

TITLE

PCV2 GENOTYPE DISTRIBUTION IN ORGAN SAMPLES COLLECTED FROM PCVD CLINICAL CASES IN FLANDERS

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CONTENT

Background and objectives

Porcine circovirus type 2 (PCV2) is an economically important swine pathogen causing a wide range of clinical problems, collectively named Porcine Circovirus Diseases (PCVD). Since the discovery of the virus, 2 major genotype shifts have been described. The prevalent PCV2a genotype was replaced by the PCV2b genotype in the mid-2000s. In recent years, the PCV2d genotype has been increasing in prevalence in many regions around the world. The aim of this study was to investigate the PCV2 genotype distribution in samples collected from PCVD clinical cases in Flanders.

Materials & methods

In order to identify the current PCV2 field strains causing PCVD, samples were selected from the Flemish Animal Health Service (DGZ Vlaanderen) sample bank. The samples were organs submitted for analysis with PCV2 quantitative PCR (July 2017 – Sept 2018). Samples were used for sequencing in case of a viral load $\geq 1,00 \text{ E}+08$ DNA copies/g. The PCV2 genotypes were identified by full genome sequencing at Ceva-Phylaxia (Hungary).

Results

In total, 54 viruses were sequenced, originating from 19 weaned piglets and 35 fattening pigs from 54 different Flemish swine farms. 35 samples originated from lung tissue, 16 from lymph node tissue, 1 from heart tissue, 1 from spleen tissue and 1 from a mixture of lung and lymph node tissue. The PCV2 viral load detected in the organs ranged from $1,82 \text{ E}+08$ to $7,56 \text{ E}+15$ DNA copies/g. Of the 54 sequenced PCV2 viruses, 7 strains (13,0%) were identified as PCV2a, 2 strains (3,7%) were identified as PCV2b and 45 strains (83,3%) were identified as PCV2d genotype (9 as PCV2d-1 and 36 as PCV2d-2).

Discussion & Conclusion

The results of this study confirm the presence and emergence of PCV2d in Flanders and are indicative that PCV2d might be the predominant PCV2 genotype involved in PCVD clinical cases.