

Complete Genomic Sequence of a Novel Porcine Circovirus 2 Strain, CC12

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The genome sequence of a novel porcine circovirus 2 strain (CC12) is composed of 1,767 nucleotides, with two major open reading frames (ORFs). ORF1 encodes two replication-associated proteins (Rep and Rep') with the unique mutation N186S, and ORF2 encodes a viral capsid protein (Cap) with two rare mutations, R59K and A190T.

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Porcine circovirus 2 (PCV2), a single-stranded circular DNA virus and a member of the virus family *Circoviridae*, is etiologically associated with postweaning and multisystemic wasting syndrome (PMWS), porcine dermatitis and nephropathy syndrome, porcine respiratory disease complex, granulomatous enteritis, necrotizing lymphadenitis, reproductive failure, exudative epidermitis, and congenital tremors (1–8). PCV2 infection was first reported in Canada in 1997 and later identified in the United States, France, Japan, and other countries (9, 10). Recently, this infection has become one of the most severe diseases affecting pig production in China (11–14).

PCV2 has been isolated from many countries, and three major genotypes (PCV2a, 2b, and 2c) have been proposed based on the genetic variations of isolates (13–20). PCV2b was demonstrated to be the prevalent form with an enhanced pathogenicity. We have isolated a PCV2 strain, named CC12, from a pig farm with an outbreak of PMWS in the Jilin province of China. Sequencing the genome of CC12 strain showed that it contains 1,767 nucleotides and consists of two major open reading frames (ORFs), ORF1 and ORF2. ORF1 encodes two replication-associated proteins (Rep and Rep'), and ORF2 encodes a viral capsid protein (Cap). Phylogenetic analysis showed that the CC12 strain is clustered to PCV2b, a predominant genotype affecting the world's swine industry since 2003. Alignment analysis by the Clustal W method revealed a very unique amino acid mutation/substitution from asparagine to serine (N186S) in the Rep protein and two rare mutations in the Cap protein, one a change from arginine to lysine (R59K) and the other from alanine to threonine (A190T), in relation to PCV2 genomic sequences in GenBank. Whether these novel mutations are of significance in altering either the biological function of ORF1-encoded Rep protein or the antigenicity of the ORF2-encoded Cap protein is not clear. This will be the subject of a future investigation.

Our findings revealed a novel PCV2 strain with a unique mutation in its Rep protein and two rare mutations in the Cap protein. These data will facilitate the future investigation of the mo-

lecular pathogenesis of PCV2 and contribute to the elucidation of the functions of PCV2 proteins.

Nucleotide sequence accession number. The complete genome sequence of CC12 has been deposited at DDBJ/EMBL/GenBank under the accession no. [KC859451](https://www.ncbi.nlm.nih.gov/nuccore/KC859451).

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REFERENCES

1. Clark EG. 1997. Post-weaning multisystemic wasting syndrome, p 499–501. *In* Proceedings of the American Association of Swine Practitioners, 28th Annual Meeting, Quebec City, Canada.
2. Smith WJ, Thomson JR, Done S. 1993. Dermatitis/nephropathy syndrome of pigs. *Vet. Rec.* 132:47. <http://dx.doi.org/10.1136/vr.132.2.47-b>.
3. Halbur PG. 1998. Porcine respiratory disease, p 1–10. *In* Proceedings of the 15th International Pig Veterinary Society Congress, Birmingham, England.
4. Thacker EL. 2001. Porcine respiratory disease complex what is it and why does it remain a problem? *Pig J.* 48:66–70.
5. Josephson G, Charbonneau G. 2001. What's your interpretation? Case report of reproductive problems in a new startup operation. *J. Swine Health Prod.* 9:258–259.
6. Kim J, Chae C. 2004. Concurrent presence of porcine circovirus type 2 and porcine parvovirus in retrospective cases of exudative epidermitis in pigs. *Vet. J.* 167:104–106. <http://dx.doi.org/10.1016/j.tvjl.2003.09.011>.
7. Ladekjaer-Mikkelsen AS, Nielsen J, Storgaard T, Bøtner A, Allan G, McNeilly F. 2001. Transplacental infection with PCV-2 associated with reproductive failure in a gilt. *Vet. Rec.* 148:759–760.
8. O'Connor B, Gauvreau H, West K, Bogdan J, Ayroud M, Clark EG, Konoby C, Allan G, Ellis JA. 2001. Multiple porcine circovirus 2-associated abortions and reproductive failure in a multisite swine production unit. *Can. Vet. J.* 42:551–553.
9. Mankertz A, Domingo M, Folch JM, LeCann P, Jestin A, Segalés J, Chmielewicz B, Plana-Durán J, Soike D. 2000. Characterisation of PCV-2 isolates from Spain, Germany and France. *Virus Res.* 66:65–77. [http://dx.doi.org/10.1016/S0168-1702\(99\)00122-7](http://dx.doi.org/10.1016/S0168-1702(99)00122-7).
10. Wellenberg GJ, Stockhofe-Zurwieden N, Boersma WJ, De Jong MF, Elbers AR. 2004. The presence of co-infections in pigs with clinical signs

