

Complete Genome Sequences of Two Newcastle Disease Virus Strains Isolated from a Wild Duck and a Pigeon in Russia

Marsel R. Kabilov,^a Tatyana Y. Alikina,^a Kseniya S. Yurchenko,^b Alexandra V. Glushchenko,^b Konstantin V. Gunbin,^{c,d} Alexander M. Shestopalov,^b Natalya V. Gubanova^{c,d}

SB RAS Genomics Core Facility, Institute of Chemical Biology and Fundamental Medicine, Siberian Branch of the Russian Academy of Sciences, Novosibirsk, Russia^a; FSBSI Research Institute of Experimental and Clinical Medicine, Novosibirsk, Russia^b; Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, Novosibirsk, Russia^c; Novosibirsk State University, Novosibirsk, Russia^d

M.R.K. and T.Y.A. contributed equally to this work.

Here, we report the complete genome sequences of two Newcastle disease virus (NDV) isolates, Adygea/duck/12/2008, from a wild duck in Russia, and Altai/pigeon/777/2010, from a pigeon in Russia. Based on comparative sequence analysis of the F gene, these strains were classified as NDV class II, genotypes VIIId and VIb/2, respectively.

Received 9 October 2016 Accepted 14 October 2016 Published 8 December 2016

Citation Kabilov MR, Alikina TY, Yurchenko KS, Glushchenko AV, Gunbin KV, Shestopalov AM, Gubanova NV. 2016. Complete genome sequences of two Newcastle disease virus strains isolated from a wild duck and a pigeon in Russia. *Genome Announc* 4(6):e01348-16. doi:10.1128/genomeA.01348-16.

Copyright © 2016 Kabilov et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Marsel R. Kabilov, kabilov@niboch.nsc.ru.

Newcastle disease is a highly contagious viral disease of birds caused by virulent avian paramyxovirus serotype 1 (APMV-1), also known as Newcastle disease virus (NDV) (1). Antigenic variants of NDV have also appeared in pigeons (2) and wild duck (3).

In the present study, we report the complete genome sequences of two NDVs: Adygea/duck/12/2008, isolated from a wild duck in the Southern Federal District (Adygea) of Russia in 2008, and Altai/pigeon/777/2010, isolated from a rock dove (*Columba livia*) from Southern Siberia (Altai Republic) in Russia in 2010.

The NDV strains were propagated in the allantoic cavities of nine-day-old embryonated hen eggs obtained from nonvaccinated chickens. NDVs have been categorized into velogenic (highly virulent), mesogenic (intermediately virulent), and lentogenic (nonvirulent) pathotypes according to standard pathogenicity tests (1, 4). Strain Adygea/duck/12/2008 was classified as a velogenic NDV with a mean death time (MDT) of 50 h and with an intracerebral pathogenicity index (ICPI) of 1.55. Strain Altai/pigeon/777/2010 belongs to the mesogenic pathotype with an MDT of 75 h and an ICPI of 0.61.

RNAs were isolated from 100 to 400 μ L of chicken allantois fluid with cultured viral particles using a GeneJET viral DNA/RNA purification kit (Thermo Fisher Scientific) and were treated with TURBO DNase (Thermo Fisher Scientific). Up to 40 ng of RNA were used for the DNA library, which was prepared using a TruSeq RNA sample preparation kit version 2 (Illumina). The DNA libraries were sequenced using the MiSeq platform (2 \times 300-bp cycles; Illumina). The full-length genomes were assembled *de novo* with CLC Genomics Workbench version 8.5 (Qiagen). The complete genomes of NDV Adygea/duck/12/2008 and Altai/pigeon/777/2010 have been found to be 15,190 and 15,192 nucleotides in length, respectively.

The comparative analysis of the F protein-coding gene revealed that both NDV Altai/pigeon/777/2010 and Adygea/duck/12/2008

strains belong to NDV class II (4) and contain a polybasic amino acid sequence (¹¹²KRQKRF¹¹⁷ and ¹¹²RRQKRF¹¹⁷, respectively) at the F protein cleavage site. It was shown that the F gene from Altai/pigeon/777/2010 is similar to NDV isolate Pi/Rus/Kemerovo/0267/09 (98% sequence similarity), which belongs to the VIb/2 genotype (5). Genotype VI includes viruses that have been isolated from multiple avian species (6–10). Viruses of this genotype are particularly important because of their frequent association with doves and pigeons and the consequent risk for introduction into poultry flocks (6, 11, 12, 13).

The F gene of strain Adygea/duck/12/2008 is homologous to NDV strain Muscovy GI 227460816 (97.47% sequence similarity) (4), which belongs to the VIIId genotype of NDV class II. Currently, genotype VII is the genotype most frequently associated with outbreaks of Newcastle disease in the Middle East and Asia (14), and outbreaks caused by these viruses are of particular concern given that some strains have shown increased virulence in poultry, while others have expanded their host range and are now able to cause disease in geese (9, 15). Additionally, an outbreak of Newcastle disease in South America has been recently attributed to a genotype VII virus, indicating that these viruses are spreading to other locations around the world (16).

Accession number(s). The complete genome sequences of NDV Adygea/duck/12/2008 and Altai/pigeon/777/2010 have been deposited in GenBank under the accession numbers [KP189357](https://www.ncbi.nlm.nih.gov/nuclot/KP189357) and [KT962979](https://www.ncbi.nlm.nih.gov/nuclot/KT962979), respectively.

