Genetic parameters and predicted response to selection for lean growth in an Australian commercial nucleus pig herd

Nguyen Hong Nguyen [A], *Cam P. McPhee* [B], *Claire M. Wade* [A], *and Brian G. Luxford* [C]

[A] The School of Veterinary Science and Animal Production,
The University of Queensland, Qld 4072, Australia.
[B] Animal Research Institute, Queensland Department of Primary Industries,
Locked Mail Bag No. 4, Moorooka, Qld 4105, Australia.
[C] Bunge Meat Industries, PO Box 78, Corowa, NSW 2646, Australia.

Abstract.   Genetic parameters for performance traits in a pig population were estimated using a multi-trait derivative-free REML algorithm. The 2590 total data included 922 restrictively fed male and 1668 *ad libitum* fed female records. Estimates of heritability (standard error in parentheses) were 0.25 (0.03), 0.15 (0.03), and 0.30 (0.05) for lifetime daily gain, test daily gain, and P2-fat depth in males, respectively; and 0.27 (0.04) and 0.38 (0.05) for average daily gain and P2-fat depth in females, respectively. The genetic correlation between P2-fat depth and test daily gain in males was –0.17 (0.06) and between P2-fat and lifetime average daily gain in females 0.44 (0.09). Genetic correlations between sexes were 0.71 (0.11) for average daily gain and –0.30 (0.10) for P2-fat depth. Genetic response per standard deviation of selection on an index combining all traits was predicted at $AU120 per sow per year. Responses in daily gain and backfat were expected to be higher when using only male selection than when using only female selection. Selection for growth rate in males will improve growth rate and carcass leanness simultaneously.

Additional keywords: restricted feeding, *ad libitum*, selection response.

Introduction

Separation of that part of the pig population used in genetic improvement programs from that part used in the production of slaughter stock is becoming more widespread. This is exemplified by multi-national breeding companies with breeding nucleus herds in temperate Western countries supplying production stock to tropical Asian countries. In this case, interaction between genotype and environment could prevent genetic gains in the breeding nucleus being fully realised by the slaughter generation. One component of the environment that can vary between breeding and production sectors is the level of feeding. Responses in growth to selection for efficient lean growth on *ad libitum* feeding have been associated with increases in food intake (Woltmann *et al.* 1992). Selection for lean growth rate on restricted feeding has been found to emphasise increased food efficiency (McPhee *et al.* 1988). A number of selection experiments in pigs (McPhee *et al.* 1988; Cameron and Curran 1995) demonstrated that greater response in lean content was obtained from selection under restricted feeding than from similar programs under *ad libitum* feeding. Such a selection scheme is preferable for a long-term genetic improvement strategy where progeny are expected to be reared under commercial feeding regimes (Cameron 1998).

Interaction between genotype and environment on pig performance has been attributed to sire effects (Merks 1988). It is important to select potential replacement boars accurately in nucleus herds because of their significant contribution to genetic improvement in the next generation. Often candidate boars for breeding are individually penned and on restricted feeding and gilts group-housed and fed *ad libitum*. Differences in testing environments between boars and gilts necessitate the separate estimation of genetic parameters for each sex.

The present study aims to estimate genetic parameters of performance traits for restrictively fed males and *ad libitum* fed females, and to predict response to selection based on indexes combining the performance traits.

Materials and methods

Animals and data structure

Analysis was performed on 2590 performance data from pigs of Bunge Meat Industries (Table 1). The breeding herd consisted mainly of terminal sire lines synthesised from several breeds (Large White, Duroc, and Hampshire) which were generally free of, or had a low incidence of, the halothane gene. Mating, replacement, and culling procedures were practiced as in commercial production.

