COMBINED GENETIC EVALUATION OF PUREBREDS AND CROSSBREDS IN YORKSHIRE AND LANDRACE PIGS

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INTRODUCTION

For almost pig breeding programs, the genetic evaluation is predominantly based on purebreds. In some practical conditions, due to the effects of interaction by genetic and environment, the best purebred animals selected at nucleus herds are not sure to result in the best crossbred ones at the multiplier level. As indicated in some studies (Wei and Van Der Werf, 1994; Lutaaya et al, 2001; Lutaaya et al, 2002), goals of joint genetic evaluation include increased accuracy of prediction for purebreds, reciprocal recurrent selection for the improvement of crossbreds, and combined purebred and crossbred selection. The aim of this study is to estimate the genetic correlations between purebreds (Yorkshire and Landrace) and crossbreds (reciprocal Y x L); the breeding values and accuracy of prediction for number born alive, 21 days-litter weight, days to liveweight 90kg, and backfat thickness at liveweight 90kg.

MATERIALS AND METHODS

The data obtained from 4,811 growing pigs and 5,570 litters in purebred Yorkshire; from 5,663 growing pigs and 5,561 litters in purebred Landrace; and from 5,770 growing pigs and 20,241 litters in crossbred (reciprocal Yorkshire x Landrace) were collected from Phu Son pig breeding farm between 2001 and 2010. Then, records were adjusted to number born alive (NBA), 21 days-litter weight (WT21), days to 90kg liveweight (D90) and backfat at 90kg liveweight (BF90) using the recommendations of National Swine Improvement Federation, United States (NSIF, 2002). The same traits in two herds (purebreds and crossbreds) were treated as two different traits and then genetic correlations were estimated by REML using VCE5 software (Groeneveld, 2003). Breeding values of traits were estimated by BLUP procedure using PEST software (Groeneveld, 2003). Reliabilities ($r_{A\hat{A}}$) were obtained by inversion using the formula:

$$r_{A\hat{A}} = \sqrt{1-(PEV/V_A)}$$ where, PEV: prediction error variance ; V_A: additive genetic variance
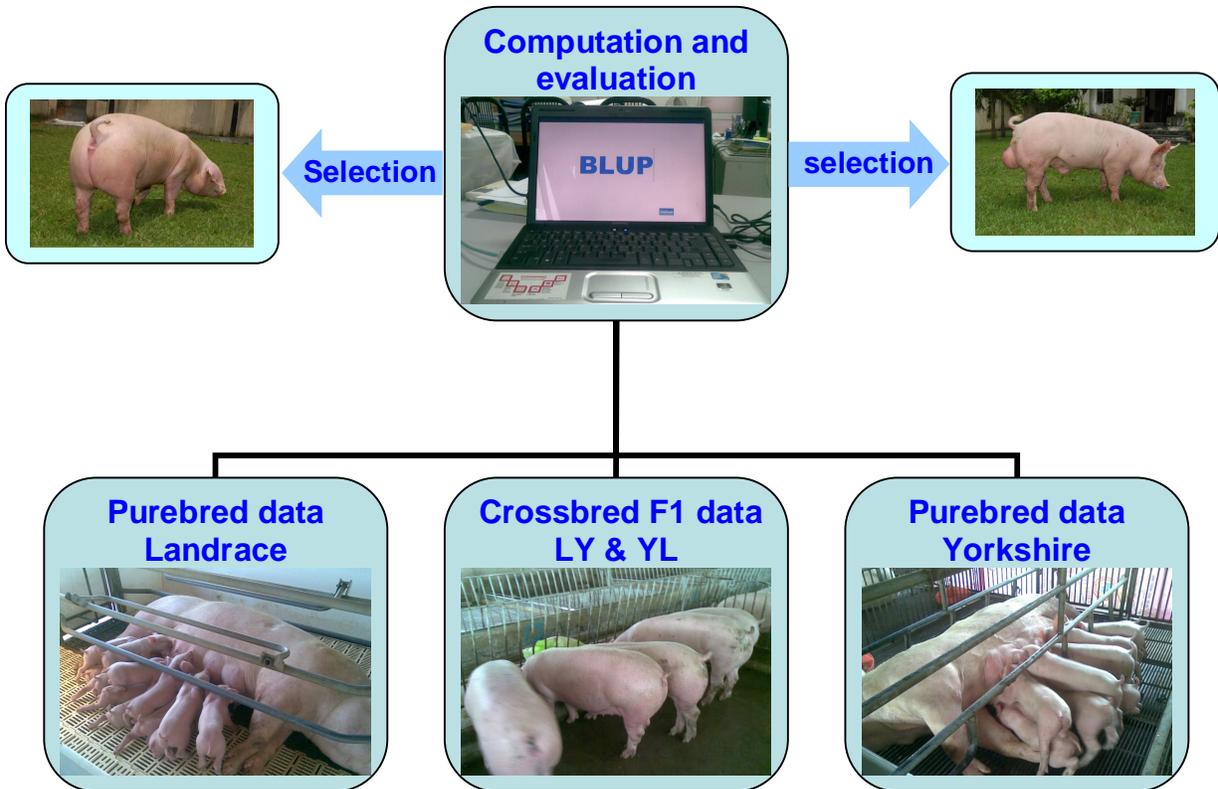
RESULTS

