

A particular genotype-class within PCV2b dominates the PMWS epizooty in Switzerland

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Key words

PMWS, epizooty, PCV2a, PCV2b, genetic drift, pig, Switzerland

Aim of the study

Postweaning multisystemic wasting disease (PMWS) has developed over the last years into an economically meaningful pig disease. Many questions about the disease are still unanswered. Thus, porcine circovirus type 2 (PCV2) was found in all PMWS cases, however, most infections proceed subclinically. Pig tissue blocks from the time period before and during the Swiss PMWS epizooty, helped to analyze the occurrence of different genetic PCV2 variants. We speculate these mutations within the PCV2 genome may have triggered the PMWS epizooty.

Material and methods

Formalin fixed and paraffin embedded lymphatic tissue from 131 before and 156 pigs during the PMWS epizooty (from 1973-2005) were analyzed for PCV2 genetic variants occurrence by immune-histochemistry (IHC) and PCR. Supernatant from clone F217 was used for IHC. A primer pair flanking a heterogenous region of 137 bp within ORF2 was chosen for PCV2 specific PCR. Animal health status was defined according to international criteria as diseased or subclinically infected. IHC negative animal cases, however, positive in the PCR reaction were also defined as subclinically infected.

Results and significance

We found 13 different PCV2 sub-genotypes, which could be grouped according to the signature motif (Cheung et al. 2007) into PCV2a or PCV2b genotypes. From the NCBI GenBank at least 18 other PCV2 subgenotypes would be feasible, which were not found in Swiss pigs. Two subgenotypes, defined by a small PCR fragment, were identical in the amino acid sequence of the short PCR amplificate. These were separately classified and newly named PCV2b-CH by us. 42% of IHC negative animal cases were positive by PCR analysis and, hence, defined as subclinically infected. PCV2 is not a new virus in the Swiss pig population, in fact, subclinical infection could be found even in samples dating back to 1979.

Before the epizooty there were few sporadic diseased cases mostly associated with PCV2a genotypes. Nevertheless, during the epizooty PCV2b-CH genotype dominated. However this variant represented by the small PCV2b-CH PCR fragment was already present in low amounts in healthy pigs long before 2003 but emerged abundantly in diseased pigs in the epizooty. The impressive shift to the PCV2b-CH genotype during the epizooty is best explained by increased virulence of preexisting viruses through genomic mutational adaptation. Identification of the critical PCV2 genomic mutations is part of ongoing studies.

Publications, posters and presentations

Wiederkehr DD, Sydler T, Bürgi E, Hässig M, Zimmermann D, Pospischil A, Brugnera E, Sidler X. A new emerging genotype subgroup within PCV-2b dominates the PMWS epizooty in Switzerland. *Vet Microbiol.* 2009 Apr 14;136(1-2):27-35.

Posters and presentations at 3 international congresses

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