RESEARCH ABSTRACT
ANIMAL SCIENCE

Title: Genome-Wide Association Study for Sow Feed Efficiency and Reproduction and Genomic Selection using Low Density Panels – **NPB #11-056**

Investigator: Jack C. M. Dekkers jdekkers@iastate.edu

Institution Dept. Animal Science, Iowa State University

Co-Investigator: Max Rothschild mfrothsc@iastate.edu
Collaborators and students: Stoycho Mediev, Trakia University, Bulgaria
Zhiqiang Du, Iowa State University
Dinesh Moorkatttukarathekkoot, Iowa State University
Jennifer Young, Iowa State University

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Scientific Abstract
The objective of this study was to conduct a genome wide association study (GWAS) to identify SNPs / chromosomal regions associated with reproductive traits and sow lactation efficiency. The Illumina porcine 60k SNP chip was used to genotype 512 purebred Yorkshire sows from the ISU Residual Feed Intake (RFI) lines, which were divergently selected for high and low RFI during finishing. After quality control, 48,521 SNPs were used for analysis. The traits included the following in each of parity 1 and parity 2: total number farrowed (TNF), number born alive (NBA); total born (TB), number weaned by sow (NWBS), number weaned from sow (NWFS), total litter birth weight of all non-mummified piglets (LBW), average litter birth weight (ALBW), total birth weight of all pigs born alive (LPBW), average live piglet birth weight (ALPBW), total weaning weight of piglets nursed by sow (WWTBS), total weaning weight of piglets born to sow (WWTFS), average weaning weight of piglets born to sow (AWWTFS) in each of the first two parities, lactation feed intake (FI), RFI, estimated maintenance requirements (MR), energy balance (EB) and lactation efficiency (LE), along with sow body weight (BWW), fat mass (FMW), and protein mass (PMW) at the time of weaning. Lactation efficiency and energy utilization of sows and piglets was calculated based on on-farm measurements of sow body weight, back fat and loin muscle area before farrowing and at the time of weaning, sow feed intake during lactation, and piglets weights at birth, death and weaning. The GWAS was implemented separately for each trait using method Bayes B of GENSEL software. The present study is the first attempt to study the genetic architecture of lactation efficiency traits using a genome wide association analysis. We report the associations of informative QTL and the genes within the QTL for each trait in different parities. These results provide evidence of gene effects having temporal impacts on reproductive traits in different parities. Different QTL and genes have different impact on reproductive and feed efficiency traits in first and second parity. Some QTL identified in this study are new for pig reproductive traits. On first parity about 50% of genes located in the

identified important QTL regions were predicted to be involved in placental functions. The QTL containing a gene important for modulation of two very potent angiogenic factors responsible for blood flow, fetal growth, survival and neonatal weight (e.g. PPP3CA) was associated with TNF, TB, NWFS, LBW, ALBW, LPBW and ALPBW. The genomic regions containing genes important for maternal-fetus interface vascular development (e.g. RNU5A-1), implantation and angiogenesis (e.g. ARHGEF17), regulation of fat and energy metabolism and parallel contribution of normal reproduction (e.g. KLF17, UCP2/3, MRPL48, GLO1, MKK6) and role in embryogenesis (e.g. CXXC) were associated with LBW, ALBW, LPBW and ALPBW. The QTL containing gene related to cooper homeostasis and embryo development (e.g. SCO1) was associated with TNF, TB, NBA and NWFS.

On second parity genomic regions containing genes important for ovarian development, still births and low birth weight (e.g. ZCCHC7), optimal endometrium development (e.g. LRIG3), oocyte and embryo competence (e.g. TIGD1) and embryonic development (e.g. member of TCP-1 family) were associated with TNF, TB, NBA and NWFS. The QTL with genes related to placental function, early embryonic lethality (e.g FTL) and maternal stress and nursing behavior
(e.g NGF1A) were associated with litter weight traits at birth and at weaning.

For feed efficiency traits, the proportion of phenotypic variance explained by markers was 0.12 for LE, 0.28 for FI, 0.09 for RFI and EB, 0.49 for MR, 0.57 for BWW, 0.51 for FMW and 0.43 for PMW. These estimates were comparable to pedigree-based estimates of heritability. Although there were no regions that explained a large proportion of variance for LE or RFI, several informative regions were identified for traits such as PMW that are components of LE. The proportion of variance explained by the most important regions varied widely by trait. E.g., for PMW, six 1 Mb windows (86 SNPs) together explained ~20% of genetic variance and for MR seven windows (166 SNPs) explained ~ 12%. Across the genome, for all traits analyzed, more than 80 1 Mb windows explained at least 1% of the genetic variance. Some regions on SSC 8 and SSC18 were associated with multiple traits. Nearly all important regions differed between parties but were little affected by removing line as a fixed effect. Overall, this GWAS revealed several genomic locations and markers associated with sow reproduction and lactation feed efficiency and associated traits, which can provide a road map for future research and application. Further validation studies on large populations are warranted to improve our understanding of the complex genetic architecture for pig reproductive traits.