Genotype by environment interactions between pig populations in Australia and Indonesia

Tiffany Mote[1], Susanne Hermesch[1] and Julius van der Werf[2]

[1]*Animal Genetic and Breeding Unit;* [2]*Department of Animal Science,*
University of New England, Armidale. N.S.W. 2351.

Introduction

Genetic improvement programs are becoming more global in their nature with animals expected to perform in diverse environments. Different environments such as tropical and temperate environments may have different effects on different genotypes. These effects may change the ranking of genotypes between environments such that the best genotype in one environment is not the best in another environment (Falconer and Mackay, 1996). This is termed a genotype by environment interaction (G x E). Another type of G x E occurs when the difference between the animals is greater in one environment than in another but the animals are still ranked in the same order (Goddard, 1985).

Genetic parameters for performance traits have been estimated in many studies for temperate environments but only a limited number of studies are available for tropical environments. Genotype by environment interactions (G x E) may exist between these two types of environments and need to be investigated. If G x Es do exist then what is thought to be the same trait in the two environments could in fact be two genetically different traits. Substantial differences in genetic parameters may exist between temperate and tropical environments. In this case, breeding value estimation will require specific genetic parameters for tropical environments.

Aim of the Project

This project focused on a tropical and temperate environment, which were genetically linked by sending semen from the temperate environment (Australia) to the tropical environment (Indonesia). Genetic parameters for growth rate, backfat and number of piglets born alive were estimated in the two environments. To determine whether G x E exist, each trait was treated as a separate trait in the two environments. Genetic correlations were then estimated, for example, between growth rate in Indonesia and growth rate in Australia. If the genetic correlation deviated from one, a G x E was found. Ranking of boars based on estimated breeding values within each environment was also studied to further illustrate existence of a G x E and whether re-ranking of boars occurred between the Australian and Indonesian environment.

Design of Project

Semen was collected from 22 service sires at Bunge Meat Industries (BMI), situated at Corowa, Australia. Part of this semen was sent to Culindo, situated on Bulan Island in

Indonesia. These boars were also used in the Large White and Landrace nucleus lines at BMI thus providing a genetic link between the two piggeries. Of the 22 common service (CS) sires, 14 were Large White and 8 were Landrace. The first progeny from these CS sires were born in July 1997 at BMI and May 1998 at Culindo. Farrowing records were collected from January 1997 to August 1999 at both piggeries. At BMI only artificial insemination was used. Farrowing information from 6097 litters were analysed in this project. Of these farrowings, 584 were from matings using semen from the CS sires. Progeny were performance tested at slaughter age at BMI between July 1997 and August 1999. Of the 19,304 animals performance tested, 2,117 were progeny of the CS sires.

At Culindo, both natural matings and artificial insemination were used. A total of 4083 farrowing records were analysed. Of the 4083 farrowings, 542 were from matings using semen from the CS sires. Performance data from 5102 animals was also collected at slaughter age of the animals at Culindo between May 1998 and July 1999. In total, 1514 CS sire progenies were performance recorded.

Description of the two Environments

Temperatures ranged from 3 to 32°C and from 22 to 32°C in Australia and Indonesia, respectively. Average humidity was 60% in Australia and 84% in Indonesia. Large differences exist for rainfall, with Australia averaging 700 mm per year and Indonesia averaging 2400mm per year. Due to the differences in temperature and humidity, differences in housing structures were evident. Sheds at BMI had solid concrete walls with blinds whereas at Culindo, sheds had no walls with metal barred pens allowing a greater flow of air through the sheds. Pigs were fed a diet of 16.7% (boars) or 15.5% (gilts) crude protein at BMI with either 13.5 or 13.8 MJ/kg of digestible energy, respectively. At Culindo, the diet contained 16.9% crude protein and 13.5 MJ/kg of digestible energy for both sexes.

Breeding Objective Traits in the two Environments

Two performance traits and one reproductive trait were measured in each environment. Growth rate from birth to 23 weeks of age (BMI) or 28 weeks of age (Indonesia) and live animal fat depth measured at the P2 site were the two production traits recorded. The reproductive trait recorded was the number of piglets born alive for each sow.

