Proc. Assoc. Advmt. Anim. Breed. Genet. 22:237-240

EXTENSION OF ENVIRONMENTAL DESCRIPTORS USED TO ANALYSE SIRE BY ENVIRONMENT INTERACTION FOR GROWTH OF PIGS

S.Z.Y. Guy[1], J. Harper[2], L. Li[3], P.C. Thomson[1,3] and S. Hermesch[3]

[1]School of Life and Environmental Sciences, University of Sydney, NSW, 2006
[2]Rivalea Australia, Corowa NSW, 2646
[3]Animal Genetics and Breeding Unit, a joint venture of NSW Department of Primary Industries and University of New England, University of New England, Armidale, NSW 2351, Australia

SUMMARY

Environmental descriptors based on contemporary group estimates of average daily gain (ADG), backfat (BF), daily feed intake (DFI) and muscle depth (MD) were used to evaluate sire by environment interactions (S×E) for growth rate of pigs. Further, these descriptors were combined using principal component analysis and the first principal component (PC1) was used as an overall environmental descriptor. Use of the environmental descriptors based on MD, BF and DFI did not detect any S×E for growth. However, significant S×E was detected using the environmental descriptor based on ADG and also the overall descriptor based on PC1, where the S×E variance components accounted for 2.1% and 1.8% of the phenotypic variance. While an environmental descriptor that encompasses more traits is expected to capture more environmental variation, use of the environmental descriptor based on ADG alone may be adequate to describe phenotypic variability attributed to S×E for growth.

INTRODUCTION

Environments can be quantified by contemporary group (CG) estimates of performance traits, adjusted for systematic and genetic effects. Environmental descriptors based on CG estimates of multiple production traits have been used in dairy cattle, which have been applied to the evaluation of genotype by environment interaction for fertility traits (Strandberg *et al.*, 2009). In pigs, estimates of CG effects based on number born alive and numbers weaned have been used to quantify disease environments affecting sow reproductive performance (Herrero-Medrano *et al.*, 2015). Meanwhile, use of CG estimates to describe growth rate of the pig has been limited to lifetime average daily gain (ADG) and backfat (BF) (Guy *et al.*, 2015; Li and Hermesch, 2016).

The objective of this study was to extend the traits used to derive environmental descriptors, to also include daily feed intake (DFI) and muscle depth (MD). These environmental descriptors will be used individually, as well as combined into an overall descriptor, to describe variation in the growth performance of sire progeny across different environments, i.e. sire by environment interaction (S×E) for growth. It is hypothesised that use of more traits will capture additional variation in the environment, and hence the ability to detect S×E will improve.

MATERIALS AND METHODS

Data. Pedigree and production records were available from a commercial piggery, located in the Riverina region of NSW, Australia. Only pigs that had records for all traits of interest were included in the study. Feed intake was only recorded from between 2004 and 2010 for entire males from 2 lines. These boars were housed in the normal production environment until 112 days of age on average, then moved to pens equipped with electronic feeders. After an adjustment period of 5-7 days, boars were weighed and classified 'on test'. Only boars with a test age of between 109 and 133 days were included in analysis. The average weight at start of test was 71.3 ± 7.6 kg (mean ± SD). Boars were on test for an average of 36 days. For analysis, DFI was defined as the average amount of feed consumed per day during the testing period (kg/day). Measurements for BF (average of measurements at last rib and base of tail, mm) and MD (between the 3rd and 4th last ribs, mm) were taken at the end of the test period with real-time ultrasound. For inclusion in the analysis, all production traits were restricted to within 4 standard deviations of the raw mean.

Boars that were tested in the same week and year were assumed to be under the same managerial and environmental conditions, and were therefore allocated to the same CG. The minimum size of the CGs was set at 15 pigs, giving a total of 255 CGs. The CG sizes ranged from 16 to 107 pigs, with an average of 30 pigs. There were on average 11 sires represented in each CG.

After data cleaning, there were 7,746 individual records, representing 448 sires and 2,565 dams from 4,245 litters. The average weight at the end of the test period was 102.5 ± 10.7 kg, at an average age of 157 ± 7 days.

Analysis. In the first step of analysis, environmental descriptors were derived from animal models for the 4 production traits using ASReml (Gilmour *et al*., 2009):

$$\mathrm{ADG}_{ijklm} = \mu + \mathrm{Line}_i + \mathrm{Season}_j + \mathrm{Animal}_k + \mathrm{Litter}_l + \mathrm{CG}_m + \varepsilon_{ijklm}$$

$$\mathrm{BF}_{ikmn} = \mu + \mathrm{Line}_i + \beta_1\mathrm{EndWeight}_n + \mathrm{Animal}_k + \mathrm{CG}_m + \varepsilon_{ikmn}$$

$$\mathrm{DFI}_{ijklmp} = \mu + \mathrm{Line}_i + \mathrm{Season}_j + \beta_1\mathrm{StartWeight}_p + \mathrm{Animal}_k + \mathrm{Litter}_l + \mathrm{CG}_m + \varepsilon_{ijklmp}$$

$$\mathrm{MD}_{ikmn} = \mu + \mathrm{Line}_i + \beta_1\mathrm{EndWeight}_n + \mathrm{Animal}_k + \mathrm{CG}_m + \varepsilon_{ikmn}$$

where μ is the overall mean for the trait of interest. All models contained the fixed effect of the i^{th} Line (2 levels), and random additive genetic effect of the k^{th} animal, random effect of the m^{th} test week-year CG and random residual effect ε, which was unique to each trait. Litter_l as a random effect was significant only for ADG and DFI. Additional fixed effects included Season_j (4 levels) for ADG and DFI, covariate of weight at end of test period ($\mathrm{EndWeight}_n$) for BF and MD, and covariate of weight at start of test period ($\mathrm{StartWeight}_p$) for DFI.

