GENOTYPE BY ENVIRONMENT INTERACTIONS FOR GROWTH AND BACKFAT THICKNESS TRAITS IN YORKSHIRE AND LANDRACE PIGS

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ABSTRACT

Genotype by environment interactions (GxE) may reduce the response of performance traits. The aim of this study is to estimate the genetic correlation of the same traits between two genetically linked farms of Binh Thang and Dong A. The total of 10 boars, 15 gilts and 442 semen dozes of Yorkshire and Landrace boars had been exchanged between two farms from 2000 to 2007. Records of individual performance test were obtained from 881 Landrace and 652 Yorkshire pigs in Binh Thang, and 835 Landrace and 1326 Yorkshire pigs in Dong A. Measurements were adjusted to days to 90kg (D90) and backfat (mm) at 90kg liveweight (BF90) referred on the recommendations of NSIF (2002). For Landrace pigs, genetic correlations of the same trait between two environments estimated using REML method in VCE5 software were 0.51 and 0.63 for D90 and BF90 traits, respectively. For Yorkshire pigs, these values were higher, 0.93 for D90 and 0.99 for BF90, respectively. Thus, the evidence of genotype by environment interactions was found in Landrace pigs for measured traits D90 and BF90, while this was not presented in Yorkshire pigs. This means the adaptation to alternative environments in Landrace pigs is worse than in Yorkshire pigs.

Key words: genetic correlation, GxE interaction, production traits, pigs

INTRODUCTION

The effect of GxE is resulted from the lack of adaptation of particular genotypes to specific environments (Montaldo, 2001). It is difficult to specify a specific environmental factor in GxE. Therefore, differences between two environments may be considered as husbandry circumstances in general between farms or herds.



The GxE for a trait may be represented by a genetic correlation between genotypic values of trait in different environments (Falconer and Mackay, 1996). In order to assess the effect of GxE in a breeding program, the same trait in two environments has to be treated as two different traits and consequently genetic correlation between the genotypic values of trait in different environments must be obtained.



Previous studies on the different aspects of GxE have been focused on the estimation of genetic correlations between the same traits measured across various herds (Merks, 1988), between purebred and crossbred performance (Merks and Hanenberg, 1998; Boesch et al, 1998; Brandt and Taubert, 1998), purebred performance in nucleus herds versus commercial crossbred (Van Steenbergen and Merks, 1998), and purebred performance in tropical versus temperate environment (Mote, 2000). The aim of this study is to estimate the genetic correlation of the same traits between two pig breeding farms linked genetically in South Vietnam.

MATERIALS AND METHODS

Data: Records on individual production with full pedigree of Landrace and Yorkshire pigs were obtained from breeding farms, Binh Thang (BT) and Dong A (DA), between 2000 and 2007. Genetic linkages across two farms have been created by sending 10 boars (5 Yorkshire and 5 Landrace), 18 gilts (10 Yorkshire and 5 Landrace) and 442 semen dozes from 12 service sires of Yorkshire and 12 service sires of Landrace to DA from BT between 2000 and 2007. The most important difference between two environments across two farms is about housing environment for individual performance test. Growing pigs for performance test were housed in individual pens at DA, while they were tested in groups of 12 -15 animals using chip cards at BT. Other conditions like feeding

regime, ratio, started and finished age were nearly the same. The initial weight was 35 kg and final weight was around 90 kg. Production records were adjusted to days to 90kg (D90) and backfat at 90kg liveweight (BF90) based age finished, weight finished, backfat at age finished and sex, using the recommendations of National Swine Improvement Federation, United States (NSIF, 2002). After adjusting for all measurements, data structure is indicated as in Table 1.



Landrace lactating sow

Table 1. Data structure of traits D90 and BF90 in Yorkshire and Landrace pigs between 2000 -2007

Farms/Bre	No. of	D90	ML90
eds	records	(Mean ±SD)	(Mean±SD)
Farm: BT			
Landrace	881	184.8 ± 21.0	8.9 ± 1.0
Yorkshire	652	184.7 ± 19.8	8.7 ± 1.0
Farm: DA			
Landrace	835	174.0 ± 12.9	11.5 ± 1.4
Yorkshire	1326	175.4 ± 12.5	11.3 ± 1.9

Statistical analysis. The same traits in two environments at BT and DA were treated as two different traits and then genetic correlations were estimated by REML using VCE5 software (Groeneveld, 2003) by the mixed animal models as follows: $\mathbf{Y}_{ijkl} = \boldsymbol{\mu} + \mathbf{hys_i} + \mathbf{s_j} + \mathbf{a_k} + \mathbf{e}_{ijkl}$ Where, \mathbf{y}_{ijkl} : phenotypic observations;

