

TITLE: CHARACTERIZATION OF CLOACA 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 may be potential reservoirs, carriers and/or transmitters of pathogens to other species. Here, a study was performed to investigate the cloaca virome of pigeons by high throughput sequencing (HTS). For this study, cloaca swab samples were collected from 69 pigeons from four municipalities of Rio Grande do Sul state (Gravataí, Taquara, São Leopoldo and Rio Grande). Samples were separated by region of capture and pooled. Then, they were then submitted to viral 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 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 923,738 to 1,200,096. Reads were compared to the database of viral sequences at the protein level using BLASTn and BLASTx. Contigs corresponding to viral genomes were classified into 6 viral families. In the samples from Gravataí/Cachoeirinha, the main viral families found were *Adenoviridae*, *Circoviridae* and *Picornaviridae*; in Rio Grande, *Circoviridae*, *Coronaviridae*, *Parvoviridae* and *Reoviridae*; in São Leopoldo the most frequent families were *Adenoviridae* and *Circoviridae*; finally, in Taquara the families found were *Adenoviridae*, *Astroviridae*, *Circoviridae*, *Parvoviridae* and *Picornaviridae*. The frequencies of viral genomes related to viral families in the study were *Circoviridae* 17.99%, *Adenoviridae* 43.91%, *Parvoviridae* 11.80%, *Picornaviridae* 15.09%, *Coronaviridae* 4.45%, *Reoviridae* 5.99% and *Astroviridae* 0.77%. Preliminary results reveal that pigeons carry viruses from several viral families. Further studies of these genomes are needed through phylogenetic analyses, in addition to evaluating the complete genomes obtained. The

potential impact of such findings on human and animal health needs further investigation.

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

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