

TITLE: CHARACTERIZATION OF THE SERA VIROME OF FREE-LIVING PIGEONS (*Columba livia*) FROM SOUTHERN BRAZIL

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Pigeons (*Columba livia*) are, originally, wild birds that remarkably adapted to urban environments, and pigeons may be potential reservoirs, carriers and/or transmitters of pathogens to other species. Here, a study was performed to investigate the sera virome of pigeons by high throughput sequencing (HTS). For this study, blood samples were collected from 137 pigeons from seven Brazilian municipalities. Samples were separated by region of capture and pooled, which were then submitted to DNA and RNA extraction for high throughput sequencing. The reads obtained were filtered through the Trimmomatic program, reassembled using Spades software 3.10.1 and analyzed with the of the Blast2GO bioinformatics tool. The contigs were analyzed and mapped by reference in Geneious software version 8.1.3. The total number of reads sequenced per sample pool ranged from 325,182 to 1,243,436. Reads were compared to the database of viral sequences at the protein level using BLASTx. On average, 43.0% of the reads showed similarity to viral sequences deposited in GenBank. Among the viral contigs, 90.8% presented similarity to eukaryotic viral genomes. Most of the viral reads corresponded to nucleotide sequences with high similarity to previously reported columbid circoviruses. Contigs corresponding to viral genomes of animal interest were classified into 6 viral families: *Circoviridae*, *Flaviviridae*, *Anelloviridae*, *Adenoviridae*, *Parvoviridae* and *Coronaviridae*. The viral agent whose genome was more often identified in pigeon's sera was PiCV, of which six full genomes were retrieved. In conclusion, a great diversity of genomes of viruses, representatives of distinct viral families, was detected. The potential impact of such findings on human and animal health needs further investigation.

Keywords: Pigeons, *Columba livia*, virome, high throughput sequencing (HTS)

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