RESEARCH ABSTRACT
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ANIMAL SCIENCE

Title: Identification of SNP Markers Associated with Number Born, Number Weaned and Weaning to Estrus Interval in Commercial First Parity Sows – **NPB #09-091**

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Scientific Abstract:

The objective of this research was to identify genetic markers that would be predictive of first parity reproductive performance and rebreeding in an effort to improve the percentage of gilts retained for breeding that actually contribute to the breeding herd. Three commercial cooperators were identified and biological samples for 706 boars used in the industry, along with the performance data from their daughter's first parity were acquired. Data from 123 boars used at USMARC were included. Phenotypic traits evaluated were number born alive, number born dead, total number born and weaning to estrus interval. Performance data analyzed were the average daughter deviations (daughter performance – contemporary group mean) for each boar. Boars were required to have a minimum of 4 daughter records for litter traits and 3 daughter records for weaning to estrus interval. DNA was extracted from each boar and genotypic data were collected using the recently developed Illumina Porcine 60K BeadChip. Genotypes were called for 59,895 single nucleotide polymorphism (SNP) markers spanning the entire porcine genome. Approximately 48 million genotypes were analyzed representing a 96.4% call rate. Association analyses were performed using PLINK to identify significant associations between SNP markers and performance traits. Only 3 SNP were significant using a Bonferroni adjusted threshold representing 2 different genomic regions on SSC 1 and 3, both for number born dead. Evaluation of all results significant at $P < 0.001$ in subsets of the data partitioned by breed revealed several locations that likely possess segregating quantitative trait loci (QTL). In total, 14 different genomic regions (including the two previously mentioned regions) were associated with a measure of reproductive performance. Two locations, presented as chromosome (SSC) and base position (in millions of bases, Mb), were associated with number born dead (SSC1:138.1 Mb and SSC3:57-60 Mb), nine locations were associated with number born alive (SSC1:177-182 Mb; SSC4:60-66 Mb; SSC4:93-101 Mb; SSC7:54-60 Mb; SSC7:116-120 Mb; SSC8:30.5-33.5 Mb; SSC8:109-115 Mb; SSC11:62-66 Mb and SSC15:54-62 Mb) and two locations were associated with weaning to estrus interval (SSC4:65-75 Mb and SSC14:8-12.5 Mb). None of the regions appeared to be associated with measures of growth rate or backfat depth in the USMARC composite population. The approach of using daughter deviations appears to be quite powerful and an economical approach to using the Illumina Porice 60K BeadChip. These results have the potential to improve first parity reproductive performance in commercial herds, but should be validated in other commercial pigs first.

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