EVALUATION OF PIG FLIGHT TIME, AVERAGE DAILY GAIN AND BACKFAT USING RANDOM EFFECT MODELS INCLUDING GROWER GROUP

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SUMMARY

Records for flight time, average daily gain and backfat were analysed from 9,638 pigs measured between April 2004 and November 2007. Genetic parameters were estimated for the three traits using alternative animal models, fitting combinations of additive genetic, common litter and grower group effects fitted as random terms. Log likelihood ratio tests showed that all three random effects were significant for the three traits analysed. Heritability estimates were 0.15±0.02 for flight time, 0.22±0.03 for average daily gain and 0.40±0.04 for backfat. Estimates for common litter (c^2) and grower group (g^2) effects were small (0.02 to 0.05) for flight time and backfat. Conversely, for growth rate estimates of c^2 and g^2 were 0.08±0.01 and 0.17±0.01, respectively. It is recommended that grower group be recorded for further investigations of social genetic effects. Flight time was genetically correlated with backfat (0.21±0.09) but had no significant genetic relationship with growth rate (0.14±0.11). Overall, little correlated response is expected in flight time resulting from selection for higher growth and lower backfat.

INTRODUCTION

Flight time, an objective measure of temperament has been analysed and found heritable in pigs (Hansson *et al.* 2005). It is likely that selection for calmer pigs should be beneficial to animal welfare and possibly also ease stock handling, lowering occupational health and safety risks. In addition, reducing pig stress levels could be beneficial to pork quality by reducing the incidence of pale soft exudative and dark firm dry pork (Guardia *et al.* 2005).

It is likely that the temperament of an individual pig influences the performance of other pigs housed in the same group. In one pig population Bergsma *et al.* (2008) found that social effects contributed the vast majority of heritable variance for growth rate and feed intake. Bergsma *et al.* (2008) used the variance of true breeding values (TBVs) among individuals as the definition of heritable variance. Bijma *et al.* (2007) defined TBVs as the sum of an individual's direct additive variance and n-1 times (n=the number of animals within the group) the individuals social additive variance. Fitting group as an additional random effect without fitting social genetic effects explicitly accounts for heritable and environmental social effects (Bijma, pers. comm.). It was the aim of this study primarily to evaluate various random effect models for flight time, average daily gain and backfat and secondly to estimate genetic correlations between flight time and growth rate or backfat.

MATERIALS AND METHODS

Data from Belmont, a farrow to finish commercial piggery located in Queensland, Australia, were recorded between April 2004 and November 2007 on three purebred breeds of grower pigs (6,072 Large White, 2,795 Landrace, 771 Duroc). Pigs were recorded for backfat (**BF**) at the P2 site using ultrasound, average daily gain (**ADG**) and flight time (**FT**) at 103 (±9.4) kg liveweight (Table 1). In pigs, flight time is the time taken to clear a one metre distance between light sensitive start and stop diodes set 0.25 and 1.25 meters from a weigh scale exit (Crump *et al.* 2005). Pigs were also scored from one to five (by six staff) for the assistance required to move them past the

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stop diode. Pigs were housed in one shed and grown in one of 16, 8m by 3m pens. Pens one to eight predominantly housed boars and were fed a higher energy diet (14.5-14.7 MJ DE/kg) than pigs in the other pens (14.0-14.2 MJ DE/kg) which predominantly housed gilts. Animals in the same pen did not always complete their testing at the same time. Grower groups (n=353) were constructed from the date of test (n=128) with animals tested from the same pen within a 15 day period combined into single grower groups. Post editing grower group size ranged from 22 to 37 pigs which were confirmed to match farm group sizes. These data were merged with 35,582 pedigree records extending to January 1995.

Table 1. Characteristics of data including coefficients of variation (CV).