- of PMWS in The Netherlands: a case-control study. *Res. Vet. Sci.* 77: 177–184. <http://dx.doi.org/10.1016/j.rvsc.2004.03.007>.
11. Wang F, Guo X, Ge X, Wang Z, Chen Y, Cha Z, Yang H. 2009. Genetic variation analysis of Chinese strains of porcine circovirus type 2. *Virus Res.* 145:151–156. <http://dx.doi.org/10.1016/j.virusres.2009.05.015>.
 12. Li W, Wang X, Ma T, Feng Z, Li Y, Jiang P. 2010. Genetic analysis of porcine circovirus type 2 (PCV2) strains isolated between 2001 and 2009: genotype PCV2b predominate in postweaning multisystemic wasting syndrome occurrences in eastern China. *Virus Genes* 40:244–251. <http://dx.doi.org/10.1007/s11262-009-0438-y>.
 13. Guo LJ, Lu YH, Wei YW, Huang LP, Liu CM. 2010. Porcine circovirus type 2 (PCV2): genetic variation and newly emerging genotypes in China. *Virology* 403:273–277. <http://dx.doi.org/10.1016/j.virusres.2010.07.003>.
 14. Wen L, Guo X, Yang H. 2005. Genotyping of porcine circovirus type 2 from a variety of clinical conditions in china. *Vet. Microbiol.* 110:141–146. <http://dx.doi.org/10.1016/j.vetmic.2005.07.003>.
 15. Nawagitgul P, Morozov I, Bolin SR, Harms PA, Sorden SD, Paul PS. 2000. Open reading frame 2 of porcine circovirus type 2 encodes a major capsid protein. *J. Gen. Virol.* 81:2281–2287.
 16. Grau-Roma L, Crisci E, Sibila M, López-Soria S, Nofrarias M, Cortey M, Fraile L, Olvera A, Segalés J. 2008. A proposal on porcine circovirus type 2 (PCV2) genotype definition and their relation with postweaning multisystemic wasting syndrome (PMWS) occurrence. *Vet. Microbiol.* 128:23–35. <http://dx.doi.org/10.1016/j.vetmic.2007.09.007>.
 17. Fenaux M, Halbur PG, Gill M, Toth TE, Meng XJ. 2000. Genetic characterization of type 2 porcine circovirus (PCV-2) from pigs with postweaning multisystemic wasting syndrome in different geographic regions of Northern America and development of a differential PCR-restriction fragment length polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2. *J. Clin. Microbiol.* 38: 2494–2503.
 18. Dupont K, Nielsen EO, Baekbo P, Larsen LE. 2008. Genomic analysis of PCV2 isolates from Danish archives and a current PMWS case-control study supports a shift in genotypes with time. *Vet. Microbiol.* 128:56–64. <http://dx.doi.org/10.1016/j.vetmic.2007.09.016>.
 19. Choi KS, Chae JS. 2008. Genetic characterization of porcine circovirus type 2 in Republic of Korea. *Res. Vet. Sci.* 84:497–501. <http://dx.doi.org/10.1016/j.rvsc.2007.05.017>.
 20. Olvera A, Cortey M, Segalés J. 2007. Molecular evolution of porcine circovirus type 2 genomes: phylogeny and clonality. *Virology* 357: 175–185. <http://dx.doi.org/10.1016/j.virol.2006.07.047>.