

Genome Wide Association Studies for Residual Feed Intake Traits in Pigs

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Suneel Onteru, Postdoctoral Research Associate;
Danielle Gorbach, Graduate Student; Jennifer Young,
Postdoctoral Research Associate; Dorian Garrick, Professor;
Jack Dekkers, Professor; Max Rothschild, Distinguished
Professor, Department of Animal Science

Summary and Implications

Residual feed intake (RFI), a measure of feed efficiency, is the difference between observed feed intake and the expected feed requirements computed based on growth and maintenance of the pig. Efficient animals with low RFI can be selected at an early age with genetic markers. Hence, the present study in 1400 pigs used several statistical methods to find the associations between more than 50,000 genetic markers and RFI, and its related traits such as average daily feed intake (ADFI), average daily gain (ADG), back fat (BF) and loin muscle area (LMA). Associations were observed for a combination of genetic markers on chromosomal regions containing insulin release genes (e.g., *GLPIR*, *CDKAL*, *SGMS1*) with RFI and ADFI, energy balance (e.g., *MC4R*, *PGMI*, *GPR81*) and muscle growth related genes (e.g., *TGFBI*) with ADG, fat related genes (e.g., *ACOXL*, *AEBPI*) with BF and skeletal muscle development genes (e.g., *KLHL31*) with LMA. Overall, these studies identified important chromosomal regions for further scrutiny to consider them for selection of pigs for RFI and its related traits.

Introduction

One of the measures for feed efficiency is residual feed intake (RFI), which is the difference between actual feed intake and the feed requirements predicted based on the animal's growth and maintenance. Efficient pigs have low RFI values with efficient feed utilization for profitable pig production systems. The feed requirement is generally predicted based on certain parameters called metabolic body weight, average daily gain (ADG) and back fat (BF). Several studies have supported that RFI is an important trait for selection of pigs to improve feed efficiency, along with selection for increased growth rate and reduced BF. Although RFI is an important trait, its measurement requires collection of average daily feed intake (ADFI), which is expensive and difficult. Hence, identification of genes or markers associated with RFI and its related traits will be useful in applying genetic marker based selection for feed efficiency at an early age with lower cost than can be achieved measuring ADFI. To understand the biological and genetic aspects of RFI, Iowa State University (ISU) has

been developing a resource population of pigs with high and low RFI genetic lines for over a decade.

Large-scale association studies called genome wide association studies are powerful approaches to identify the genetic markers associated with RFI and its related traits such as ADFI, ADG, BF and LMA. Using various statistical methods, these studies perform association analyses between more than 50,000 genetic markers spanned through out the pig genome and the traits to be studied.

Materials and Methods

A total of 1,433 animals from generations 0 to 8 of low and high RFI genetic lines were included in these studies. The low RFI line was developed for decreased RFI (increased efficiency) for all 8 generations. The high RFI line was randomly mated until generation 4 and was selected for increased RFI (decreased efficiency) starting in generation 5. The animals demonstrated a difference in RFI of 117 g/day between the two lines in generation 8. The RFI, ADFI, ADG, BF and LMA were measured with established methods.

The genetic material or chromosomal DNA was isolated from tail tissues of all pigs. DNA was sent to GeneSeek, Inc. (Lincoln, NE, USA) for analyzing each animal's DNA for the types of genetic markers called single nucleotide polymorphisms (SNP) by using Illumina (San Diego, CA, USA) PorcineSNP60 BeadChip. A total of 50,953 SNPs for each animal were considered in the association analyses after several quality control measures. Statistical approaches such as allele frequency differences at generation 8, and single and combined SNP association analyses were implemented with the PLINK and GenSel software.

Results and Discussion

Allele frequency differences at generation 8 identified that RFI selection lines likely differ in genes related to insulin and leptin regulation as well as metabolism in the liver and gastrointestinal tract. Single and combined SNP associations were observed on chromosomal regions containing insulin release genes (e.g., *GLPIR*, *CDKAL*, *SGMS1*) with RFI and ADFI, energy balance (e.g., *MC4R*, *PGMI*, *GPR81*) and muscle growth related genes (e.g., *TGFBI*) with ADG, and fat related genes (e.g., *ACOXL*, *AEBPI*) with BF and skeletal muscle development genes (e.g., *KLHL31*) with LMA.

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