ACKNOWLEDGMENTS

This work was supported by the Russian Foundation for Basic Research (grant no. 14-04-01196) and Federal Fundamental Scientific Research Programs for 2013–2020 (VI.53.1.4, VI.62.1.3). This study was performed on the base of the SB RAS Genomics Core Facility (ICBFM SB RAS, Novosibirsk, Russia).

FUNDING INFORMATION

This work, including the efforts of Marsel R. Kabilov, Alexandra V. Glushchenko, Kseniya S. Yurchenko, Alexander M. Shestopalov, Konstantin V. Gunbin, and Natalya V. Gubanova, was funded by Russian Foundation for Basic Research (RFBR) (14-04-01196). This work, including the efforts of Marsel R. Kabilov, Tatyana Y. Alikina, Konstantin V. Gunbin, and Natalya V. Gubanova, was funded by Federal Fundamental Scientific Research Programs for 2013–2020 (VI.53.1.4 [0324-2015-0003], VI.62.1.3 [0309-2014-0007]).

REFERENCES

1. World Organisation for Animal Health. 2012. Manual of diagnostic tests and vaccines for terrestrial animals, 7th ed. Office International des Epizooties, Paris, France.
2. Yurchenko KS, Sivay MV, Glushchenko AV, Alkhovsky SV, Shchetin 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>.
3. 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. <http://dx.doi.org/10.1128/genomeA.01414-15>.
4. Diel DG, da Silva LH, Liu H, Wang Z, Miller PJ, Afonso CL. 2012. Genetic diversity of avian paramyxovirus type 1: proposal for a unified nomenclature and classification system of Newcastle disease virus genotypes. *Infect Genet Evol* 12:1770–1779. <http://dx.doi.org/10.1016/j.meegid.2012.07.012>.
5. Pchelkina IP, Manin TB, Kolosov SN, Starov SK, Andriyasov AV, Chvala IA, Drygin VV, Yu Q, Miller PJ, Suarez DL. 2013. Characteristics of pigeon paramyxovirus serotype-1 isolates (PPMV-1) from the Russian Federation from 2001 to 2009. *Avian Dis* 57:2–7. <http://dx.doi.org/10.1637/10246-051112-Reg.1>.
6. 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>.
7. Czeglédi A, Ujvári D, Somogyi E, Wehmann E, Werner O, Lomniczi B. 2006. Third genome size category of avian paramyxovirus serotype 1 (Newcastle disease virus) and evolutionary implications. *Virus Res* 120:36–48. <http://dx.doi.org/10.1016/j.virusres.2005.11.009>.
8. 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>.
9. Liu XF, Wan HQ, Ni XX, Wu YT, Liu WB. 2003. Pathotypical and genotypical characterization of strains of Newcastle disease virus isolated from outbreaks in chicken and goose flocks in some regions of China during 1985–2001. *Arch Virol* 148:1387–1403. <http://dx.doi.org/10.1007/s00705-003-0014-z>.
10. Wehmann E, Czeglédi A, Werner O, Kaleta EF, Lomniczi B. 2003. Occurrence of genotypes IV, V, VI and VIIa in Newcastle disease outbreaks in Germany between 1939 and 1995. *Avian Pathol* 32:157–163. <http://dx.doi.org/10.1080/0307945021000071623>.
11. Kim LM, King DJ, Guzman H, Tesh RB, Travassos Da Rosa AP, Bueno R, Jr, Dennett JA, Afonso CL. 2008. Biological and phylogenetic characterization of pigeon paramyxovirus serotype 1 circulating in wild North American pigeons and doves. *J Clin Microbiol* 46:3303–3310. <http://dx.doi.org/10.1128/JCM.00644-08>.
12. Kommers GD, King DJ, Seal BS, Brown CC. 2001. Virulence of pigeon-origin Newcastle disease virus isolates for domestic chickens. *Avian Dis* 45:906–921. <http://dx.doi.org/10.2307/1592870>.
13. Kommers GD, King DJ, Seal BS, Carmichael KP, Brown CC. 2002. Pathogenesis of six pigeon-origin isolates of Newcastle disease virus for domestic chickens. *Vet Pathol* 39:353–362. <http://dx.doi.org/10.1354/vp.39-3-353>.
14. Miller PJ, Decanini EL, Afonso CL. 2010. Newcastle disease: evolution of genotypes and the related diagnostic challenges. *Infect Genet Evol* 10:26–35. <http://dx.doi.org/10.1016/j.meegid.2009.09.012>.
15. Huang Y, Wan HQ, Liu HQ, Wu YT, Liu XF. 2004. Genomic sequence of an isolate of Newcastle disease virus isolated from an outbreak in geese: a novel six nucleotide insertion in the non-coding region of the nucleoprotein gene. *Arch Virol* 149:1445–1457. <http://dx.doi.org/10.1007/s00705-004-0297-8>.
16. Perozo F, Merino R, Afonso CL, Villegas P, Calderon N. 2008. Biological and phylogenetic characterization of virulent Newcastle disease virus circulating in Mexico. *Avian Dis* 52:472–479. <http://dx.doi.org/10.1637/8276-022908-Reg.1>.