



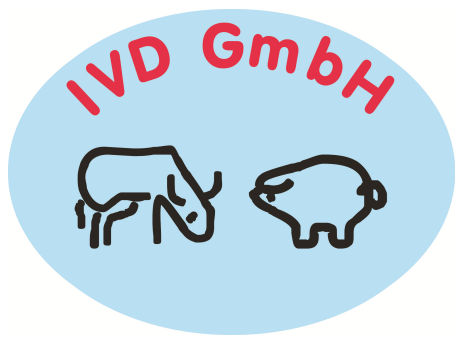
# AN OVERVIEW OF THE MOST FREQUENTLY FOUND PATHOGENS IN ALTERED SLAUGHTER LUNGS FROM FOUR EUROPEAN COUNTRIES

E. De Jonghe<sup>1</sup>, S. Van Colen<sup>1</sup>, C. Soeckler-Lionetti<sup>2</sup>, M. Koechling<sup>2</sup>, H. Marks<sup>2</sup>, N. Schreiner<sup>2</sup>, C. Waehner<sup>2</sup>, K. Strutzberg-Minder<sup>3</sup>, V. Cvjetkovic<sup>2</sup>

<sup>1</sup>Ceva Santé Animale S.A./N.V., Brussels, Belgium

<sup>2</sup>Ceva Tiergesundheit GmbH, Düsseldorf, Germany

<sup>3</sup>IVD GmbH, Innovative Veterinary Diagnostics, Seelze, Germany

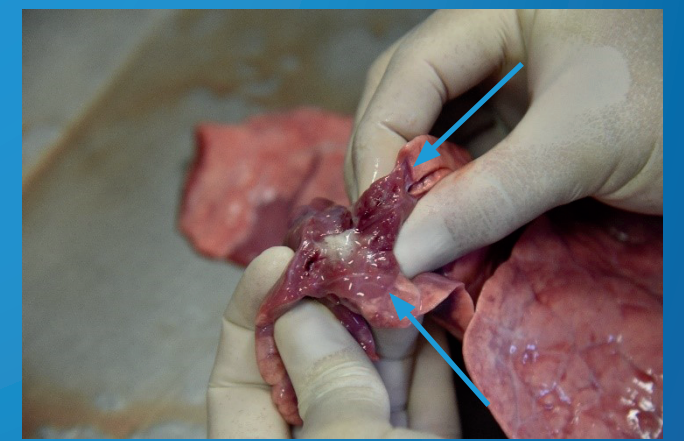


## Background and Objectives

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 was 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

