



UPDATED REGIONAL ASSESSMENT IN FOUR EUROPEAN COUNTRIES OF PRDC PATHOGENS USING LUNG LESION SCORING AND SCREENING PCR

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Introduction and Objectives

To effectively tackle Porcine Respiratory Disease Complex (PRDC), it is often essential to assess lung lesions at slaughter and identify causative pathogens. This study combines pathoanatomical lung examination with PCR to detect key PRDC agents in slaughter pigs from Germany, the Netherlands, Belgium, and Austria. It serves as an update to regional findings from 2024 [1].

Material and Methods

In total, 459 farms with low to high respiratory problems were included. Lungs were scored according to a standardized lung scoring methodology [2]. 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* (M. hyo), Betaarterivirus suis 1 + 2 (PRRSV 1+2), Swine influenza A virus (swIAV) and Porcine circovirus type 2 (PCV2). The latter pathogen was genotyped at ct-values ≤ 32.

Results and Discussion

As shown in Fig. 1, M. hyo was found on average in 354 (77.1%) farms, followed by PCV2 (223; 48.6%), PRRSV1 (167; 36.4%), App (42; 9.2%), PRRSV2 (18; 3.9%) and swIAV (22; 4.8%). Co-infections were quiet common, as shown in Fig.2. Dual infection with M.hyo + PCV2 was the most frequent type in 97 farms (23%), followed by M.hyo and PRRSV (61; 15%). Most frequent triple infection was M.hyo + PCV2 + PRRSV also found in 61 farms. In total, 91 farms (19.8%) were sequenced for PCV2. Most prominent genotype was PCV2d (80.2%), followed by PCV2a (14.3%) and PCV2b (5.5%; Fig. 3).

