RESEARCH REPORT
SWINE HEALTH

Title: Rational Design of a New Generation of PRRSV Differential (Marker) Vaccines – **NPB # 05-159**

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Abstract

This project is based on two main premises: 1) the conviction that the use of vaccines will always be a cost-efficient method and the preferred approach to control PRRSV infections, and 2) the notion that the best type of immunogen against PRRSV has been shown to be, so far, a live, replicating vaccine. Live vaccines present the antigens to the pig's immune system in a similar way as wild-type PRRSV. Therefore our ultimate goal is to develop a live, replicating vaccine that would be safe, efficacious and compatible with eradication. Our overall objectives are addressed to find answers to the following specific questions**: 1. What is the molecular basis of attenuation of virulence in PRRSV? 2. Can we molecularly attenuate PRRSV and obtain a replicating vaccine of unprecedented efficacy and safety? 3. Can we engineer this product to be a "marker" vaccine so that we can integrate robust vaccination together with efficient cleansing of PRRSV infection?** To achieve these goals, we are successfully applying the technology of reverse genetics [infectious clone, IC] developed in our laboratories to identify the genes responsible for virulence in PRRSV and precisely engineer an attenuated vaccine candidate. In this particular year of the project we have been able to show that two of the major PRRSV structural genes that are major determinants of virulence are ORF 5 (coding for GP5) and ORF2 (coding for GP2) . Likewise we have conducted a primary identification of small segments of PRRSV proteins (epitopes) that can be deleted from the vaccine so that could then be used as serologic diagnostic markers of infection (DIVA). These studies should continue with: 1) the identification of a major cluster of virulence detected in non-structural proteins that will permit to obtain full molecular attenuation of PRRSV 2) identification of the single aminoacids that determine the virulence and that should be targeted for mutations and 3) the establishment of a marker deletion and test for DIVA differentiation.