Genetic and Phenotypic Correlations for Maternal and Post-weaning Traits from a Seedstock Swine Breeding System

A.S. Leaflet R2644

Caitlyn Abell, research assistant;
Kenneth Stalder, professor, Department of Animal Science;
John Mabry, professor, Department of Animal Science,
Iowa State University, Ames, IA

Summary and Implications

The purpose of this study was to determine the genetic and phenotypic correlations between maternal and post-weaning traits from a seedstock swine breeding system. The strongest phenotypic correlation was between percent lean and backfat at -0.72 (P<0.05). The genetic correlations between annualized farrowing interval and each of the post-weaning traits (BF, PCL, and D100) were 0.41, -0.53, and 0.49 (P<0.05), respectively. The correlations between annualized farrowing interval and post-weaning traits suggest that selecting based on annualized farrowing interval would negatively impact the post-weaning traits in the herd. The direction of the correlation between number born alive and post-weaning traits could not be concluded from this study.

Introduction

Determining the genetic correlations among traits can help breeders evaluate the expected affects on other economically important production traits that are not included in the selection criteria. This is particularly important when considering maternal and post-weaning traits because of the undesirable genetic correlations that typically exist between maternal and post-weaning traits. When selection is based solely on maternal traits, post-weaning traits often suffer. This makes it difficult to improve both traits simultaneously

Materials and Methods

Records on 7,015 sows born from 1992 to 2009 were obtained from a seedstock breeding stock organization. Sows were Landrace, Yorkshire, and F_1 crossbreds. The traits considered were number born alive (NBA), annualized farrowing interval (AFI), adjusted back fat (BF), percent lean (PCL), and days to 100 kg (D100). Post-weaning traits were measured on those gilts that could potentially be selected to enter the breeding herd. Post-weaning trait means were 60.4%, 9.9 mm, and 164 days for PCL, BF, D100, respectively. Maternal traits were measured on all sows in the breeding herd. Maternal trait means were 2.41 and 11.4 for AFI and NBA, respectively.

ASREML was used to calculate heritabilities for each of the traits in the study. A model for AFI included breed, parity, contemporary group (herd, year, and season of last parity), status of the sow (removed, gestating, lactating, or open) as fixed effects, age in days at first service as a quadratic covariate, and sire and dam as random effects. A model for NBA included breed, parity, contemporary group (herd, year, and month), status of the sow (removed, gestating, lactating, or open) as fixed effects, age in days at first service as a quadratic covariate, and sire and dam as random effects. The model for the post-weaning traits included breed as a fixed effect and sire and dam as random affects.

Results and Discussion

The heritabilities for the traits were 0.17 for NBA, 0.04 for AFI, 0.48 for BF, 0.56 for PCl, and 0.61 for D100. The strongest phenotypic correlation was between PCL and BF at -0.72 (P<0.05). The genetic correlations between AFI and each of the post-weaning traits (BF, PCL, and D100) were 0.41, -0.53, and 0.49 (P<0.05), respectively. Table 1 shows the heritabilities, genetic correlations, and phenotypic correlations for each of the traits in the study. The genetic correlations between NBA and the post-weaning traits were small and not directionally conclusive. These results suggest that selecting for a greater AFI may have an unfavorable result on economically important post-weaning production traits unless these genetic correlations were taken into consideration.

Table 1. Heretabilities, genetic correlations, and phenotypic correlations for number born alive (NBA), annualized farrowing interval (AFI), backfat (BF), percent lean (PCL), and days to 100 kg (DAYS100)[1]

	NBA	AFI	BF	PCL	DAYS100
NBA	0.17	0.11	-0.06	-0.03	0.01
AFI	0.04	0.04	0.41	-0.53	0.49
BF	-0.00	0.02	0.48	-0.81	-0.04
PCL	-0.01	-0.02	-0.72	0.56	-0.00
DAYS100	-0.05	0.03	-0.09	0.18	0.61

[1]Heritabilities are on the diagonal, genetic correlations are above the diagonal, and phenotypic correlations are below the diagonal.