RESEARCH ABSTRACT

ANIMAL SCIENCE

Title: Genome-wide association analyses of sow reproduction and lifetime productivity – **NPB #11-070** revised

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Scientific Abstract:

We performed genome wide association studies in a discovery population resource developed at UNL to identify loci that influence reproductive and lifetime productivity traits. Combined SNP effects explained 26% of phenotypic differences in age at puberty. The contribution of SNP variation to the phenotypic variance of the lifetime number of parities was 19% whereas the contribution to litter size traits (TNB and NBA) at first parity was very limited (5%). Of the traits recorded before breeding, only age at puberty significantly affected the probability that females would produce a first parity litter. The genetic variance explained by 1 Mb windows of the sow genome, compared across traits, uncovered regions that influence both age at puberty and lifetime number of parities. Allelic variants of SNPs located on SSC5 (27-28 Mb), SSC 8 (36-37 Mb) and SSC12 (1.2-2 Mb) exhibited additive effects and were associated with both early expression of puberty and a greater than average number of lifetime parities. Combined analysis of these SNPs showed that an increase in the number of favorable alleles had positive impact on reproductive longevity, increasing number of parities with up to 1.36. The region located on SSC5 harbors non-synonymous alleles in arginine vasopressin receptor 1A (AVPR1A) gene, a G-protein coupled receptor associated with social and reproductive behaviors in voles and humans and a candidate for the observed effects. This region is characterized by high levels of linkage disequilibrium in different lines and could be exploited in marker assisted selection programs across populations to increase sow reproductive longevity.

The litter size traits were the main reproductive traits present in both UNL and ISU data sets. Combined SNP effects of the merged UNL and ISU data sets explained a relatively low proportion of the phenotypic variation of the reproductive traits, varying across parities from 1.9 % for NBA at P1 to 21.3 % at P3. The contribution of SNP variation to the phenotypic variance of the lifetime productivity was minor (0.5 and 1 %). Genomic prediction values of reproductive traits explained an important proportion of the phenotypic differences when training and prediction was performed in the UNL data set but negligible for litter size traits when training was performed in the UNL set and genomic prediction was performed in the ISU data set.