

Aves) são atacados. Diante dos fatos, o sistema de Vigilância em Saúde do município de Ananindeua programou as ações em 2012 usando as técnicas de geoprocessamento. Os mapas foram elaborados utilizando-se o sistema ARC. GIS 9.3, as bases cartográficas do Município de Ananindeua e o equipamento GPS MAP 60 CSX Garmin. Foram atendidas, 05 propriedades na Ilha João Pilatos, 01 na Ilha viçosa e 01 na Ilha Santa Rosa. Sendo capturados 35 morcegos hematófagos georreferenciados e cadastrados 06 abrigos artificiais e 03 abrigos naturais e 07 pontos de captura gerando mapa para fazer uma avaliação espacial. Certas características de uma região determinam altas populações de *D. rotundus* em áreas próximas aos rios, geralmente favorecem a existência de um número maior de abrigos Lord (1988). Os abrigos artificiais georreferenciados, a maioria são: Caeiras desativadas e casas de taipa abandonadas foram encontrados morcegos em ocos de árvores denominadas siriúba (*Avicennia nitida*) ao longo dos rios. Investigação epidemiológica sobre o caso de raiva em Augusto Corrêa relata a existência de grande população de morcegos que habitam os manguezais e abrigam-se no oco da siriubeira Ministério da Agricultura Pecuária e Abastecimento (2005). Ao se inter-relacionar as bases de dados georreferenciados e espes-las visualmente através do mapa digital, pode-se observar que os abrigos e as propriedades atacadas por morcegos localizam-se as proximidades dos rios, possivelmente os mesmos deslocam-se através dos manguezais que margeiam as ilhas. O controle da população dos morcegos hematófagos conforme o mapa, ajuda na caracterização do transmissor, identificando as comunidades mais afetadas e definindo a situação de risco, estabelecendo uma ação estratégica específica de vigilância a saúde. **Palavras-Chave:** Ananindeua, georreferenciamento, morcego hematófago, mapa Agradecemos a Dra Ivete Gadelha Vaz Secretária de Saúde de Ananindeua pelo apoio, e os agentes de endemias Artemis, J.Theodósio, Aviz, Augusto, Erivaldo e Edmilson por suas dedicações na captura.

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PHYLOGEOGRAPHY OF THE RABIES VIRUS ISOLATED FROM CANIDS IN THE NORTH AND NORTHEAST OF BRAZIL

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Antigenic variant 2 of the Rabies Virus (RABV), typically found in dogs in Brazil, still circulates in the North and Northeast of Brazil in spite of mass vaccination campaigns against rabies in domestic animals. Previous studies have shown that this variant is made up of two main genetic lineages: one found in dogs (*Canis familiaris*) and another typically found in wild canids, particularly the crab-eating fox (*Cerdocyon thous*), which is known in Brazil as *cachorro do mato*. *C. thous* is currently the only wild land species in which RABV is continually isolated, with an average of 20 cases/year. Although previous studies and phylogenetic analyses of the N and G genes and intergenic G-L region all confirmed the existence of these two genetic lineages, the way in which the lineages had dispersed temporally and spatially remained to be elucidated. We sequenced a 1388 nucleotide-long region of the RABV N gene from 53 typical canid samples. The phylogeography of the dataset obtained was determined using the BEAST (Bayesian Evolutionary Analysis Sampling Trees) program with the following data for the script: Evolutionary Model K3Puf+G4; Partitioning into codon positions (1+2)+3; Molecular clock relaxed uncorrelated lognormal; Demographic model coalescent exponential growth; Dispersion model relaxed random walking (RRW). The results can be summarized as follows. The common ancestor of the RABV in the samples analyzed became established around 1900 in the border region between the states of Paraíba and Pernambuco

and diversified into the lineages typically found in *C. familiaris* and *C. thous*. Around 1910 the original *C. thous* lineage diversified into two main sublineages in the same area, one of which migrated to the south and the other to the north. Then, around 1930 the southern sublineage diversified even further and moved in two directions: toward the state of Bahia and toward the state of Pernambuco. In approximately 1945 the northern sublineage of *C. thous* also diversified, resulting in a sublineage that remained in the state of Pernambuco and another that diversified even further and moved toward the state of Piauí. The lineage typically found in *C. familiaris* diversified around 1945 and moved toward the north and south. However, around 1970 it underwent a major diversification when one of the 1945 sublineages divided into two sublineages, one of which migrated to the states of Pernambuco, Sergipe and Alagoas and the other to the states of Pará and Piauí. Analysis with the RRW model allowed us to infer not only the movement of the virus lineages isolated from *C. familiaris* and *C. thous* among the municipalities sampled, but also the probable location where dispersion of the lineages occurred. Further studies covering a longer period and using more samples are required to confirm the pattern of movement of the virus described here so that its geographic spread can be predicted and blocked. Financial Support: Instituto Pasteur, São Paulo, Brazil.

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A PRELIMINARY ANALYSIS OF THE GLYCOSYLATION PATTERN OF SERUM IgG FOLLOWING PRE-EXPOSURE SCHEME FOR HUMAN RABIES VACCINE

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Introduction: The currently recommended by WHO for prevention individuals exposed to rabies virus (RV) is pre-exposure prophylaxis (PEP) through the administration of three doses of rabies vaccine by intradermal (ID) or intramuscular (IM) route. The previous study showed that the persistence of protective antibodies titer in the IM schedule is more long-lived, suggesting a different clearance mechanism of antibody. It known that carbohydrate modification of antibodies could induce accelerated clearance or modulate of antibody effector functions. All endogenous IgG antibodies contain an N-linked glycan in the Fc region and about 20% contain glycans elsewhere on the molecule to maintain the two heavy chains of the Fc in an open conformation required for interactions with activating Fcγ receptors (FcγRs). **Objective:** Based on these data, we compared the glycosylation patterns of serum IgG of individuals who received the PEP schedule by ID or IM route. **Methods:** The Purified Vero Cell Vaccine (PVCV) (Sanofi /Pasteur Laboratory) was utilized, with a minimum of 2.5 IU per dose. Sera of individuals who previously received the PEP by the IM (n= 15; 0.5 mL per vaccine dose) or by the ID (n= 19; 0.1 mL /dose) route were collected to IgG detection and its subclasses (IgG1, IgG2, IgG3 and IgG4) by antigen-specific ELISA and to measured RV neutralizing antibodies by rapid fluorescent focus inhibition test (RFFIT). The N-linked oligosaccharide chain of purified IgG antibodies from serum was evaluated by a lectin enzyme-linked immunosorbent assay. **Results:** All 34 persons tested developed titers of antibody ≥ 0.5 IU/mL, with a maximum geometric mean titer of 18.0 IU/mL. There was no statistically significant relation between neutralizing antibody titer and route of administration. Similarly, the majority of the anti-rabies humoral responses were restricted to the IgG1 subclass in both groups. However, the lectin-binding assay showed difference on the monosaccharide content, mainly of galactose, neuraminic acid, mannose and fucose between serum IgG1