

HERD HEALTH MANAGEMENT AND ECONOMY

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AN OVERVIEW OF THE MOST FREQUENTLY FOUND PATHOGENS IN ALTERED SLAUGHTER LUNGS FROM FOUR EUROPEAN COUNTRIES

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Background and Objectives

Tackling the Porcine Respiratory Disease Complex (PRDC) relies on ameliorating farm management and implementing correct treatment and prophylactic measures. These can only be successfully conducted if the pathogens leading to PRDC are diagnosed properly, and a part of this strategy can rely on examining slaughter lungs. The goal of this study is to identify main pathogens present in PRDC-affected lungs from herds located in Germany (DE), the Netherlands (NL), Belgium (BE) and Austria (AT).

Material and Methods

In total, 61 farms with low to high respiratory problems were included. Lungs were scored according to Ceva Lung Program methodology. Within each batch, the investigator selected up to five lungs and sampled the transition area between healthy and affected parenchyma. Pooled samples were then analyzed by a screening-PCR for following pathogens: *Actinobacillus pleuropneumoniae* (App), *Mesomycoplasma hyopneumoniae* (Mhyo), Betaarterivirus suid 1 + 2 (PRRSV), Swine influenza A virus (swIAV) and Porcine circovirus type 2 (PCV2).

Results

Mhyo was found on average in 90.2% of all farms, followed by PRRSV1 (47.5%), PCV2 (45.9%), App, PRRSV2 and swIAV respectively (3.3%). There were low differences in the presence of Mhyo between the regions, with high values ranging from 85.7% (NL) – 100% (BE). PCV2 was found in most Belgian herds (80%), followed by NL (42.9%), AT (66.7%) and Germany (35.3%). Most prominent genotype was PCV2d (69.2%), followed by PCV2a and PCV2b respectively (15.4%).

Discussion and Conclusion

We can conclude that the present method of sampling and analysis was practical and efficient for finding latter mentioned pathogens. Most importantly, we demonstrated that PCV2 was detected in PRDC lungs from almost every second herd, with a higher rate for PCV2d. The impact of PCV2 and especially PCV2d in PRDC as an immune-suppressive and co-infective agent should be evaluated in future studies.