Sample Young Scholar Recognition Program Abstract Submission (from the ASAS Midwest Section)

O187 Genetic basis of host response to PRRSv infection. N. J. Boddicker [1,*], J. K. Lunney [2], B. R. R. Rowland [3], D. J. Garrick [1], J. M. Reecy [1], [1]Animal Science, Iowa State University, Ames, [2]USDA, ARS, BARC, Beltsville, [3]Kansas State University, Manhattan.

Host genetics is an additional tool for controlling the costly disease of Porcine Reproductive and Respiratory Syndrome (PRRS). The objective of this work was to discover the genetic basis of host response to PRRS virus infection by estimating genetic parameters and conducting a genome-wide association study. Eight groups of ~200 commercial crossbred pigs were infected between 25 and 35 days of age with virus isolate NVSL 97-7985. Breeds represented in the crosses included Large White, Landrace, Yorkshire, Duroc, and Pietrain. Blood samples and body weights were collected up to 42 days post infection (dpi). Experimental pigs and their parents were genotyped with Illumina's Porcine 60k Beadchip. Phenotypes analyzed were viral load (VL = area under the curve for logtransformed qRT-PCR based serum virus from 0-21 dpi) and weight gain from 0-42 dpi (WG). Viral load data was only available for the first 7 trials. Heritabilities estimated using pedigree were moderate at 0.41 for VL and 0.29 for WG. Single-nucleotide polymorphism (SNP) associations were identified using Bayes-B of GenSel software. A 1 Mb region on chromosome 4 (SSC4) explained 14.6% of the genetic variance for VL and 9.1% for WG. Effects of the most significant SNP in the region, WUR10000125 (WUR), acted in a dominant manner, with the favorable allele estimated to decrease VL by 4 units (0.53 phenotypic sd) and increase WG by 2 kg (0.49 phenotypic sd). The effect was present irrespective of parental breeds involved in the crosses. All haplotypes that carried the favorable allele (11 of 77) of SNP WUR also had the desirable phenotype. In conclusion, the 1 Mb region on SSC4 explained a sizable proportion of genetic variation in response to experimental challenge with a specific strain of the virus. Heritability estimates were moderate and, with a frequency of 0.15 for the favorable allele, genetic improvement of host response to PRRSv infection is possible. Identification of other genomic regions associated with PRRSv response is underway. This work was supported by PRRS CAP, USDA ARS and NIFA Award 2008-55620-19132, NRSP-8 Swine Genome and Bioinformatics projects, National Pork Board and the breeding companies of the PRRS Host Genetics Consortium.

Key Words: genome-wide association study, PRRSv