 μ : population mean; hys_i: farm x year x season; s_j: sex effect; a_k: random additive genetic effect and e_{iikl}: residual effect

RESULTS AND DISCUSSION

When genetics were sent from BT to DA, there was a specific change in environment for individual performance test as indicated in previous section. The alternative environment influenced a little on heritability estimates for measured traits at different levels (Table 2). Estimates of heritability for D90 in both Landrace and Yorkshire pigs were nearly the same between two farms (0.31 - 0.34). For BF90 in Landrace, heritability under DA environment (0.53) was slightly lower than under BT environment (0.59). In contrast for this trait in Yorkshire, heritability under DA conditions (0.64) was slightly higher than under BT conditions (0.59). This showed that there is an advantage for genetic improvement by selection for BF90 trait in Landrace under BT environment Yorkshire under conditions and in environment conditions.



Yorkshire lactating sow

In pigs, the studies on practical implications of GxE showed that the presence of GxE or low genetic correlation among environments are very important (Brascamp et al, 1985; Webb and Curran, 1986) in animal breeding programs. The economic consequence of animal importation may be negative if genetic correlation between the two environments is less than one due to reduced accuracy of estimated breeding values optimal (Montaldo. 2001) or changed composition of the selection and rejected groups across environments (Cooper and DeLacy, 1994). However, according to Robertson (1959), the serious reductions in the efficiency of animal breeding programs may occur when the genetic correlation between environments is lower than 0.8. In current study (Table 2), genetic correlations between two environments BT and DA for D90 and BF90 traits in Yorkshire pigs were high and not significantly different from one (0.93-0.99). But in Landrace pigs, genetic correlations between two environments for these traits were not very high, varying from 0.51 for D90 to 0.63 for BF90 trait. These figures indicated that the presence of GxE for D90 and BF90 in Landrace pigs is very significant and should be considered for the design of acrossherds genetic valuation.

Table 2. Heritability and genetic correlations between farms for D90 and BF90 in Landrace and Yorkshire pigs

1 orksime pigs				
Breeds	Traits	Heritability at BT	Heritability at DA	Genetic correlations between
		$(h^2 \pm SE)$	$(h^2 \pm SE)$	BT and DA $(r_G \pm SE)$
Landrace	D90	0.34 ± 0.06	0.32 ± 0.07	0.63 ± 0.16
	BF90	0.59 ± 0.07	0.53 ± 0.05	0.51 ± 0.15
Yorkshire	D90	0.31 ± 0.08	0.32 ± 0.06	0.93 ± 0.18
	BF90	0.58 ± 0.09	0.64 ± 0.05	0.99 ± 0.17

CONCLUSIONS

Genetic correlations between environments (Binh Thang and Dong A pig breeding farm) for

the traits of days to 90kg and backfat thickness at 90kg were very closed to one in Yorkshire pigs and not high in Landrace pigs. Therefore, the current study suggested that the influence of genotype with environment interactions for these measured traits is quite clear and should be interested in the pig breeding programs.

REFERENCES

- Brascamp, E.W., J.W.M., Merks, and J.B.M., Wilmink, 1985. Genotype-environment interaction in breeding programs: Methods of estimation and relevance of the estimates. *Livest. Pro. Sci.*, 13:135-146
- Cooper, M., and I.H., DeLacy, 1994. Relationships among analytical methods used to study genotypic variation and genotype-by-environment interaction in plant breeding multi-environment experiments. *Theor. Appl. Genet.* 88:561-572
- Falconer, D. S. and T. F. C. Mackay, 1996. Introduction to quantitative genetics. Fourth edition. Pearson Education Limited, Edinburgh Gate, Harlow, Essex CM20 2JE, England. 462 pages

- Montaldo, H. H., 2001. Genotype by environment interactions in livestock breeding programs: a review. Interciencia, vol. 26, No 6.
- Merks, J.W.M., 1988. Genotype x environment interaction in pig breeding programs. VI. Genetic relations between performances in central test, on-farm test and commercial fattening. *Livest. Pro. Sci.*, 22:325-339
- Mote, T.G., 2000. Genotype by environment interaction between pig populations in Australia and Indonesia. *Thesis (Abstract)*. University of New England, Australia.
- Robertson, A., 1959. The sampling variance of the genetic correlation coefficient. Biometrics, 15: 469-485
- Van Steenbergen, E., and J.W.M., Merks, 1998. Estimates of genotype x environment interaction and their impact on pig breeding programs. 46th Annual Meeting European Association for Animal Production. Warsaw, Poland.
- Webb, A.J., M.K., Curran, 1986. Selection regime by production system interaction in pig improvement: a review of possible causes and solutions. *Livest. Pro. Sci.*, 14:41-54