The total number of performance records used in data analysis is shown in Table 1 for BMI and Culindo along with means and phenotypic standard deviations. Animals were performance tested at significantly different ages in the two piggeries (BMI: 162 days; Culindo: 196 days). The mean values for growth rate, backfat and weight were significantly greater at BMI than Culindo. The lower P2 at Culindo was more favourable than the value for P2 at BMI. However, a higher GR at a younger age at BMI was more favourable than the GR and age of the animals at Culindo.

Table 1. Means and standard deviations (S.D.) for performance records collected at Bunge Meat Industries (BMI) and Culindo

Herd	No. of records	GR* (g/day)	S.D.	P2 (mm)	S.D.	Weight (kg)	S.D.	Age (days)	S.D.
BMI	19,304	594	65.4	13.5	2.90	96.5	13.2	162	10.6
Culindo	5,102	478	65.3	9.45	2.20	93.6	12.9	196	7.50

*Abbreviations: GR – growth rate; P2 – backfat;

The mean total number of piglets born alive (NBA) at BMI (9.70 piglets) was significantly greater than total NBA for Culindo (8.59 piglets). At Culindo, sows are retained longer, sometimes up to parity ten, while sows are kept to a maximum of parity six at BMI. Means and standard deviations for parities one, two, and three and above at BMI and Culindo are shown in Table 2. When comparing NBA between the two piggeries, NBA recorded for each parity at BMI was significantly greater than the value for the corresponding trait at Culindo. Due to the low numbers of records for each parity, all parities were pooled for genetic parameter estimation.

Table 2. Means and standard deviations (S.D.) for number of piglets born alive (NBA) and age at farrowing recorded in parities one, two, and three and above at BMI and Culindo

Herd	Parity	No. of records	NBA	S.D.	Age at Farrowing (days)	S.D.
BMI	1	3120	9.14	2.66	335	18.4
	2	1372	9.89	2.85	487	21.5
	3+	1605	10.6	2.81		
Culindo	1	1153	8.32	2.47	357	26.7
	2	717	8.29	2.95	507	33.4
	3+	2213	8.83	2.80		

Model

The model for the BMI performance data included the breed of the animal, the feeding system in which the animal spent its finisher period and a management group. The data included two breeds, Large White and Landrace. Feeding systems included conventional pens with ad libitum feeding, pens equipped with electronic feeders and ad libitum feeding or pens equipped with electronic feeders restricting feed to 85% of the ad libitum diet. The management group incorporated sex of the animal and the week when animal was performance tested. Age of the animal was fitted as a linear covariable for both GR and P2, while weight was only fitted for P2.

The model for the Culindo performance data included the unit the animal was raised in, the source of the genotype (either Indonesian or Australian derived) and also a management group. Age was also fitted as a linear covariable for both GR and P2. Weight was fitted as a linear covariable only for P2.

For number born alive, over all parities, the significant fixed effects for the BMI data were parity, breed of the sow, month of farrowing. The linear covariable, age of the sow

at farrowing was fitted. For the Culindo data, parity, month of farrowing and the origin of the sire (either BMI or Culindo) were fitted as significant fixed effects.

Variance components were estimated using the program DFREML (Meyer, 1997). Litter was fitted as a random effect for GR and P2. It accounted for common environmental effects and possible maternal effects between littermates. The permanent environmental effect of the sow was fitted for NBA to take repeated records into account.

Genetic Parameters

Heritabilities and variance components estimated for the three traits are shown in Table 3. The heritability for GR was 0.25 for both environments. These results are in agreement with results found by Hall et al. (1999) in a temperate environment. In tropical environments, the heritability for GR was in the range found by Carellino and Siewerdt (1992). Litter effects were also similar for GR in each environment (c^2: 0.10 and 0.09).

