

# Complete Genome Sequence of Genotype Ib Newcastle Disease Virus Isolated from a Mallard (*Anas platyrhynchos*) in Russia

Kseniya S. Yurchenko, Ivan A. Sobolev, Alexandra V. Glushchenko, Alexander M. Shestopalov

FSBSI Research Institute of Experimental and Clinical Medicine, Novosibirsk, Russia

**We report here the complete genome sequence of a Newcastle disease virus isolate, NDV/Yakutiya/mallard/852/2011, isolated from a mallard in Russia. On the basis of phylogenetic analysis, this strain was clustered into class II genotype Ib.**

Received 12 October 2015 Accepted 16 October 2015 Published 3 December 2015

**Citation** Yurchenko KS, Sobolev IA, Glushchenko AV, Shestopalov AM. 2015. Complete genome sequence of genotype Ib Newcastle disease virus isolated from a mallard (*Anas platyrhynchos*) in Russia. *Genome Announc* 3(6):e01414-15. doi:10.1128/genomeA.01414-15.

**Copyright** © 2015 Yurchenko et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Kseniya S. Yurchenko, xenia7yurch@rambler.ru.

Newcastle disease (ND) is a highly contagious viral disease caused by virulent avian paramyxovirus serotype 1 (APMV-1), also known as Newcastle disease virus (NDV) (1). There is also an antigenic variant of NDV, which has appeared in pigeons (2). The causative agent, which has a single-stranded negative-sense RNA genome, belongs to the genus *Avulavirus* (3).

NDV pathotypes are based on clinical signs in infected chickens: velogenic, mesogenic (intermediate), and lentogenic with mild infection (1, 4). However, the clinical signs of viral infections by different pathotypes can vary with the bird species. Wild ducks are regarded natural reservoirs of avirulent NDV strains and in most cases display few or no symptoms consistent with ND (5, 6). Nonetheless, several strains might be more virulent in chickens after passing from infected to healthy birds (7, 8).

In the present study, we report the complete genome sequence of NDV/Yakutiya/mallard/852/2011 strain, initially isolated from a clinical healthy wild mallard (*Anas platyrhynchos*) in the Russian Far East (Republic of Sakha [Yakutiya]) in fall of 2011.

Nine-days-old embryonating chicken eggs were used for viral propagation. Standard pathogenicity assays were performed, including determinations of the mean death time (MDT) and intracerebral pathogenicity index (ICPI) (9). NDV/Yakutiya/mallard/852/2011 is classified as mesogenic in chickens, with an ICPI of 1.04 and MDT of 116 h.

Viral RNA was extracted from allantoic fluid using TRIzol LS (Invitrogen, USA). cDNA was synthesized using random hexamer primer with RevertAid Premium (Thermo Scientific, USA). The second DNA chain was synthesized using the NEBNext mRNA second-strand synthesis module (NEB, USA), in accordance with the manufacturer's instructions. DNA libraries were made using TruSeq DNA sample prep kits version 2 (Illumina, USA), as specified by the manufacturer. The DNA sequence of the libraries was made using MiSeq (Illumina, USA) with the reagent kits version 2 (300 paired-end [PE]), according to the manufacturer's instructions. Bioinformatic analysis was conducted using the CLC Genomics Workbench 5.5 software (CLC bio, USA).

The complete genome of NDV/Yakutiya/mallard/852/2011 has been sequenced and found to be 15,186 nucleotides (nt) in length. The fusion (F) protein cleavage site is one of the main

determinants of NDV pathogenicity (1), for which sequence analysis shows that NDV/Yakutiya/mallard/852/2011 contains the typical avirulent type sequence 112G-K-Q-G-R116, with leucine at residue 117. A phylogenetic tree classified the strain into class II genotype Ib. Viruses of this genotype are mainly of low virulence and are often detected in wild and domestic waterfowl. It is supposed that water-bird isolates from the Far East of separate sublineage Ib are the possible transmission between the wild and domestic waterfowl (10).

Phylogenetic analysis of the F gene sequence showed a high similarity of NDV/Yakutiya/mallard/852/2011 with strains from South Korea (GenBank accession no. JX401405), Japan (GenBank accession no. KC503411) (11), China (GenBank accession no. KM885166) (12), and other closely related NDV isolates from the Russian Far East (GenBank accession no. KC503482) (11), North America (11, 13) and North Europe (Sweden) (14).

Thus, we first isolated genotype Ib NDV in the Republic of Sakha (Yakutiya), where there is no poultry in the region; therefore, the most likely way virus of this sublineage could appear in the present territory is by viral transmission from migratory birds.

**Nucleotide sequence accession number.** The complete genome sequence of NDV/Yakutiya/mallard/852/2011 has been deposited in GenBank under the accession no. [KJ920203](https://www.ncbi.nlm.nih.gov/nuccore/KJ920203).

