

Molecular Detection of Porcine Circovirus Type 3 in Shanxi Province, China

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Abstract

Porcine circovirus type 3 (PCV-3) had posed a potential threat to the swine industry since its discovery in the United States in 2015. The Shanxi province had a wide range of large-scale pig farms in China, but the transmission of PCV-3 was unclear. To further investigate the epidemic profile and genetic diversity of the virus, the lung samples (491) from 19 different pig slaughterhouse in 11 cities covering the whole of the Shanxi province of China were evaluated by PCR. The results indicated that the PCV-3 positive rate at the slaughterhouse level and at the individual level was 100% (19/19) and 86.76% (426/491), respectively. The PCR-positive samples were further sequenced, and eight new PCV3 isolates were identified. The complete genomes of the eight virus isolates showed 97.45%–99.90% nucleotide identity with other PCV-3 isolates available in NCBI. Phylogenetic analysis based on the complete genome and capsid gene divided the PCV-3 strains into two main groups and several subclusters. The eight identified PCV-3 strains could be divided into the same clades, according to amino acid mutations A24/V and R27/K of Cap proteins. The results could provide new insight into the prevalence and genetic variation of PCV-3 in the Shanxi province of China, as well as the possibility of transmission from this center. It also reminded me that the molecular epidemiology of this new circovirus was urgent.

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