The heritability for P2 at BMI was 0.37, which was not significantly greater than the heritability of 0.30 found at Culindo. Both heritability estimates were within the range of heritabilities (range: 0.00 to 0.60) shown in a review by Clutter and Brascamp (1998). Furthermore, the heritability for Culindo was similar to estimates presented by Duc (1998) for a tropical environment. The effect of litter was similar in the two environments (c^2: 0.04).

For NBA, heritabilities were low in both environments. At BMI, the heritability of 0.08 was similar to the mean heritability of 0.09 presented in a review by Rothschild and Bidanel (1998). The heritability for NBA at Culindo was 0.03 and was lower than estimates of NBA obtained in tropical conditions by Huang and Lee (1996).

Genetic and phenotypic variances for P2 were lower at Culindo than at BMI. At BMI, higher additive genetic variance could be due to the higher mean for P2. These differences in variances indicate a G x E for P2 according to the definition of a G x E by Goddard (1985).

Table 3. Heritabilities (h^2) and permanent environment of the litter (c^2) and the sow(pe_{sow}) along with variance components for growth rate (GR), backfat (P2) and number of piglets born alive (NBA) at BMI and Culindo

Herd	Trait	h^2	c^2/pe_{sow}	σ^2_a	σ^2_c	σ^2_e
BMI	GR*	0.25 (0.02)	0.10 (0.01)	913	390	2412
	P2	0.37 (0.02)	0.04 (0.01)	2.13	0.25	3.32
	NBA$_{total}$	0.08 (0.02)	0.10 (0.02)	0.57	0.73[+]	6.14
Culindo	GR	0.25 (0.04)	0.09 (0.02)	891	299	2317
	P2	0.30 (0.04)	0.04 (0.02)	1.00	0.15	2.16
	NBA$_{total}$	0.03 (0.02)	0.08 (0.03)	0.25	0.57[+]	6.56

*Abbreviations: σ^2_a – additive genetic variance; σ^2_c – litter variance; σ^2_e – residual variance; +variance due to the permanent environmental effect of the sow.

The genetic correlation estimated between GR and BF was –0.05 at BMI (Table 4). This result was similar to results found by Bryner et al. (1992). This genetic correlation is not significantly different from zero. At Culindo, the genetic correlation between GR and BF was 0.16. Other estimates of genetic correlations in tropical conditions have been obtained under restricted feeding and can not be directly compared to the results found in this study. The genetic correlation estimated for Culindo is unfavourable indicating that selection for GR will also increase P2. However, these genetic correlations between GR and P2 estimated for each piggery are not significantly different from each other. Genetic correlations were also estimated between NBA and the performance traits. These correlations ranged between 0.17 and 0.20 with high standard errors. These results agree with a review by Haley et al (1988) where genetic correlations between NBA and performance traits have usually not been significantly different from zero.

Table 4. Genetic correlations between growth rate (GR), backfat (P2) and number born alive (NBA) at BMI and Culindo

| Herd | Trait | BMI | | Culindo | | |
		P2	NBA	GR	P2	NBA
BMI	GR	-0.05 (0.06)	0.20 (0.10[+])	*0.96 (0.10)*		
	P2		0.17 (0.08[+])		*0.78 (0.16)*	
	NBA					*0.31 (0.15[+])*
Culindo	GR				0.16 (0.11)	0.20 (0.22[+])
	P2					0.20 (0.20[+])

[+]Standard errors calculated according to Robertson (1959).

The genetic correlation estimated between GR at BMI and GR at Culindo was 0.96. This correlation was not significantly different from one indicating that no G x E existed for GR. For P2 the genetic correlation was 0.78. The high standard error indicates that this correlation is not significantly different from one. A G x E was found for NBA with the genetic correlation of estimated as 0.31. Although this estimate indicated that NBA was a different trait in the two piggeries it is most likely not very reliable given that it was not possible to estimate a standard error as a result of limited data for these traits.

