



EMERGING AND IMPACT OF PORCINE CIRCOVIRUS TYPE 2D IN DENMARK

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Background and Objectives

Porcine circovirus type 2 is a small DNA-virus, which can be divided into genotypes based on genetic differences. During recent years, a new genotype (genotype d) has evolved to be the most prevalent genotype in Asia and North America. Furthermore, some studies have indicated that this genotype induces more severe clinical signs and has been related to vaccine failures in the field. The objective of this study was to investigate the genotypes presently circulating in Denmark and to relate the genotype to clinical signs and/or decreased efficacy of PCV2 vaccines.

Materials and Methods

Archived samples from herds collected between 2014 and 2018 were included. These samples had previously been tested positive for a moderate to high level of PCV2 by qPCR. In addition, samples received in 2017-2018 from case herds with PCV2 associated clinical signs (wasting, un-thriftiness, poor performance) or typical pathological signs (enlarged lymph nodes, wasting) were included. PCV2 was genotyped by full genome SANGER sequencing of PCR products followed by phylogenetic analysis including representative virus sequences retrieved from GeneBank.

Results

The sequencing revealed that PCV2b was the only genotype identified in 2014-2016, whereas both PCV2b and PCV2d genotypes were detected in 2017-2018. In two herds, both PCV2b and PCV2d were identified in the same sampling. Interviews with owners of the case herds revealed in all cases that the PCV2 related problems had been controlled either by change in management or by vaccination.

CONCLUSION

This study revealed that PCV2d is evolving also in Denmark but did not confirm that PCV2d has been associated with more severe disease in Danish pig herds. Furthermore, the available vaccines seem to be effective, also towards the PCV2d genotype.

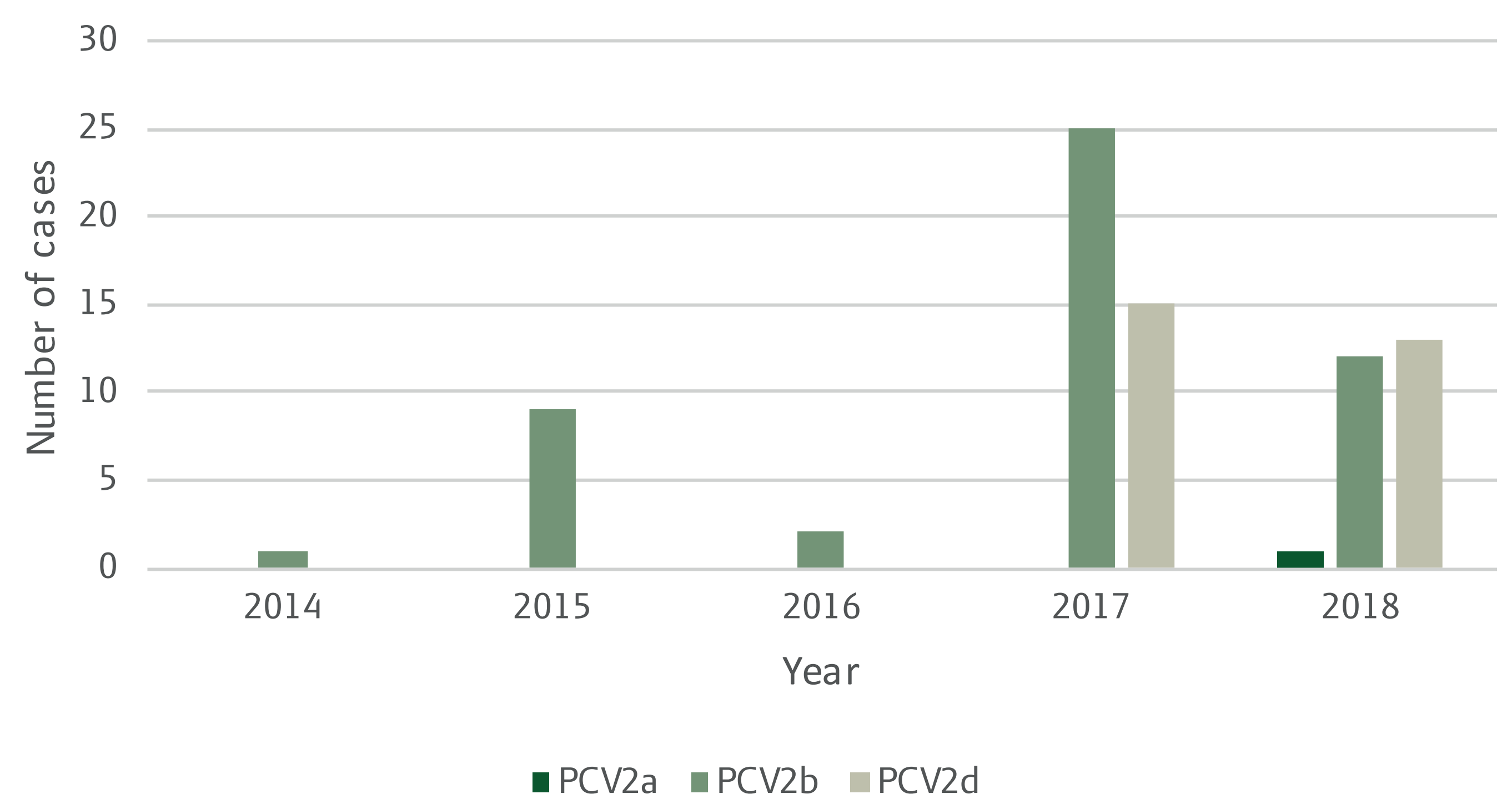


FIGURE 1 Genotypes identified in Danish herds

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