Whole Genome Association Study for Lactation Feed Efficiency in Yorkshire Sows Selected for Residual Feed Intake during Finishing

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Summary and Implications

Sow feed intake and efficiency during lactation is an important component associated with sow productivity, longevity and efficiency, which are important traits for pork producers. The difficulty in collecting accurate phenotypes that are required to estimate lactation efficiency, and the high replacement rate of sows in the nucleus herds, highlight the importance of using genomic tools to examine the underlying genetics of these traits. The goal of this project was to conduct genome wide association studies of traits related to lactation efficiency on sows from the ISU RFI selection lines using the 60k SNP marker chip. More than 80 regions across the genome that explained at least 1% of the genetic variance of the traits under study were identified. These results can provide an effective resource to future research and application to marker assisted or genomic selection to improve sow productivity and efficiency.

Introduction

Over the past decades, the productivity of sows has increased substantially and this has resulted in higher energy requirements and greater mobilization of body reserves, leading to prolonged negative energy balance during lactation, which can negatively impact longevity and future production performance. To counteract this, feed intake of sows during lactation must be increased. However, as a result of selection for leaner pigs with improved feed conversion ratio during finishing, appetite and feed intake capacity of sows shows a declining trend. Thus, efforts are needed to increase feed efficiency during lactation, i.e. increase milk output per unit of energy obtained from feed and body reserves. Genetic improvement of sows for lactation efficiency is, however hampered by the need to collect accurate feed intake and body composition data during lactation. This limitation could be overcome if genetic markers associated with lactation efficiency could be identified. Thus the objective of this study was to conduct a genome wide association analysis to identify genetic markers or chromosomal regions associated with sow lactation feed efficiency.

Materials and Methods

Purebred Yorkshire sows from the Iowa State University (ISU) residual feed intake (RFI) lines, which were divergently selected for high and low RFI during finishing, were used for this study. A total of 512 sows from these lines were genotyped using Illumina porcine 60k SNP chip and after quality control, 48,521 genetic markers were used for analysis. The traits included in this study were feed intake during lactation, RFI during lactation, estimated maintenance requirements of the sow, energy balance, and lactation efficiency, along with sow body weight, fat mass, and protein mass at the time of weaning.

Lactation efficiency and energy utilization of sows and piglets were 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 piglet weights at birth, death and weaning. Prior to farrowing, the sows were fed with 2.8 kg /day and after farrowing they were fed twice a day to appetite.

The genome-wide association analysis was implemented separately for each trait using method Bayes B of the GenSel software developed at Iowa State University, with genetic variances and proportions of markers with non-zero effects estimated using Bayes C. The fixed effects of line (high and low RFI), generation (7 levels), and parity (2 levels) were included in the model.

Results and Discussion

The proportion of phenotypic variance explained by markers was 0.12 for lactation efficiency, 0.28 for feed intake, 0.09 for RFI and energy balance, 0.49 for maintenance requirements, 0.57 for body weight, 0.51 for fat mass and 0.43 for protein mass. These estimates were comparable to pedigree-based estimates of heritability. Although there were no regions that explained a large proportion of variance for lactation efficiency or for RFI, several informative regions were identified for traits such as protein mass that are components of lactation efficiency. The proportion of variance explained by the most important regions varied widely by trait. E.g., for protein mass, six 1 Mb windows (86 SNPs) together explained ~20% of genetic variance and for maintenance requirements, seven windows (166 SNPs) explained ~ 12%. Across the genome, for all traits analyzed, more than 80 1 Mb windows were identified that explained at least 1% of the genetic variance for one of

the traits studied. Some regions on chromosomes 8 and 18 were associated with multiple traits. Nearly all important regions differed between first and second parity but were little affected by removing line as a fixed effect. Overall, this study revealed several genomic locations and markers associated with sow lactation feed efficiency and associated traits, which can provide a road map for future research and application.

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