RELATIONSHIPS BETWEEN GROWTH AND LITTER TRAITS IN PIG DAM LINES

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SUMMARY

Genetic relationships between growth traits and litter size were estimated in two dam lines from two farms. Analyses were by REML using a multiple trait animal model. Heritabilities of growth traits were moderate to high (.28 to .55) and h^2 of total number born was low (<.14) with repeatability near .20. Most genetic correlations between growth traits and total number born were small in magnitude (<.25) and were inconsistent between lines and farms. Average daily feed intake had the largest genetic correlations with total number born (-.25 to .20). Genetic correlations tended to be larger when only first parity litter records were included. If multiple trait evaluations are performed within each line and farm, accuracy of breeding values for number born may be increased by including growth traits. However, if average estimates are used, including growth traits would have little impact on the accuracy of evaluations for number born since average correlations are near zero.

INTRODUCTION

Multiple trait BLUP estimation of breeding values has become commonplace in many species of livestock. These analyses take into account correlations among the traits involved and thus require estimates of genotypic and environmental parameters. Multiple trait BLUP is becoming more widely used in swine evaluations for growth and carcass traits (e.g., growth rate, backfat, feed intake), and to a lesser extent litter traits (e.g., litter size, 21-day litter weight). Currently, Pig Improvement Company, Inc. (PIC) evaluates growth traits using a multiple trait evaluation and separately evaluates litter size using a single trait model. Estimated breeding values are then combined in an index using appropriate economic values. This method assumes that the genetic correlation between growth and litter traits is zero. No estimates are available in the literature where modern techniques have been employed to investigate these relationships in pigs (e.g., animal model, REML). Therefore, the objective of this study is to investigate genetic relationships between growth and litter traits in two dam lines using a multiple trait animal model.

MATERIALS AND METHODS

Data for this study were from two PIC dam lines (L02, L03) each at two different genetic nucleus (GN) farms located in the southern (DWR) and northern (MFR) U.S. L02 is a white line derived from a Landrace base and L03 is a white line derived from hyperprolific selection in a Large White population (Bichard and David, 1985; Legault, 1985). Growth traits were measured at completion of a 12-week test period at the GN farms between 1984 and 1993. Male pigs provided data for average test daily gain (ADG), ultrasonic P_2 backfat (BF), and average test daily feed intake (ADF). Data from female pigs were ADG, BF, and total number born (NB), which includes live piglets and stillborns. Females did not have individual feed intake records. In addition to litter data from the GN farms, litter data were also used from thirteen daughter nucleus farms. Up to three parities were included in the litter data.

All analyses were by Restricted Maximum Likelihood using bivariate animal models with full relationships. DFREML programs (Meyer, 1988, 1989; Boldman and VanVleck, 1991) were used to estimate (co)variance components. Each analysis contained one growth trait in addition to total number born. Different models were used for the two traits. For growth traits, fixed effects included week off-test, sex-regime (male or female, group or individual), a covariate for starting weight, and random effects of animal and error. Sex-regime was eliminated from analyses involving ADF since only individually tested males had observations for this trait. The repeatability model for total number born included fixed effects of farm-month-farrowed, and service type (natural or AI), a covariate for age at

farrowing, and random effects of animal, permanent environment, and error. Residual covariances between ADF and NB were fixed at zero since it was impossible for these two traits to be recorded on the same animal. Analyses were repeated using only first parity litter records with the above models except that the permanent environmental effect was removed.

RESULTS

Table 1 shows numbers of observations and averages for the traits considered in this study. A total of 83,383 records were used from 69,204 animals. Sixteen percent of animals had ADF information and 18.8 percent had litter records. Average number of litters per sow was 2.1.

Table 1. Number of observations, means and standard deviations for growth traits and total number born (values in parentheses include first parity only).