Estimated Breeding Values

No G x E was found for GR in the two environments according to the estimated genetic correlation. When estimated breeding values (EBVs) for the CS sires were plotted for GR, some re-ranking of sires occurred between the environments (Figure 1). In Figure 1, sires have been ranked according to their BMI EBV because the animals were first selected at BMI for use in the Culindo herd. Only boars with an accuracy of above 80% were graphed in Figure 1 reducing the number of sires to 13. Accuracies were approximated from the number of progeny for each sire and the heritability of the trait. If the top 10% of sires were selected at BMI for GR, then sires 1 and 2 would be selected. At Culindo, sire 3 would be selected first and then sire 2. The top 50% of sires (seven sires, 1-7) at BMI rank 3, 2, 1, 7, 8, 10, 4 in Culindo. Although re-ranking of the animals has occurred differences in EBVs are not significant.
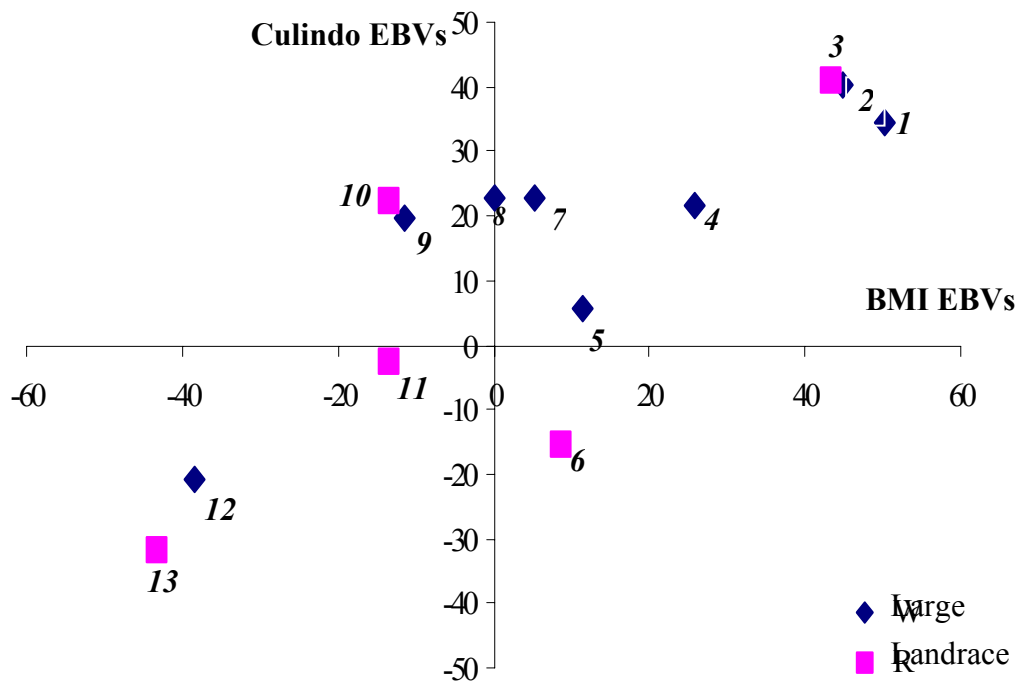
Figure 1. Estimated breeding values (EBVs) for growth rate obtained at BMI and Culindo for common sires (standard error of EBVs: 7-16)