Table 1. Number of sires and dams in each data file

	Male data	Female data
No. of records	922	1668
Sires	55	49
Dams	378	472
No. of common sires	26	
No. of common dams	246	

Performance test

Pigs were performance tested over a period of 6 weeks for males and from birth to finishing for females during test. Males were individually penned, and restrictively fed approximately 85% of *ad libitum* intake (CV = 6.8%) after reaching 70 kg. The daily food allowance for males for Weeks 1–6 was 1.8, 1.9, 2.0, 2.3, 2.5, and 2.7 kg, respectively. Females were performance tested on *ad libitum* feeding in groups comprising 40 individuals to an average weight of 89 kg. Animals were offered a standard grower diet with dietary protein of 146 g/kg, digestible energy of 14 MJ DE/kg, and lysine of 0.55 g/MJ DE. Average lifetime daily gain, daily liveweight gain on test, P2 fat, and food conversion ratio were measured in males. In females, average lifetime daily gain (FADG) from birth to finishing and P2 fat (FFT) were recorded. For males, test daily gain (MTDG) was calculated by the ratio of finishing weight minus starting weight to days on test. P2 fat (MFT) was ultrasonically measured at the end of test.

Analyses

Additive genetic and environmental variance and covariance components for performance traits were estimated using a restricted maximum likelihood procedure (REML) applied using the multi-trait derivative-free REML algorithm to allow simultaneous estimation of multiple random effects (ASREML) (Gilmour *et al.* 1999).

Preliminary analyses for variance of growth rate and fat were carried out using the Mixed Model Least Square and Maximum Likelihood Computer Program (LSMLMW) (Harvey 1987) to determine the significance of fixed effects.

The same model was used for the REML analysis. The random effect for each trait was the additive genetic effect of each animal. Fixed effects were pen (9 classes) and month × year. The REML analysis of bivariate models (Juga and Thompson 1990) was applied to estimate genetic correlations between homologous traits measured in the two sexes, with sex also included as fixed effect. Final weight was fitted as linear covariate for P2-fat depth.

Response prediction

The breeding objective was to increase profit, as determined by growth rate and P2-fat depth under an *ad libitum* feeding regime. The selection criteria were growth rate and backfat measured under restricted feeding for males and *ad libitum* feeding for females and combined into a linear selection index. The indexes were constructed in the traditional way according to Cunningham (1972). Economic values are derived from a bioeconomic model of a typical Australian pig herd defined by statistics given in the annual Australian Pig Industry Handbook. The same economic values are used in the National Pig Improvement Program (Macbeth 1999). Profit is the difference between maximum possible returns and the variable costs per sow per year. Returns are obtained from the sale of growers and culled breeders. Grower price depends on slaughter weight, dressing percentage, and carcass grade. Culled breeders are priced on slaughter weight and dressing percentage. Costs are mainly incurred in feed, and the cost of breeding stock replacement. An increase in average daily gain of 0.1 kg was expected to increase profit by \$AU441 per sow per year. A reduction in P2 fat by 1 mm was expected to gain \$31 per sow per year.

Results

Estimates of genetic parameters

Heritability estimates, and phenotypic and genetic correlations, are shown in Table 2. Heritabilities for lifetime daily gain and P2-fat depth were similar in males and females. In males, the genetic and phenotypic correlations between male average daily gain (MADG) and MTDG with MFT were negative. In females, FADG was positively correlated with FFT at both the genetic and phenotypic levels. The genetic correlations between daily gain and P2-fat depth between the sexes were low. In males the heritability estimate of 0.16 obtained for food conversion ratio (MFCR) was similar to that of MTDG. Both the genetic and phenotypic correlations of MTDG with MFCR were close to –1, and these coefficients between MFT and MFCR were positive (i.e. favourable).

Table 2. Heritability (on the diagonal), and phenotypic and genetic correlations (above and below diagonal, respectively)

MADG, average daily gain (male); MTDG, test daily gain (male); MFT, P2-fat depth (male); MFCR, food conversion ratio (male); FADG, average daily *lifetime* gain (female); FFT, P2-fat (female). Standard errors in parentheses

