



VIRAL DISEASES

VVD-041

PCV2 GENOTYPES : EPIDEMIOLOGICAL SURVEY IN THE WEST OF FRANCE

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Introduction

Since 2004 a worldwide shift of porcine circovirus type 2 (PCV2) genotypes was observed from PCV2a towards PCV2b and more recently PCV2d (since 2012).

Material and methods

In order to identify the current PCV2 field strains, samples were selected from LABOCEA 22's sample bank, a public diagnostic laboratory set in Ploufragan, France. (period: May 2016 - June 2017).

The samples were piglets sera or organs submitted for PCV2 PCR. The viral load needed was 10^7 copies/ml (sera) or g (organs). The approach was made by total virus sequencing.

Results

The survey concerned 37 farms. More than 20 Field vets took part and 32 viruses were sequenced: 14 viruses were belonging to genotype b and 18 to genotype d.

30 case history could be gathered retrospectively: Field Vets observed global symptoms of PCVD in 8 PCV2b infected farms out of 12, and in 17 PCV2d infected farms out of 18.

The average clinical score was apparently higher when strain d was isolated: 7.8 on a scale of 10 (6.2 for strain b, difference not significant). Weight loss/wasting away was mainly associated with strain d (Chi square, p: 0.016) . No statistical differences between strains were observed for the other clinical signs i.e mortality, respiratory disorders and heterogeneity.

In farms where no PCV2 vaccine was recently used, strains b or d were observed in the same proportion.

Among the 7 vaccinated farms showing clinical signs, strain d was isolated in 6 farms using a PCV2 vaccine on piglets (on the contrary, strain b was isolated only in 1 farm).

Conclusion

In this study Weight loss/wasting away seems to be significantly linked to higher occurrence of PCV2d.

The correlation between PCV2 genotype, acute clinical symptoms and vaccine protection needs to be further investigated.