system hamper the identification of the disease. The mild symptoms may also go unnoticed when these individuals come in contact with different species or strains of lower virulence. Thus, our results suggest the circulation of hantavirus in residents of peri-urban area of Jataí city. Therefore, there is a need to intensify surveillance activities and education of the local people to prevent this viral infection. Financial support: FAPEG, CNPq

VV1296 - PHYLOGENETIC ANALYSIS OF BRAZILIAN ORF VIRUS FROM SHEEP AND GOATS

Schmidt, C., Cargnelutti, J.F., Traesel, C.K., Martins, M., Weiblen, R., Flores, E.F.

1. **FEPAGRO Saúde Animal, FEPAGRO - IPVDF, Estrada do Conde, 600. Eldorado do Sul-RS**
2. **Universidade Federal do Rio Grande do Sul, UFRGS, Rua Sarmento Leite, 500. Porto Alegre-RS**
3. **Universidade Federal de Santa Maria, UFSM, Avenida Roraima, 1000. Santa Maria-RS E-mail: candy86.vet@gmail.com**

We herein describe the partial nucleotide sequencing and phylogenetic analysis of the B2L gene of twenty Brazilian Orf viruses (ORFV). Seventeen viruses were recovered from outbreaks of contagious ecthyma in sheep and goats in four states in Southern and Northeast country and three from commercial vaccines. Most analyzed viruses were associated with cases/outbreaks of classical contagious ecthyma, with lip, nostrils and labial commissure involvement, yet udder/teat, feet, vulvar and disseminated lesions were also reported in some cases. Nucleotide sequence analysis revealed a high degree of B2L similarity among sheep sequences (>99%) regardless the geographic origin, and a remarkable high identity for the two goat isolates (>99.8%), with similarity dropping to below 99% when comparing viruses from the two species. A phylogenetic tree grouped most sheep and goat viruses on different branches. In addition, sequence alignment allowed for the identification of up to six scattered nucleotide changes that were predominant and more consistent in goat isolates, including a number of sequences from other continents. Thus, in spite of the high nucleotide similarity, different degrees of similarity and discrete nucleotide changes in the B2L gene may help in grouping ORFV viruses according to host species. Financial support:CNPq and CAPES

VV1297 - FULL GENOME SEQUENCING OF A HUMAN-LIKE H1N2 SWINE INFLUENZA VIRUS

Schaefer, R., Cantão, M.E., Sá Rocha, C., Gava, D., Ciacci Zanella, J.R.

Embrapa Suínos e Aves, CNPSA, BR153, KM 110, Concordia, SC E-mail: rejane.schaefer@embrapa.br

Influenza is an acute respiratory disease of swine caused by influenza A virus (IAV). IAV has a negative-sense segmented RNA genome, allowing the occurrence of genetic exchange or reassortment among distinct influenza viruses during mixed infections. After the detection of pandemic H1N1 (pH1N1) influenza virus in pigs, reassortant viruses containing genes

of pandemic virus and endemic swine viruses have been detected in pigs around the world. Herein we describe the full genome sequencing of a novel human-like H1N2 influenza virus isolated in pigs in Paraná state in 2011. Influenza virus isolated from lung tissue samples resulted positive to pH1N1 influenza virus Matrix (M) gene by reverse-transcription real-time PCR. Nucleotide sequencing was performed for all eight viral gene segments with primers retrieved from the literature. Nucleotide sequences were aligned with other influenza virus sequences available in GenBank and evolutionary analysis was conducted in MEGA5. Evolutionary history was inferred by using the Maximum Likelihood method based on nucleotide and aminoacid sequences. According to phylogenetic analysis, the HA and NA genes clustered with influenza viruses of human lineage (H1_cluster delta) whereas the M gene clustered into pH1N1 group. The internal genes (NP, NS, PB1, PB2 and PA) showed a high similarity (99%) to pH1N1 influenza virus circulating in humans and pigs. This is the first full genome sequencing of a swine influenza virus in Brazil. Moreover, the analyzed virus is a reassortant virus containing the external genes (HA and NA) derived from human influenza virus and the internal genes derived from pH1N1 influenza virus. The detection of a reassortant human-swine influenza virus shows the importance of performing full genome sequencing of pig isolates in order to enhance genetic information about influenza virus circulating in pigs. Financial support: CNPq (process no. 578102/2008-0)

VV1298 - TORQUE TENOSUS VIRUS 1AND 2: VIRAL LOADS AND ITS ASSOCIATION WITH POSTWEANING MULTISYSTEMIC WASTING SYNDROME (PMWS)

Teixeira, T.F., Schmidt, C., Varela, F.C.P., Scheffer, C.M., Cibulski, S.P., dos Santos, H.F., Franco, A.C., Roehe, P.M.

1. **FEPAGRO Saúde Animal, FEPAGRO - IPVDF, Estrada do Conde, 600. Eldorado do Sul-RS**
2. **Universidade Federal do Rio Grande do Sul, UFRGS, Rua Sarmento Leite, 500. Porto Alegre-RS**

Torque teno viruses (TTVs), are small, non-enveloped agents with a circular single-stranded DNA genome. In domestic pigs, two distinct species have been reported: Torque tenosus virus 1 (TTSuV1) and 2 (TTSuV2). Associationsof such viruses with the occurrence of post weaning multisystemic wasting syndrome (PMWS), a multifactorial condition where the main infectious agent involved is porcine circovirus type 2 (PCV2), have been reported with controversial results. To further examine the role for TTSuVs in PMWS, a SYBR Green-based quantitative PCR (qPCR) was designed to detect and quantify TTSuV1 and TTSuV2 genomes. The test wasapplied on samples from 49 PMWS-affected and 132 healthy pigs (including 50 piglets, 50 adults and 32 SPF animals). The frequency of detection of TTSuV1 and TTSuV2was high (97.8%)and did not differ significantlybetween diseased and control groups.In addition, no significant association was detected between the frequency of detection of TTSuV1 and TTSuV2 DNA and the age range of the sampled animals.