

ANIMAL SCIENCE

Title: Large-Scale Association Analyses of Candidate Genes for Feed Efficiency Traits in Pig – NPB #08-011

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Scientific Abstract

Residual feed intake (RFI) measures how much feed an animal consumes compared to how much would be expected based on maintenance and growth requirements. Iowa State University developed two lines of Yorkshire pigs. The select line was selected for reduced RFI over 6 generations. A control line that originated from the same population was randomly selected for 5 generations prior to 1 additional generation of selection for increased RFI. A total of 730 animals (395 select, 335 control) were genotyped with the PorcineSNP60 BeadChip. After removing fixed markers and SNPs with call rates below 80%, a total of 55,533 SNPs remained for analyses with genomic positions based on the Sscrofa9 genome build. Genetic effects were fitted using a Bayesian model averaging approach (Bayes-C) that simultaneously fitted various combinations of 250-300 SNPs. Many SNPs were fitted more often than expected by chance, reflecting associations with the traits analyzed. For RFI, SNPs near *SLC5A12* on SSC2 and *SUCLG1* on SSC3 showed association, for example. Several SNPs near the *MC4R* gene on SSC1 showed some of the largest effects on both average daily feed intake (ADFI) and average daily gain (ADG), though other significant regions were also identified for both traits. An unmapped SNP had the largest SNP effect on 10th-rib backfat (BF), accounting for over 3% of the estimated genetic variance. Markers on chromosomes 13 and 15 had the largest effects on BF. More research needs to be done to validate the new significant regions, but results look promising based on the combination of previously identified genes and new candidate regions.

These research results were submitted in fulfillment of checkoff-funded research projects. This report is published directly as submitted by the project's principal investigator. This report has not been peer-reviewed.

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