different production categories in pig herds of Brazil. The results indicated that PBoV infection has widespread in all pig-producing categories. Suckling piglets presented lower percentage of PBoV detection than animals from other categories. However, the presence of PBoV in young piglets revealed that these animals had early contact with the virus, which raises questions regarding the routes of PBoV transmission. PBoV infection was higher in recently weaned pigs, likely due to the decrease in the titres of maternal antibodies in addition to the mixing of young piglets of different litters. After this period, infection with this virus became endemic in older animals, as seen in the results from finisher pigs. All animals included in this study were asymptomatic at the moment of fecal collection and, therefore, PBoV infection was not associated with disease occurrence. Further studies are necessary to investigate whether the virus presence is related to PBoV-induced diseases in Brazil. Financial Support: FINEP, CAPES, CNPq, and Fundação Araucária/PR.

VV334 - MOLECULAR DETECTION AND GENOTYPING OF BOVINE PAPILLOMAVIRUS IN SERGIPE STATE, NORTHEASTERN BRAZIL

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Bovine papillomavirus (BPV) is a potentially oncogenic virus group, which mainly affects individuals from the species *Bos taurus*. In contrast to other types of papillomavirus, BPV is not species-specific. Studies have shown that BPV were found in other ruminants, such as giraffes, bison, buffalo, and equines. BPV still causes great concern to livestock producers, especially the dairy ones, since it affects the growth of papillomas in teats, which affects the production of milk, and could progress to cancer. Today, 13 BPV types are known, which belongs to three different genera. As long as some BPV types are associated to cancer and others are not, it is very important to understand which types of BPV are circulating in Brazil. However, information about the diversity of BPV in Sergipe state, Northeastern Brazil, is still unknown. Sergipe has a dairy region with a big local economic relevance and large number of cows. Therefore, the knowledge about BPV types in this area has a great economic importance, and could be applied in order to develop better prevention treatment methods. In this context, the objective of this study was to assess the diversity of BPV types infecting cattle in the state of Sergipe. In order to do this, lesions were collected from cattle in different regions of Sergipe state. Histopathological analysis were carried out to characterize BPV lesions. Next, DNA was extracted from the samples. A fragment of L1 gene was amplified using polymerase chain reaction with the primers FAP59/64. The amplified product was analyzed in agarose gel electrophoresis. All positive samples were purified and sequenced. Local sequence alignments were carried out with BLAST to identify the BPV types. We were able to detect BPV DNA in all samples tested, which shows that BPV is widespread over the state of Sergipe. Sequencing analysis showed that different types of BPV were circulating in Sergipe, which shows that there is a great genetic diversity of BPV in this region. This is the first report of the occurrence of BPV in cutaneous lesions in Sergipe state. The knowledge of the distribution of BPV types is essential to serve as the basis for diagnostic and treatment methods development. Although this study contributes to increase the understanding about the diversity of these viruses in Brazil, further studies are needed in order to shed light on the correlation between these viruses and risk factors. Financial Support: CNPq, CAPES and FAPITEC/SE.

VV335 - GENETIC DIVERSITY OF PORCINE CIRCOVIRUS TYPE 2 CAUSING CLINICAL DISEASE IN BRAZILIAN PIG HERDS CONCOMITANT WITH PCV2 VACCINATION

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Porcine Circovirus type 2 (PCV2) belongs to the *Circoviridae* family and four distinct genotypes have been described; PCV2a and PCV2b, which have been detected worldwide; PCV2c, identified from archived samples in Denmark; and PCV2d, isolated initially in China in 2010 and in U.S in 2012, which carries an ORF2 elongation by one amino acid. Postweaning Multisystemic Wasting

Syndrome, the most common clinical manifestation of Porcine Circovirus Diseases (PCVD), was first described in 1996 in Canada and in 2000 in Brazil. PCVD has caused economic losses with high mortality rate in Brazilian pig farms until the introduction of a PCV2 vaccine in 2008. However, since 2012, PCVD has been reported in nursery pigs from vaccinated pig herds. Aiming to diagnose and characterize PCV2 infection in PCV2 vaccinated pig herds, lymph node, kidney and lung tissue samples from 12 clinically affected pigs from seven farms were submitted to histopathology (H&E), nested-PCR and immunohistochemistry (IHC) test. DNA sequencing was performed by the Sanger method. The obtained sequences were analyzed and assembled with Phred/Phrap/Consed softwares. Phylogenetic analyses of the whole genome and the ORF2 gene (capsid protein) were performed by Neighbor-Joining method in MEGA 6 software. PCv2 infection was demonstrated in all samples by H&E and confirmed by IHC and nested-PCR. Sequence analysis revealed one PCV2a, nine PCV2b, and two PCV2d. These results show the detection of distinct PCV2 genotypes causing clinical disease in PCV2 vaccinated pigs. Moreover, only PCV2a and PCV2b have been identified in Brazilian herds until now. PCV2a was mainly detected until 2003, and in 2004 a new genotype, PCV2b, emerged worldwide. Multiple factors are involved in vaccine efficacy, including the interference by maternal derived antibody, the presence of co-infecting agents, level and frequency of challenge, management practices, and also the presence of isolates that are more virulent due to antigenically silent mutations. Molecular modelling studies applied to the capsid protein of these isolates are ongoing. These studies aim to elucidate possible modifications in the viral protein conformation which could have caused an inefficient antibody binding recognition that was observed in the apparent vaccination failure. Financial Support: EMBRAPA (02.11.01.006.00).

VV337 - IDENTIFICATION OF CANINE PARVOVIRUS 2B IN A CRAB-EATING FOX *Cerdocyon thous* (LINNAEUS, 1766) WILDLIFE IN BRAZIL

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Canine parvovirus (CPV) belongs to *Parvoviridae* family and is the causal agent of one of the most dangerous infectious disease in young dogs and it is responsible for large numbers of animal deaths worldwide. The CPV has a linear ssDNA genome that codifies two structural proteins (VP1/VP2) and two non-structural proteins (NS1/NS2). The CPV2 emerged as a variant of feline panleukopenia virus (FPV) which is adapted to the canine host by wild carnivores such as mink and foxes and spread rapidly. A few years later, CPV2a emerged and replaced completely the CPV2. After a new type called CPV2b emerged and co-circulated with CPV2a. In 2000, the CPV2c was discovered and is co-circulating with CPV2a and CPV2b. The Crab-eating Fox (*Cerdocyon thous*) is present in all Brazilian biomes and in some countries of South America. The viral disease constitutes 56% of the pathogens that threaten populations of wild carnivores worldwide. The aim of this study was to detect the causal agent of diarrhea in a Crab-eating Fox. The Medical and Research Center for Wild Animals (CEMPAS) of the Universidade Estadual Paulista (UNESP) - Botucatu, received a Crab-eating Fox with 21 days old with diarrhea. The animal died and organ fragments (CNS, gut, kidney, heart, lung, tonsil, liver, and spleen) were collected. The viral DNA extraction was performed using a combination of phenol/chloroform/isoamyl alcohol and silica/guanidinium isothiocyanate nucleic acid methods. The DNA extracted was submitted to PCR assay that amplifies a fragment with 583 bp (nt 4003-4585) of the VP2 gene. The PCR product was sequenced in ABI3500 Genetic Analyzer sequencer using the same primers used in the PCR assay. Nucleotide and amino acid sequence alignment (Clustal W) and the phylogenetic tree were performed in MEGA software. The sequence identity matrix was performed in BioEdit software. Just the heart out of eight organ fragments evaluated was positive to CPV2 in PCR assay. In the sequence