Traits	Males				Females	
	MADG	MTDG	MFT	MFCR	FADG	FFT
MADG	**0.25** (0.03)	0.27 (0.03)	0.16 (0.05)	–0.15 (0.03)		
MTDG	0.02 (0.00)	**0.15** (0.03)	–0.09 (0.04)	–0.98 (0.03)		
MFT	–0.06 (0.01)	–0.17 (0.06)	**0.30** (0.05)	0.12 (0.04)		
MFCR	0.26 (0.09)	–0.94 (0.05)	0.78 (0.23)	**0.16** (0.03)		
FADG	0.71 (0.11)	0.11 (0.07)	0.05 (0.07)		**0.27** (0.04)	0.42 (0.02)
FFT	0.21 (0.15)	0.08 (0.01)	–0.30 (0.11)		0.44 (0.09)	**0.38** (0.05)

Table 3. Predicted response to selection per standard deviation of indexes combing all traits or pairs of traits in males and females
R_{IG}, correlation of index and aggregate genotype; σ_I, standard deviation of index

Gain/trait	All traits	Males	Females
MTDG (kg)	0.154	0.018	—
MFT (mm)	–0.030	–0.337	—
FADG (kg)	0.121	-	0.164
FFT (mm)	0.085	-	0.095
R_{IG}	0.46	0.42	0.50
σ_I	119.85	90.38	69.70

Predicted response to selection indexes

Selection indexes were constructed using all traits in both sexes or pairs of traits measured in either males or females. Changes in these traits with improvement in 1 unit of these indexes are given in Table 3.

The change in daily gain and backfat produced from 1 standard deviation change of selection index ranged from 0.018 to 0.164 kg and from –0.337 to 0.095 mm, respectively. A 1 standard deviation change in index value combining all traits was expected to result in an economic change of $120 per sow per year. Using all male traits predicted a genetic gain of $90.38 per sow per year, whereas all female traits gave a genetic gain of $69.70 per sow per year. The male selection index reduced fat, reflecting the negative genetic correlation between fat and gain in that sex.

Discussion

Heritability estimates obtained for performance traits in the present study fell within the normal range of the values reported in the literature, although admittedly the normal range is expansive: 0.03–0.5 for daily gain, 0.12–0.74 for backfat, and 0.12–0.58 for food conversion ratio (Clutter and Brascamp 1998). The current heritability estimate for MTDG was relatively low. Two reasons have been proposed for this. Firstly, since the final weight of some males was as high as 120 kg, some may have suffered growth disturbance associated with the attainment of puberty. Secondly, the growth period for the male test was much shorter than the whole of the life test used to estimate ADG in females. Moreover, the variation in food intake was relatively large for boars: CV = 6.8% compared with only 0.02% observed by McPhee *et al.* (1988). The heritability of FCR is similarly low, but this was to be expected as a result of there being a low phenotypic variation in food intake.

Although these results are lower than earlier estimates reported in studies involving experimental populations, they are in good agreement with recent reports obtained from field data. Investigating 3 New Zealand nucleus herds of Large White, Landrace, and Duroc, Skorupski *et al.* (1996) indicated that heritabilities for ADG ranged from 0.16 to 0.20. The estimates obtained by Crump *et al.* (1997) varied from 0.05 to 0.23 in males and from 0.10 to 0.27 in females

with univariate analysis, and when bivariate analysis was applied between sexes they ranged from 0.07 to 0.20.

Growth rate has been found to be strongly associated with food intake (Whittemore 1986). Restriction of feeding aims to eliminate genetic variation in growth associated with variation in intake and to expose variation caused by more efficient feed utilisation, such as that favouring lean tissue deposition over the deposition of fat. By removing one aspect of variation (variation in feed intake), restricted feeding is also expected to result in lower heritabilties for performance traits than *ad libitum* feeding (Cameron *et al.* 1988).

