GENETIC PARAMETERS FOR PERFORMANCE TRAITS RECORDED IN BOARS AND GILTS

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SUMMARY

Genetic parameters were estimated for performance traits recorded in 3680 boars and 3893 gilts. Data included Large White and Landrace pigs. Both sexes were raised and performance recorded in the same commercial conditions using electronic feeders in group pens. Heritabilities did not differ between sexes for growth rate and feed intake. However, heritabilities and variance components were lower in boars than in gilts for feed conversion ratio and backfat. Lower means in these traits in boars than in gilts might explain differences in variances. Feed intake was more strongly genetically correlated with growth rate in boars than in gilts. Among the five analysed traits only growth rate during test had a genetic correlation significantly different from one indicating a genotype by sex interaction. Further analysis will evaluate possible genotype by sex by feeding regime interactions using multivariate analyses.

Keywords: Pigs, genetic parameters, performance traits, genotype by sex interaction

INTRODUCTION

Pig production aims at producing quality lean pork efficiently and consistently. Breeding programs have therefore focussed on genetic improvement of efficient lean meat growth and have made good progress overall. However, testing facilities are often limited and it is not possible to performance record all animals. Therefore, boars are performance recorded more often than gilts since more emphasis is being placed on correct selection for boars than on gilts. This selection procedure assumes that performance traits are genetically the same trait in both sexes and that genetic improvement achieved in boars will also be realised in gilts. It is well known that on the phenotypic level at least the sex of an animal influences its growth performance and body composition (van Lunen and Cole 1998). Consequently, a number of studies have estimated genetic parameters for traits recorded in each sex in order to determine possible genotype by sex interactions (for a discussion see Crump *et al.* 1997). However, environments and testing procedures often differed between sexes, and estimated genotype by sex interactions may actually have been genotype by environment interactions.

The aim of this study was to estimate genetic parameters for boars and gilts, both performance recorded in the same commercial environment using electronic feeders to examine genotype by sex interactions.

MATERIAL AND METHODS

Data were recorded at Bunge Meat Industries between February 1996 and October 1998. The project aimed for a balanced design between both sexes and two feeding regimes which was achieved given practical limitations (Table 1). This paper presents important performance traits which include growth rate before test (ADG1) and growth rate (ADG2), daily feed intake (FDINT) and feed conversion ratio (FCR) during test as well as backfat at the P2 site recorded with real time ultrasound on the live animal (LP2). For a description of these traits see Hermesch *et al* (1999). The data included 7,573 Large White and Landrace pigs from 187 sires and 2,545 dams. It was anticipated to have an equal number of boars and gilts from each sire and dam (Hermesch *et al.* 1999).

Table 1. Number of pigs within each sex by feeding regime group

Feeding regime	Boars	Gilts	Total
Ad libitum	2,187	1,763	3,950
Restricted	1,493	2,130	3,623
Total	3,680	3,893	7,573

Each week 60 to 90 animals grouped in two or three pens were performance recorded. Boars and gilts were kept in the same environment in order to avoid confounding of sex with other management factors. Pigs were fed either ad libitum or restricted and the level of restriction was slightly higher in gilts (Hermesch *et al.* 1999). However, the overall mean feed intake did not differ significantly between sexes. The fixed effect model for each trait was described in Hermesch *et al* (1999) and did not differ between sexes. Fixed effects included management group and breed. Weight of the animal at start and finish of test were fitted as linear covariables for feed conversion ratio and backfat. The computer package VCE4.25 (Groeneveld 1998) was used to obtain genetic parameters. Random effects analysed included additive genetic, litter and residual effects.

RESULTS AND DISCUSSION

Heritability estimates did not differ between boars and gilts for both growth rate traits and feed intake (Table 2). However, heritabilities and variance components were lower in boars than in gilts for feed conversion ratio and backfat. Lower variance components may be related to lower means in both traits in boars. Heritabilities differed between sexes and between management groups within sexes in the study by Crump *et al* (1997). However, these differences were not consistent and may in large part reflect sampling effects (Crump *et al.* 1997).

Correlations. Genetic and environmental correlations between performance traits within each sex are presented in Table 3. In both sexes, growth rate before and within test are lowly correlated (rg: 0.38) which indicates that growth at an earlier weight is genetically a different trait than growth rate during the later growth stage. A similar genetic correlation was found by Hermesch (1996) between these two traits for boars single penned during test.

Genetic correlations between feed intake and growth rate traits were lower in gilts than in boars. Furthermore, feed intake had a higher genetic correlation with feed conversion ratio in gilts (rg: 0.39) than in boars (rg: 0.08). It is well known that boars and gilts have physiological differences which influence growth performance and body composition (van Lunen and Cole 1998). However, genetic correlations between sexes for the same performance trait are required in order to investigate genotype by sex interactions (Table 4).

