Complete Genome Sequence of Porcine Circovirus Strain 102 with a Novel Mutation, Isolated from Hunan Province, China

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Porcine circovirus 2 (PCV2) strain 102 belongs to the PCV2b-1C subtype, and its sole structural protein (Cap) exhibits high homology with that of other PCV2b isolates reported in South Korea, China, and the United States. Strain 102 contains a new mutation (R37H) in the domain of the nuclear localization signal (NLS) of the Cap.

Recently, a series of mutated strains of PCV2b were discovered worldwide (12–16). Some amino acid mutations have been found in the Caps of these strains; specifically, an extra lysine (K) is present at the end of the Caps in some of the new emerging mutants and is thought to elevate PCV2 virulence (12, 16). As a consequence of the mutations in PCV2, vaccination failure in the field has been reported in the United States and South Korea (13, 14). Compared to the strain with accession no. KJ133547 found in South Korea, strain 102 has a mutation of arginine to histidine at position 37 in the Cap NLS. The same mutation in the NLS has also been found in another PCV2 strain we isolated (GenBank accession no. KJ867553). Thus, strain 102 is a candidate mutant strain behind the vaccination failures in field studies. Although it is unclear whether the new mutation has functional biological or antigenic significance, this finding facilitates the analysis of the PCV2 genomics and antigenicity.

Nucleotide sequence accession number. The complete genome sequence of strain 102 has been submitted to GenBank under the accession no. KP112484.

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