Symposium: Recent Advances in Swine Genomics

689 Pigs, feed intake, and genes. J. P. Cassady*[1], S. Jiao[1], C. Maltecca[1], K. A. Gray[2], and J. W. Holl[1], *[1]North Carolina State University, Raleigh, [2]Smithfield Premium Genetics.*

The objective of this research was to develop genomic strategies for improving nutrient utilization by identifying genomic regions affecting feed intake, growth rate, and ultrasound traits in a Duroc terminal sire population. Individual feed intake, growth rate, and ultrasound data were available on 1022 Duroc boars. Boars were genotyped at GENESEEK using the Illumina Porcine SNP60 BeadChip. The criteria for screening the genomic data was a call rate per animal of 0.9, call rate per SNP marker of 0.9, Hardy Weinberg equation test with $P < 0.001$, and minor allele frequency >0.01. After editing, 40,008 SNPs were retained for genome wide association analysis. The Bayes B and C options in GenSel 4.0.1 were used with pen and contemporary group included as fixed effects for all traits. A preliminary analysis of average daily feed intake, intramuscular fat, and muscle depth was completed. Regions on chromosomes 1, 6, 9, 10, 12, 15, and X were identified affecting average daily feed intake, intramuscular fat, and muscle depth. Additional regions affecting average daily feed intake were found on chromosomes 3, 4, 5, 7, 8, 11, 13, and 17. The markers explained 16% of the total variance for average daily feed intake, 44% for intramuscular fat, and 49% for muscle depth. Analyses of ADG and feeding behavior are currently in progress. Markers identified on chromosome 1 effecting average daily feed intake were in the general region of MC4R. Several other markers were also located in regions where QTL have previously been reported. It was concluded that opportunities exist to use genomic markers to increase accuracy of selection in a Duroc terminal sire population.

Key Words: denomics, SNP, Duroc

690 A review of swine genome-wide association studies at USMARC. J. F. Schneider,* *USDA, ARS, USMARC, Clay Center, NE.*

Reproductive efficiency has a great effect on the economic success of pork production. Traits including age at puberty (AP), ovulation rate, number born alive (NBA), and average piglet birth weight (ABW) contribute greatly to reproductive efficiency. To better understand the underlying genetics of reproductive efficiency, a series of GWAS were undertaken. Samples of DNA were collected and tested using the Illumina PorcineSNP60 BeadChip (Illumina Inc., San Diego, CA). The first analysis included total number born (TNB), NBA, number born dead (NBD), number still born, mummies, litter birth weight (LBW), and ABW taken from 1,152 first parity females. Chromosome and position assignments were based on Build 10. A total of 41,151 SNP were tested using a Bayesian approach. Beginning with the first 5 SNP on SSC1 and ending with the last 5 SNP on the SSCX, SNP were assigned to groups of 5 consecutive SNP by chromosome-position order and analyzed again using a Bayesian approach. These selected 5-SNP non-overlapping groups were defined as QTL. Of the available 8,814 QTL, 124 were found to be statistically significant ($P < 0.01$). Multiple testing was considered using the probability of false positives. QTL were found for litter traits on SSC1, SSC4, SSC6, SSC10, SSC11, SSC13, SSC14, SSC15, and SSC17. QTL were found for LBW and ABW on all chromosomes except SSC16 and SSCX. Several candidate genes have been identified that overlap QTL locations among TNB, NBA, NBD, and ABW. A second analysis measured AP on 752 gilts that showed estrous before 230 d of age. Chromosome and position assignments were made based on Build 10.2. Seventy-two QTL were found to be statistically significant ($P < 0.01$) and were found on all chromosomes except SSC17. One hundred fifty-seven gilts that failed to reach puberty were added to the data set and the 909 gilts were analyzed as a binomial trait. A similar number of QTL were found on all chromosomes except SSC11, SSC16, and SSC18. The results of these analyses demonstrate that opportunities exist to introduce QTL into genetic improvement programs designed to improve reproductive efficiency. USDA is an equal opportunity provider and employer.

Key Words: Bayes, GWAS, reproduction

691 The genetic basis of host response to experimental infection with the PRRS virus in pigs. J. Dekkers*[1], N. Boddicker[1], E. Waide[1], J. K. Lunney[2], R. R. R. Rowland[3], D. J. Garrick[1], and J. Reecy[1], *[1]Iowa State University, Ames, [2]USDA, ARS, BARC, Beltsville, MD, [3]Kansas State University, Manhattan.*

Porcine reproductive and respiratory syndrome (PRRS) represents the most costly disease in the US pig industry. Caused by an RNA virus, vaccination strategies have generally been ineffective. Thus, to investigate opportunities for genetic improvement of pigs for increased resistance or tolerance to the PRRS virus, the PRRS Host Genetics Consortium (PHGC) was established. Among others, the PHGC involves experimental challenge of piglets provided by commercial breeding companies with a specific strain of the PRRS virus shortly after weaning, evaluating piglet response in terms of viremia and weight gain, genotyping each piglet with the Porcine 60K SNP panel, and conducting genome-wide association studies to identify genomic regions associated with host response. The purpose of this presentation will be to review results of the first 6 challenge trials of 200 piglets each, with specific reference to a major QTL identified on chromosome 4, and to discuss future plans and implications. This work is supported by the PRRS CAP, USDA NIFA Award 2008-55620-19132, the National Pork Board, USDA ARS and the NRSP-8 Swine Genome and Bioinformatics Coordination projects.

Key Words: porcine reproductive and respiratory syndrome (PRRS), genetic markers, swine