RESEARCHABSTRACT

ANIMAL SCIENCE

Title: Increased Accuracy of Selection for Nutrient Utilization in Duroc Pigs by Application of Genomic Tools – NPB #11-076

Revised

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Scientific Abstract

Efficiency of producing saleable products in the pork industry is largely determined by feed costs and by the amount and quality of lean meat produced. The objective of this study was to identify genomic regions associated with variation in feed efficiency and several related production traits in a Duroc terminal sire population. Traits studied were ADFI (Average daily feed intake), ADG (Average daily gain), FCR (Feed conversion ratio), RFI (Residual feed intake), ultrasound back fat (BF), muscle depth (MD), inner muscle fat (IMF), birth weight (BW) and weaning weight (WW). Individual feed intake and serial pig body weights were recorded using the FIRE system on 1047 individuals and edited by linear mixed model to adjust errors of individual visits to the feeders and subsequent body weight measures were estimated from both linear and robust regression. Heritabilities were 0.50 ± 0.102, 0.32 ± 0.096, 0.08 ± 0.057, 0.10 ± 0.054, 0.59 ± 0.086, 0.39 ± 0.087, 0.54 ± 0.011, 0.65 ± 0.10 and 0.64 ± 0.11 for ADG, ADFI, FCR, RFI, BF, MD, IMF, BW and WW estimated using animal model by ASReml3.0 and were used as prior for following analysis. All phenotypes were pre-adjusted for fixed effects using linear models before GWAS. Genotyping was performed using Illumina PorcineSNP60K BeadChip. After quality control 40,008 SNPs remained for analysis. Single trait association analyses were performed using a Bayes-B model. The proportion of phenotypic variance explained by markers was 0.182 for ADFI, 0.278 for ADG, 0.187 for FCR, 0.054 for RFI, 0.506 for BF, 0.348 for MD, 0.267 for IMF, 0.241 for BW and 0.370 for WW. Significant regions were identified by using three different significance tests; posterior windows variance, Bayes factor and bootstrapping. Significance was declared for regions where test's significance overlapped. Regions associated with ADFI were mapped to SSC 1 and 10; with ADG mapped to SSC 1, 4, 11, and 14; FCR on SSC 4, BF on SSC 1, 14 and 18, MD on SSC 13 and 23, WW on SSC 8, 16, 17 while no QTL were identified for RFI, IMF and BW. Genes associated traits within the informative QTL regions were annotated. In conclusion, we have identified several genomic regions associated with traits affecting nutrient utilization that could be considered for future genomic prediction to improve feed utilization.