



# Complete Genome Characterization of Novel Chinese Porcine Deltacoronavirus Strain SD

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**ABSTRACT** A porcine deltacoronavirus (PDCoV) was isolated and identified from feces of diarrheic piglets in Shandong Province of the Chinese mainland, and the complete genome of the Chinese PDCoV strain, SD, was sequenced and analyzed to further characterize PDCoV circulating in China.

Porcine deltacoronavirus (PDCoV) is an enveloped, single-stranded, positive-sense RNA virus belonging to the fourth genus, *Deltacoronavirus*, in the family *Coronaviridae* of the order *Nidovirales* (1, 2). PDCoV was detected mostly in the entire small intestine, especially the jejunum and ileum, where it causes severe enteritis, accompanied by diarrhea and vomiting, in piglets. Since 2013, the prevalent PDCoV virus has been detected in the United States, South Korea, China, Japan, Europe, and other places (3–7).

Since the discovery of PDCoV in the United States, we have conducted a surveillance study to detect the presence of PDCoV in China. Fifty-six fecal and intestinal samples from the Hebei, Henan, Shandong, Guangdong, and Shaanxi provinces were collected and tested. Molecular testing was positive for PDCoV and negative for porcine epidemic diarrhea virus (PEDV), transmissible gastroenteritis virus (TGEV), and porcine rotavirus (PRotAV). Subsequently, the complete genome sequence of PDCoV strain SD was generated using a previously described method (5).

The complete genomic sequence of PDCoV SD is 25,414 nucleotides (nt) in length, excluding the 3' poly(A) tail. The genomic organization of this Chinese PDCoV is the same as that of the better-known PDCoV HKU15-155. The genome consists of a 5' untranslated region (UTR), open reading frame 1a/1b (ORF1a/1b); the genes encoding the proteins spike (S), envelope (E), membrane (M), and nonstructural protein 6 (NS 6), nucleocapsid (N), and nonstructural protein 7 (NS 7); and a 3' UTR.

Analysis of PDCoV SD with the basic local alignment search tool (BLAST) demonstrated that strain SD shares nucleotide identity percentages of 98.97%, 99.06%, and 99.13% with HKU15-155, CH/Sichuan/S27/2012, and CH-HB-2014, respectively (8). Moreover, this analysis revealed a 6-nt (TTTGAA) deletion at positions 1739 to 1744 (corresponding to the HKU15-44 sequence) in the Nsp-2 region and a 9-nt (TCGGCAATG) deletion at positions 2810 to 2818 in the Nsp-3 region.

The data presented here will facilitate future research on the epidemiology and diagnosis of disease caused by PDCoV infection in China. Further study remains to be conducted to develop effective measures to control this disease.

**Accession number(s).** The genome sequence of the porcine deltacoronavirus strain SD was deposited in GenBank with the accession no. [MF431743](https://www.ncbi.nlm.nih.gov/nuclot/MF431743).

Received 27 July 2017 Accepted 11 August 2017 Published 5 October 2017

**Citation** Liu C, Zhang X, Zhang Z, Chen R, Zhang Z, Xue Q. 2017. Complete genome characterization of novel Chinese porcine deltacoronavirus strain SD. *Genome Announc* 5:e00930-17. <https://doi.org/10.1128/genomeA.00930-17>.

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## REFERENCES

1. Lee S, Lee C. 2015. Functional characterization and proteomic analysis of the nucleocapsid protein of porcine deltacoronavirus. *Virus Res* 208: 136–145. <https://doi.org/10.1016/j.virusres.2015.06.013>.
2. Ma Y, Zhang Y, Liang X, Oglesbee M, Krakowka S, Niehaus A, Wang GP, Jia AQ, Song HH, Li JR. 2016. Two-way antigenic cross-reactivity between porcine epidemic diarrhea virus and porcine deltacoronavirus. *Vet Microbiol* 186:90–96. <https://doi.org/10.1016/j.vetmic.2016.02.004>.
3. Wang L, Byrum B, Zhang Y. 2014. Detection and genetic characterization of deltacoronavirus in pigs, Ohio, 2014. *Emerg Infect Dis* 20:1227–1230. <https://doi.org/10.3201/eid2007.140296>.
4. Ma Y, Zhang Y, Liang X, Lou F, Oglesbee M, Krakowka S, Li J. 2015. Origin, evolution, and virulence of porcine deltacoronaviruses in the United States. *mBio* 6:e00064-15. <https://doi.org/10.1128/mBio.00064-15>.
5. 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. <https://doi.org/10.3201/eid2008.140526>.
6. Lee S, Lee C. 2014. Complete genome characterization of Korean porcine deltacoronavirus strain KOR/KNU14-04/2014. *Genome Announc* 2(6): e01191-14. <https://doi.org/10.1128/genomeA.01191-14>.
7. 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:e00278-14. <https://doi.org/10.1128/genomeA.00278-14>.
8. Wang YW, Yue H, Fang W, Huang YW. 2015. Complete genome sequence of porcine deltacoronavirus strain CH/Sichuan/S27/2012 from mainland China. *Genome Announc* 3(5):e00945-15. <https://doi.org/10.1128/genomeA.00945-15>.