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VVD – Virology and Viral Diseases

INVESTIGATION OF PORCINE CIRCOVIRUS TYPE 2, TYPE 3 AND TYPE 4 IN SWINE CLINICAL SAMPLES IN BRAZILR. Miotto ¹, C. Pissetti ², C. Reck ³, M. Martelo ³, Á. Menin ⁴, L.C. Bordin ⁵, J. Ciacci Zanella ⁵¹Federal Institute of Education, Science and Technology, Concórdia, SC, Brazil²Center for Animal Health Diagnoses (CEDISA) BR 153, km 110, SC, 89715-899, Distrito de Tamanduá, Concórdia, SC, Brazil³Department of Research and Innovation, VERTÁ Laboratórios, Curitiba, SC, Brazil⁴Department of Biosciences and Unified Health - Federal University of Santa Catarina, Curitiba, SC, Brazil⁵Brazilian Agricultural Research Corporation (EMBRAPA), Concórdia, Brazil**Background and Objectives**

Porcine circovirus (PCV), includes PCV1, PCV2, PCV3, and PCV4 that can infect pigs. PCV2 causes PCV disease (PCVD) which can be controlled by vaccination and management practices. However, new genotypes and co-infections with other PCVs can aggravate PCVD. This work studied the etiology of PCVD in PCV2 vaccinated herds by characterizing PCV2 genotypes, and PCVs coinfections. Also, verified the presence of PCV3 and PCV4 in samples from PCV2 positive herds.

Material and Methods

PCVD clinical cases samples diagnosed with PCV2 in 2021 and 2022 were used. DNA from 333 samples (serum, uterus, kidney, lung, lymph node, intestine, fetuses, brain) from 333 PCV2 vaccinated pigs, 191 farms (all production phases) and 8 Brazilian states was extracted. PCV2, PCV3 and PCV4 genome detection was carried out using real-time PCR (qPCR) assay as previously described. For PCV2 genotyping, a PCR aimed the PCV2 ORF2 region, having each sample tested for PCV2a, PCV2b and PCV2d.

Results

PCV2b and PCV2d genotypes were the most prevalent genotypes from all Brazilian states examined. PCV2b was the most prevalent genotype, detected in 151 out of 266 genotyped samples. PCV2b was most common genotype in nurseries, but PCV2d was more frequent in finishing and sow's herd. Finishing phase had the largest number of PCV2 positive samples, possibly due to decreased vaccine protection. Since the majority of vaccines used in Brazil are for PCV2a genotype, PCV2a was not found in any clinical samples. Co-infections between genotypes (PCV2b and PCV2d) was detected in 27 samples and between PCV3 and PCV2 in 26 samples from our study. In 320 samples analyzed, none was positive in qPCR tests for PCV4.

Discussion and Conclusion

PCVD is an important disease for Brazilian and global pig farming. Challenges include the control of known infectious agents, but also the identification new viruses, mainly in mixed infections in vaccinated herds. This study found that PCV2b is prevalent in Brazilian swine herds, with an increase in PCV2d detection. Coinfections between PCV2 genotypes and PCV3 are observed. PCV4 or PCV2a DNA were not identified in tested herds. Monitoring vaccine effectiveness and the emergence of clinical circovirus is crucial.