

Poster topic 10

Poster 1

Use of dna sequencing and phylogenetic analysis to investigate a bovine rabies outbreak in Minas Gerais Brazil

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Bovine rabies in Brazil is transmitted by hematofagous bat (*Desmodus rotundus*). Since the first report, in 1900, many aspects about rabies epidemiology have been elucidated by DNA sequencing, genetic and phylogenetic analysis. Most recent epizootics affecting livestock took place in Sao Paulo state between years 1997-2002 with possible expansion to neighbor areas of Minas Gerais. There is scarce information about genetic diversity of rabies virus isolates in this state. Considering background, present work is intended to analyze potential epidemiological connections among 22 bovine rabies cases in 12 municipalities of Minas Gerais (during 2000 to 2009) and Sao Paulo's epidemics to contribute to current surveillance rabies program. RNA extraction, reverse transcription, PCR and sequencing reaction were performed according to Sato *et al.* 2004. For genetic analysis a phylogenetic tree was constructed based on of rabies virus glycoprotein segment of 540 nucleotides using Neighbor-joining method with software – MEGA, fixing Kimura 2 parameters evolution model with a bootstrap level of 1000 replications. Results suggest that the same viral sublineage is involved in Sao Paulo epizootics and Minas Gerais cases. Although genetic distance is subtle among Brazilians isolates it is possible to observe that bovine rabies virus in the border region of the aforementioned states are distinguishable from the rest of the country. Vaccination is recommended for livestock concomitantly with mapping of bat shelters and reinforcement of control *D. rotundus* population.