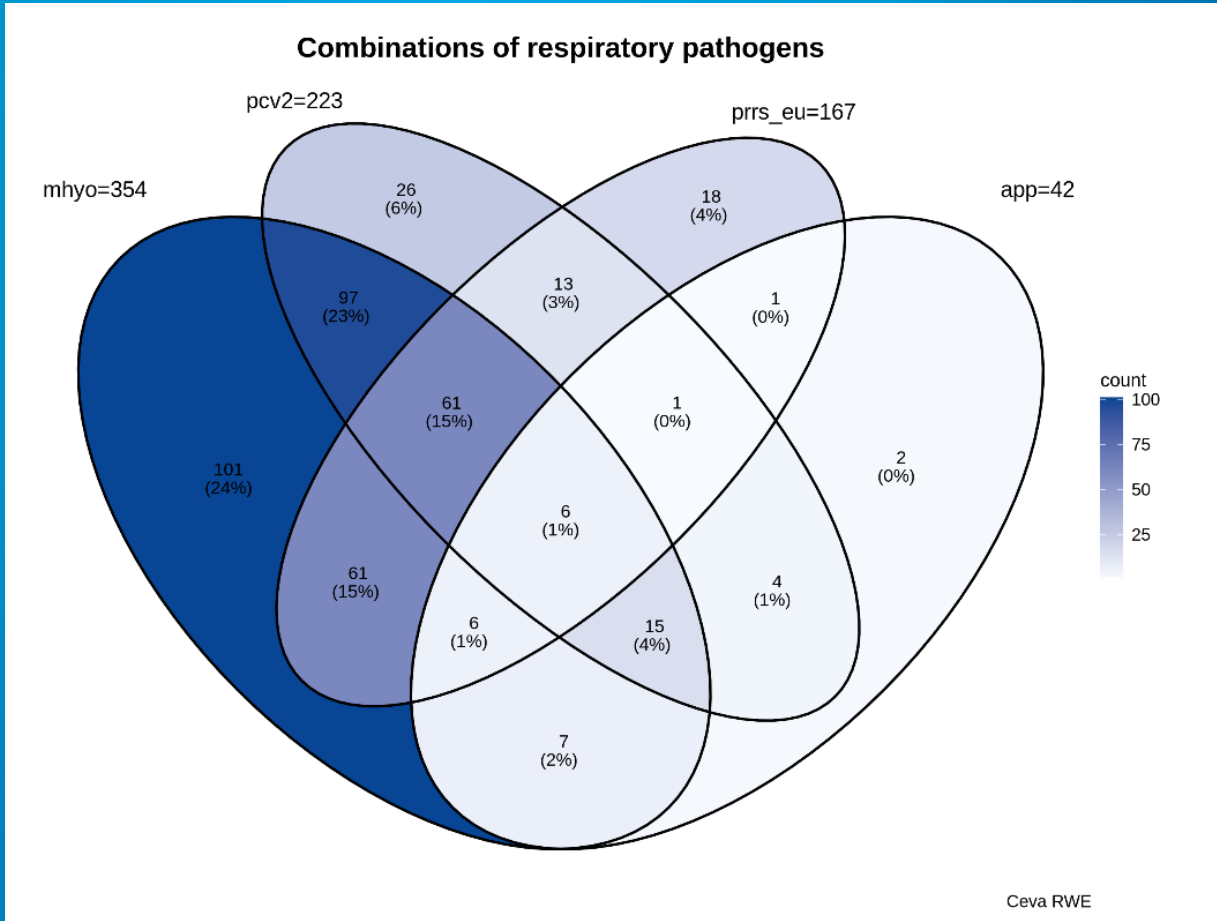


Fig. 2 Venn diagram showing the distribution and overlap of co-infections among respiratory pathogens

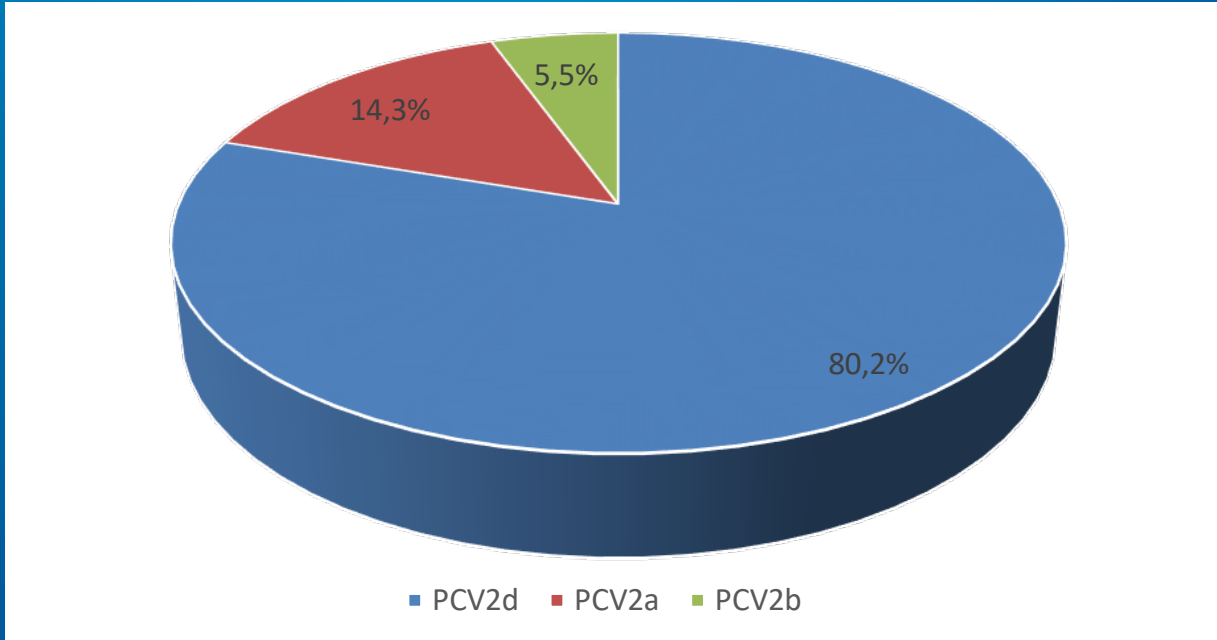


Fig. 3 Percentage of PCV2-genotypes detected in farms with sequenceable isolates (n=91)

