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 with conventional nested-PCR (nPCR). The standard curve of qPCR was linear ranging from 6×10^6 genome copies equivalent/mL (gce/mL) to 2×10^3 gce/mL with a 0.98 square of correlation coefficient (R^2 value). The specificity assay was positive only using PPV1 strains and negative with related viruses. The comparative analysis of both amplification techniques resulted in 11 positive samples in both tests, but the nPCR detected four additional samples. The concordance, sensitivity and specificity between the techniques were 98%, 73% and 100%, respectively. The qPCR reproducibility presented a coeficient of variation of 1.3% to 1.6% in intra-assay and 1.5 to 1.8% in inter-assays. qPCR displayed advantages as rapidly, high reproducibility, precision, quantification and do not require post-PCR analysis, although the nPCR presented higher sensitivity. Therefore, the established qPCR protocol is a useful tool for diagnosis and quantification of PPV1 in serum samples that can be used for epidemiological studies and monitoring PPV1 infection in swine herds. Financial Support: CNPq, FAPERGS and Simbios Biotecnologia.