## RABIES IN CHIROPTERS: TYPIFICATION AND EPIDEMIOLOGICAL STUDY.

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Epidemiological surveillance is of utmost importance in the study of the different cycles of rabies, as well as in the determination of antigenic variants.

To learn more about the aerial cycle of rabies and the possible interrelationships among the different species of chiropters, 50 strains were isolated and studied between 1994 and 1998. These strains were from bats from urban and wild areas: forty-eight from the state of São Paulo, one from the state of Rio de Janeiro and another from the state of Pará, in the north of Brazil. All the samples were genetically characterized using the panel of nucleocapsid monoclonal antibodies made in the CDC-Centers for Disease Control and Prevention, Atlanta, USA and pre-stablished by the Pan-American Health Organization (PAHO) for the study of strains isolated in the Americas. Twenty-two of the samples were also analyzed through the phylogenetic comparison of a fragment of N gene from the rabies virus. Of these samples, six were from hematophagous bats *Desmodus rotundus*; eighteen from phytophagous bats of the species *Artibeus lituratus* and *Artibeus planirostris*; twenty-five were insectivorous species such as the Myotis nigricans, Myotis albicens, Molossus ater, Molossus molossus, Nyctinomops laticaudatus, Nyctinomops macrotis, Eumops auripendulus, Epitesicus diminutus, Lasiurus borealis, Lasiurus ega, Lasiurus cinereus and Tadarida brasiliensis; and one from a non-hematophagous bat that could not be identified.

All the hematophagous bats presented the antigen variant 3 (*Desmodus rotundus*). Three of these strains were also genetically characterized. The frugivorous group presented variant 3 (*Desmodus rotundus*) and variant 4 (*Tadarida brasiliensis*), 6 (*L.cinereus*) and another 4 antigenic profiles different from the ones present in the panel. The sample 4113 obtained from an *Epitesicus diminutus*, showed no close genetic relationship to any of the Brazilian samplesused in this comparison. It segregated in an independent branch of the phylogenetic tree. It could be representative of a genetic variant maintained in an independent endemic cycle by *Epitesicus diminutus* or other currently unknown bat reservoir. This same antigenic profile could not be observed more than once in two other species, the *Nyctinomops laticaudatus* and the *Eumops auripendulus*, both from the same region.

The fact that variant 3 (*Desmodus rotundus*) has been isolated in seven of the fifteen different species of non-hematophagous bats suggests that this hematophagous bat plays an important role not only in the rural cycle in domestic animals, but also in the aerial cycle, interrelating with other species of phytofagous and insectivorous bats, in both rural and urban environments. It is important to call attention to the diversity of genetic variants that are adapted to different species of bats.