Epidemiological surveillance in reservoir animal – one health practice to avoid spillover
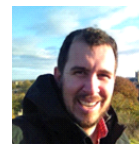
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Abstract

The key to control emerging infectious diseases is to perform active epidemiological surveillance to identify the main healthy reservoir animals into each ecosystem. In this sense, Tadarida brasiliensis bats specie is widely distributed in the American Continent and the species and occur in the most populated areas of Brazil. This specie is adapted to urban areas, enabling contact and spread of several viral agents to humans, domestics and production animals. Some viral families like Coronavirus (CoV) stands out for sanitary and epidemiological surveillance, since highly pathogenic virus strains have evolved from bats like SARS in 2002, MERS in 2013 and probably SARS-2 current epidemic. The aim is to characterize the Coronavirus species and its phylogenetic relationships using viral metagenomics in T. brasiliensis bats' specie, a typical specie distributed into Americas. We used anal and oral swabs of bats' specimens collected in Jequitibás Wood, Central region of Campinas City, São Paulo State, Brazil in 2011. Samples were subjected to Next Gen-Sequencing (NGS) using the Illumina platform HiSeq 2500. Phylogenetic analyzes were performed in MEGA. The BLAST similarity search was conducted from different databases and matches were obtained with sequences of viral origin of great interest for health surveillance like unclassified Alphacoronavirus. Phylogenetic analyzes only for coronavirus matches included representative sequences of all genus of Orthocorovirinae subfamily – alpha, beta, gamma and deltaCoV and were performed using maximum likelihood methods (ML) and neighbor-joining (NJ). We identify sequences phylogenetically related AlphaCoV-like, Appalachian Ridge Cov.2, Porcine Epidemic Diarrhea Virus (PEDV), HCoV-NL63, Bat Coronavirus 1B, the viruses of importance to one health. One sample was validated using RT-PCR and Sanger Sequencing and was similar to PEDV. Considering the zoonotic impact of many CoV, our results contribute greatly to a better understanding of the molecular eco-epidemiology in the evolution of these viral agents before epidemics spillover.

Biography:

Paulo Vitor Marques Simas is Bachelor at Biological Sciences (2007) when developed the research titled Analysis of seasonal distribution of Human Respiratory Syncytial Virus in children younger than 6 years old related to climatic factors in Sao Jose do Rio Preto, Sao Paulo, Brazil; Master at Microbiology (2008), Virology area studying Genetic variability of Human Respiratory Syncytial Virus isolated from hospitalized and day care children. Both, bachelor and Master degree, at Sao Paulo State University, Sao Jose do Rio Preto, Sao Paulo State, Brazil. PhD in Genetic and Molecular Biology (2015), Virology area with the thesis Metavirome of Tadarida brasiliensis bats at University of Campinas, Sao Paulo State, Brazil. A dedicated professional with extensive experience in Genetic and Molecular Biology in the Virology area.

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