Trait[a]	Line	Farm	n	$\bar{X}$	SD
ADG (g/d)	L02	DWR	14,298	868.2	116.2
		MFR	16,825	838.9	105.4
	L03	DWR	18,887	838.0	113.3
		MFR	19,193	770.4	97.8
P_2 (mm)	L02	DWR	14,298	13.7	3.5
		MFR	16,825	11.6	3.5
	L03	DWR	18,887	14.7	3.1
		MFR	19,193	12.0	3.3
ADF (g/d)	L02	DWR	1,807	2170	284
		MFR	3,330	2310	288
	L03	DWR	2,768	2197	289
		MFR	3,106	2164	228
NB (pigs)	L02	DWR	4,345 (2,250)	10.1 (10.0)	3.0 (3.0)
		MFR	6,482 (3,110)	10.0 (10.0)	3.0 (2.8)
	L03	DWR	7,961 (3,727)	10.4 (10.1)	3.3 (3.2)
		MFR	8,430 (3,807)	10.8 (10.2)	3.1 (3.1)

[a]ADG = average daily gain, P_2 = ultrasonic backfat, ADF = average daily feed intake, NB = total number born.

Table 2 shows estimates of heritabilities (h^2), repeatability (R), genetic (r_g) and phenotypic (r_p) correlations between growth traits and total number born. Heritability and repeatability of NB are averages of the three pairwise analyses. In the multi-parous analyses, h^2 estimates were similar among lines and farms for ADG (.33 to .41) and P_2 backfat (.51 to .55). Heritabilities of ADF (.28 to .49) and NB (.08 to .14) were more variable than for ADG and P_2. Approximate standard errors were less than .003 for all h^2 estimates. Heritability estimates of growth traits from the single parity analyses were similar, if not identical to those from multiple litter analyses, as expected. Heritabilities of growth traits and number born are consistent with literature estimates (Lamberson, 1989; Stewart and Schinckel, 1989). Repeatability of number born ranged from .17 to .23 across farms and lines, but within a farm and line estimates of R were identical in each of the pairwise analyses.

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Table 2. Estimates of heritability (h^2), repeatability (R), genetic (r_g) and phenotypic (r_p) correlations for growth traits with total number born (values in parentheses include first parity only).

Line	Farm	Trait[a]	$h^{2 b}$	R	r_g with NB [b]	r_p with NB
L02	DWR	ADG	.33 (.33)	-	.04 (.08)	.08 (.07)
		P_2	.55 (.55)	-	-.12 (.03)	-.08 (-.06)
		ADF	.28 (.34)	-	.17 (.20)	.02 (.04)
		NB	.08 (.12)	.17	-	
L02	MFR	ADG	.37 (.37)	-	.23 (.19)	.06 (.06)
		P_2	.51 (.51)	-	-.03 (.07)	-.03 (-.03)
		ADF	.49 (.49)	-	-.12 (-.19)	-.02 (-.03)
		NB	.07 (.06)	.20	-	
L03	DWR	ADG	.41 (.42)	-	-.15 (-.08)	-.01 (.03)
		P_2	.52 (.52)	-	.06 (.11)	.02 (.02)
		ADF	.33 (.34)	-	-.02 (.20)	.00 (.03)
		NB	.14 (.06)	.23	-	
L03	MFR	ADG	.37 (.36)	-	.05 (.02)	.04 (.05)
		P_2	.52 (.52)	-	-.08 (-.10)	.01 (.00)
		ADF	.37 (.37)	-	-.22 (-.25)	-.03 (-.04)
		NB	.09 (.08)	.19	-	

[a] ADG = average daily gain, P_2 = ultrasonic backfat, ADF = average daily feed intake, NB = total number born.

[b] Standard errors of h^2 <.003 and standard errors of r_g <.03.

