

SWINE HEALTH

Title: Year 2 funding support for the PRRS Host Genetics Consortium: A proposal to study the role of host genetics and resistance to PRRSV – **NPB #09-208**

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Scientific Abstract

The PRRS Host Genetics Consortium (PHGC) is a national effort developed with input from PRRS researchers, NC1037/NRSP8 genome researchers, members of the NPB Swine Health and Animal Science Committees, veterinarians, AASV, producers, and commercial partners. It was funded by NPB starting in December 2007. The PHGC incorporates a nursery pig model to assess pig responses to acute PRRSV infection and to study of the relationship between host genes and the resistance/susceptibility of pigs to primary PRRSV infection. Blood and other samples (e.g. oral fluids) and weight measurements are collected regularly for phenotypic data. Tonsil is collected at the end of the study to measure persistent infection. Phenotypic measurements include virus load, weight gain, antibody responses, and cytokine levels in serum. Serum samples are collected at 10 time points for all pigs, which provides the opportunity to create “deep phenotypes” of the anti-PRRS response. All samples are catalogued and distributed to appropriate testing labs and stored for use in future studies. The data are collected into a secure PHGC relational database, housed at Iowa State University and maintained by James Reecy, a CoPI on the project. DNA recovered from each pig is genotyped using funding from a separate PRRS CAP grant and through resources provided by national NRSP-8 swine genome. Blood is collected for total RNA analysis of host gene expression, which is supported by a separate NIFA grant. Oral fluid samples are collected for the purpose of developing improved PRRS surveillance methods.

Deliverables of the PHGC include:

- Genetic and blood tests that can be used to predict how pigs respond to PRRSV infection.
- Determination of alleles in genomic regions, single nucleotide polymorphism (SNP), or candidate genes [and source pig genetics] which are correlated with PRRS resistance/susceptibility or PRRSV persistence.
- Identification of quantitative trait loci (QTL) to develop selection procedures to lower the effects of PRRS and prevent persistence of PRRSV virus in pigs.
- Discovery of unique PRRSV resistance mechanisms and virus-host interactions.
- Development of a resource of samples and data for studies of PRRS genetics, diagnostics and pathogenesis.
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These research results were submitted in fulfillment of checkoff-funded research projects. This report is published directly as submitted by the project's principal investigator. This report has not been peer-reviewed.

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