi.nlm.nih.gov/nuccore/KP089979).

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