Estimates of genetic correlation between purebreds and crossbreds

As indicated in table 1, genetic correlations between purebreds and crossbreds were lower than "1' for all four traits. However, the different traits had different merits of genetic correlation. In some papers, it was reported that the trait of backfat thickness had a large additive variance and a very small dominant variance (Cullbertson et al, 1998; Lutaaya et al, 2001), so the effects of changed environment between purebreds and crossbreds on this trait were very little. This means that genetic correlations between purebreds and crossbreds were usually larger for backfat thickness trait. In curent study, this merit of genetic correlation was 0.96 between YY and YL/LY, and 0.98 between LL and LY/YL.

Otherwise, some research reported that traits of NBA, WT21 and D90 with small additive variances and large dominant variancesare influenced very large by changing the environmental among herds. Therefore, smaller genetic correlations (0.40-0.78) between purebreds and crossbreds as presented in table 1 for these traits was reasonable and agreed with the paper of Boesch et al (1998) for NBA trait (0.59-0.81). Low genetic correlations indicate the presence of interaction by genetic and environment even in the same farm, but between breeding levels. This means that boars and gilts ranked best as purebreds are not necessarily breeding the best crosbreds. Hence, the combined evaluation of purebreds and crossbreds will result in the advantage for both purebred and crossbred improvement, if genetic correllations between purebreds and crossbreds are less than 0.8 (Wei and Van der Werf, 1994; Bijma and Van Arendonk, 1998).

Also indicated in table 1, genetic correlations were different in absolute merit between purebreds Landrace and Yorkshire versus reciprocal crossbreds for the same traits. This showed that the gene frequency affecting to traits of NBA, WT21, D90 and BF90 had been different between the purebreds Landrace and Yorkshire in this study. The lager genetic correlation for litter traits is with Yorkshire and the larger genetic correlation for D90 trait is with Landrace. This is an advantage for mutual complementarity when crossbreeding.

Table 1. Genetic correlation ($r_G \pm SE$) between purebreds (Landrace-LL and Yorkshire - YY) and crossbreds (reciprocal Yorkshire x Landrace-YL/LY) for the traits of NBA, WT21, D90 and BF90

Traits	LL vs. LY/YL	YY vs YL/LY
1. NBA	0.47 ± 0.01	0.59 ± 0.05
2. WT21	0.48 ± 0.05	0.78 ± 0.06
3. D90	0.69 ± 0.08	0.40 ± 0.03
4. BF90	0.98 ± 0.05	0.96 ± 0.07

Estimated breeding values using the joint evaluation of purebreds and crossbreds

Table 2 presented average breeding values and mean reliability of prediction from the top ten of purebreds for the traits of NBA, WT21, D90 and BF90 using purebred data compared to joint data of purebreds and crossbreds. Average breeding values predicted from the joint data of purebreds and crossbreds were smaller than from purebred data for all four traits. Average breeding values for litter traits predicted from the joint data of purebreds and crossbreds decreased much more than for D90 and BF90 because of different information in amount from crossbreds added (Kuhlers et al 2001). Conversely, the mean reliability of prediction increased by 0.02-0.07 when using combined data of purebreds and crossbreds. This indicates that the improvement in reliabilities of purebred evaluation when adding crossbred data was really remarkable. Therefore, the purebred evaluation can be performed better with the combined use of purebred and crossbred data. However, optimal use of these evaluations may require some changes in the breeding schemes because purebred animals identified as the best in crossbred evaluation may no longer be available (Lutaaya et el, 2001).

Table 2. Average breeding values (EBV) and mean reliability ($r_{A\hat{A}}$) of prediction from the top ten of the best purebreds for the joint evaluation of purebreds and crossbreds for the traits of NBA, WT21, D90 and BF90

Traits	From purebred data		From combined purebred and crossbred data	
	EBV	$r_{A\hat{A}}$	EBV	$r_{A\hat{A}}$
1. NBA	1.310	0.68	1.029	0.71
2. WT21	2.145	0.66	1.129	0.73
3. D90	-20.67	0.45	-17.04	0.52
4. BF90	-1.457	0.58	-1.346	0.60

CONCLUSIONS

For the herds of Landrace and Yorkshire in this study, genetic correlations between purebreds and crossbreds were lower than assumed correlation of "1". The dominance effect and different management of purebreds and crossbreds could be causes for these results. Therefore, the genetic improvement of purebreds just based on purebred evaluation would result in less improvement of crossbreds than expected.

The accuracy of predicted breeding values increased by 0.02-0.07 when the genetic evaluation included data on both purebreds and crossbreds. Therefore, in this case, it is better to evaluate purebreds based on the joint evaluation of purebreds and crossbreds. However, there may be some changes in the breeding schemes in order to ensure that purebred animals identified as the best in crossbred evaluation may be available.