VV490 - SEROLOGICAL SURVEY WITH NEGATIVE RESULT OF SMALL RUMINANT LENTIVIRUSES IN PARAÍBA STATE

Moura, G.S., Araújo, S.A.C., Assis, R.N., Ribeiro, J.A.C., Pinheiro, R.R., Melo, V.S.P.

Universidade Federal da Paraíba; UFPB; Campus II Areia -PBEmbrapa Caprinos; Embrapa Caprinos; Sobral - CE

Among the infectious diseases, small-ruminant lentiviruses (SRLV) has been a reason of concern for both goat and sheep producers. The disease is considered of difficult control, mainly because of its dissemination and the inexistence of vaccines or treatments. Therefore, the objective of this study was to perform a serological survey of two SRLV, Caprine Arthritis Encephalitis and Maedi-Visna, in Paraíba State, Brazil. We collected 500 blood samples, being 250 samples from each animal species. Samples were obtained by jugular puncture of males and females older than 12 months and of several breeds. Samples were centrifuged in the Laboratory of Microbiology of the Federal University of Paraíba, Campus II, Areia. After centrifugation, serum aliquots were stored at - 20 ºC until analysis. Antibodies against SRLV were detected by agar gel immunodiffusion test (AGID) following manufacturer's instructions. IDGA data analysis demonstrated that there were no positive samples among the studied animals. The absence of seropositive animals could be justified by the occurrence of delayed seroconversion in the SRLV. In SRVL, viruses present the capacity to integrate themselves to the genome of the host cells, infecting them in a latent form. Moreover, the extensive animal raising associated to the absence of farm technification reduces not only the direct contact between animals but also the fomites, reducing the probability of virus transmission. However, negative results for SRLV following IDGA test should be analyzed with precaution due the possibility of occurrence of false negatives.

VV491 - DETECTION OF PORCINE ROTAVIRUS BY RT-PCR TARGETED FOR GENE ENCODING NSP5.

Marconi, E.C.M.[1], Barbosa, B.R.P.[1], Bernardes, N.T.C.G.[1], Beserra, L.A.R.[1], Brandão, P.E.[1], Carmo, A.C.V.[3], Giovanni, D.N.S.[2], Mori, E., Tonietti, P.O., Gregori, F.

1. Faculdade de Medicina Veterinária e Zootecnia - USP; FMVZ-USP; Av. Prof. Dr. Orlando Marques de Paiva, 87 CEP 05508 270 - Cidade Universitária
2. Laboratório de Parasitologia, Instituto Butantan, São Paulo/; IB; Av Vital Brasil, 1500 São Paulo, SP, Brasil
3. Laboratório de Tecnologia de Cultivo Celular; UFSCar; UFSCar, São Carlos, SP, Brasil

The Rotavirus is a major viral agents causing diarrhea among several animal species. The NSP5 protein plays a key role in the viroplasma formation in infected cells and has regions of high degree of nucleotide sequence conservation among different porcine rotavirus strains, which has made this region the choice for primer selection in transcription and amplification by PCR. The aim of this study was to develop a RT-PCR targeted for gene encoding NSP5 and the method was validated by applying it to the detection of the agent in 48 samples collected from different pig farms. The primers were designed, using the software Netprimer, by multiple alignments of homologous NSP5 sequences retrieved from GenBank. In all samples was added 0.260 DO600nm MDBK cells. The RNA extraction was performed with Trizol, following the manufacturer's instructions. RT-PCR was performed using random primers and PCR was made with primers that generate the 137 bp product. As a positive PCR control by NSP5 gene was used the porcine Rotavirus 32/00 strain. As an internal exogenous control the mRNA coding for subunit 5 of the bovine mitochondrial NADH dehydrogenase gene (191 bp) was used. The detection threshold test enabled the detection of at least 100.2161 TCID50%. After the standardization of RT-PCR conditions, we found that 16 of 48 field samples were positive (33.3%). This method should be an alternative approach to porcine rotavirus diagnosis, and has potential use in real-time PCR. As it was demonstrated the high frequency of occurrence of porcine rotavirus, the early diagnosis of this agent can play a key role in development of prophylactic measures.

Financial Support: Research Grant FAPESP 2011/10846-9; Fellowship by CNPq 830657/1999-1

VV492 - MOLECULAR DIVERSITY OF BRAZILIAN EQUID HERPESVIRUS TYPE 1 ABORTOGENIC AND NEUROTROPIC STRAINS BASED ON GD, ICP4 (ORF64) AND DNA POLYMERASE (ORF30) GENES

Mori, E.[1], Marconi, E.C.M.[1], Lara, M.C.C.[2], Cunha, E.M.[2], Villalobos, E.M.[2], Mori, C.M.[1], Castro, A.M.M.[1], Soares, R.M.[1], Brandão, P.E.[1], Richtzenhain, L.J.[1]

1. Faculdade de Medicina Veterinária e Zootecnia - USP; FMVZ-USP; Av. Prof. Dr. Orlando Marques de Paiva, 87 CEP 05508 270 - Cidade Universitária
2. Instituto Biológico, São Paulo/SP; IB; São Paulo, SP, Brasil

Four EHV 1 Brazilian strains (A3/97, A4/72, A9/92 and Iso07/05) and two clinical abortion visceral tissues samples (Iso11/06 and Iso33/06) were PCR-positive for glycoprotein B (gB) of EHV-1. A sequence analysis of the glycoprotein D (gD), ICP4 (ORF64) and ORF30 (DNA polymerase) genes from these strains suggested that among Brazilian EHV 1 strains, the gD gene is highly conserved, and the ICP4 gene showed high nucleotide and amino acid identities when compared with genotype P strains, suggesting that the EHV 1 Brazilian strains belonged to the same group. All the EHV-1 Brazilian strains were classified as non-neuropathogenic variants (N752) based on the ORF30 analysis. These findings indicate a high conservation of the gD, ICP4- and ORF30-encoding sequences. Different