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TITLE

PREVALENCE OF PCV2 GENOTYPES IN ORAL FLUID SAMPLES ORIGINATING FROM GERMAN AND AUSTRIAN PIG FATTENING FARMS

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CONTENT

Quantitative measuring of PCV2 in serum samples is the golden method for monitoring PCV2 infections in growing and finishing pigs. However, over the last years, oral fluid (OF) sampling has gained more attention since it´s less invasive and more animals can be sampled at once. The aim of this study was to measure the amount of PCV2 in OF and if possible, categorize the main genotypes.
In total 20, well described fattening farms were selected for the analysis. Two ropes were placed into two different pens for a period of approx. 30 minutes, without directly coming into contact with feed, water or excretions. Both ropes were subsequently centrifuged and the OF pooled into one sample. PCV2 quantitative analysis was performed by a real-time multiplex polymerase chain reaction (rt-PCR), positive samples (? E+05 copies/ml) were then sequenced using the Sanger chain-termination method. Alignment and phylogenetic analysis were performed using the software BioEdit and Mega 5.
Out of the 20 samples, 14 were positive for PCV2 with an average value of 9,14E+06 copies/ml. Seven had a value of ? E+05/ml (mean 1,83E+07/ml), out of which five were sequenced: Four belonged to PCV2 genotype a (three PCV2-vaccinated herds, one PCV2-unvaccinated) and one to PCV2b (PCV2-vaccinated herd). One sample showed fragment lengths and nucleotide sequences similar to either PCV2d or PCV2e and therefore couldn´t be differentiated.
Under the conditions of this study, monitoring of PCV2 through OF was shown to be efficacious at revealing PCV2 presence, quantity and if possible, the respective PCV2 genotype. High PCV2 copies in OF should always be considered together with clinical (subclinical) symptoms and if necessary, they can open the door for further diagnostic steps including serological, virological and pathological investigations.