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The roles of age at puberty and energy restriction in sow reproductive longevity: a genomic perspective

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that genetic variants explaining differences in age at puberty also explain differences in sow reproductive longevity was tested. Phenotypes, genotypes, and tissues from the UNL resource population ($n > 1700$) were used in genome-wide association analyses, genome, and RNA sequencing to uncover functional polymorphisms that could explain variation in puberty and reproductive longevity. A BeadArray including 56,424 SNP explained 25.2% of the phenotypic variation in age at puberty in a training set ($n = 820$). Evaluation of major windows and SNPs of subsequent batches of similar genetics ($n = 412$) showed that if all SNPs located in the major 1-Mb windows were tested, they explained a substantial amount of phenotypic variation (12.3 to 36.8%). Due to differences in linkage disequilibrium status, the most informative SNP from these windows explained a lower proportion of the variation (6.5 to 23.7%). To improve genomic predictive ability, the limited capability of BeadArray was enhanced by potential functional variants uncovered by genome sequencing of selected sires ($n = 20$; $>20\times$). There were 11.2 mil. SNPs and 2.9 mil. indels discovered across sires and reference genomes. The role of gene expression differences in explaining phenotypic variation in age at puberty was investigated by RNA sequencing of the hypothalamic arcuate nucleus (ARC) in gilts ($n = 37$) with different pubertal statuses. Seventy genes, including genes involved in reproductive processes, were differentially expressed between gilts with early and late puberty status ($P_{adj} < 0.1$). Dietary restriction of energy 3 mo before breeding delayed puberty by 7 d but improved the potential of a sow producing up to three parities ($P < 0.05$). Energy restriction was associated with differential expression in 42 genes in the ARC, including genes involved in energy metabolism. This integrated genomic information will be evaluated in commercial populations to improve the reproductive potential of sows through genomic selection. This project is supported by AFRI Competitive grant no. 2013-68004-20370 from the USDA-NIFA. USDA is an equal opportunity provider and employer.

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027 The roles of age at puberty and energy restriction in sow reproductive longevity: a genomic perspective. Hiruni R. Wijesena¹, Clay A. Lents², Melanie D. Trenhaile-Grannemann¹, Jean-Jack Riethoven¹, Brittney N. Keel², Jennifer F. Thorson², Phillip S. Miller¹, Rodger K. Johnson¹, Matthew L. Spangler¹, Stephen D. Kachman¹, and Daniel C. Ciobanu^{1*}, ¹University of Nebraska-Lincoln; ²USDA-ARS, U.S. Meat Animal Research Center, Clay Center, NE

Approximately 50% of sows are culled annually with more than one-third due to poor fertility. Our research demonstrated that age at puberty is an early pre-breeding indicator of reproductive longevity. Age at puberty can be measured early in life, has a moderate heritability, and is negatively correlated with lifetime number of parities. Detection of age at puberty is tedious and time consuming and is therefore not collected by the industry, which limits genetic progress. Genomic prediction is a viable approach to preselect gilts that will express puberty early and have superior reproductive longevity. The hypothesis