

ESTIMATION OF GENETIC PARAMETERS FOR THAI PIG POPULATIONS

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SUMMARY

Data on 883 Duroc (Du), 1924 Large White (Lw) and 2290 Landrace (Lr) pigs performance tested in Thailand from 1994 to 2002 were used to estimate genetic parameters for production traits applying a multiple trait animal model procedure. The heritability estimates for Du, Lw and Lr were 0.21, 0.24 and 0.39 for average daily gain from birth to the end of test (ADG), 0.32, 0.21 and 0.34 for average daily gain over the test period (TDG), 0.26, 0.35 and 0.41 for ultrasonic back fat depth (BF) and 0.31, 0.10 and 0.26 for feed conversion ratio (FCR), respectively. Genetic correlations between ADG and TDG were relatively high (0.72 to 1.00), between ADG and BF were low (0.03 to 0.29), between ADG and FCR were moderately to highly negative (-0.42 to -0.89) and between BF and FCR were low (-0.07 to 0.20). Overall, these results agree well with estimates presented in previous studies

Keywords: Pigs, genetic parameters, heritability, genetic and phenotypic correlations

INTRODUCTION

Genetic parameter estimates are essential in setting up breeding programs. There have been numerous studies on genetic parameters for pigs in temperate environments. However, there have only been a limited number of studies estimating genetic parameters of commercial European pig breeds raised in tropical environments (Mote, 2000). Estimated genetic parameters have been found to differ across studies and environmental factors such as housing, climates, breeds and feeding regimes. The aim of this study was to estimate genetic parameters for production traits of the pig population in Thai government farms consisting of three major breeds; Duroc (Du), Large White (Lw) and Landrace (Lr).

MATERIALS AND METHODS

Growth performance records of 883 Du, 1924 Lw and 2290 Lr pigs were collected from four government breeding centres in Thailand from April 1994 to March 2002. Both male and female pigs were fed *ad libitum* and individually performance tested from approximately 30 kg to 90 kg of liveweight. Feed intake, body weight, ultrasonic back fat depth and measurement dates were recorded for each animal during the test together with a pedigree record and date of birth. Pedigrees of the Du, Lw and Lr breeds contained 1241, 2560 and 3032 identities; 115, 192 and 251 sires and 285, 466 and 578 dams, respectively. All statistical analyses were performed within breed.

The traits ADG, TDG, BF and FCR were analysed using the GLM SAS procedure (SAS 1988) to ascertain an appropriate fixed effects model. Herd-year-season (HYS), sex and selection line within breed were included as fixed effects in the mixed model analyses for all traits and weight at the end of test was fitted as a covariate for BF. The season was formed as 4-month intervals on the basis of date of birth. Individual animal model residual maximum likelihood analyses were performed using the average

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information algorithm as implemented by Gilmour *et al.* (2002). The direct additive genetic effect of the animal and permanent environmental effect of litter were fitted as random effects in the mixed model analyses for all breeds. A series of univariate and bivariate analyses were performed, with the results of these being used as starting values for the multivariate analyses. Variance components, heritabilities and genetic and phenotypic correlations from the multivariate analyses are reported for Du and Lr breeds. The results from bivariate analyses are reported for Lw breed as its estimates from multivariate analyses were outside the parameter space although results from bivariate and multivariate analyses were similar.

RESULTS AND DISCUSSION

Coefficients of variation (CV) for the traits analysed ranged from 6.9 to 182 % (Table 1). Backfat had the highest coefficient of variation for all breeds, followed by TDG, FCR and ADG. The same pattern of the CV was observed for all breeds. The fixed effects accounted for between 30% and 55% of the total variation in the traits. All fixed effects included in the mixed model analyses were significant for all traits ($P < 0.001$).

Table 1. Number of records (N), mean, coefficient of variation (CV) and coefficient of determination (R^2) for the full model of fixed effects including sex, line, herd-year-season for all traits and final weight for BF

Breed	Trait	Unit	N	Mean	CV(%)	R^2 (%)
Du	ADG	g/day	883	564.01	6.9	51.93
	TDG	g/day	883	782.10	11.3	42.12
	BF	mm	877	13.47	15.3	35.06
	FCR	g/g	883	2.52	9.4	54.52
Lw	ADG	g/day	1923	562.55	7.6	47.27
	TDG	g/day	1924	770.46	11.9	35.03
	BF	mm	1924	12.79	18.2	32.48
	FCR	g/g	1909	2.58	10.6	43.39
Lr	ADG	g/day	2290	610.40	7.73	42.73
	TDG	g/day	2290	838.96	11.8	36.63
	BF	mm	2290	12.34	16.6	39.80
	FCR	g/g	2290	2.45	9.8	52.45