Genetic correlations between growth traits and number born were low in magnitude, ranging from -.22 to .23 for multi-parous analyses and -.25 to .20 for parity one analyses. Correlations were not consistent across lines or farms. For ADG, r_g was -.15 for L03 at DWR and .23 for L02 at MFR. For P_2, r_g was -.12 for L02 at DWR and .06 for L03 at DWR. For ADF, r_g was -.22 for L03 at MFR and .17 for L02 at DWR. Nonetheless, three out of the four analyses revealed positive genetic correlations between ADG and NB, while three out of the four estimates were negative for P_2 or ADF and NB. Estimates of genetic correlations were also not consistent within farm or line. Average daily feed best demonstrates this as L02 at DWR had a genetic correlation with NB of .17 and L02 at MFR had a genetic correlation with NB of -.12. At DWR, genetic correlations between all growth traits and number born differed in sign between L02 and L03. However, all genetic correlations with NB were similar in sign between L02 and L03 at MFR. Estimates of genetic correlations for L03 at DWR are similar to previous estimates from fewer data (E. Groeneveld, unpublished data). Approximate standard errors for genetic correlations were less than .03. Phenotypic correlations between growth traits and NB were all near zero (-.08 to .08).

Genetic correlations in the single parity analyses were similar to those from the multiple parity analyses. Almost all correlations had the same sign and similar magnitude to the multiple parity estimates. Exceptions were r_g between P_2 and NB in L02 at DWR (-.12 vs. .03) and MFR (-.03 vs. .07), and ADF and NB in L02 at MFR (-.12 vs. .19) and L03 at DWR (-.02 vs. .20). Most of the correlations were small in magnitude. Genetic correlations were more consistent across farms for L02 in the single parity analyses, although for L03 all correlations differed in sign. Phenotypic correlations were near zero for all single parity analyses (-.04 to .07).

DISCUSSION

Heritability estimates of growth traits were moderate to high, whereas h^2 of total number born

were low. Selection on growth traits could also affect response in litter size since many of the genetic correlations were non-zero. When averaged across lines and farms in the multiple parity analyses, genetic correlations with number pigs born were .04 for ADG, -.04 for P_2 backfat, and -.05 for ADF. Even though the magnitude of the correlations is small, the signs are favorable indicating that selection for increased gain, lower backfat, and lower feed intake could either have no effect or slightly improve litter size. Averaged across lines in the single parity analyses, the sign of the genetic correlations between P_2 (.03) and ADF (.09) with number born are slightly positive, however, indicating an adverse relationship.

Deciding which parameters to use in an across line and farm multiple trait genetic evaluation is difficult when estimates are inconsistent. If lines are evaluated separately, individual parameter estimates should be used. Since most of the individual estimates are in the favorable direction, assuming no genetic correlation would not be detrimental to the response in number born. One of the primary reasons for multiple trait analyses is to increase the accuracy of the evaluations, especially for traits with low heritability. However, when correlations among traits are low, multiple trait analyses will have little impact on the accuracy of breeding values for the lowly heritable traits. Therefore, if average parameters are used, including growth traits will not have a large impact on the accuracy of evaluations for number of pigs born.

Annual rates of genetic improvement over the last 10 years are shown in Table 3. Genetically, P_2 backfat has decreased nearly .6 mm/year, ADG has increased between 15 and 22 g/year, and ADF has remained essentially unchanged. While the growth traits have consistently improved, number born has also shown a small annual improvement over the same period. This favorable correlated response is indicative of the average genetic correlations between the growth traits and number born. Until 1990, breeding values used for selection were based on traditional selection index methods, and only for growth traits. Best Linear Unbiased Prediction (BLUP) was initiated in 1990 for growth traits and 1991 for number born. Selection in these lines now includes number born in addition to growth traits. It is unknown what affect selection on BLUP breeding values for both growth and litter traits will have on the relationships between them. When sufficient data from pigs selected on BLUP for growth and litter size are accumulated, these relationships will be reestimated to determine if genetic parameters assumed in the base populations have changed.

Table 3. Annual rates of genetic improvement for growth traits and number born.

Trait[a]	L02		L03	
	DWR	MFR	DWR	MFR
P_2 (mm)	-.6	-.6	-.6	-.6
ADG (g)	22	15	18	16
ADF (g)	13	-2	6	4
NB (pigs)	.01	.01	.01	.00

[a]ADG = average daily gain, P_2 = ultrasonic backfat, ADF = average daily feed intake, NB = total number born.

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