PCR performed using primers that amplify 288 base pairs (bp) of the 5' UTR. For BoHV-1 and 5 detection, total DNA was extracted and, after a first generic PCR, two specific nested-PCRs were performed to differentiate BoHV-1 and 5, respectively. It was obtained 7.69 % (3/39) and 2.56 % (1/39) positive FF pools for BVDV and BoHV-1, respectively. The presence of these viruses may be detrimental in culture systems, causing a reduction in rates of maturation, fertilization and/or development, and may infect recipient females. The results for BVDV are higher than previously reported while the one for BoHV-1 are similar. These results reinforce the need for check for the presence of these viruses before fertilization in vitro.

Financial support: CAPES and CNPq

VV449 - SEROLOGICAL AND MOLECULAR DETECTION OF SWINE HEPATITIS E VIRUS (HEV) IN BRAZILIAN EASTERN AMAZON

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Hepatitis E virus (HEV) is an enterically transmitted agent that causes acute hepatitis in humans. HEV shows an endemic distribution in many regions of the world and is classified into four genotypes (1 to 4). All genotypes infect humans while only genotypes 3 and 4 also infect other mammals, particularly pigs, which have been reported as the main source of human infection in non-endemic areas. In this study, HEV infection was investigated in 151 adult pigs slaughtered from April to October 2010 in the metropolitan region of Belém, Pará, Brazil. From each animal, serum, stool and liver samples were collected. Serological diagnosis was carried out by testing for the presence of IgM and IgG anti-HEV with commercially available methods (RecomWell HEV - Mikrogen®) and with confirmatory testing by immunoblot (RecomLine HEV - Mikrogen®). The presence of HEV RNA was analyzed in serum, stool and liver samples by nested RT-PCR using 3 sets of primers that amplify two genomic regions: ORF1 and ORF2. Genotype was characterized by phylogenetic analysis in positive samples. Anti-HEV IgG was found in 8.6% (13/151) of the animals and none showed positivity for IgM antibodies. HEV RNA was detected in 4.6% (21/453) of the samples and the prevalence of positive pigs was 9.9% (15/151). Phylogenetic analysis of sequences from ORF1 and ORF2 (348 bp) indicated that all isolates belong to genotype 3; however, subtypes 3c and 3f were identified in the same sample when the ORF1 or ORF2 were analyzed. In conclusion, our results showed for the first time that HEV circulating among swine herds in Eastern Amazon of Brazil and that genotype 3 is the most prevalent in this region. The detection of divergent subtypes in the same animal suggests co-infection with multiple viral populations and/or the presence of recombinant virus. These results should raise concerns about the presence of HEV genotype 3 in Brazilian pigs and the possible zoonotic potential of these isolates.

Financial support: FAPESP (2010/50081-9); CAPES/UFPA; IEC/SVS/MS

VV450 - MOLECULAR CHARACTERIZATION OF GENE ENCODING NON-STRUCTURAL PROTEIN 5 (NSP5) OF SWINE ROTAVIRUS IN THE CURRENT STATE OF SÃO PAULO, BRAZIL.

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Rotavirus is responsible for the occurrence of diarrhea in several animal species and humans, with economic, animal health and public health implications. The nonstructural protein 5 (NSP5) of rotavirus is encoded by segment 11 by the viral genome and contains 667 base pairs. This protein plays a key role in the formation of viroplasma, within which occurs the rotavirus replication and early morphogenesis of new viral particles. The objective of this study was to characterize the gene encoding the NSP5 of rotavirus circulating in pigs farms in the São Paulo State and determine their phylogenetic relationships with other isolates, using Neighbor-Joining, Maximum Composite Likelihood as substitution model and 1,000 bootstrap repetitions. Two strains had the gene fully defined, with nucleotide identity of 96.2% and 96.9% in terms of amino acids. These strains were grouped with other homologous samples belonging to the genotype H1, in turn, described both in pigs and in humans. These data are useful for a broader surveillance of rotavirus circulating, being a key point in understanding the pathogenesis, epidemiology and disease prevention.

Financial support: FAPESP (processo nº 2010/13652-8)

VV451 - DETECTION AND PHYLOGENETIC ANALYSIS OF PORCINE HOKOVIRUS IN PIGLETS WITH POSTWEANING MULTISYSTEMIC WASTING SYNDROME

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