

**DETECTION OF CORONAVIRUS BY RT-PCR AND NESTED-PCR IN WILD BIRDS FROM
NORTHEASTERN SÃO PAULO STATE, BRAZIL**

*(DETECÇÃO DE CORONAVÍRUS POR TÉCNICAS MOLECULARES DE RT-PCR E NESTED-PCR
EM AVES SILVESTRES DA REGIÃO NORDESTE DO ESTADO DE SÃO PAULO, BRASIL)*

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Coronaviruses are among the most important viral pathogens causing infectious diseases in mammals and birds, particularly avian coronaviruses, such as infectious bronchitis viruses (IBV). A broad knowledge of the genotypic and phenotypic characteristics for coronaviruses derived from poultry is widely available. However, in the case of wild birds, little is known, especially in Brazil, even though it has been shown that some bird species can be asymptomatic carriers of these viruses, including IBV, which is an important pathogen for domestic hens especially those for poultry industry. Thus, it is important to understand better the role of wild birds in the epidemiology of avian coronavirus infection. Thus, this study aims at investigating the presence of group 3 coronavirus using molecular techniques such as RT-PCR and Nested-PCR while having as amplification targets the hypervariable region of the S1 gene and 3'-untranslated region along the viral genome (3'-UTR) in 29 wild birds in northeastern São Paulo, distributed in 18 species and 12 families. The results showed that 3 of the 29 bird species belonging to *Coragyps atratus* (Black Vulture), *Passer domesticus* (House Sparrow) and *Zenaida auriculata* (Eared Dove) were positive for the presence of a coronavirus similar to IBV. In conclusion, our findings suggest that these species of wild birds may play a role in the epidemiology of avian coronavirus infection, especially regarding transmission to poultry, and should be considered in the control programs devised to contain infections with these viruses.

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