Porcine Reproductive and Respiratory Syndrome Virus (PRRSV)

This PhD thesis presents the diversity of Porcine Reproductive and Respiratory Syndrome viruses (PRRSV) circulating in the Danish pig population. PRRS is a disease in pigs caused by the PRRS virus resulting in reproductive failures in sows and gilts and respiratory diseases in pigs. Due to genetic heterogeneity, PRRSV is divided into two genotypes, Type 1 and Type 2. Type 1 PRRS viruses are further divided into at least 3 subtypes. The virus evolves rapidly and reports of high pathogenic variants of both Type 1 and Type 2 appearing in Europe, North America, and Asia have been reported within recent years. This abrupt occurrence of highly pathogenic PRRSV strains emphasizes the significance of monitoring the diversity of circulating strains around the world both in respect to the sensitivity and specificity of diagnostic tests as well as efficacy of available vaccines.

The aims and objectives of the PhD project will be introduced in the objectives section together with a short introduction to the situation of PRRSV in Denmark at the start of this study. The background chapter will provide a review on PRRSV with the emphasis on genetic diversity.

The results of the work performed during the PhD are presented in the four manuscripts included in the PhD thesis and a short summary of each manuscript is depicted below:

Manuscript I is focusing on the development of methods for complete genome sequencing of PRRSV. The sequencing strategy was based on the production of long range PCR fragments covering the PRRSV genome in two or four fragments with full-length cDNA as template. The sequencing of the PCR fragments was performed using Next Generation Sequencing (NGS) technologies and three different platforms were used. A total of 18 complete PRRSV genomes were obtained using this new method.

Manuscript II is focusing on the diversity of Type 1 PRRSV in Denmark. For the first time genetic and antigenic examinations of complete genomes of Danish isolated Type 1 PRRSV was conducted. Furthermore, extensive studies of ORF5 and ORF7 sequences were performed from 44 viruses collected from 2003 to February 2013. The diversity study confirmed that only Type 1 subtype 1 PRRSV is circulating in the Danish pig population. The examination of the Danish PRRS field viruses confirmed that there is a high overall diversity among Type 1 viruses in Europe. The phylogenetic study also indicated the presence of two Danish virus clusters, one dominating vaccine/LV like and one resembling an early introduced strain.

Manuscript III is focusing on the diversity of Type 2 PRRSV in Denmark. For the first time examinations of complete genomes of European isolated Type 2 PRRSV were performed. Furthermore, ORF5 and ORF7 sequences obtained from 57 viruses collected in the years 2003-2012 were examined. The diversity study confirmed that Danish Type 2 PRRS viruses share high genetic similarity to the vaccine strain and there was no obviously reason to believe that new Type 2 PRRSV strains have been introduced. However, a few viruses showed both a higher diversity to the other Danish viruses and to the vaccine strain and one virus harbored the largest deletion in NSP2 reported in Danish Type 2 PRRSV.

Manuscript IV is focusing on an experimental infection study in pigs with a Type 2 PRRS virus causing significant clinical disease in the field. Genetic and antigenic examination of ORF5 and partial NSP2 sequences obtained from the case virus revealed several variations compared to the vaccine strain. However, complete genome comparison of the case virus to the vaccine strain showed high genetic similarity and no obvious virulence maker was found. The results of the experimental infection study revealed that the strain induced only sparse clinical symptoms and the magnitude and duration of viraemia was comparable to an older Danish Type 2 strain. The results emphasized that infections in the field is often more severe than in experimental studies due to the multifactorial nature of PRRSV. Furthermore, the study underlined the need for more research on virulence markers of PRRSV.