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PREVALENCE OF PCV-2 GENOTYPES CIRCULATING ON VACCINATED COMMERCIAL FARMS IN BRAZIL, COLLECTED IN 2021 AND 2022

Franz KA
Zoetis INC. – Brazil

Costa AE
Department of Preventive Veterinary Medicine - Universidade Federal de Minas Gerais, Belo Horizonte – MG

Debortoli LH
Zoetis INC. – Brazil

Fernandes V
Zoetis INC. – Brazil

Franco EG
Zoetis INC. – Brazil

Veit DC
Zoetis INC. – Brazil

Tres DP
Zoetis INC. – Brazil

INTRODUCTION

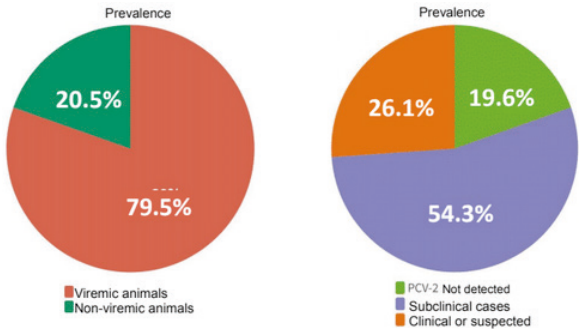
Porcine circovirus type 2 (PCV-2) is one of the most widespread viral infections in pigs and draws attention because it is an ssDNA virus and has a high evolutionary rate, leading to the emergence of variants with different biological and epidemiological behaviors, expressing in the field four conditions: systemic disease, subclinical infection, reproductive disease and dermatitis syndrome associated with nephropathy (1,2,6). To date, nine PCV-2 genotypes have been proposed (PCV-2a to PCV-2i), with the PCV-2a genotype predominating in the 2000s, switching to PCV-2b until 2014 and subsequently increasing the representation of the PCV-2d genotype (6). Therefore, the present study aims to verify the prevalence of PCV-2 genotypes found on commercial farms in Brazil, in the years 2021 and 2022, and evaluate their genetic evolution behavior.

MATERIALS AND METHODS

In 2021 and 2022, a total of 1601 animals were sampled, in seven states: SC, RS, PR, MG, MT, DF and GO and coming from 20 pig production systems, for screening purposes and subsequent genotyping of positive samples. The samples were grouped into ages of 30, 45, 60, 90, 120 and 150 days of life, with all production systems being vaccinated for PCV-2. Total DNA from the samples was extracted using the mini spin DNA extraction kit (Kasvi, Brazil). Initially, all samples were subjected to real-time PCR, which amplifies the conserved part of the PCV-2 ORF1 gene, for detection and quantification of PCV-2 genomic copies, according to the protocol described in 2003 (5). After the screening carried out on all samples, only those that had the highest quantifications of genomic copies from the production unit in question (>4 Log/ml) were selected, therefore totaling 260 samples that were subjected to genotyping. For genotyping of PCV-2a, PCV-2b and PCV-2d, specific primers were used that amplify part of the gene that encodes ORF2 of each PCV-2 genotype according to a 2017 study (3). The amplicons were analyzed by electrophoresis in a 1.5% agarose gel, stained with ethidium bromide and visualized using a UV transilluminator.

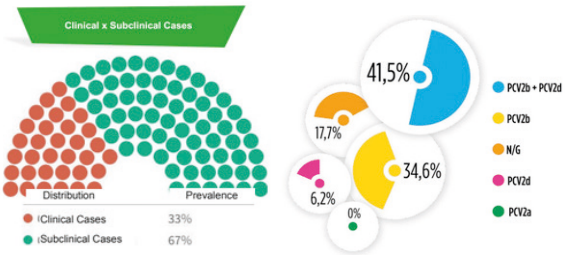
RESULTS

Of the total of 1601 animals sampled for screening purposes, 20.5% (328/1601) were samples from animals with clinical signs suggestive of circovirus and 79.5% (1273/1601) came from animals without clinical signs, of which, through from the detection and quantification of genomic copies of PCV-2, 19.6% (314/1601) of absence of circulating PCV-2 was obtained, where the majority of animals 54.3% (870/1601) had a suggestive viremic load of subclinical infection and 26.1% (417/1601) of the animals had high quantifications, suggesting suspicion and positivity of disease associated with porcine circovirus type 2.



After screening, 66.5% (173/260) of the samples intended for genotyping analysis came from animals without clinical signs and with good zootechnical performance and 33.5% (87/260) collected from animals with clinical signs suggestive of PCV-2. The results reveal that no sample was of the PCV-2a genotype (0/260), 34.6% (90/260) for PCV-2b, 6.2% (16/260) for PCV-2d and 41.5% (108/260) of the animals had PCV-2b +

PCV2d co-infection. Another interesting fact is that 17.7% (46/260) of the animals, even with high antigenic loads, did not fit into any of the researched genotypes (N/G).



CONCLUSION

Animals without clinical signs suggestive of circovirus have genomic copies of PCV-2 in subclinical presentation, characterizing the presence of the agent in this animal category. The PCV-2a genotype was not identified in the samples, with only PCV-2b and PCV-2d being found, with a large participation in co-infections. Sequencing the genetic material of samples that did not qualify for the primers used is necessary to understand whether there is a new genotype circulating in Brazil, or whether these are small mutations in the ORF2 fraction, therefore requiring constant research and diagnostics in the field.

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