

Complete Genome Characterization of Korean Porcine Deltacoronavirus Strain KOR/KNU14-04/2014

Sunhee Lee, Changhee Lee

Animal Virology Laboratory, School of Life Sciences, BK21 Plus KNU Creative BioResearch Group, Kyungpook National University, Daegu, Republic of Korea

In April 2014, porcine deltacoronavirus (PDCoV) was first identified in feces from diarrheic piglets in South Korea and found to be closely related to other PDCoV strains. The complete genome of the Korean PDCoV strain, KOR/KNU14-04/2014, was sequenced and analyzed to characterize PDCoV circulating in South Korea.

Received 5 October 2014 Accepted 17 October 2014 Published 26 November 2014

Citation Lee S, Lee C. 2014. Complete genome characterization of Korean porcine deltacoronavirus strain KOR/KNU14-04/2014. *Genome Announc.* 2(6):e01191-14. doi:10.1128/genomeA.01191-14.

Copyright © 2014 Lee and Lee. 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 Changhee Lee, changhee@knu.ac.kr.

Coronaviruses are enveloped, single-stranded, positive-sense RNA viruses belonging to the family *Coronaviridae* of the order *Nidovirales*, which are further divided into 4 genera, *Alphacoronavirus*, *Betacoronavirus*, *Gammacoronavirus*, and *Deltacoronavirus* (1, 2). Viruses of the *Alphacoronavirus* and *Betacoronavirus* genera have been detected in swine (3). The fifth porcine coronavirus was identified in 2012 in an investigation to discover new deltacoronaviruses in mammals and birds from China (2). In February 2014, the presence of porcine deltacoronavirus (PDCoV) was first announced in Ohio, United States, and since then, this novel coronavirus has been reported in 17 U.S. states (4–7).

Since the discovery of PDCoV in China, we have conducted a surveillance study to identify the presence of PDCoV and tested a total of 108 fecal and 5 intestinal homogenate samples from pigs with diarrheal disease. These samples were initially negative for transmissible gastroenteritis virus (TGEV), porcine epidemic diarrhoea virus (PEDV), and rotavirus, or positive for at least one of three viruses. Two fecal samples received from different pig farms in April and June of 2014, each of which had been positive for rotavirus and negative for all three viral pathogens, respectively, tested positive for PDCoV by reverse transcription (RT)-PCR followed by sequencing confirmation of PCR amplicons. To further investigate the genetic relationship of the Korean and previously reported Chinese and U.S. strains, the complete genome of a representative PDCoV strain, KNU14-04, was sequenced using rapid amplification of cDNA ends (RACE) and next-generation sequencing (NGS) as described previously (8–10). The KNU14-04 NGS reads were assembled using the full-length PDCoV reference genomes from GenBank (4, 5).

The complete genomic sequence of KNU14-04 is 25,422 nucleotides (nt) in length, excluding the 3' poly(A) tail and consists of the 539-nt 5' untranslated region (UTR), the 18,803-nt replicase gene (nt 540 to 11,414 for 1a and nt 11,414 to 19,342 for 1b), the 3,483-nt spike (S) gene (nt 19,324 to 22,806), the 252-nt envelope (E) gene (nt 22,800 to 23,051), the 654-nt membrane (M) gene (nt 23,044 to 23,697), the 285-nt nonstructural gene 6 (NS 6) (nt 23,697 to 23,981), the 1,029-nt nucleocapsid (N) gene (nt

24,002 to 25,030), the 603-nt NS7 gene (nt 24,096 to 24,698), and the 392-nt 3' UTR.

The full-length PEDV genome of KNU14-04 has nucleotide identities of 98.8 to 99.0% and 99.6 to 99.8% to 2 Chinese strains (GenBank accession numbers JQ065042 and JQ065043) and 8 United States strains (accession numbers KJ462462, KJ481931, KJ567050, KJ569769, KJ601777, KJ601778, KJ601779, and KJ601780), respectively. Comparing the complete genome of KNU14-04 to the Chinese strain HKU15-155, a 3-nt insertion was observed in each of the S genes and the 3' UTR of strain KNU14-04, which is also present in strain United States/IA/2014/8734 (4).

