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GENOME ANNOUNCEMENT

Complete Genome Analysis of Porcine Enterovirus B Isolated in Korea

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The complete genome sequence of porcine enterovirus B (PEV-B) from a Korean isolate was analyzed. The genome size was 7,393 bp. Previously, full genome sequences of PEV-B had been reported from the United Kingdom, Hungary, and China. The Korean PEV-B isolate presented polyprotein gene nucleotide sequence similarities of 77.9, 73.7, 78.9, and 80.3%, respectively, to PEV-B UKG/410/73, LP54, PEV15, and Chinese strains (Ch-ah-f1).

Porcine enterovirus B (PEV-B) is a single-stranded RNA virus that belongs to the genus *Enterovirus* of the family *Picornaviridae*. PEV-B consists of two serotypes, PEV-9 and PEV-10 (5). Although PEV infection is commonly asymptomatic, various clinical signs due to some virulent strains have been reported. Unlike porcine teschovirus (PTV) or PEV-A, which causes reproductive disorders, diarrhea, or pneumonia, PEV-B is reported to cause cutaneous lesions (3). Full genome sequences of PEV-B from skin or fecal samples were reported in the United Kingdom (4), Hungary (2), and China (6). In Korea, there were no known PEV-B reports, while isolation and serotyping of PTV-3 and PEV-A were reported (7).

Korean PEV-B was isolated at a commercial farm from a healthy nursery pig that had neither diarrhea nor skin lesions. Its complete genome sequence was determined by primer walking and rapid amplification of cDNA ends (RACE) for the 5′ and 3′ ends using the 5′ RACE System for Rapid Amplification of cDNA Ends, version 2.0 (Invitrogen), and the SMARTer RACE cDNA amplification kit (Clontech). The size of the novel Korean PEV-B isolate's genome was 7,393 bp, excluding the poly(A) tail. We deduced 2,169 amino acids from the polyprotein gene. This sequence contains an 811-bp 5′ untranslated region (UTR) and a 34-bp 3′UTR.

The Korean PEV-B isolate presented polyprotein gene nucleotide similarities of 77.9, 73.7, 78.9, and 80.3% to the PEV-B UKG/410/73 (Y14459), LP54 (AF363455), PEV15 (JN807387), and Ch-ah-f1 (HM131607) strains, respectively, and 87.2, 82.3, 88.8, and 89.6% PEV polyprotein amino acid sequence similarities, respectively. The most variable region, the antigenic determinant VP1, presented 65.1, 64.6, 75.1, and 67.4% nucleotide similarities and 64.1, 66.2, 83.9, and 68.7% deduced amino acid similarities to PEV-B UKG/410/73, UKG/LP54/, PEV15, and Ch-ah-f1, respectively. Although our Korean PEV-B isolate showed greater complete amino acid sequence similarity than any of the other four strains to Ch-ah-f1 (89.6%), the Hungarian isolate presented the highest amino acid similarity (83.9%) in the VP1 region among the four reference strains. This genome sequence is the first Korean PEV-B sequence. The complete genome sequence of the Korean PEV-B isolate could be useful in research on genetic diversity. The latest publications have reported genetic variations in Hungarian (1) and Chinese (6) PEV-B strains PEV-3H/PEV-14 (HQ702854) and Ch-ah-f1 (HM131607), respectively. Moreover, the clinical characteristics of the Korean isolate might be investigated through animal experiments.

Nucleotide sequence accession number. The complete sequence of the Korean PEV-B isolate was submitted to GenBank and assigned accession no. JQ818253.

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REFERENCES

1. **Boros A, et al.** 2012. Characterization of a novel porcine enterovirus in wild boars in Hungary. Arch. Virol. **157**:981–986.
2. **Boros A, Pankovics P, Reuter G.** 2011. Characterization of a novel porcine enterovirus in domestic pig in Hungary. Infect. Genet. Evol. **11**:1096–1102.
3. **Knowles NJ.** 2006. Porcine enteric picornaviruses, p 337–344. *In* Straw BE, Zimmerman JJ, Taylor DJ, D'Allaire S (ed), Disease of swine, 9th ed. Iowa State University Press, Ames.
4. **Knowles NJ, Buckley LS, Pereira HG.** 1979. Classification of porcine enteroviruses by antigenic analysis and cytopathic effects in tissue culture: description of 3 new serotypes. Arch. Virol. **62**:201–208.
5. **Racaniello VR.** 2007. Picornaviridae: the viruses and their replication, p 796–802. *In* Knipe DM, et al. (ed), Fields virology, 5th ed, **vol 2**. Lippincott Williams & Wilkins, Philadelphia, PA.
6. **Ren L, et al.** 6 April 2012, posting date. Sequencing of a porcine enterovirus strain prevalent in swine groups in China and recombination analysis. Vet. Microbiol. (Epub ahead of print.) doi.org/10.1016/j.vetmic.2012.03.036.
7. **Shin T, Lee C, Kwon H, Knowles NJ.** 1987. Serological classification of porcine enteroviruses isolated in Korea. Korean J. Vet. Res. **27**:223–226.

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