RESEARCH ABSTRACT

SWINE HEALTH

Title: Rational design of a broadly protective vaccine against porcine reproductive and respiratory syndrome virus - **NPB #13-155** revised

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Scientific abstract

Substantial genetic variation among PRRSV strains represents a major obstacle for the development of a broadly protective vaccine. We describe here a novel approach to generate a PRRSV vaccine strain that could confer broad cross-protection against divergent PRRSV isolates. We initially obtained a set of 60 non-redundant, full-genome sequences of type-II PRRSV. After that, we generated the consensus genome (designated as PRRSV-CON) by aligning the 60 PRRSV full-genome sequences, followed by selecting the most common nucleotide found at each position of the alignment. Our analysis demonstrates that the PRRSV-CON has the highest degree of sequence identity to the PRRSV field-isolates when compared to any current PRRS vaccine strains, both at the full-genome level and the individual gene level. Next, we chemically synthesized the PRRSV-CON genome and assembled it into a bacterial plasmid under the control of the T7 promoter. The resulting PRRSV-CON cDNA clone is fully infectious. Viable virus is consistently produced after MARC-145 cells are transfected with the RNA transcript produced from the PRRSV-CON cDNA clone. Moreover, the PRRSV-CON virus replicates as efficiently as our prototype PRRSV strain FL12, both *in vitro* and *in vivo*. Importantly, primary infection of pigs with PRRSV-CON virus confers significantly broader protection than the prototype PRRSV strain FL12 when tested upon subsequent challenge with a third unrelated heterologous PRRSV strain. Collectively, our data demonstrate that the PRRSV-CON virus can serve as a potential vaccine candidate for the development of a novel PRRS vaccine with broader cross-protection.