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Genome sequence characterization of pigeon circoviruses in China

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Highlights

Pigeon circovirus (PiCV) was prevalent in China.

PiCV genome can be sequenced using next-generation sequencing platform.

Based on phylogenetic tree analysis, the 48 sequences isolated in this study could be further divided into five clades (A–E).

Abstract: Pigeon circovirus (PiCV) was detected by PCR in pigeons from China. Altogether, 48 out of 244 pigeons tested positive for PiCV (positive rate, 19.67%), suggesting that the virus was prevalent in China. From the 48 PiCV-positive samples, about 2040 bp complete genome fragments were obtained by full length genome amplification and sequenced with a next-generation sequencing platform. Characteristics of the ORFs from different PiCV strains tested in this study were analyzed. Several insertion, deletion or substitutions were discovered during the analysis of the nucleotide sequence compared with sequences reported previously. In phylogenetic tree analysis, 48 sequences isolated in this study could be further divided into five clades (A, B, C, D, and F), clade E includes reference sequences only. Two major groups were found in the six clades, distinguished by ATA and ATG initiation codons. Most of the viruses isolated in the study were in the ATG group, with fewer in the ATA branch.

Keywords: Pigeon circovirus; epidemiology; genetic variation; molecular evolutionary; initiation codon

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