

Technical University of Denmark



The diversity of Porcine Reproductive and Respiratory Syndrome Virus Type 1 and 2 in Denmark

Kvisgaard, Lise Kirstine; Hjulsager, Charlotte Kristiane; Kristensen, Charlotte Sonne; Brar, Manreetpal Singh ; Leung, Frederick Chi-Ching; Larsen, Lars Erik

Publication date:
2013

[Link back to DTU Orbit](#)

Citation (APA):

Kvisgaard, L. K., Hjulsager, C. K., Kristensen, C. S., Brar, M. S., Leung, F. C-C., & Larsen, L. E. (2013). The diversity of Porcine Reproductive and Respiratory Syndrome Virus Type 1 and 2 in Denmark. Abstract from International Porcine Reproductive and Respiratory Syndrome Symposium (PRRS 2013), Beijing, China.

DTU Library

Technical Information Center of Denmark

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

The diversity of Porcine Reproductive and Respiratory Syndrome Virus Type 1 and 2 in Denmark

Lise K. Kvisgaard^{1*}, Charlotte K. Hjulsager¹, Charlotte Sonne Kristensen², Manreetpal Singh Brar³, Frederick Chi-Ching Leung^{3,4}, and Lars E. Larsen¹

¹National Veterinary Institute, Technical University of Denmark, DK-1870 Frederiksberg C, Denmark, ²Pig Research Centre, Danish Agriculture & Food Council, DK-8620 Kjellerup, Denmark, ³School of Biological Sciences, University of Hong Kong, Hong Kong, China, ⁴Bioinformatics Center, Nanjing Agriculture University, Nanjing, China

Abstract

Both Type 1 and Type 2 PRRS viruses are circulating among Danish pigs. The first appearance of Type 1 PRRSV in Denmark was in 1992 whereas the Type 2 PRRSV was introduced in 1996 after the use of a live attenuated vaccine that reverted to virulence. Since then, vaccination to control the disease for both PRRSV genotypes has been widely used in Denmark and it is therefore highly relevant to monitor the diversity of currently circulating PRRSV strains. Only subtype 1 of the Type 1 PRRSV strains and vaccine-like Type 2 PRRSV strains were previously detected in Denmark, however, only few Danish PRRSV strains were sequenced. Denmark exports more than 50.000 living pigs each month. A portion of these pigs inevitably harbor PRRSV. Thus, the diversity of PRRSV in Denmark is of interest to other countries besides Denmark. The main objective of the present study was to close the gap in knowledge on the genetic diversity of currently circulating PRRSV strains in Danish pigs by sequencing ORF5 and ORF7 of approximately 41 Type 1 and 50 Type 2 strains isolated between 2003 and 2013. Furthermore, full genome analysis was performed on nine Type 1 and nine Type 2 selected strains. The preliminary assessment of the results showed that the Type 1 strains all belonged to subtype 1. Based on the ORF5 sequences, the Danish Type 1 viruses clustered into two groups. These two groups shared 84 % to 92 % and 94 % to 99 % nucleotide identity to the Lelystad virus, respectively. The sequenced Type 2 viruses showed a significant higher level of identity in that the ORF5 sequences were 94 - >99 % identical at the nucleotide level. Most of the Type 2 viruses, shared high level of identity to the VR2332 vaccine strain (Ingelvac MLV), but a few more diverse isolates were also identified, including strains with interesting deletions in NSP2 and other genes. The full genome sequences of Danish strains showed an overall nucleotide identity of 88-98 % (Type 1) and 94 % to >99 % (Type 2). The impact of these results will be discussed.

Acknowledgement: The work in this study was funded by the 7th Framework Program: New tools and approaches to control Porcine Reproductive and Respiratory Syndrome in the EU and Asia (PoRRSCon). www.porrscon.ugent.be