RESEARCH ABSTRACT

SWINE HEALTH

Title: Using genomic tools to link PRRSV quasispecies to disease severity in pigs infected with contemporary virulent isolates. **NPB #18-156**

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Scientific abstract

Porcine reproductive and respiratory syndrome virus (PRRSV) is the etiological agent of PRRS. It is a member of the *Arteriviridae* family of positive single stranded rapidly evolving RNA viruses. Arteriviruses have the ability to establish either mild chronic or severe infections in domestic swine. Ever since the primary introduction, PRRSV continues to evolve and new genetic variants re-emerge routinely throughout the US and Europe. Here we compare two virulent PRRSV isolates, MN30100 (MN) and OK/2016 (OK), that were reported to have unique disease severity outcomes observed under field conditions. We describe the quasispecies nature of these twoinfections, over time and from different cell types and sources, with both isolates showing increased heterogeneity in genomic variants in tissue over serum samples. Whole genome sequencing revealed a greater genetic variation in the 5' region of both genomes, notably in the non-structural protein coding region. For example, OK/2016 had a 1,151 bp deletion in the orf1a gene. Nonetheless, the majority of changesresulted in synonymous mutations. The genetic variation in Orf5 was atypical of the changes observed across the whole of the PRRSV genome. Due to the lack of sequence depth for MN30100, especially across the 5' non-structural protein encoded genes for all sources of material, we could not assign function to any differences that could be attributed to specific tissue type or time of sampling. This type of analysis is still feasible but it requires a larger financial and personnel investment. We nonetheless did observe genetic variation within animal over a small window of time (up to 14 days post infection), which was less when comparing sample type. This study emphasizes once again the potential whole genome comparative analysis can make towards a deeper understanding of the pathology associated with a rapidly evolving virus such as PRRSV.