Table 2. Proportion of variation explained by fixed effect model (R2), estimates of heritabilities (h2) and litter effects (c2), both with standard errors (s.e.) and variance components, for performance traits in boars and gilts

Trait	R^2	h^2	s.e. h^2	c^2	s.e. c^2	σ^2_a *	σ^2_c	σ^2_e
Boars								
ADG1	0.14	0.23	0.03	0.11	0.02	661	301	18,87
ADG2	0.27	0.14	0.02			2,397		15,361
FDINT	0.41	0.20	0.03			0.014		0.056
FCR	0.31	0.07	0.02			0.014		0.183
LP2	0.34	0.42	0.03	0.07	0.02	2.18	0.36	2.61
Gilts								
ADG1	0.21	0.20	0.03	0.20	0.02	546	544	1,620
ADG2	0.35	0.12	0.02			1,632		11,393
FDINT	0.47	0.21	0.03			0.012		0.045
FCR	0.42	0.16	0.03			0.034		0.185
LP2	0.37	0.54	0.03			3.57		3.03

* σ^2_a : additive genetic variance, σ^2_c : variance due to litter effect, σ^2_e : environmental variance

Table 3. Genetic correlations (first row) and environmental correlations (second row) with standard errors (in brackets) between performance traits recorded in boars (below diagonal) and gilts (above diagonal)

	ADG1		ADG2		FDINT		FCR		LP2	
ADG1			0.38	(0.10)	0.10	(0.10)	-0.40	(0.10)	0.19	(0.07)
			-0.13	(0.02)	0.00	(0.03)	0.04	(0.03)	0.17	(0.03)
ADG2	0.38	(0.09)			0.41	(0.09)	-0.68	(0.06)	-0.14	(0.08)
	-0.03	(0.02)			0.47	(0.02)	-0.77	(0.00)	-0.07	(0.02)
FDINT	0.37	(0.09)	0.74	(0.06)			0.39	(0.10)	0.43	(0.07)
	0.07	(0.03)	0.49	(0.01)			0.12	(0.02)	0.12	(0.03)
FCR	-0.48	(0.11)	-0.61	(0.09)	0.08	(0.12)			0.50	(0.08)
	-0.13	(0.03)	-0.76	(0.01)	0.13	(0.02)			0.14	(0.03)
LP2	-0.17	(0.08)	0.04	(0.08)	0.44	(0.07)	0.49	(0.10)		
	0.03	(0.13)	0.04	(0.03)	0.22	(0.03)	0.14	(0.02)		

Among the five traits analysed only growth rate during test had a genetic correlation significantly different from one (rg: 0.77, Table 4). The significance of this difference was additionally tested with a log likelihood ratio test (Meyer 1993) This might reflect differences in potential lean meat growth between boars and gilts, in particular during the later growth stage when animals reach puberty. However, in general the results agree with Crump *et al* (1997) who also found little evidence for genotype by sex interactions in the same traits analysed in this study when tested in the same environment.

Table 4. Genetic correlations with standard errors (in brackets) for performance traits between sexes

	G_ADG1		G_ADG2		G_FDINT		G_FCR		G_LP2	
B_ADG1	0.92	(0.05)	0.40	(0.10)	0.18	(0.09)	-0.39	(0.10)	0.07	(0.08)
B_ADG2	0.07	(0.09)	0.77	(0.08)	0.63	(0.08)	-0.43	(0.10)	-0.04	(0.08)
B_FDINT	-0.08	(0.10)	0.30	(0.10)	0.95	(0.04)	0.36	(0.09)	0.37	(0.07)
B_FCR	-0.01	(0.12)	-0.78	(0.10)	0.31	(0.12)	0.96	(0.07)	0.50	(0.10)
B_LP2	-0.19	(0.06)	-0.27	(0.09)	0.38	(0.07)	0.70	(0.07)	0.94	(0.04)

* G_trait_name: performance trait recorded in gilts; B_trait_name: performance trait recorded in boars

CONCLUSIONS

Genetic parameters were obtained for performance traits recorded in boars and gilts. Both sexes were raised under the same conditions which allowed estimation of genotype by sex interactions. Heritabilities and variance components were higher in gilts for feed conversion ratio and backfat. Genetic correlations between feed intake and growth rate traits were lower in gilts than in boars. Only growth rate during test at a later age had a genetic correlation between sexes of less than unity. All other traits showed little evidence for genotype by sex interactions. Within this study, boars and gilts were pooled over two feeding regimes, *ad libitum* and restricted feeding. Further analysis will evaluate possible genotype by sex by feeding regime interactions using multivariate analyses.

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