Veterinary Virology: VV

UFRGS; UFRGS

Porcine hokovirus (PHoV) is a new virus closely related to human and bovine hokovirus, but there is no data about the presence and prevalence of PHoV in the American continent. PHoV has been detected in pigs with porcine reproductive and respiratory syndrome virus (PRRSV) and may be involved in Postweaning Multisystemic Wasting Syndrome (PMWS) that affects swine industry and presents multiple viral infections. The aim of the present study was to detect and perform a phylogenetic analysis of PHoV in piglets with PMWS. The PCR detection of porcine circovirus type 2 (PCV2) and PHoV were performed in pooled tissues (lymph nodes, lungs, liver, spleen and kidneys) of 30 piglets of each herd displaying PMWS from 8 herds. Also, eight overlapping fragments that cover hypothetical structural protein of PHoV were sequenced. The Bayesian Inference (BI) using MrBayes 3.1.2 was conducted to perform a phylogenetic analysis. Selective pressure was determined by the ratio of non-synonymous to synonymous substitutions (dN/dS) using Nei Gojobori- Jukes Cantor method, Mega 4.0. All the samples were PCR positive for PCV2 and PHoV was 55.3% co-detected in 7 of 8 herds. The kidney, lung, spleen and lymph node samples presented more positives (75%, 62.5%, 57.1% and 50%) than liver samples (28.6%), respectively. Six hypothetical structural protein sequences of PHoV were obtained and compared with PHoV sequences available in Genbank. The phylogenetic tree indicated that the three Brazilian PHoV sequences were closely related to European sequences and three formed distinct clades. The (dN/dS) ratio within PHoV sequences was low (0.05) suggesting that most amino acids residues of hypothetical structural protein have been subjected to purifying selection. These results indicate that piglets displaying PMWS are PCV2 infected and can be co-infected with other virus, as PHoV. Further studies are required to understand the prevalence and commercial importance of PHoV in swine herds. CNPq / Fapergs.

VV452 - COMPARISON OF HEMAGGLUTINATION INHIBITION TEST AND ELISA TO DETECT PORCINE PARVOVIRUS ANTIBODIES

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Porcine parvovirus (PPV) causes reproductive failure in swine, characterized by embryonic and fetal death, mummification and stillbirths. Clinical diagnosis of infection is difficult and laboratory confirmation is required. Hemagglutination inhibition (HI) test is the gold standard and despite HI is a relatively inexpensive serologic assay, the labor intensiveness is a major obstacle to its use on a large scale. Recently, a commercial ELISA has been developed, and an agreement between these two tests is therefore of great interest. The aim of the present study was to compare the HI test with a commercial ELISA (Ingezim PPV 1.1.PPV.K.1®, Ingenasa) for detection of antibodies to PPV. A hundred eighty samples were selected, according to the age (gilts and piglets) and vaccination status (unvaccinated, one dose of PPV vaccine and two doses of PPV vaccine). For HI test, the samples were considered negative when the titers were ≤32, undefined =64 and positive ≥128. For ELISA test, the S/P rate was calculated and the cut-off values were given by the manufacturer: ≤0.300 was negative and >0.300 was positive. To determine the cut-off of ELISA and HI test, maximizing the sensibility (SE) and specificity (SP) values, a ROC curve with 95% of confidence interval was fitted using the equation y= a + bx, where y= OD and x= HI natural logarithm (ln). The correlation was also determined using the correlation coefficient (ρ) of Spearman Rank, with 95% of confidence interval. There was a general agreement between ELISA and HI. The ROC curve had the cut-off in OD at 0.340, resulting in a 93.8% of SE and 98.5% of SP (R2= 0.67). The Spearman's correlation coefficient (ρ) was 0.89. Based on that, ELISA test showed to be as efficient as HI to detect PPV antibodies, and can be a good tool to estimate the herd PPV antibody status. CNPq – Processo 481718/2009-5.

VV453 - DETECTION AND QUANTIFICATION OF PORCINE PARVOVIRUS 1 USING A TAQMAN-BASED REAL-TIME PCR FOR NS1 GENE

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Porcine parvovirus 1 (PPV1) is present worldwide and is an important causative agent of reproductive failures that generate significant economic losses to the swine industry. Gilts are the most susceptible class in which infection causes stillbirth, mummified fetuses, small litters and infertility. Although the disease is subclinical in non-pregnant pigs, PPV1 infection has been associated with Postweaning Multisystemic Wasting Syndrome (PMWS) as a cofactor that enhances clinical effects of this syndrome. The aim of the present study was to develop a real-time PCR (qPCR) using a TaqMan probe based on the NS1 gene for detection and quantification of PPV1 in serum samples. The specificity, sensitivity, reproducibility and quantitative range of qPCR were evaluated and compared