

# Complete Genome Sequence of an NADC30-Like Strain of Porcine Reproductive and Respiratory Syndrome Virus in China

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**The most recently emergent porcine reproductive and respiratory syndrome virus strains in China are characterized by 393 nucleotide deletions in the nonstructural protein 2 (NSP2) region and are known as NADC30-like strains. Here, we report the complete genome sequence of the NADC30-like HNjz15 strain that was isolated in 2015.**

Received 2 March 2016 Accepted 7 March 2016 Published 21 April 2016

**Citation** Ji G, Li Y, Tan F, Zhuang J, Li X, Tian K. 2016. Complete genome sequence of an NADC30-like strain of porcine reproductive and respiratory syndrome virus in China. *Genome Announc* 4(2):e00303-16. doi:10.1128/genomeA.00303-16.

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Porcine reproductive and respiratory syndrome virus (PRRSV) is a major swine pathogen causing huge economic losses in the swine industry worldwide. PRRSV belongs to the order *Nidovirales*, family *Arteriviridae*, and can be divided into European genotype 1 and North American genotype 2. PRRSV has shown remarkable genetic variation through mutation and recombination, resulting in new isolates with different levels of pathogenicity and virulence. Highly pathogenic PRRSV (HP-PRRSV) with a discontinuous 30-amino acid (aa) deletion has been circulating and predominating in the field since 2006 and has affected >2 million pigs in China (1, 2). Recently, several field isolates of PRRSV that are genetically similar to the NADC30 strain, a type 2 PRRSV that was isolated in United States in 2008, were designated NADC30-like PRRSV and caused the outbreaks of severe PRRS (3–5). Here, we report the complete genome sequence of the NADC30-like variant HNjz15.

The HNjz15 strain was isolated in 2015 from the serum samples of diseased pigs using porcine pulmonary alveolar macrophages. The first passage of virus was used for genomic sequencing. Basically, 12 primer pairs were used to generate overlapping amplicons by reverse transcription-PCR (RT-PCR). The 5' and 3' regions were obtained by rapid amplification of cDNA ends (RACE) using a RACE kit (TaKaRa, China). The PCR products were cloned into pEASY-Blunt vector (TansGen Biotech, China), sequenced three times, and assembled into the full-length sequence using the DNASTar (Lasergene) software. The genome of HNjz15 was 15,019 nucleotides in length, excluding the poly(A) tail.

Genome analysis results showed that HNjz15 shared the highest similarity with NADC30 (95.6%) compared to other PRRSV strains. Like other NADC30-like isolates, HNjz15 had the same discontinuous amino acid deletions in the nonstructural protein 2 (NSP2) region as those in NADC30 (GenBank accession no. JN654459). These deletions were identified as 1 aa at position 303, 111 aa at positions 323 to 433, and 19 aa at positions 501 to 519. In addition, it is noteworthy that HNjz15 had 2 amino acid mutations at sites 12447 (G to A) and 13067 (A to G), which led to an early termination of the GP2 protein code and a delayed termination of the GP3 protein code. Consequently, the number of amino acids of the GP2 protein of HNjz15 was 1 amino acid less than that

of NADC30, and the number of amino acids of GP3 protein was 12 amino acids more than that of NADC30. The significance of these amino acid changes on the pathogenicity of NADC30 is worth further investigation.

The genome data of HNjz15 will help us to understand the epidemiology and evolution of PRRSV in pigs.

**Nucleotide sequence accession number.** The complete genome sequence of the HNjz15 strain is available in GenBank under the accession no. [KT945017](https://www.ncbi.nlm.nih.gov/nuclseq/KT945017).

## ACKNOWLEDGMENTS

This work was supported by a grant from the National Natural Science Foundation of China (grant no. 3149600031), the Major Science and Technology Program in Henan Province (grant no. 131100110200), Innovation Scientists and Technicians Troop Construction Projects of Henan Province (grant no. 142101510001), Talents Plan for Scientific and Technological Innovation in Henan Province (grant no. 144200510002), and Science and Technology Innovation team in Henan Province (team no. C20130005).

## REFERENCES

1. Tian K, Yu X, Zhao T, Feng Y, Cao Z, Wang C, Hu Y, Chen X, Hu D, Tian X, Liu D, Zhang S, Deng X, Ding Y, Yang L, Zhang Y, Xiao H, Qiao M, Wang B, Hou L. 2007. Emergence of fatal PRRSV variants: unparalleled outbreaks of atypical PRRS in China and molecular dissection of the unique hallmark. *PLoS One* 2:e526. <http://dx.doi.org/10.1371/journal.pone.0000526>.
2. Shi YJ, Hu ZB, Xiong ZH, Zhou YJ, Jin X, Gu CQ, Hu XY, Cheng GF, Song NH, Zhang WP. 2013. Analysis of molecular variation of porcine reproductive and respiratory syndrome virus in central China from 2006 to 2012. *Arch Virol* 158:717–721. <http://dx.doi.org/10.1007/s00705-012-1542-1>.
3. Zhou L, Wang ZC, Ding YP, Ge XN, Guo X, Yang HC. 2015. NADC30-like strain of porcine reproductive and respiratory syndrome virus, China. *Emerg Infect Dis* 21:2256–2257. <http://dx.doi.org/10.3201/eid2112.150360>.
4. Zhao K, Ye C, Chang XB, Jiang CG, Wang SJ, Cai XH, Tong GZ, Tian ZJ, Shi M, An TQ. 2015. Importation and recombination are responsible for the latest emergence of highly pathogenic porcine reproductive and respiratory syndrome virus in China. *J Virol* 89:10712–10716. <http://dx.doi.org/10.1128/JVI.01446-15>.
5. Zhou F, Zhao J, Chen L, Chang HT, Li YT, Liu HY, Wang CQ, Yang X. 2015. Complete genome sequence of a novel porcine reproductive and respiratory syndrome virus that emerged in China. *Genome Announc* 3(4):e00702-15. <http://dx.doi.org/10.1128/genomeA.00702-15>.