

SWINE HEALTH

Title: Do capsid mutants with the PCV-2 genotype variations induce virulence differences in vitro and in vivo? - **NPB # 08-268**

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Scientific abstract

The porcine circovirus of type 2 (PCV-2) is the causal agent of post-weaning multisystemic wasting syndrome (PMWS) and is associated to other diseases grouped under the term porcine circovirus associated diseases. Two main genogroups a and b were identified during the outbreaks of PMWS in 2005 in North America, and it was speculated that PCV-2b isolates were more virulent than those of PCV-2a. This work was aimed to investigate if PCV-2 genetic variations were responsible of virulence and check if a motif specific of each PCV-2 genogroup located in the capsid protein contributes to a difference in virulence. Two clones, PCV-2a and PCV-2b, representative of the PCV-2 genogroups were produced as well as two mutants, PCV-2a (PCV-2b motif) and PCV-2a (PCV-2b motif) displaying an inversion of the capsid genogroup-specific motif into the backbone of the parental strains. Both clones and mutants were infectious *in vitro*. The experimental trial on SPF piglets demonstrated that the PCV-2b clone was more virulent than the PCV-2a one and that the PCV-2a (PCV-2b motif) was highly attenuated while the PCV-2b (PCV-2a motif) was moderately attenuated in virulence. These results suggest that the amino acids between positions 86 and 91 of the viral protein are involved in the virulence of PCV-2 and that this motif is thereby a putative biomarker of virulence between the two genotypes.

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