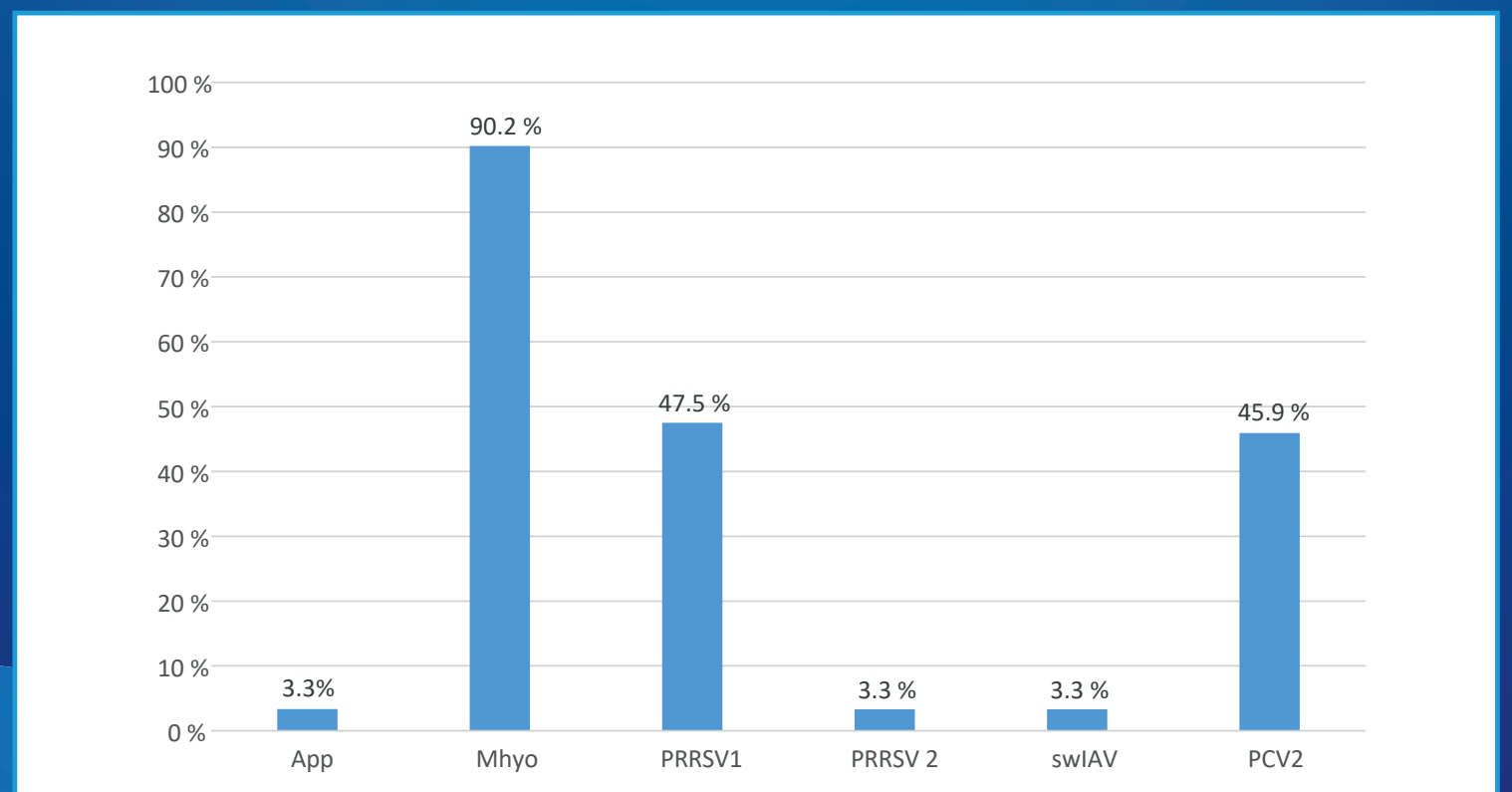
In total, 61 farms with low to high respiratory problems were included. Lungs were scored according to Ceva Lung Program methodology [1]. Within each batch, the investigator selected up to five lungs and sampled the transition area between healthy and acutely affected parenchyma (Fig. 1) by extracting approx. 0.125 cm<sup>3</sup> of tissue, with a maximum of two such samples per lung: pooled samples were then stabilized in plastic tubes with 2 ml of viral media (Virocult<sup>®</sup>, Medical Wire & Equipment Co Ltd), shipped between 2-8°, and subsequently analyzed by a screening-PCR (IVD Gesellschaft für Innovative Diagnostik GmbH) for following pathogens: *Actinobacillus pleuropneumoniae* (App), *Mesomycoplasma hyopneumoniae* (Mhyo), Betaarterivirus suid 1+ 2 (PRRSV 1+2), swine influenza A virus (swIAV) and porcine circovirus type 2 (PCV2).



**Figure 1:** Left cardiac lobe acutely affected by a mucopurulent cranioventral consolidation. Sampling of parenchyma was ideally conducted between affected and non-affected areas (indicated with arrows)

## Results

Mean EP-index values were the lowest in NL (0.45), followed by BE (1.73), DE (2.88) and Austria (2.93). 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 AT (66.7 %), NL (42.9 %), and Germany (35.3 %). Most prominent genotype was PCV2d (69.2 %), followed by PCV2a and PCV2b respectively (15.4 %).



**Figure 2:** Average detection rate of screened pathogens per farm (N=61)

## Discussion and Conclusion

We can conclude that the present method of sampling and analysis was practical and efficient for finding latter mentioned pathogens. As shown in previous studies, EP-like lesions are highly suggestive of Mhyo [2]. Furthermore, even in batches with low EP-index values, we were able to find (bronchopneumonic lungs with) Mhyo, indicating that both parameters should always be interpreted together when evaluating the level of control against Mhyo. Most importantly, we also demonstrated that PCV2 was detected in PRDC lungs from almost every second herd, with a higher rate for PCV2d. This is especially interesting, since PCV2d has a better binding capacity than both PCV2a and PCV2b, and shows a more effective replication in lymphoblasts [3, 4]. The impact of PCV2, and especially PCV2d in PRDC as an immune-suppressive and co-infective agent, should be evaluated in future studies.

## References

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3. Wei, R., N. Van Renne, and H.J. Nauwynck, *Strain-Dependent Porcine Circovirus Type 2 (PCV2) Entry and Replication in T-Lymphoblasts*. LID - 10.3390/v11090813 [doi] LID - 813. (1999-4915 (Electronic)).
4. Wei, R.A.-O., et al., *Changes on the viral capsid surface during the evolution of porcine circovirus type 2 (PCV2) from 2009 till 2018 may lead to a better receptor binding*. (2057-1577 (Print)).