The estimates of litter effect for ADG were greater than its estimates for TDG for all breeds, meaning that litter effects had a greater impact on growth rates before test than growth rates over the test period. The litter effects estimated for production traits from this study were higher than estimates from the study of Mote (2000, 0.09 to 0.13 for growth rate traits and 0.04 to 0.06 for BF). Different patterns of heritability estimates were observed in different breeds. In Du breed, the heritability estimate for TDG was highest whereas in Lw and Lr breeds, the estimates for BF were the highest. Heritability estimates for ADG and TDG in this study were similar to the estimates from pigs with *ad libitum* or semi-*ad libitum* access to feed (0.03 to 0.49) reviewed by Clutter and Brascamp (1998) despite some differences in performance testing across studies, such as performance testing having been conducted either on a weight basis or an age basis, different test lengths, and testing at different stages of growth. The heritability estimates for

growth rate traits (ADG and TDG) were mostly moderate suggesting that the traits will respond to selection. The estimates also agree well with those from tropical studies of pigs in commercial farms (0.23 to 0.47) by Mote (2000), Duc (1999) and Dzama and Mugate (1998). Heritabilities for BF estimated from this study were similar to the average of the estimates (0.49) reviewed by Clutter and Brascamp (1998) and estimates from tropical studies (0.32-0.42) by Duc (1997) and Mote (2000). As well as high heritability estimates, BF had the highest coefficient of variation of the four traits (Table 1). This suggests that genetic improvement for BF in the pig population studied is achievable. For FCR, the heritability estimates were moderate in Du and Lr breeds and low in Lw. The estimates in Du and Lr breeds were within the range reported by Clutter and Brascamp (1998) of 0.12 to 0.58 with an average of 0.30 and similar to estimates (0.21 to 0.44) for pigs in Vietnam by Duc (1997). In Lw breed, the estimate for FCR was lower than those estimates from previous studies.

Table 2. Results of multivariate animal model REML analyses for production traits of Du, Lw and Lr pigs (r_p , r_g , c^2 and se are phenotypic correlation, genetic correlation, permanent environmental effect of litter and standard errors, respectively)

Breed	Trait	Unit	Phenotypic Variance	Heritability (on diagonal) and correlation estimates (r_g below and r_p above diagonal) $\times 100 \pm se$				$c^2 \times 100 \pm se$
				ADG	TDG	BF	FCR	
Du	ADG	g/day	1666	21±11	74±02	17±05	-42±04	28±06
	TDG	g/day	8555	72±15	32±11	18±04	-57±03	21±05
	BF	mm×10	467	29±33	16±28	26±11	04±04	22±06
	FCR	g/g×100	608	-89±20	-77±14	-07±29	31±11	03±05
Lw	ADG	g/day	2025	24±08	91±01	10±03	-45±02	30±04
	TDG	g/day	8995	100±02	21±08	14±03	-61±02	25±04
	BF	mm×10	600	03±21	04±22	35±07	10±03	10±03
	FCR	g/g×100	774	-57±23	-28±33	14±27	10±06	19±04
Lr	ADG	g/day	2487	39±06	67±02	08±03	-39±02	33±03
	TDG	g/day	10740	78±07	34±07	09±03	-57±02	25±03
	BF	mm×10	450	10±12	18±14	41±06	13±03	07±03
	FCR	g/g×100	628	-42±13	-63±11	20±15	26±07	18±03

High standard errors associated with the correlation estimates preclude detailed discussions. Genetic and phenotypic correlations between pairs of production traits were similar in direction and magnitude across breeds. The exceptions to this were the genetic correlation between BF and FCR in the Du breed which was slightly negative while these correlations were moderately positive in both Lw and Lr breeds. The genetic and phenotypic correlations between ADG and TDG were relatively high. The high genetic correlations between ADG and TDG especially in Lw suggest that either can be used as a selection criterion for growth to the end of the test period.

The estimates of genetic correlations between growth rate traits (ADG and TDG) and BF differ widely between the breeds, which agree with the review of Clutter and Brascamp (1998) where correlations

between ADG and BF differed across studies. The results agree well with a study in Indonesia which reported moderate and unfavourable genetic correlation estimates of 0.10 and 0.27 for Lw and Lr breeds (Mote, 2000) but disagree with a study in Vietnam which reported favourable estimates of -0.23 and -0.27 (Duc, 1997). The disagreement of the findings among the tropical countries suggests that factors other than climate contribute to relationships between growth rate and BF in pigs. The genetic correlation between growth rates and BF in the Lw population in this study was slightly positive or close to zero suggesting that selection on growth rate for this breed will not effect BF. The genetic correlations between growth traits and FCR were highly negative and agree well with the estimates (-1.24 to 0.35 with an average of -0.53) reviewed by Clutter and Brascamp (1998) and were similar to the estimates (-0.57 and -0.61) for Lw and Lr in Vietnam (Duc 1997). The estimated genetic correlations between BF and FCR were moderate and positive in Lw and Lr and agree well with studies reviewed by Clutter and Brascamp (1998, range of 0.10 to 0.44) and the tropical study of Duc (1997, range of 0.25 to 0.36). However, the correlation estimate for Du was negative and lower than most of the previous studies.

CONCLUSIONS

It was anticipated that genetic parameter estimates in this study may have differed from those found in studies in temperate regions because of the tropical climate of Thailand, the diversity of the populations used to found the populations studied and the long period required to obtain the relatively small data sets analysed. However, the pigs were tested in government farms where the environment and management were similar to those in commercial farms in many countries and this may account for the overall similarity of genetic parameter estimates with those from other studies.

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