The ranking of sires based on their EBV for P2 is shown in Figure 2. Fourteen sires have an approximated accuracy of greater than 80%. The top 10% of these sires based on their EBV for P2 at BMI would be sire 1 and 2. These sires rank 1 and 3 in Culindo. When selection is extended to 50% of the sires at BMI, sires 1 to 7 would be selected. At Culindo, the order of sires selected would be 1, 3, 4, 8, 14, 7, 10. However, these differences in EBVs between herds are not significant for the majority of sires.
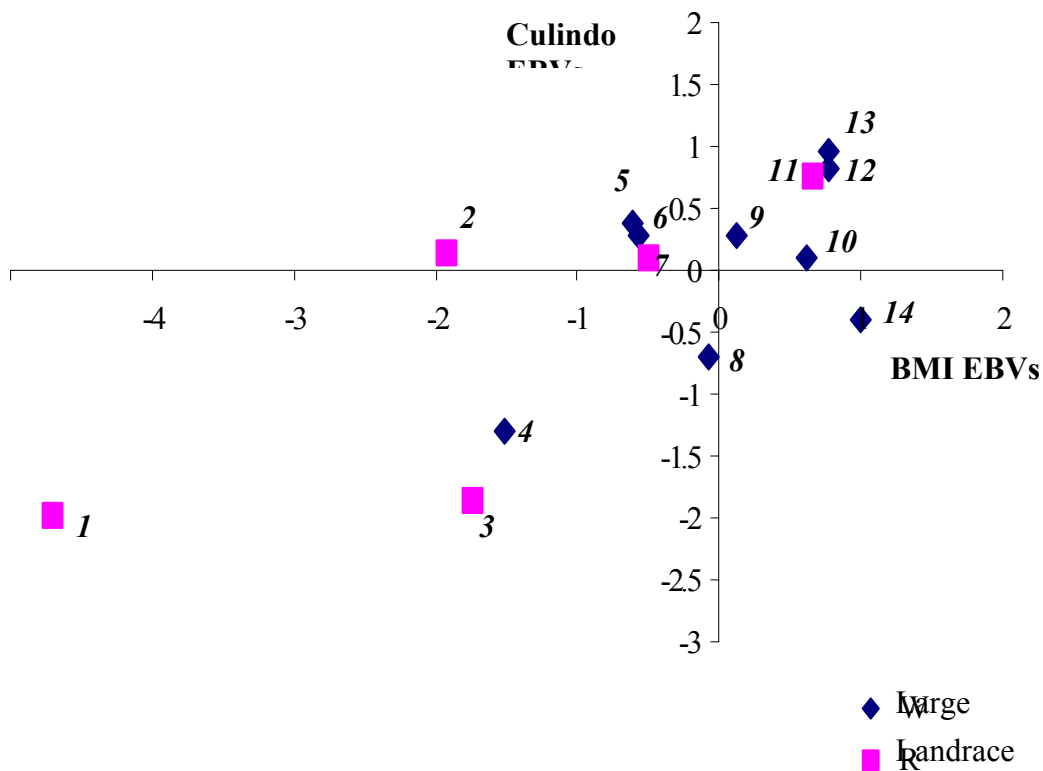
Figure 2. Estimated breeding values (EBVs) for backfat obtained at BMI and Culindo for common sires (standard error of EBVs: 0.22-0.62)

Figure 3 shows EBVs obtained for both herds for all 22 CS sires for NBA. None of the sires had an accuracy of above 80%. Low accuracies were caused by the limited number of daughters with performance records for NBA available for each CS sire. For BMI EBVs for NBA show considerable variation. In contrast, many of the boars are grouped around an EBV of zero in Culindo. This low variation in EBVs for NBA at Culindo is due to the low heritability and the limited reproductive records of the CS sire daughters indicating that the data is not sufficient to reliably analyse a G x E for NBA between BMI and Culindo.
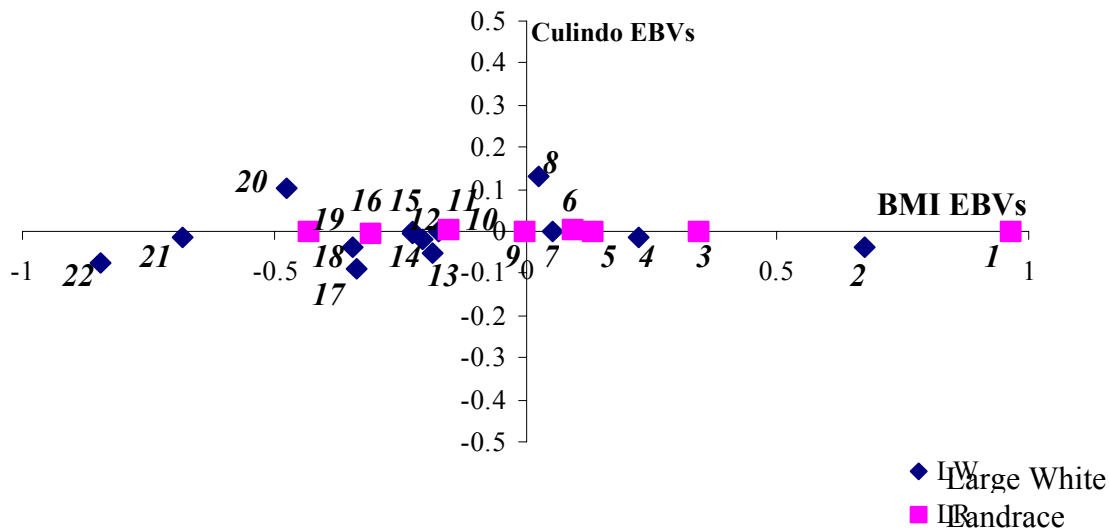
Figure 3. Estimated breeding values (EBVs) for number of piglets born alive obtained at BMI and Culindo for common sires (standard errors of EBVs: 0.22-0.57)

