

Full-Length Genome Sequence of Porcine Deltacoronavirus Strain USA/IA/2014/8734

Ganwu Li,^a Qi Chen,^a Karen M. Harmon,^a Kyoung-Jin Yoon,^a Kent J. Schwartz,^a Marlin J. Hoogland,^b Phillip C. Gauger,^a Rodger G. Main,^a Jianqiang Zhang^a

Department of Veterinary Diagnostic and Production Animal Medicine, College of Veterinary Medicine, Iowa State University, Ames, Iowa, USA^a; Murphy-Brown LLC, Algona, Iowa, USA^b

Porcine deltacoronavirus (PDCoV) was detected in feces from diarrheic sows during an epidemic of acute and transmissible diarrhea. No transmissible gastroenteritis virus or porcine epidemic diarrhea virus was detected. The PDCoV USA/IA/2014/8734 from the herd was sequenced for full-length genomic RNA to further characterize PDCoV in U.S. swine.

Received 13 March 2014 Accepted 25 March 2014 Published 10 April 2014

Citation Li G, Chen Q, Harmon KM, Yoon K-J, Schwartz KJ, Hoogland MJ, Gauger PC, Main RG, Zhang J. 2014. Full-length genome sequence of porcine deltacoronavirus strain USA/IA/2014/8734. *Genome Announc.* 2(2):e00278-14. doi:10.1128/genomeA.00278-14.

Copyright © 2014 Li 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/3.0/).

Address correspondence to Ganwu Li, liganwu@iastate.edu, or Jianqiang Zhang, jqzhang@iastate.edu.

Coronaviruses (CoVs) are enveloped, single-stranded, positive-sense RNA viruses belonging to the order *Nidovirales* and the family *Coronaviridae*. Three genera, *Alphacoronavirus*, *Betacoronavirus*, and *Gammacoronavirus*, were proposed to replace the traditional group 1, 2, and 3 coronaviruses (1–3). The fourth genus, *Deltacoronavirus*, has recently been described by a research group in Hong Kong (4, 5). By use of a molecular tool, they detected deltacoronaviruses in various species, including at least nine avian CoVs and two porcine CoVs (HKU-15-44 and HKU-15-155).

In late February of 2014, we received a submission for diagnostic investigation from a 2,500-sow herd in Iowa with a history of acute severe diarrhea. The epidemic started in one breeding barn and progressed throughout the breeding and gestation barns over a 7-day period. Acute diarrhea started in the farrowing rooms (sows and piglets) approximately 8 to 9 days after the initial onset of clinical signs in the breeding barn. Viral enteritis was suspected based on clinical impression and gross and microscopic lesions. Molecular testing did not detect porcine epidemic diarrhea virus, transmissible gastroenteritis virus, or porcine rotaviruses. Bacterial culture yielded mixed and inconsistent populations of expected flora with no significant pathogens consistently identified. Unexpectedly, all fecal samples tested positive for porcine deltacoronavirus (PDCoV) by a pan-*Coronaviridae* PCR (6) followed by sequencing confirmation of PCR amplicons, as well as by a PDCoV-specific real-time reverse transcription (RT)-PCR assay with cycle threshold (C_T) values ranging from 14 to 19.

Since the full-length genomic sequences of PDCoV in U.S. swine have not been previously reported, complete genomic sequencing of PDCoV (USA/IA/2014/8734) was attempted using next-generation sequencing technology on an Illumina MiSeq platform following the procedures established in our laboratory (7). Sequences were mapped to all known coronaviruses and *de novo* assembled and then analyzed using the DNASTar Lasergene 11 Core Suite.

The genomic sequence of the PDCoV USA/IA/2014/8734

strain is 25,422 nucleotides (nt) in length, excluding the 3' poly(A) tail. The genomic organization of this U.S. PDCoV is similar to what was previously described for PDCoV HKU15-44 and HKU15-155 (4). The genome arrangements are as follows: 5' untranslated region (UTR), open reading frame 1a/1b (ORF1a/1b), spike (S), envelope (E), membrane (M), nonstructural protein 6 (NS 6), nucleocapsid (N), nonstructural protein 7 (NS 7), and 3' UTR.