Trait	N	Means	Standard deviations	Min-Max	CV
Flight time (s)	9,460	2.1	1.1	0.3-9.4	54.3
Average daily gain (g/day)	9,606	672	68.6	463-881	10.2
Backfat (mm)	9,468	11.4	2.1	7-18	18.5
Test weight (kg)	9,622	103	9.4	75-132	9.1
Test age (days)	9,638	154	8.3	130-190	5.4

Records exceeding three standard deviations from the mean were deleted as were flight time records equalling exactly eight seconds, which were caused by an equipment failure. Fixed effect models were derived using the GLM procedure (SAS 1999) only retaining significant effects and their interactions. Breed and test month within year were fitted for all traits. Further fixed effects were encouragement score within staff (27 levels) for flight time as well as sex and diet for growth rate and backfat. The model for backfat also included weight as a linear covariate. Variance component estimates for all traits were obtained with univariate animal model analyses using the ASReml software (Gilmour *et al.* 2006). Random effects fitted were a combination of additive genetic, common litter and grower group. The significance of individual random effects was evaluated using a log likelihood ratio test. In addition, log likelihood values were generated for a range of estimates of two random effects by alternatively fixing either common litter or grower group effects at their estimated values. Genetic correlation estimates were obtained from one tri-variate analysis fitting all three random effects.

RESULTS AND DISCUSSION
The heritability of flight time was (0.15±0.02, Table 2) which was similar to previously reported heritability estimates (Hannson *et al*. 2005). Heritability estimates were 0.22±0.03 for growth rate and 0.40±0.04 for backfat. All three random effects were significant for the three traits analysed. Estimates of the ratios of common litter effect (c^2) and group effect (g^2) variances over phenotypic variance were low (0.02 to 0.05) for flight time and backfat. The low g^2 estimate of 0.02±0.005 for flight time (Table 2) implies that this behavioural trait is reasonably independent of the group that the animal was raised in. Conversely, for growth rate the estimates of c^2 and g^2 were 0.08±0.009 and 0.17±0.009, respectively. This relatively large g^2 estimate for ADG is indicative of the group expressing a considerable influence on this trait. Fitting pen as a fixed effect in the growth rate model did not alter the estimates. Using an equivalent model, Bergsma *et al.* (2008) found a larger g^2 effect of 0.27 for growth rate and a similar g^2 effect of 0.04 for backfat. However, in their study, fitting group as an additional random effect for growth rate reduced the heritability estimate from 0.36 to 0.25, whereas heritability estimates were not affected significantly in the current study. Various models were applied to simulated data with additive genetic effects, genetic social effects and group effects by Van Vleck and Cassady (2005). When genetic social and group effects were ignored, as models usually used in pig breeding do, additive genetic variances were

increased slightly but residual variances were substantially inflated, especially in data sets with large simulated group effects. Residual variances in this study were also higher for models that excluded group effects although additive genetic variances were minimally increased. Including grower group in models could reduce the likelihood of inflated residual variances and possibly inflated additive variances by improving variance partitioning.

In addition, Van Vleck and Cassidy (2005) did not expect the large overestimation of group variance when genetic social effects were ignored. The increase in group variance observed by Van Vleck and Cassidy (2005) corresponded well with the theoretical expectation of group variance of twice the covariance between the additive direct and additive social genetic effects plus (n-2) times the genetic social variance where n is the number of penmates (Bijma pers. comm.). Social genetic effects were not fitted explicitly in our study and group represents both additive and environmental social effects.

In models with multiple parameters, change in one parameter will often lead to a corresponding change in other parameters. Figure 1 illustrates the relative robustness of the parameter estimates providing some confidence that the g^2 effect is not a result of a confounding with c^2. These ranges illustrate the possible substitution between random effects until the log likelihood was changed significantly.

Table 2. Heritabilities (h^2), litter (c^2) and grower group (g^2) effects and log likelihoods (LogL) as well as residual and phenotypic variances for flight time (FT), average daily gain (ADG) and backfat (BF) for model 1 (M1: h^2+c^2), model 2 (M2: h^2+g^2) and model 3 (M3: $h^2+c^2+g^2$).

