

## PT.301

### INVESTIGATING THE FECAL VIROME OF PASSERINE BIRD FROM SERRA DO MAR STATE PARK, SÃO PAULO, BRAZIL

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Wild birds can be key reservoirs of avian viruses, affecting poultry and wildlife conservation. An unusual 10-segment dsRNA pattern was detected by polyacrylamide gel electrophoresis in one fecal sample from *Troglodytes musculus* (Curruira) during a virological survey of passerines in Serra do Mar State Park, São Paulo, 2022-2024. In an attempt to identify this virus, a fecal virome investigation was conducted. Total nucleic acid was extracted using the AllPrep PowerViral DNA/RNA Kit, followed by reverse transcription and dsDNA synthesis. Library preparation was performed and sequenced on Illumina NextSeq 500. Data was preprocessed, assembled with SPAdes, classified using CAT\_pack, and genetically analyzed with BLASTx and IQ-TREE. Of 41.669 contigs *de novo* assembled, 166 were classified as viruses. About 43% were unclassified at any taxonomic level, while 95 contigs (>200bp) were classified at the order or family level, including ssDNA viruses *Genomoviridae* (410bp–2161bp) and *Parvoviridae* (225bp–601bp); +ssRNA viruses *Iflaviridae* (230bp–805bp) and *Astroviridae* (5663bp–6706bp); and dsRNA viruses *Reovirales* (4201bp–4298bp). We recovered two potential novel viruses: an *Avastrovirus* with 6706bp that remained in a divergent clade in phylogenetic analysis and showed 47% amino acid identity in ORF2 with wild bird isolate (MW735969.1); and a dsRNA segment of 4298bp encoding a reovirus RdRp (possibly the virus initially identified in the sample) with 26% identity to the Rice ragged stunt virus RdRp (O92604.1). These findings from a single sample highlights the unknown viral diversity in wild birds and underscores the importance of virome studies.

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