



## VIRAL DISEASES

VVD-025

### **GENETIC DIVERSITY OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV) ISOLATES IN THE NETHERLANDS FROM 2014-2016**

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#### **Introduction**

Porcine reproductive and respiratory syndrome (PRRS) is the most significant swine disease worldwide and is endemic in many countries, including the Netherlands. It is caused by the PRRS virus which shows remarkable genetic variation. Epidemiological and molecular analysis of circulating PRRS-viruses is key to modern farm management and essential to review current diagnostic tools. Since the early nineties no epidemiological or molecular study has been performed on circulating PRRS-viruses in the Netherlands. To determine the genetic diversity of PRRS isolates in the Netherlands, the sequences of circulating field viruses were compared.

#### **Material & Methods**

Seventy-eight PRRS-virus isolates collected in the Netherlands from 2014-2016 were sequenced from and including ORF2 to ORF7. Phylogenetic analysis was performed using the MEGA 6.06 software and sequences were compared with sequences available on GenBank.

#### **Results**

All investigated isolates belong to the European type I viruses including twelve Lelystad-like viruses. Most isolates showed only approximately 90% similarity with published sequences in GenBank and suggest a complete Dutch cluster in the phylogenetic tree. Sequence comparison of the individual ORFs of the viruses with the Lelystad strain showed that ORF3 (84-89%) and ORF5 (82-89%) are the most diverse ORFs, whereas ORF2 (90-95%), ORF6 (88-97%) and ORF7 (89-97%) showed the highest similarity with the Lelystad strain. Furthermore, comparison of individual ORFs suggested that some of the isolates may have originated from strains with a different genetic background.

#### **Discussion & Conclusion**

PRRS viruses isolated in the Netherlands in 2014-2016 show a high variation in their sequences. Most isolates belong to a distinct phylogenetic cluster within the type I viruses. The finding that some isolates have different origins when looking at the different ORFs suggests that recombination between different PRRS viruses may occur.