The genome of PDCoV USA/IA/2014/8734 has 271 nt differences (98.9% nt identity) from the HKU15-44 strain (GenBank accession no. JQ065042) and 209 nt differences (99.2% nt identity) from the HKU15-155 strain (JQ065043). The majority of nt differences were located in the ORF1a/1b and S genes. There were no insertions or deletions between USA/IA/2014/8734 and HKU15-44. However, compared to HKU15-155, USA/IA/2014/8734 has six nucleotide insertions (a 3-nt AAT insertion at positions 19477 to 19479, corresponding to the S gene, and a 3-nt GTT insertion at positions 25047 to 25049, corresponding to the 3' UTR).

The PDCoV USA/IA/2014/8734 sequence data will facilitate future research on the epidemiology and evolutionary biology of PDCoVs in U.S. swine. Further study remains to be conducted to determine the clinical significance of PDCoV.

Nucleotide sequence accession number. The complete genome sequence of PDCoV strain USA/IA/2014/8734 has been deposited in GenBank under the accession number [KJ567050](https://www.ncbi.nlm.nih.gov/nuclseq/KJ567050).

ACKNOWLEDGMENTS

This study was supported by Iowa State University Veterinary Diagnostic Laboratory.

We thank Wendy Stensland, Amy Chriswell, Derek Dunn, and Sarah Abate for technical assistance in casework.

REFERENCES

1. Curtis KM, Yount B, Baric RS. 2002. Heterologous gene expression from transmissible gastroenteritis virus replicon particles. *J. Virol.* 76: 1422–1434. <http://dx.doi.org/10.1128/JVI.76.3.1422-1434.2002>.

2. Woo PC, Huang Y, Lau SK, Yuen KY. 2010. Coronavirus genomics and bioinformatics analysis. *Viruses* 2:1804–1820. <http://dx.doi.org/10.3390/v2081803>.
3. Woo PC, Lau SK, Huang Y, Yuen KY. 2009. Coronavirus diversity, phylogeny and interspecies jumping. *Exp. Biol. Med.* 234:1117–1127. <http://dx.doi.org/10.3181/0903-MR-94>.
4. Woo PC, Lau SK, Lam CS, Lau CC, Tsang AK, Lau JH, Bai R, Teng JL, Tsang CC, Wang M, Zheng BJ, Chan KH, Yuen KY. 2012. Discovery of seven novel mammalian and avian coronaviruses in the genus *Deltacoronavirus* supports bat coronaviruses as the gene source of *Alphacoronavirus* and *Betacoronavirus* and avian coronaviruses as the gene source of gammacoronavirus and *Deltacoronavirus*. *J. Virol.* 86:3995–4008. <http://dx.doi.org/10.1128/JVI.06540-11>.
5. Woo PC, Lau SK, Lam CS, Lai KK, Huang Y, Lee P, Luk GS, Dyrting KC, Chan KH, Yuen KY. 2009. Comparative analysis of complete genome sequences of three avian coronaviruses reveals a novel group 3c coronavirus. *J. Virol.* 83:908–917. <http://dx.doi.org/10.1128/JVI.01977-08>.
6. Moës E, Vijgen L, Keyaerts E, Zlateva K, Li S, Maes P, Pyrc K, Berkhout B, van der Hoek L, Van Ranst M. 2005. A novel pancoronavirus RT-PCR assay: frequent detection of human coronavirus NL63 in children hospitalized with respiratory tract infections in Belgium. *BMC Infect. Dis.* 5:6. <http://dx.doi.org/10.1186/1471-2334-5-6>.
7. Chen Q, Li G, Stasko J, Thomas JT, Stensland WR, Pillatzki AE, Gauger PC, Schwartz KJ, Madson D, Yoon KJ, Stevenson GW, Burrough ER, Harmon KM, Main RG, Zhang J. 2014. Isolation and characterization of porcine epidemic diarrhea viruses associated with the 2013 disease outbreak among swine in the United States. *J. Clin. Microbiol.* 52:234–243. <http://dx.doi.org/10.1128/JCM.02820-13>.