

Table 3 Sequence analysis of genome sequences of *Pigeon circovirus* (PiCV) strains.

Selected strains	Genome sequence	<i>cap</i> gene sequence		<i>rep</i> gene sequence	
	Nucleotide	Nucleotide	Amino acids	Nucleotide	Amino acids
Identity of the PiCV strains identified in our study	84.2%–100%	71.9%–100%	71.7%–100%	90.3%–100%	92.7%–100%
Compared with Chinese PiCV reference strains	83.0%–97.8%	73.0%–99.6%	72.3%–100%	89.0%–99.2%	89.2%–99.6%
Compared with PiCV reference strains from other countries	82.0%–98.3%	68.8%–98.4%	63.6%–100%	89.5%–98.3%	90.5%–99.3%

Note. The GenBank accession no. of the identified PiCV strains, the Chinese PiCV reference strains and PiCV reference strains from other countries

was shown in Table 2, S1 and S2.