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PRRSV PREVALENCE AND CIRCULATING PRRS STRAINS IN DUTCH FARMS BASED ON RESPiG® TEST RESULTS

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Introduction

ResPig® program includes biannual serological and saliva-PCR PRRS tests of all production groups. PRRSv is further characterized upon request. PRRSv prevalence and dynamics is summarized in the database.

Material and methods

The analysis at farm level includes weaner and nursery groups in 2016 (n=124). Saliva qPCR are classified as negative or positive. PRRSv prevalence at weaning and nursery was calculated. PRRSv PCR+ samples between 9-2016 and 9-2017 were typed via a differentiating DV-PCR (Porcilis® PRRS pigs) or ORF-5 nucleotide sequence. A sequence with ≥98% homology is defined as phylogenetically related. Together with the vaccination history, the PRRSv dynamics can be followed. Twenty nine (29) sequences and 63 PRRS DV-PCR’s were completed.

Results

Piglet vaccination-rate was 29%, with PRRSv prevalence in weaners and nursery 25% and 46%, respectively. The ORF-5 homology (Lelystad Virus) of circulating field strains varied between 84%-97% (n=13). The detected genotype-2 strains (n=4) were closely related to VR2332 strain and found on non US-MLV vaccinating farms. The DV related strains (n=5) were only detected in recently Porcilis® PRRS vaccinating farms. Six (6) out of 7 94881 related strains were detected in recently 94881-strain vaccinating farms. A total of 35/63 DV-PCR tests were positive.

Conclusion

Compared with previous studies, PRRSv prevalence in weaners increased, which is influenced by increased piglet vaccination rate. Still, ±30% of PRRSv (-) weaner batches are infected in the nursery indicating the importance of biosecurity. ORF-5 LV homology distribution does not change over time and there is no evidence of drift towards more heterologous strains. In contrast to other vaccines, Porcilis® PRRS-positive samples always originated from recently vaccinated pigs, which is of importance when PRRSv eradication of farms or outflow is a goal besides control.