GENETIC CORRELATIONS BETWEEN THE PERFORMANCE OF PUREBRED AND CROSSBRED PIGS

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SUMMARY
Genetic correlations between purebred Duroc (DU), Large White (LW) and Landrace (LR) pigs and their crossbreds LW×LR, LR×LW, DU×(LW×LR) and DU×(LR×LW) were estimated for production and reproduction traits. Performance test and litter records from Government pig breeding stations in Thailand were used. REML bivariate animal models were used to estimate genetic correlations for each trait measured in purebreds and in crossbreds. Production traits tended to have very high genetic correlations (0.66 – 0.96) between purebreds and crossbreds, whereas reproduction traits tended to have low to moderate genetic correlations (0.21 – 0.52). The breeding procedure to improve production traits of crossbred pigs using genetic evaluation and selection based on purebred records is verified by the results of this study due to the high genetic correlations. However, for reproduction traits, purebred records seem to be less relevant for use to improve crossbred reproduction traits because of low genetic correlations between purebreds and crossbreds. Therefore, a joint genetic evaluation of purebred and crossbred records is recommended to improve reproduction traits in crossbred sows.
Keywords: Genetic correlations, production traits, reproduction traits, purebreds and crossbreds

INTRODUCTION
In pig improvement programs, genetic evaluation has been based predominantly on purebred data but crossbreds are the end product to be improved and raised at the commercial level. Based on selection index theory, Wei and Van der Werf (1994) found that a combined crossbred and purebred selection method was always better than either pure-line selection or crossbred selection methods alone. Estimates of genetic correlations between purebreds and crossbreds and crossbred heritabilities for economically important traits are needed to verify genetic evaluation procedures for integrated pig breeding programs aiming to improve both purebreds and crossbreds (Wei and Van der Werf, 1994). Despite an increase in interest, genetic evaluation of purebreds using crossbred information has been limited due to the lack of a recording system and performance test records for crossbred animals. However, contemporary performance test and litter records from both crossbreds and purebreds are available from Thai Government pig breeding stations. These records have been used here to estimate genetic correlations between purebred and crossbred animals for production and reproduction traits in this study.

MATERIALS AND METHODS
In order to estimate genetic correlations between two traits, one measured on purebreds and the other on crossbreds, the two measurements were treated as different traits. Purebred animals had their own purebred traits but were given missing values for the corresponding crossbred traits, and vice versa. The genetic correlations between purebreds and crossbreds for production and reproduction performance were

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estimable through common parents and ancestors providing genetic links between purebred and crossbred individuals in the pedigree. The production and reproduction data were collected from Thai Government breeding stations from 1993 to 2003. The performance test data consisted of 7666 purebred records (1431 Duroc (DU), 2712 Large White (LW) and 3523 Landrace (LR)), and 1409 crossbred records (464 LR×LW, 498 LW×LR, 197 DU×(LR×LW) and 250 DU×(LW×LR). Three hundred and eighty purebred records (5%) and 345 crossbred records (24.5%) came from the offspring of 39 common sires. The reproduction data consisted of 10,558 purebred sows' litters (1133 DU, 4573 LW and 4852 LR) from 3399 sows, and 1265 crossbred sows' litters (534 LR×LW and 731 LW×LR) from 509 sows. Nine hundred and thirty two purebred records (9%) and 442 crossbred records (35%) came from the offspring (sows) of 21 common maternal grand sires. The production traits in this study were test daily gain from approximately 30 to 90 kg body weight (TDG), average daily gain from birth to the end of the performance test (ADG), feed conversion ratio (FCR), ultrasonic backfat thickness (BF) and body length (BL). The reproduction traits included total number of pigs born (NPB), number of pigs born alive (NBA), litter weight at birth (LWB) and at 3 weeks (LW3W), litter size at 3 weeks (LS3W) and gestation length (GL).

Bivariate individual animal model analyses were performed using residual maximum likelihood as implemented in the program ASREML by Gilmour *et al.* (2002). Fixed effects included in the mixed models for production traits were breed, sex, and contemporary group of herd-year-season for 4-month periods. Initial age was fitted as a linear covariate in the analysis of TDG and final weight was fitted as a linear covariate in the analyses of BF and BL. Random effects of direct additive genetic of the animal and common litter environment were included in the genetic analyses of production traits. For reproduction traits, repeatability animal models were used. Fixed effect of breed, contemporary group of farrowing herd-year-season (4-month periods), age class of farrowing dams (1 year increments from 1 year of age to ages more than 10 year in the same class), parity number and litter breed were included. Random effects of animal direct additive genetic effect and permanent environmental effect of repeated records of the sow were included in the analyses of reproduction traits. Log likelihood ratio tests (LRT) were used to test if the genetic correlations were different from unity (1.00).

RESULTS AND DISCUSSION
The estimates of genetic correlations for production traits between purebreds and crossbreds (Table 1) were moderate to high for all production traits and not significantly different from 1.00 unity. However, standard errors associated with the estimates were also high reflecting the small numbers of informative records, especially from crossbreds. Genetic correlations for growth traits TDG and ADG were 0.78 and 0.84, which are high enough to expect that selection on purebred animals will achieve a strong correlated response in crossbred progeny. The genetic correlation for ADG (0.84) is in the range of the correlation estimates of 0.99 and 0.62 obtained by Lutaaya *et al.* (2001). Those genetic correlations were estimated from 2-way terminal crossbred data where traits from two different purelines and crossbreds were treated as three separate traits so that genetic correlations between a specific pureline and crossbred could be estimated. In our study, traits were separated only as either crossbred or purebred, because the numbers of records were not sufficient to yield reasonable genetic correlation estimates for a specific purebred line and crossbred genotypes. Our genetic correlation estimate for BF (0.96) is higher that those (0.32 and 0.70) from Lutaaya *et al.* (2001). Differences in genetic backgrounds of the pig populations studied may contribute to the differences in the genetic parameter estimates.

