Title: Development of next generation sequencing methodology for full genome characterization of porcine reproductive and respiratory syndrome virus (PRRSV) from oral fluids and nasal swabs - NPB#14-204

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Scientific Abstract:

Porcine reproductive and respiratory syndrome virus causes one of the most significant swine diseases with near worldwide distribution. In the U.S., open reading frame 5 (ORF5) is commonly sequenced to investigate viral epidemiology. While glycoprotein 5 (GP5) is the major protein on the surface of the virion found as a heterodimer with the membrane protein, the minor glycoproteins GP2a, GP3 and GP4 exhibit similar genetic diversity and form a heterocomplex responsible for receptor binding. To increase our understanding of PRRSV diversity and evolution, 66 genome sequences were determined directly from serum samples using viral metagenomic methodology. Phylogenetic analysis identified five, four, seven, seven and six well-supported clades for ORF2a, ORF3, ORF4, ORF5 and ORF6, respectively, which encompassed nearly all strains. Intraclade genetic distance was approximately 0.00-0.12 while interclade distances were 0.10-0.21. Similar genetic diversity was observed for ORF2a, ORF3, ORF4 and ORF5 while ORF6 was more conserved. Topological incongruences were noted in the 3’ end of the genome (ORF2a to 3’-terminus) using the genetic analysis recombination detection algorithm with five breakpoints identified with statistical significance ($P<0.05$). Thirteen gene combinations with respect to ORF2a, ORF3, ORF4, ORF5 and ORF6 clade composition were identified. Recombination detection program identified two representatives from these gene combinations as recombinants with high confidence. This study identified more diversity in the PRRSV structural proteins than previously recognized, possibly due to direct sequencing of clinical samples as opposed to selection for growth in vitro.