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Title: Genetic and antigenic drift of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) in a closed population evaluated by full genome sequencing

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Abstract: Porcine Reproductive and Respiratory Syndrome (PRRS) viruses are divided into two major genotypes (Type 1 and Type 2) based on their genetic diversity. Type 1 PRRSV is further divided into at least 3 subtypes, but until now only subtype 1 has been detected in Western Europe and North America. Both genotypes are circulating in Denmark and since gilt vaccinations are widely used it is essential to monitor the diversity of circulating PRRS viruses. Prior to the present study, however, the diversity of circulating viruses in Denmark was virtually unknown. The main objective was to assess the diversity of circulating PRRS viruses in Danish pigs and to investigate the genetic drift of the virus in a closed population with very limited introductions of new animals. The study included phylogenetic analysis of full genome sequences of eight Type 1 and nine Type 2 PRRS viruses, including the very first Danish isolated Type 1 virus and the very first Danish Type 2 PRRS virus isolated from a non-vaccinated pig herd. Furthermore, by sequencing ORF5 and ORF7 of 43 Type 1 and 57 Type 2 viruses isolated between 2003 and 2013, the level of genetic diversity was assessed. The results showed a very high genetic diversity among the Danish viruses throughout the genome within the same genotype. A global phylogenetic analysis showed that the Danish Type 1 PRRSV formed two major clusters, one vaccine (Porcilis)-like clade exclusively containing viruses isolated after the Porcilis vaccine was introduced and another distinct clade consisting mainly of viruses isolated in Denmark. Phylogenetic analysis in a global Type 2 PRRSV framework classified all Danish Type 2 viruses to a single cluster (sub-lineage 5.1) which comprised viruses closely related to the Type 2 prototype isolate VR2332. Both Type 1 and Type 2 harbored deletions in the region encoding nsp2 and some significant amino acid changes were also seen in antigenic sites. Acknowledgement: The study was supported by EU Grant n° 245141 (New tools and approaches to control Porcine Reproductive and Respiratory Syndrome in the EU and Asia (PoRRSCon) coordinated by Prof. H. Nauwynck.