Trait	Model	LogL	h^2	c^2	g^2	Residual variances	Phenotypic variances
FT	1	-5890.23	0.14±0.02	0.03±0.008		1.09±0.02	1.33±0.02
FT	2	-5912.65	0.17±0.02		0.02±0.005	1.07±0.02	1.35±0.02
FT	3	-5884.97	0.15±0.02	0.02±0.007	0.02±0.005	1.07±0.02	1.34±0.02
ADG	1	-3699.63	0.26±0.03	0.12±0.010		2522±89	4062±89
ADG	2	-3391.92	0.31±0.03		0.17±0.014	2248±83	4335±109
ADG	3	-3356.09	0.22±0.03	0.08±0.009	0.17±0.009	2243±78	4207±103
BF	1	-9846.37	0.41±0.04	0.05±0.008		1.93±0.09	3.55±0.09
BF	2	-9803.40	0.45±0.03		0.04±0.006	1.89±0.09	3.63±0.09
BF	3	-9780.22	0.40±0.04	0.04±0.007	0.04±0.006	1.83±0.09	3.57±0.09
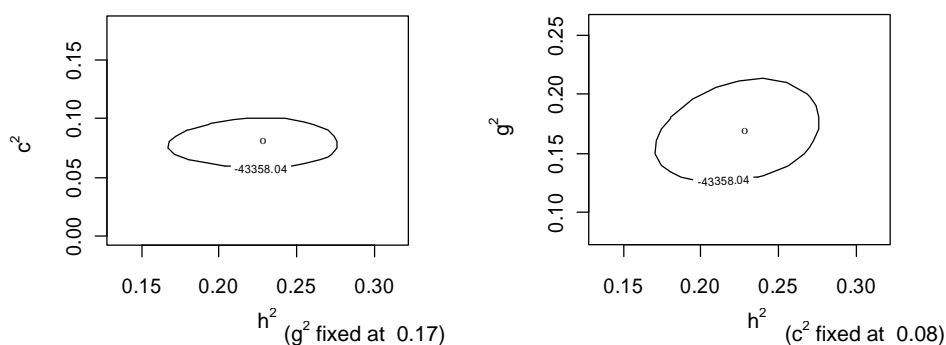
Figure 1. Log likelihood contour lines, illustrating where parameter estimates differ significantly from those obtained when the log likelihood is maximised (Model3) and either group (g^2) or litter (c^2) effects are fixed (trait=ADG).

Flight time was genetically correlated with backfat (0.21±0.09) but had no genetic relationship with growth rate (Table 3) confirming results by Hansson *et al.* (2005). Bunter (2005) also estimated positive genetic correlations between flight time and growth rate (0.34±0.16) or backfat (0.14±0.16). Adjusting flight time for weight did not significantly reduce the genetic correlation with growth rate (0.14±0.11 to 0.02±0.11). Overall, little correlated response is expected in flight time resulting from selection for higher growth and lower backfat.

In beef cattle, flight time is used as a selection criterion for tenderness. Bunter (2005) reported a significant genetic correlation between flight time and pH recorded 24 hour *post mortem* of -0.53±0.21. High final pH indicates dark, firm and dry pork and this genetic correlation suggests that selection for higher flight time would lead to a reduced incidence of dark, firm and dry pork.

Table 3. Genetic and phenotypic correlations between flight time, backfat and average daily gain.

Traits	Genetic	Phenotypic
Flight time – Average daily gain	0.14 ± 0.11	0.08 ± 0.01
Flight time – Backfat	0.21 ± 0.09	0.03 ± 0.01
Average daily gain - Backfat	0.13 ± 0.09	0.10 ± 0.02

CONCLUSIONS

The random additive genetic, litter (c^2) and group (g^2) effects were significant for flight time, growth rate and backfat, although estimates for c^2 and g^2 effects were low (0.02 to 0.05) for flight time and backfat. The g^2 estimate of 0.17 for growth rate indicates that this trait is affected by social effects and further analyses should fit genetic social effects explicitly. In addition, grower group should be recorded to enable analyses of genetic social effects. Flight time was heritable and had low positive genetic correlations with growth rate (not significant) and backfat. Little correlated response is expected in flight time resulting from selection for higher growth and lower backfat.

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