The high estimates of genetic correlations suggest that there was little effect of an additive genetic interaction between breeds involved in growth rate and body measurement traits. FCR had the lowest heritability and genetic correlation estimates between purebreds and crossbreds. The heritability estimates from this study were well within the range of the heritability estimates reviewed by Clutter and Brascamp (1998), thus supporting the validity of the genetic correlation estimates between purebreds and crossbreds that were obtained from the same analyses as the heritability estimates in this study.

Table 1. Estimates of genetic correlations (r_g) between purebred (pure) and crossbred (cross) data, heritabilities (h^2), common litter effect (c^2) and standard errors of the estimates for production traits in pigs

Trait	r_g	h^2 (pure)	c^2 (pure)	h^2 (cross)	c^2(cross)
TDG	0.78 ± 0.49	0.25 ± 0.03	0.24 ± 0.02	0.12 ± 0.09	0.60 ± 0.05
ADG	0.84 ± 0.22	0.29 ± 0.03	0.32 ± 0.02	0.44 ± 0.10	0.37 ± 0.05
FCR	0.66 ± 0.30	0.15 ± 0.03	0.23 ± 0.02	0.33 ± 0.09	0.05 ± 0.04
BF	0.96 ± 0.35	0.33 ± 0.04	0.10 ± 0.02	0.18 ± 0.08	0.15 ± 0.04
BL	0.74 ± 0.23	0.38 ± 0.03	0.12 ± 0.01	0.26 ± 0.08	0.10 ± 0.04

TDG: test daily gain; ADG: average daily gain; FCR: feed conversion ration; BF: ultrasonic backfat; BL: body length

For all reproduction traits studied (Table 2), the genetic correlations between purebreds and crossbreds were low to moderate. This agrees well with a review by Wei and Van der Steen (1991) in that the genetic correlations between purebred and crossbred animals were lower for traits showing more dominance, as could be expected for reproduction traits from this study. However, no estimates of genetic correlations for reproduction traits between purebred and crossbred pigs have been reported. The highest genetic correlation was found in gestation length (0.52) and the lowest in NPB and LS3W (0.21).

Table 2. Estimates of genetic correlations (r_g) between purebred (pure) and crossbred (cross) data, heritabilities (h^2), repeatability (r) and standard errors for reproduction traits in pigs

Trait	r_g	h^2 (pure)	r (pure)	h^2 (cross)	r (cross)
NPB	0.21 ± 0.41	0.09 ± 0.02	0.14 ± 0.01	0.10 ± 0.07	0.12 ± 0.04
NBA	0.37 ± 0.53	0.10 ± 0.02	0.15 ± 0.01	0.05 ± 0.06	0.11 ± 0.04
LS3W	0.21 ± 0.44	0.09 ± 0.02	0.15 ± 0.01	0.08 ± 0.06	0.11 ± 0.04
LWB	0.32 ± 0.32	0.11 ± 0.02	0.16 ± 0.01	0.16 ± 0.07	0.17 ± 0.04
LW3W	0.33 ± 0.39	0.10 ± 0.02	0.19 ± 0.01	0.13 ± 0.04	0.13 ± 0.04
GL	0.52 ± 0.35	0.12 ± 0.02	0.19 ± 0.01	0.18 ± 0.09	0.32 ± 0.04

NPB: number of pigs born; NBA: number of pigs born alive; LS3W: litter size at 3 weeks; LWB: litter weight at birth; LW3W: litter weight at 3 weeks; GL: gestation length

The low to moderate genetic correlations between purebreds and crossbreds for reproduction traits imply significant genetic by genetic interaction effects between breeds, or dominance effects, which may be high in lowly heritable traits such as reproduction traits, as compared with production traits. Higher standard errors of the estimates of heritabilities and repeatabilities for crossbred sows were associated with the smaller number of available litter records from crossbred sows.

A genetic correlation between purebreds and crossbreds less than 0.8 indicates an advantage of selection using combined purebred and crossbred records over pure-line selection when the goal is crossbred improvement (Lutaaya *et al.* 2001). In this case animals ranked best as purebreds are not necessarily best for crossbred performance and information from crossbreds is needed for re-ranking. The low genetic correlation estimates for reproduction traits indicate that the improvement of reproduction traits such as litter size and weight would benefit from a joint genetic evaluation of purebred and crossbred sows. This is supported by Bijma and Van Arendonk (1998) who found that the benefit of using crossbred information was largest when the genetic correlation between purebred and crossbred performance was low. However, a combined genetic evaluation of purebreds and crossbreds to improve crossbred production traits may not be as advantageous, because performance testing of crossbred animals would add cost to a pig breeding program, and genetic correlations between purebred and crossbred are already high. That is, performance testing of purebreds only is sufficient to improve production traits in both purebreds and crossbreds.

CONCLUSIONS

Relatively high genetic correlations between purebreds and crossbreds for production traits verify the conventional genetic evaluation and breeding procedure. That is, performance testing and selection on purebreds will improve production traits in both purebred and crossbred progeny. The low genetic correlation estimates between purebreds and crossbreds for production traits suggest that a joint multi-trait genetic evaluation using both purebred and crossbred data may be more appropriate for the genetic improvement of reproduction traits in crossbred sows. However, due to the high standard errors associated with the estimates of genetic correlations between purebred and crossbred performance for reproduction traits additional data and further investigation are required to validate this conclusion.

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