

**Phylogenetic analysis of rabies virus glycoprotein of herbivorous isolated from north Brazil**

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Rabies is an acute viral encephalitis that can infect all warm-blooded animals. This disease has a worldwide distribution and causes important economic losses to livestock. Analysis of the gene G may improve the understanding of the epidemiology and prevention measures of rabies in South America. The aim of this study was to characterize genetically isolated samples from North Brazil based on glycoprotein gene. Rabies virus from cattle (5), equine (3) and buffalo (1), obtained between 2006 and 2008, from Para (4), Rondonia (2) and Tocantins (3) States were investigated. A RT-PCR targeting a glycoprotein-coding gene (914 nucleotides) were performed. Obtained amplicons were sequenced for genetic analysis. Phylogenetic analysis suggests presence of five main subclusters. Subcluster I, composed of one samples from Tocantins which are related to isolates of *Desmodus rotundus* and *Diphilla ecaudata* from São Miguel Tapuio Piauí. Subcluster II, the samples from Tocantins which are related to isolates of *D. rotundus* from Goiás State. Subcluster III, composed for one isolate from southeastern region of Pará related to one isolated from Colina (Tocantins). Subcluster IV composed of isolated from Rondonia and one sample from Ipora (Goiania). Subcluster V, grouping samples from Northeast Pará related to human rabies cases occurred in Maranhão, showing circulation of rabies virus among hematophagous bats, livestock and humans in this region. Evidence of genetic proximity of isolates from different geographic areas should be interpreted taking in consideration livestock migration attending to food availability and consequent bat migration to more favorable conditions. Chiropterans have high mobility, hematophagous bats visit neighbor colonies, promoting rabies dissemination among livestock, humans and other bat species.