

reservoirs are haematophagous bats. In the State of Rio Grande do Sul (RS), southern Brazil, urban rabies has not been detected since 1988. Nevertheless, rabies remains endemic in haematophagous and non haematophagous bat species. The present work reports the first phylogenetic analyses on RABV isolates from the State of RS, for that, a total of 30 rabies virus (RABV) isolates sent to rabies diagnosis were analyzed. The isolates were recovered from different bat species (*Tadarida brasiliensis*, *Myotis nigricans* and *Histiotus velatus*), from herbivores (bovines and buffalo) and carnivores (domestic dog and cat). The bat species were identified with the aid of a morphological dichotomous key. For the phylogenetic analysis, total RNA was extracted from original brains (herbivores and carnivores) or infected mice (bats) with Trizol and submitted to reverse transcription/polymerase chain reaction (RT-PCR) with primers targeting a initial portion of the nucleoprotein gene (N). Phylogenetic analysis of the sequenced fragments revealed the occurrence of four RABV lineages, named after its natural hosts: *Desmodus rotundus* (haematophagous bat), *Tadarida brasiliensis* (insectivorous bat), *Myotis nigricans* (insectivorous bat) and *Histiotus velatus* (insectivorous bat). All RABV isolates from herbivores belonged to the haematophagous bat *Desmodus rotundus* lineage. The two RABV isolates from carnivores clustered within the *Tadarida brasiliensis* lineage, revealing two occasional spillovers from insectivorous bats to domestic pets, thus not compromising the status of “urban rabies free” of the area. These findings highlight the importance of the identification of RABV lineages and its value as an aid to support rabies surveillance. Financial support: Instituto Pasteur.

CO.40

SITUACIÓN EPIDEMIOLÓGICA DE LA RABIA EN CHILE. 2000-2011

Yung V¹, Favi M¹, Fernandez J¹ – ¹Instituto de Salud Pública de Chile

En Chile, el año 1990, se detecto el último caso de rabia identificado como variante canina desde entonces esta variante no circula en el país, la importancia de los animales silvestres en la transmisión de la rabia fue reconocida en 1985, cuando se detectó por primera vez rabia en murciélagos insectívoros de la especie *Tadarida brasiliensis*. El reconocimiento de los murciélagos como reservorio de la enfermedad hizo que se ampliaran las acciones de vigilancia epidemiológica hacia esas especies caracterizándose el patrón epidemiológico de la rabia por una epidemia en quirópteros. Desde el año 2000 al 2011, se analizaron un total de 32802 muestras para diagnóstico de rabia, de estas 979 fueron positivas (3,0%), 976 murciélagos insectívoros, 2 gatos y 1 perro. Según la distribución geográfica de casos, estos se registraron en las regiones centrales del país, y no se han encontrado muestras positivas al virus rábico en las regiones extremas. A través de tipificación antigénica y genética se han identificado 4 variantes virales que son las responsables de la transmisión de la rabia, los principales reservorios silvestres circulando en el país son murciélagos de la especie *Tadarida brasiliensis*, *Myotis chiloensis*, *Lasiurus cinerius* y *borealis* y finalmente *Histiotus macrotus*. La especie *Tadarida brasiliensis* representa el 91,1% de los casos positivos. Los estudios de caracterización antigénica y genética nos han permitido tener un conocimiento más amplio de la epidemiología de la rabia. El Programa de Control de Rabia contempla la educación de la población para evitar el contacto con murciélagos y el reporte de cualquier mamífero sospechoso, la eliminación de colonias de murciélagos se realiza solamente en casos de detección de especímenes positivos, en razón del importante rol que esta especie desarrolla en la mantención del equilibrio ecológico y dado el bajo porcentaje de positividad a rabia (alrededor de 2%) en capturas masivas de esta especie.

CO.41

MOLECULAR CHARACTERIZATION OF RABIES VIRUS AND OTHER VIRAL AGENTS ISOLATED FROM BATS IN VENEZUELA.

BOYER L¹, PUJOL F², HIDALGO M¹, PAPO S³ – ¹National Institute of Agricultural Research (INIA) – Rabies Laboratory, ²Venezuelan Institute of Scientific Investigation (IVIC) – Molecular Virology Laboratory, ³National Institute of Integral Agricultural Health (INSAI) – Department of control and prevention of Rabies wildlife

Bats (Chiroptera) are reservoirs for zoonotic diseases, including Rabies, Hendra, Nipah, SARS-CoV, Ebola virus. Hence their importance as a potential reservoir hosts of viruses affecting human and animal health. In our country, there is no knowledge of bats as reservoir for viruses except rabies. The aim of this investigation was the molecular characterization of rabies virus and other viral agents, isolated from bats in Venezuela. The molecular characterization was based on: viruses with impact in public health, persistence in hosts and endemic areas. A total of 54 bats were collected in different states and years. Those were identified and classified into: 12 vampires, 29 frugivorous and 13 insectivorous belonging to different families, genera and species. They were autopsied to collect tissues from different organs including brain tissue of livestock positive to rabies virus. Different systems were used for PCR to detect DNA and RNA viral genomes. Samples were amplified, molecularly characterized and sequenced to identify the phylogeny of each virus. We were able to detect 8 Herpesviruses and 4 Polyomaviruses in trachea and lungs samples from different bat species and one Astrovirus in an intestine of an insectivorous bat. Eight Rabies isolates were grouped in the genus *Lyssavirus* genotype 1. Four of them characterized as antigenic variant 3 (*Desmodus rotundus*). The detection of these viral agents in the Venezuelan bats is the first and paramount information for the study of these unknown agents, which could pose great risk to humans and livestock health in our country. **Acknowledgements:** MCTI-Misión Ciencia, Venezuelan Institute of Scientific Investigation (IVIC): Molecular Virology Laboratory, National Institute of Agricultural Research (INIA): Rabies Laboratory, National Institute of Integral Agricultural Health (INSAI). **Funding:** IVIC. **Almeida M**, *Rev.Inst.Med.trop.S.Paulo*; 53:31, 2011; **Calisher C**, *Rev.Med.Vir*, 17:67, 2007; **Chen Zhue**, *J.Gen.Virol*, 90:883, 2009; **De Mattos C**, *J.Clin.Microbiol*, 34:1553, 1996; **Olivier D**, *PLoS/ONE*, 4:e2057, 2008; **Richter R**, *J.Gen.Virol*, 90:44, 2009; **Wong S**, *Rev.Med.Vir*, 17:67, 2007.

CO.43

THE SPATIAL AND TEMPORAL DYNAMICS OF RABIES IN CHINA

Tang Q¹, Yu J¹, Hao L¹, Rayner S², Liang G¹ – ¹China CDC – Institute for Viral Disease Control and Prevention, ²Chinese Academy of Sciences – Wuhan Institute of Virology

Background and Objectives: Recent years have seen a rapid increase in the number of rabies cases in China and an expansion in the geographic distribution of the virus. In spite of the seriousness of the outbreak and increasing number of fatalities, little is known about the phylogeography of the disease in China. In this study, we report an analysis of a set of Nucleocapsid sequences consisting of samples collected through the Chinese National Surveillance System as well as publicly available sequences. This sequence set represents the most comprehensive dataset from China to date, comprising 210 sequences (including 57 new samples) from 15 provinces and covering all