

ANIMAL SCIENCE

Title: Identification of markers associated with sow lifetime productivity for whole genomic selection - **NPB project #09-032**

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Scientific Abstract:

We performed genome wide association studies in a population resource well characterized to identify loci that influence traits such as growth, fatness, age at puberty, breeding performance, and sow lifetime productivity traits until completion of parity 4. Genotyping of 639 gilts of two maternal crossbreds that reached puberty was performed using the PorcineSNP60 BeadChip (Illumina) that contains assays for a total of 62,183 SNPs. Quality scores were assigned for each genotype obtained. A genotype quality score of 0.15 was used as a cutoff threshold for removing low quality genotypes. There were 57.8% of the samples with a call rate of at least 0.995. There were 58,982 SNPs with a call rate of at least 0.900. In this group of reliable marker assays there were 9,627 SNPs with a Minor Allelic Frequency (MAF) <0.05 , 6,450 SNPs with a MAF <0.01 and finally 4,147 SNPs completely fixed for one of the alleles.

The level of DNA degradation is influencing the fraction of SNPs successfully genotyped and the genotyping rate. The samples with no or low level of DNA degradation had a higher number of the SNPs genotyped ($>99.2\%$) compared to samples with advanced level of DNA degradation (87%). The number of discrepancies between called genotypes of the samples with absent and limited DNA degradation was extremely small ($<0.008\%$) compared to the samples with increased level of DNA degradation (0.1%).

A Bayesian analysis was conducted to estimate proportion of variance for each developmental, reproductive and lifetime trait accounted for by the SNPs from the PorcineSNP60 BeadChip. From all the reproductive traits, variation in the age at puberty was associated with the largest SNP effects. Clusters of SNPs associated with large effects on puberty onset were located on SSC 1 (21, 29, 88, 127 and 269 Mb regions), SSC2 (56 and 80 Mb), SSC4 (16 Mb), SSC10 (3Mb) and SSC14 (27 Mb). Lower marker effects were identified for litter size from parity 1 to parity 4 and for lifetime productive traits. Variation of sow lifetime productivity traits is potentially influenced by genes located on most swine chromosomes. Clusters of SNPs clearly associated with the largest effects on lifetime number of live-born piglets are located on SSC2, SSC8, SSC13, SSC16 and SSC17. Clear clusters of SNPs associated with lifetime number of weaned pigs are located on SSC1, SSC2, SSC3, SSC8, SSC9, SSC11, SSC12, SSC16 and SSC17. Common major loci that affect both lifetime number of live-born and weaned piglets are located on SSC1, SSC2, SSC16 and SSC17.

Combined association analysis of age at puberty and sow lifetime production traits revealed common regions/genes located on SSC1 (21, 29, 88, 127 Mb) that influence phenotypic variation of age at puberty and lifetime number of live-born and weaned piglets produced by sows. In addition,

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one of the clusters with the richest number of SNPs associated with the total number of live-born pigs and located on the distal end of SSC17 is influencing also litter size on parity 3.

Main clusters of SNPs associated with gilt weaning weights are located on proximal SSC8 and distal SSC11. Major loci influencing growth from weaning to the initiation of the treatment are located on SSC1, SSC2, SSC3, SSC4, SSC16 and SSC18. Growth during the developmental phase appeared to be influenced by major loci identified on most swine chromosomes. There are loci that potentially influence variation of growth during both developmental phases.

We are in process of assembling a panel of DNA markers associated with sow reproductive and productive longevity and identify procedures to apply the information in whole genome selection. The effects of the major markers will be validated in other commercial populations. We expect that our research will provide a panel of molecular markers that can be successfully used for reducing culling rates, sow death losses, and enhance the sow productive life.