## ACKNOWLEDGMENTS

We thank Sergey V. Alkhovsky and Alexey M. Shchetin of the D. I. Ivanovsky Institute of Virology (Moscow) and Michail Y. Shchelkanov of Pacific State Medical University (Vladivostok) for their assistance in genome sequencing from NDV the isolate.

This work was supported by RFBR Russian Federation research project no. 14-04-01196 A and USDA grant no. 58-0210-2-040F. This study was performed on the base of CCUE "Modern Optical Systems" RIECM.

## REFERENCES

- OIE. 2012. Manual of diagnostic tests and vaccines for terrestrial animals, 7th ed. Office International des epizooties, Paris, France.
- Yurchenko KS, Sivay MV, Glushchenko AV, Alkhovsky SV, Shchetinin AM, Shchelkanov MY, Shestopalov AM. 2015. Complete genome sequence of a Newcastle disease virus isolated from a rock dove (*Columba livia*) in the Russian Federation. *Genome Announc* 3(1):e01514-14. <http://dx.doi.org/10.1128/genomeA.01514-14>.
- Mayo MA. 2002. A summary of taxonomic changes recently approved by

- ICTV. Arch Virol 147:1655–1663. <http://dx.doi.org/10.1007/s007050200039>.
4. Alexander DJ. 2011. Newcastle disease in the European Union 2000 to 2009. Avian Pathol 40:547–558. <http://dx.doi.org/10.1080/03079457.2011.618823>.
  5. Cattoli G, Susta L, Terregino C, Brown C. 2011. Newcastle disease: a review of field recognition and current methods of laboratory detection. J Vet Diagn Invest 23:637–656. <http://dx.doi.org/10.1177/1040638711407887>.
  6. Dai Y, Cheng X, Liu M, Shen X, Li J, Yu S, Zou J, Ding C. 2014. Experimental infection of duck origin virulent Newcastle disease virus strain in ducks. BMC Vet Res 10:164. <http://dx.doi.org/10.1186/1746-6148-10-164>.
  7. Kang Y, Li Y, Yuan R, Li X, Sun M, Wang Z, Feng M, Jiao P, Ren T. 2014. Phylogenetic relationships and pathogenicity variation of two Newcastle disease viruses isolated from domestic ducks in southern China. Virol J 11:147. <http://dx.doi.org/10.1186/1743-422X-11-147>.
  8. Shengqing Y, Kishida N, Ito H, Kida H, Otsuki K, Kawaoka Y, Ito T. 2002. Generation of velogenic Newcastle disease viruses from a nonpathogenic waterfowl isolate by passaging in chickens. Virology 301:206–2011. <http://dx.doi.org/10.1006/viro.2002.1539>.
  9. Young M, Alders R, Grimes S, Spradbrow P, Dias P, da Silva A, Lobo Q. 2012. Controlling Newcastle disease in village chickens: a laboratory manual, 2nd ed. ACIAR Monograph no. 87 Australian Centre for International Agricultural Research, Canberra, Australia.
  10. Liu X, Wang X, Wu S, Hu S, Peng Y, Xue F, Liu X. 2009. Surveillance for avirulent Newcastle disease viruses in domestic ducks (*Anas platyrhynchos* and *Cairina moschata*) at live bird markets in eastern China and characterization of the viruses isolated. Avian Pathol 38:377–391. <http://dx.doi.org/10.1080/03079450903183637>.
  11. Ramey AM, Reeves AB, Ogawa H, Ip HS, Imai K, Bui VN, Yamaguchi E, Silko NY, Afonso CL. 2013. Genetic diversity and mutation of avian paramyxovirus serotype 1 (Newcastle disease virus) in wild birds and evidence for intercontinental spread. Arch Virol 158:2495–2503. <http://dx.doi.org/10.1007/s00705-013-1761-0>.
  12. Wu W, Liu H, Zhang T, Han Z, Jiang Y, Xu Q, Shao Y, Li H, Kong X, Chen H, Liu S. 2015. Molecular and antigenic characteristics of Newcastle disease virus isolates from domestic ducks in China. Infect Genet Evol 32:34–43. <http://dx.doi.org/10.1016/j.meegid.2015.02.016>.
  13. Kim LM, King DJ, Curry PE, Suarez DL, Swayne DE, Stallknecht DE, Slemmons RD, Pedersen JC, Senne DA, Winker K, Afonso CL. 2007. Phylogenetic diversity among low-virulence Newcastle disease viruses from waterfowl and shorebirds and comparison of genotype distributions to those of poultry-origin isolates. J Virol 81:12641–12653. <http://dx.doi.org/10.1128/JVI.00843-07>.
  14. Tolf C, Wille M, Haidar A, Avril A, Zohari S, Waldenström J. 2013. Prevalence of avian paramyxovirus type 1 in mallards during autumn migration in the western Baltic Sea region. Virol J 10:285. <http://dx.doi.org/10.1186/1743-422X-10-285>.