Conclusions

Heritabilities for GR and P2 were similar in both environments indicating that heritabilities in temperate environments could be applied to breeding programs in tropical environments. However, genetic and phenotypic variances were lower in Culindo for P2. Genetic correlations estimated for GR and P2 did not indicate a significant G x E. However, some individual sires showed considerable differences in EBVs for backfat between environment. The heritability estimate and genetic variance component was lower for NBA in Culindo. A G x E existed between the two environments according to the genetic correlation between NBA recorded in both herds. However, further plotting of EBVs for NBA in both herds showed that the data is not sufficient to reliably estimate a G x E for NBA. Growth rate is genetically the same trait in both environments. Provided measurement costs for P2 are sufficiently low in Culindo it is recommended to continue recording P2 under tropical conditions in order to monitor G x E for this trait. The low heritability for NBA in Culindo makes genetic improvement of this trait in the tropical environment difficult.

Acknowledgments

References

Bryner, S. M., J. W. Mabry, J.K. Bertrand, L.L Benyshek and L.A. Kriese, (1992). Estimation of direct and maternal heritability and genetic correlation for backfat and growth rate in swine using data from centrally tested Yorkshire boars. *Journal of Animal Science* **70**: 1755-1759.

Cardellino, R. A. and F. Siewerdt, (1992). Genetic parameters of production traits in Landrace and Large White pigs in southern Brazil. *Revista Brasileira de Genetica* **15**: 575-583.

Clutter, AC. and E.W. Brascamp (1998). Genetics of performance traits. The genetics of the pig. M. F. Rothschild and A. Ruvinsky, CAB International: 427-462.

Duc, N.V. (1998). Heritabilites and genetic correlations between production traits in Vietnamese pigs. *Proceedings of the Association of Animal Breeding and Genetics Conference* **13:**157-160

Falconer, D. S. and T. F. C. Mackay (1996). Introduction to quantitative genetics, London, Longman Scientific and Technical.

Goddard, M. E., (1985). Genotype x environment interactions in dairy cattle. *Proceedings of the Association of Animal Breeding and Genetics 5th Conference, Sydney* **1985**: 52-56.

Haley, C. S., E. Avalos and C. Smith, (1988). Selection for litter size in pigs. *Animal Breeding Abstracts* **56**: 317-332.

Hall, A. D., W. G. Hill, P.R. Bampton and A.J. Webb, (1999). Genetic and phenotypic parameter estimates for feeding pattern and performance test traits in pigs. *Animal Science* **68**: 43-48.

Huang, Y. H. and Y. P. Lee, (1996). Genetic study on reproductive performance of purebred pigs. *Journal of the Chinese Society of Animal Science* **25**: 391-402.

Meyer, K. (1997). DFREML Version 3.0 α User Notes (AGBU), UNE: Armidale).

Robertson, A. (1959). The sampling variance of the genetic correlation coefficient. *Biometrics* **15:**459-485.

Rothschild, M. F. and J. P. Bidanel (1998). Biology and genetics of reproduction. The genetics of the pig. M. F. Rothschild and A. Ruvinsky, CAB International**:** 313-343.