

Diet by Genotype Interaction in Yorkshire Pigs Divergently Selected for Feed Efficiency

A.S. Leaflet R3184

Emily Mauch, Ph.D. Candidate;
Nick Serão, Assistant Professor, Department of Animal
Science, North Carolina State University;
Jennifer Young, Swine Research Technician, Department of
Animal Sciences, North Dakota State University;
John Patience, Professor;
Nicholas Gabler, Associate Professor;
Jack Dekkers, Professor

Summary and Implications

For ten generations, purebred Yorkshire pigs were divergently selected for increased and decreased feed efficiency based on residual feed intake when fed a standard corn and soybean-meal based diet. In this study, gilts and barrows born in generations 8, 9, and 10 were fed either a standard diet or an alternative diet that incorporated by-products while reducing corn and soybean-meal, resulting in a lower energy, higher fiber diet. Genotype by diet interactions were investigated by estimating heritabilities, genetic correlations, response to selection, and genome wide associations for six traits based on these two diets. Results indicate that feed efficiency is a genetically complex trait that appears to be genetically different depending on the diet fed. Thus, genetic gains made by selection on standard diets may not be fully expressed in swine production systems that use alternative diets, particularly those incorporating by-products.

Introduction

In all animal production, feed remains the primary input cost. In the U.S. swine industry, over 50% of production costs are attributed to feed (Giamalva, 2014). In addition, prices of the main feed ingredients, such as corn and soybean-meal, saw increases in the past ten years compared to historical pricing (USDA, Feed grains database, Accessed Dec. 9, 2016). With this in mind, the objective of this study was to investigate the impact of diet on genetic components of feed efficiency in pigs.

For ten generations, purebred Yorkshire pigs were divergently selected for increased and decreased feed efficiency, based on residual feed intake (RFI), when fed a diet comprised of 97% corn and soybean-meal (Standard diet). In generations 8, 9, and 10, gilts and barrows from this selection project were fed an alternative diet that replaced 47% of the corn and soybean-meal with by-products, specifically soybean hulls, wheat middlings, and corn bran (Challenge diet). Thus, two genetically distinct lines (Low and High RFI) were fed two distinct diets (Standard and

Challenge) with the aim of investigating the presence of an interaction between genotype and diet.

Materials and Methods

For ten generations, selection for high and low RFI based on estimated breeding values (EBV) occurred, resulting in two genetically divergent lines. During selection, a corn and soybean-meal (Standard) diet was fed to 1,978 pigs ($n_{\text{LowRFI}}=1,359$ and $n_{\text{HighRFI}}=619$). In parity two of generations 8, 9, and 10 and parity one of generation 10, gilts and barrows ($n=645$) of the Low and High RFI lines ($n_{\text{LowRFI}}=329$ and $n_{\text{HighRFI}}=316$) were fed either the Standard diet or the Challenge diet ($n_{\text{Standard}}=331$ and $n_{\text{Challenge}}=314$). Line by diet treatments were balanced for sex and littermates were split between diets and pens, as possible. All pigs were genotyped for genetic markers across the genome using the Illumina PorcineSNP60 Beadchip ($n_{\text{Standard}}=1,692$ and $n_{\text{Challenge}}=311$).

The Standard diet was formulated to represent a conventional diet fed in the U.S. and was high in energy and low in fiber content (2.42 Megacalorie (Mcal) net energy (NE) per kg feed; 9.4 % neutral detergent fiber (NDF)). The Challenge diet was formulated to represent an extreme example of how by-products might replace corn and soybean-meal ingredients in a U.S. swine diet, resulting in a diet with 18 % less energy and 175 % more fiber content than the Standard diet (1.99 Mcal NE/kg feed; 25.9 % NDF). The diets were balanced for lysine to metabolizable energy ratio at 2.9 g per Mcal, resulting in lower total lysine content for the Challenge diet compared to the Standard diet. However, all diets were formulated to meet or exceed NRC (1998) requirements.

During the grow-finish phase (~40 kg to 118 kg body weight), individual feed intake, body weight every two weeks, and end of test ultrasonic backfat depth (BF) and loin muscle area (LMA) were collected. Average daily feed intake (ADFI), average daily gain (ADG), feed conversion ratio (FCR), and RFI were calculated.

Bivariate animal models were implemented in ASREML (Gilmour, 2009) to estimate heritabilities, genetic correlations, and responses to selection for all phenotypic traits for both diets. Single-SNP genome wide association analyses for each trait within diet were conducted by fitting univariate animal models in ASREML (Gilmour, 2009). Genome wide association analyses for the Standard diet were conducted by Serão and others (2016).

Results and Discussion

For both diets, feed related traits (RFI, ADFI, FCR) were moderately heritable, ranging from 0.18 to 0.45, and growth related traits (ADG, BF, LMA) were moderate to

highly heritable, ranging from 0.39 to 0.59 (Table 1). The genetic correlations for a given trait when measured on the Standard versus the Challenge diet are reported in Table 1. Genetic correlations (r_g) were positive and ranged from 0.82 to 0.99. Growth related traits appeared to be genetically the same regardless of diet fed, while feed related traits appeared to be genetically different traits depending on the diet fed. Observed response to selection in RFI on the Challenge diet was 47% less than predicted based on $r_g=0.82$. Some genomic regions associated with BF, FCR, ADG, and ADFI overlapped between the Standard and Challenge diets. Associations were observed for BF and FCR on *Sus scrofa* chromosome 2 near IGF-2, FGF4, and olfactory receptor genes. An association for both ADG and ADFI was seen on chromosome 1 near the MC4R gene. No clear overlaps of association results were observed for RFI or LMA between the Standard and Challenge diets.

In conclusion, feed efficiency, measured as RFI, is a highly polygenic trait with many genes contributing small effects. Additionally, RFI appears to be a genetically different trait depending on the diet fed. This suggests a diet by genotype interaction, and, therefore, deviations from the diet fed during selection may result in weakened expression of genetic gains obtained under the selection diet. In practice, diet by genotype interactions may be less extreme than observed here due to the higher than normal by-product inclusion rates in the Challenge diet.

Acknowledgments

We gratefully acknowledge the work of the farm staff at the Lauren Christian Swine Research Center. This project was supported by AFRI-NIFA Grant #2011-68004-3033.

Table 1: Estimates of heritabilities, h^2 (standard error), for RFI and component traits on the Standard or Challenge diet, and of genetic correlations, r_g (standard error), between diets for each trait.

Diet	RFI, kg/d	ADFI, kg/d	FCR, kg/kg	ADG, kg/d	BF, mm	LMA, cm ²
h^2 Standard	0.24 (0.05)	0.41 (0.05)	0.26 (0.05)	0.39 (0.05)	0.59 (0.06)	0.52 (0.06)
h^2 Challenge	0.35 (0.17)	0.45 (0.14)	0.18 (0.15)	0.52 (0.17)	0.46 (0.20)	0.47 (0.22)
r_g	0.82 (0.28)	0.86 (0.17)	0.92 (0.45)	0.99 (0.18)	0.99 (0.22)	0.99(0.23)