

Complete Genome Sequence of a Newcastle Disease Virus from a *Coturnix coturnix japonica* (Japanese Quail) Covey in India

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The genome of a Newcastle disease virus isolated from a Japanese quail in 2003 is reported here. The genome is 15,192 nucleotides (nt) long, as found in the recent genotypes, and grouped as genotype VIIb, with a 6-nt insertion. This is the first report on the sequence of a genotype VII Newcastle disease virus (NDV) from India.

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Newcastle disease (ND) virus, a member of the *Paramyxoviridae* family and genus *Avulavirus*, has been shown to be present on six of the seven continents, and reports indicate the susceptibility of 241 different species, which includes 27 of the 50 orders of birds, to this virus. There has been a greater understanding of the diversity of ND virus (NDV) as a result of different vaccines that have been in use and also due to the availability of the whole-genome sequence information from different countries. An analysis of the genome had enabled the classification of the virus into 11 different genotypes (1), with recent reports of a novel genotype from South Africa (2). Preliminary analysis of the sequences available at GenBank for the Indian strain indicate the prevalence of genotypes II, IV, VI, and VII (3) and suggest that India is the only country to have genotype IV strains, which had been considered to have died out (4, 5).

Currently, whole-genome sequence information that has been generated by our laboratory is available on genotype II and IV field strains of NDV from India. We report here the whole-genome sequence information for an ND virus (ND-2K35) isolated in 2003 in 10-day-old specific-pathogen-free chicken eggs from a pooled homogenate of spleen and brain samples from a Japanese quail (*Coturnix coturnix japonica*) with clinical signs of diarrhea, lethargy, and nervous symptoms. This virus is a mesogenic strain, since it had an intracerebral pathogenicity index (ICPI) value of 1.98 and a mean death time of 67 h. Genotyping based on the 374-bp region of the fusion protein gene sequence confirmed it to belong to genotype VIIb. The whole-genome information was generated following assembly of the chromatograms (using the SeqMan module of the Lasergene version 7.1 [DNASTar, Inc., WI]) from three different clones using 36 different primer pairs, as reported in our earlier study (5), with the leader and trailer generated by rapid amplification of cDNA ends (RACE), as already described (6). The genotype of the virus was confirmed by generating the phylogenetic tree by employing MEGA 6.0 with maximum likelihood fits (using the Bayesian information criterion,

maximum likelihood values, and Akaike information criterion corrected scores) (7).

The whole-genome sequence of ND-2K35/CHN/TN/2003 is 15,192 nucleotides, containing six genes in the order 3'-N-P-M-F-HN-L-5', and has a six-nucleotide insertion (TCCCAC) downstream of the untranslated region of the nucleoprotein gene, as seen in the recent genotypes. The fusion protein cleavage site of this strain was ¹¹⁷SGRRQKRF¹¹⁹, indicating it to be highly virulent, but the biological characteristics confirm the virus to be mesogenic.

All the residues that contribute to the sialic acid binding site and neutralizing epitopes as already reported were invariant in the Indian genotype VII strain. A comparison revealed isoleucine at position 69 of the fusion protein to be unique; however, this needs confirmation with more isolates (8). The predicted length of the hemagglutinin neuraminidase (HN) protein of NDV-2K35 is 571 amino acids, which is a common feature of most virulent NDV strains. Phylogenetic analysis of the 2K35/Chennai/Japanese quail whole-genome sequence also groups it in genotype VII and in the cluster of the subgroup genotype VIIb.

Nucleotide sequence accession number. The whole-genome sequence has been submitted to GenBank under the accession no. [KF740478](http://www.ncbi.nlm.nih.gov/nuccore/KF740478).

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