Genetic parameter estimates reported in the literature from selection experiments under restricted feeding do not agree well with those reported in the current study. In an analysis of performance traits from 1725 *ad libitum* fed boars and 3802 restrictively fed gilts, Cameron *et al.* (1990) obtained similar heritabilities, and genetic and phenotypic correlations between feeding regimes. In selection experiments based on the index of daily gain, backfat thickness, and eye muscle area for boars on restricted feeding and gilts on full feeding, Suzuki *et al.* (1998) fed pigs 82.1% of full feeding in the period of 30–70 kg and approximately to *ad libitum* from 70 to 90 kg and reported that heritability estimates for all observed performance traits were higher on *ad libitum* than on restricted feeding. It is difficult to define causes of this contradiction, however, due to differences in levels and stages of restriction among studies. Males in the present study were restrictively fed to 85% of *ad libitum* food intake over 6 weeks. They started testing at an average body weight of 70 kg when there may be a preference for fat deposition rather than muscle growth. Levels of restricted food intake were scaled, based on the time on test, in the study of Cameron *et al.* (1990).

In general, genetic and phenotypic correlations between growth and backfat are positive, that is, unfavourable under *ad libitum* feeding but negative or close to zero under restricted feeding. The genetic correlation of MTDG and MFT in the currently reported study is small and negative (–0.17) as may be expected under restricted feeding. A number of selection experiments have indicated greater correlated response in lean growth rate and carcass lean content under restricted feeding than under *ad libitum* feeding (Fowler and Ensminger 1960; McPhee *et al.* 1988). This implied that selection with a constraint on the amount of feeding would exploit genetic variances in partitioning of energy toward lean growth and away from fat deposition (McPhee *et al.* 1988). This was because the latter tissue deposition required higher energy cost than the former (Webster 1977).

Genetic and phenotypic correlations of FCR with daily gain and P2-fat depth from this study agreed well with results reported in the literature, indicating that selection for lean growth rate, or joint selection for increased lean growth and

reduced backfat, would achieve correlated improvement in food efficiency. However, genetic improvement in food efficiency seems to be becoming more difficult than in the past because a long history of selection for increased efficiency of lean production has been associated with a significant reduction in backfat, and satisfactory fat levels are being reached. In the meantime, direct selection for FCR has not been found to be effective.

The effect of genotype × environment (G×E) interactions in pig breeding programs may be interpreted by a genetic correlation between homologous traits measured in 2 environments. Genetic correlation estimates obtained between sexes were 0.71 for average daily gain and –0.30 for P2-fat depth. This may indicate the existence of an interaction between genotype and feeding regimes for both traits, but this is confounded with sexes. The pooled estimate for genetic correlation between the rate of gain on 2 different planes of nutrition was 0.70 (Fowler and Ensminger 1960). The corresponding value of 0.65 was obtained in the study of Suzuki *et al.* (1998). Both authors definitely concluded that G×E interaction was present for daily gain. Nevertheless, Cameron *et al.* (1988) did not detect interactions between sires and feeding regimes for ADG, BF, and FCR in either Large White or Landrace, although genetic correlation of FCR between 2 feeding regimes was estimated to be 0.42. In another study, Cameron (1993) reported genetic correlations between *ad libitum* and restricted feeding regime that ranged from 0.29 to 0.92 across traits, and concluded that G × E interaction only occurred for growth rate.

Selection for efficient lean growth under restricted feeding resulted in greater economic return than selection under *ad libitum*. Progress per generation of selection was predicted at $90.39 per sow per year in restrictively fed males in comparison with only $69.70 per sow per year in *ad libitum* fed females. Using genetic estimates from central testing station data where pigs were restrictively fed and on-farm data where *ad libitum* feeding regime was applied, McPhee (1995) showed advantages of restricted feeding performance testing over *ad libitum* testing for identifying breeding stock, which will transmit superiority in efficiency of lean growth to their progeny. Estimates of progress per generation of selection were $77/sow.year with restricted feeding in comparison with only $61/sow.year with *ad libitum* testing. But once again, level of test feeding was confounded with farm *v.* station test environments.

Conclusion

The heritability estimates for performance traits obtained from the study ranged from low to moderate. Genetic relationships of daily gain with P2-fat depth were unfavourable in *ad libitum* fed females and favourable in restrictively fed males. Low genetic correlations of daily gain and backfat between the sexes may suggest the evidence of G × E interaction. The contribution of male selection on restricted

feeding to genetic gain was likely to be greater than the female contribution selected on *ad libitum* feeding for the same selection intensity.

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