

DETECTION AND MOLECULAR CHARACTERIZATION OF CORONAVIRUS IN INSECTIVOROUS BATS OF ARGENTINA

ABSTRACT

Bats are the main hosts of coronaviruses (CoV) among mammals. Currently, the high diversity of these mammals and their wide dissemination throughout the world, in addition to their lifestyle and habits, have contributed to the appearance of a wide variety of emerging zoonotic diseases in wild and domestic animals, including humans. . For this reason, there has been great interest in identifying new bat CoVs worldwide, as this allows for better preparation for an eventual zoonotic emergency. In this work we set out to investigate the prevalence and diversity of coronaviruses circulating in insectivorous bats in Argentina during the period 2019-2021 and study the association between the positivity of the specimens and their biological and ecological variables. To carry out this research, 594 samples of rectal tissue from insectivorous bats from 9 Argentine provinces were analyzed, which were provided by the Neurovirosis Service, Department of Virology of the National Institute of Infectious Diseases ANLIS “Dr. Carlos G. Malbrán”. The estimated prevalence was 8.25%, and when studying the diversity through phylogenetic analysis, we detected only members of the α -CoV genus. We did not find a statistically significant association between the positivity rate and the biological and ecological variables studied. In the absolute descriptive graphic analysis, a peak was detected in the warm months, which coincides with greater activity associated with the reproductive season of bat populations in the southern hemisphere. Due to the impact of recent zoonotic diseases on public health, CoVs generate concern. This is why epidemiological surveillance is needed to minimize future zoonotic events.

This research contributes significantly to the understanding of the diversity and epidemiology of coronaviruses at the national and regional level. In the future, it could be improved by expanding the number of species and areas studied, as well as deepening the analysis, by exploring genomic aspects.

KEYWORDS: viruses, coronaviruses, bats, clade.