Conclusion

Compared to our previous evaluation, this study included 7.5 times more farms and revealed a lower prevalence for M. hyo (77.1% vs. 90.2%) and PRRSV1 (36.4% vs. 47.5%). App, PRRSV2, and swIAV remained the least prevalent agents. Interestingly, PCV2 was found more frequently (48.6% vs. 45.9%), with a notable increase in the identification of the PCV2d genotype (80.2% vs. 69.2%). These changes may be attributed to the larger number of farms included, differences in their geographic distribution, and a potential shift in pathogen epidemiology. Taken together, these findings suggest that PCV2, particularly the PCV2d genotype, is still on the rise, warranting close monitoring and potentially adapted control strategies. Furthermore, it plays an important role in co-infections with M.hyo and PRRSV, as shown in this study

References

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[2] Cvjetković V, Sipos S, Szabó I, Sipos W Clinical efficacy of two vaccination strategies against *Mycoplasma hyopneumoniae* pig herd suffering from respiratory disease. Porcine Health Manag. 2018 Aug 1;4:19. doi: 10.1186/s40813-018-0092-7. PMID: 30083374; PMCID: PMC6069710.

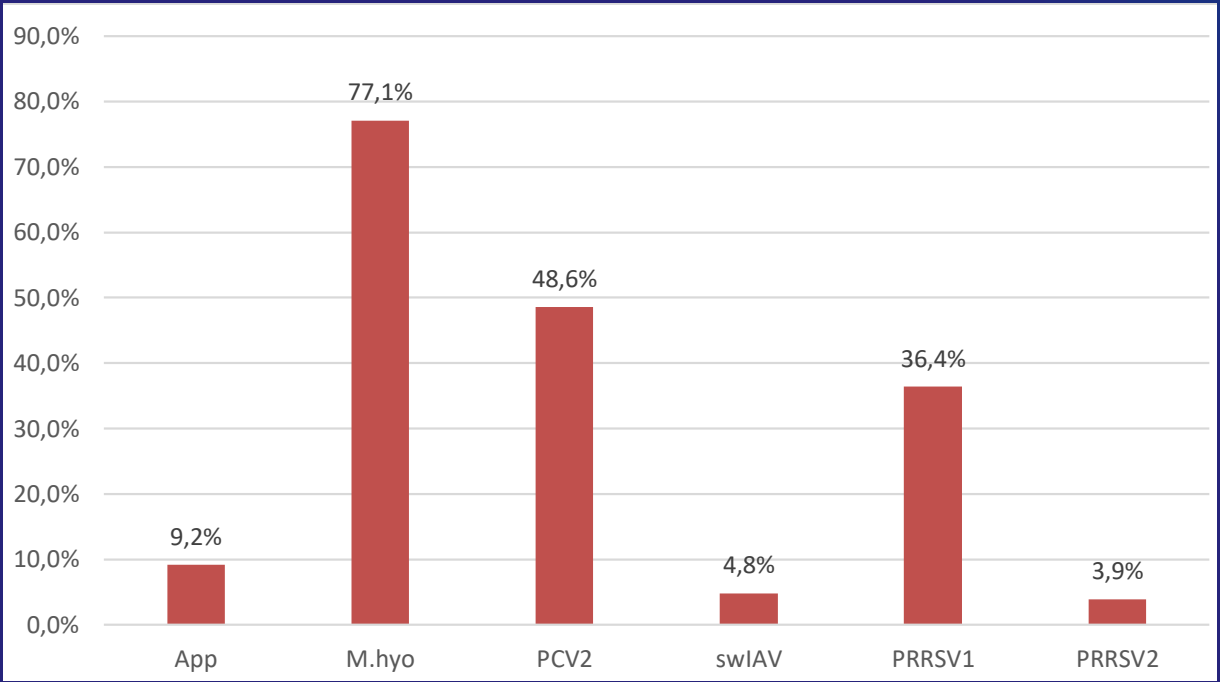


Fig.1 Percentage of farms tested positive for each pathogen (N=459)