To our knowledge, this is the first time that the complete genome sequence of PDCoV from South Korea has been determined. Our sequence data will provide further insight into the understanding of the epidemiology and evolution of PDCoV in South Korea and facilitate investigations on the genetic diversity of PDCoV worldwide.

Nucleotide sequence accession number. These KOR/KNU14-04/2014 PDCoV sequence data have been deposited in GenBank under the accession no. [KM820765](https://www.ncbi.nlm.nih.gov/nuccore/KM820765).

ACKNOWLEDGMENTS

We gratefully thank Gun-Seok Park and Jae-Ho Shin from Kyungpook National University for their technical assistance with the NGS analysis.

This research was supported by the Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Science, ICT & Future Planning (2013R1A2A2A01004355).

REFERENCES

- de Groot RJ, Baker SC, Baric R, Enjuanes L, Gorbalenya AE, Holmes KV, Perlman S, Poon L, Rottier PJM, Talbot PJ, Woo PCY, Ziebuhr J. 2012. Family *Coronaviridae*, p 806–828. In King A, Adams M, Cartens E, Lefkowitz E (ed), *Virus taxonomy: ninth report of the International Committee on Taxonomy of Viruses*. Academic Press, San Diego, CA.
- 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>.
3. Chan JF, To KK, Tse H, Jin DY, Yuen KY. 2013. Interspecies transmission and emergence of novel viruses: lessons from bats and birds. *Trends Microbiol.* 21:544–555. <http://dx.doi.org/10.1016/j.tim.2013.05.005>.
 4. Li G, Chen Q, Harmon KM, Yoon KJ, 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. <http://dx.doi.org/10.1128/genomeA.00278-14>.
 5. Marthaler D, Jiang Y, Otterson T, Goyal S, Rossow K, Collins J. 2013. Complete genome sequence of porcine epidemic diarrhea virus strain USA/Colorado/2013 from the United States. *Genome Announc.* 1(4):e00555-13. <http://dx.doi.org/10.1128/genomeA.00555-13>.
 6. Marthaler D, Raymond L, Jiang Y, Collins J, Rossow K, Rovira A. 2014. Rapid detection, complete genome sequencing, and phylogenetic analysis of porcine deltacoronavirus. *Emerg. Infect. Dis.* 20:1347–1350. <http://dx.doi.org/10.3201/eid2008.140526>.
 7. Wang L, Byrum B, Zhang Y. 2014. Porcine coronavirus HKU15 detected in 9 US States, 2014. *Emerg. Infect. Dis.* 20:1594–1595. <http://dx.doi.org/10.3201/eid2009.140756>.
 8. Lee YN, Lee C. 2013. Complete genome sequence of a novel porcine parainfluenza virus 5 isolate in Korea. *Arch. Virol.* 158:1765–1772. <http://dx.doi.org/10.1007/s00705-013-1770-z>.
 9. Lee S, Lee C. 2014. Outbreak-related porcine epidemic diarrhea virus strains similar to US strains, South Korea, 2013. *Emerg. Infect. Dis.* 20:1223–1226. <http://dx.doi.org/10.3201/eid2007.140294>.
 10. Rothberg JM, Hinz W, Rearick TM, Schultz J, Mileski W, Davey M, Leamon JH, Johnson K, Milgrew MJ, Edwards M, Hoon J, Simons JF, Marran D, Myers JW, Davidson JF, Branting A, Nobile JR, Puc BP, Light D, Clark TA, Huber M, Branciforte JT, Stoner IB, Cawley SE, Lyons M, Fu Y, Homer N, Sedova M, Miao X, Reed B, Sabina J, Feierstein E, Schorn M, Alanjary M, Dimalanta E, Dressman D, Kasinskas R, Sokolsky T, Fidanza JA, Namsaraev E, McKernan KJ, Williams A, Roth GT, Bustillo J. 2011. An integrated semiconductor device enabling non-optical genome sequencing. *Nature* 475:348–352. <http://dx.doi.org/10.1038/nature10242>.