



## VIRAL DISEASES

VVD-023

### **NORTHERN IRISH PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV) TYPE 1 ISOLATES EVIDENCE CONSIDERABLE VARIABILITY IN THE OPEN READING FRAME 5 (ORF5)**

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#### **Introduction**

PRRSv is widely spread around Northern Ireland infecting most breeding and growing pig farms. PRRSv vaccines are used in 90 to 95% of infected sow herds, while less than 15% of weaning-growing pigs receive vaccines. PRRSv is frequently involved in porcine respiratory disease complex. PRRSv infection rarely causes severe clinical signs, and a remarkable number of famers reject the use of vaccines, arguing the perceived very mild-to-nill contribution of PRRSv to respiratory problems and performance drops.

#### **Material & methods**

Between 2016 and 2017, we gathered PRRSv isolates from clinical cases of mild-to-severe respiratory disease in Northern Ireland, from which 8 samples from different farms were selected. The ORF5 gene was sequenced (Anicon, Germany). The Animal and Plant Health Agency (APHA) provided additional historical sequences from Irish samples to compare the homology between them. We built a Neighbour-joining phylogenetic tree with an additional 687 nucleotide sequences from the UK and compared the nucleotide identity.

#### **Results**

Northern Irish samples were PRRSv type 1 with >85% similar nucleotide identity with the Lelystad strain.

Variability between Northern Irish strains was noticeable with nucleotide identities as low as 84%. These strains were widely spread in the phylogenetic tree (see poster) among other British, Irish and reference isolates.

#### **Discussion & conclusion**

PRRSv from these Northern Irish cases did not belong to any single cluster based on ORF5 analysis, contrary to the beliefs of many Norther Irish producers regarding the mildness of the disease and the lack of necessity to vaccinate against PRRSv in Northern Ireland.

Predictions of disease severity and vaccine effectiveness based on ORF5 sequence are not possible. Northern Irish farms are infected by a wide range of PRRSv-1 viruses, and clinical cases do need a proper investigation to elicit the best control measures – with or without vaccines.