TITLE: COMPLETE GENOMIC SEQUENCES FROM TWO PIGEON CIRCOVIRUS RETRIEVED FROM FREE-LIVING PIGEONS OF SOUTHERN BRAZIL

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ABSTRACT: Pigeon circovirus (PiCV), also known as columbid circovirus (CoCV), is a member of the *Circovirus* genus, family *Circoviridae*. The virus contains a single stranded DNA genome of approximately 2 kb, with minor length variations among different isolates. This study describes the complete genome sequences of two identical PiCV genomes recovered from sera of domestic pigeons (*Columba livia*) from the cities of Cambará (Paraná state (PR); n=10) and Porto Alegre (Rio Grande do Sul state (RS); n=25). Specimens collected in each city were pooled; viral DNA was extracted and submitted to high throughput sequencing. Phylogenetic analyses were performed by comparing the sequences recovered in this study with other 48 complete PiCV genome sequences available at GenBank, using the maximum likelihood method with 1,000 bootstrap replicates. Recombination events were identified using seven different detection methods with aid of the software RDP4. Two identical, complete PiCV genomes were recovered (2,041 nucleotides in length), one from each pool (accession numbers KX808543 and KY114965). It is remarkable that two identical sequences were recovered from birds in localities 800 km apart; yet these clustered along with PiCVs previously reported in Europe. These findings suggest low genetic variability of PiCV; however, he relatively low number of full genome sequences so far available preclude conclusive analyses. The phylogenetic analysis showed that complete genome is more informative to examine genomic variability of the virus; however, the Cap-based classification may be used if complete genome sequences are not available. Moreover, bootscan analyses with 50 PiCV complete sequences (from the present study and from Genbank) revealed that both *Rep* and *Cap* ORFs exhibit hot spots prone to recombination events. These results are expected to contribute to future studies on genetics and evolution of circoviruses.