Estimates of CG effects were extracted from each of these models and combined through principal component analysis using the prcomp() function in R (R Core Team, 2016). Principal component analysis combines variables by producing weighted linear combinations that capture maximum variation. It is therefore dependent on scale, so CG estimates were scaled to a variance of 1. The first principal component (PC1) was used as the overall descriptor. Environments were categorised by partitioning each environmental descriptor into quintiles. Pigs were assigned an environment according to the CG they belonged to, with each pig having an environment based on the CG estimates of the 4 traits, as well as the overall descriptor.

In the second step of analysis, S×E for growth was evaluated using the environments characterised from the 5 environmental descriptors derived in the first step. A separate sire model was used for each descriptor:

$$y_{ijklmnp} = \mu + \mathrm{Line}_i + \mathrm{Season}_k + \mathrm{Sire}_l + \mathrm{S{\times}E}_{lm} + \mathrm{Litter}_n + \mathrm{CG}_p + \varepsilon_{ijklmnp}$$

where y_{ijklmn} is the ADG of the j^{th} progeny of sire l in the m^{th} environment (E). The amount of S×E for growth was quantified by the S×E variance component.

RESULTS AND DISCUSSION

Boars had a mean ADG of 653.8 ± 65.0 g/day, a mean BF measurement of 8.8 ± 1.8 mm, a mean DFI of 2.10 ± 0.37 kg/day and a mean MD of 45.5 ± 5.8 mm.

Estimates of CG effects ranged from -53.5 to 56.6 g/day for ADG, -1.66 to 2.18 mm for BF, -0.46 to 0.49 kg/day for DFI, and -5.04 to 10.49 mm for MD. Pearson's correlations between these CG estimates were all positive and less than 0.15, except for between ADG and DFI (0.39). This suggests these 4 traits capture different aspects of the environment.

Genetic parameter estimates for each trait are presented in Table 1 to assess the fitted models used to derive environmental descriptors. Heritability estimates for the 4 traits align with previous studies (Hermesch, 2008), although they were slightly lower due to the inclusion of CG variance component in the calculation of the phenotypic variance estimate. The estimated common litter effect was lower than expected, which may be due to a low average of 1.8 boars/litter tested.

Table 1. Genetic parameter estimates of average daily gain (ADG) (g/day), backfat (BF) (mm), daily feed intake (DFI) (kg/day) and muscle depth (MD) (mm), using models from which contemporary group estimates were used as environmental descriptors

Trait	$\hat{\sigma}_P^2$ ± SE	$\hat{\sigma}_\varepsilon^2$ ± SE	$\hat{h}^2$ ± SE	$\hat{c}^2$ ± SE	$\hat{i}^2$ ± SE
ADG	4063.2 ± 87.6	2328.3 ± 82.7	0.22 ± 0.03	0.06 ± 0.01	0.15 ± 0.01
BF	2.34 ± 0.06	1.16 ± 0.05	0.29 ± 0.02	-	0.21 ± 0.02
DFI	0.12 ± 0.003	0.06 ± 0.002	0.22 ± 0.03	0.04 ± 0.01	0.23 ± 0.02
MD	28.8 ± 0.95	13.7 ± 0.50	0.21 ± 0.02	-	0.31 ± 0.02

Abbreviations of estimates: $\hat{\sigma}_P^2$ = phenotypic variance, $\hat{\sigma}_\varepsilon^2$ = residual variance, $\hat{h}^2$ = heritability, $\hat{c}^2$ = proportion of phenotypic variance attributed to common litter effect, $\hat{i}^2$ = proportion of phenotypic variance attributed to contemporary group effect

The CG estimates based on the 4 traits were combined through principal component analysis. The first principal component (PC1) explained 37.5% of the variation, and the second principal component (PC2) explained 26.1%. For PC1, the greatest emphasis was placed on ADG and DFI, with loadings of 0.60 and 0.64 respectively. The PC1 loading for BF was 0.35 and 0.31 for MD. Meanwhile, PC2 placed the greatest emphasis on the carcass traits, with loadings of 0.59 for BF, 0.65 for MD, -0.40 for ADG and -0.26 for DFI. These loadings suggest associations between the descriptors based on ADG and DFI, and also between the descriptors based on BF and MD.

The environments characterised by the 5 descriptors were used in sire interaction models to evaluate S×E for growth rate, and results are presented in Table 2. Estimates of additive genetic variance using descriptors based on BF and MD were larger but not appreciably different, considering their standard errors. Other variance components, except for the S×E term, remained fairly consistent across models using different environmental descriptors.

Table 2. Genetic parameter estimates for the analysis of sire by environment interaction (S×E) for growth rate, using environmental descriptors based of average daily gain (ADG), backfat (BF), daily feed intake (DFI), muscle depth (MD), and all 4 traits combined using the first principal component (PC1)

Descriptor	$\hat{\sigma}_A^2$ ± SE	$\hat{\sigma}_{CG}^2$ ± SE	$\hat{\sigma}_{S\times E}^2$ ± SE	$\hat{\sigma}_P^2$ ± SE	$\hat{h}^2$ ± SE	$\hat{c}^2$ ± SE
ADG	1022.1 ± 173.9	532.1 ± 65.6	**87.0 ± 37.9**	4060.3 ± 87.5	0.25 ± 0.04	0.10 ± 0.01
BF	1104.9 ± 171.5	586.8 ± 68.3	12.6 ± 28.9	4099.0 ± 90.1	0.27 ± 0.04	0.11 ± 0.01
DFI	1067.5 ± 171.6	584.1 ± 68.3	32.4 ± 30.9	4095.1 ± 89.9	0.26 ± 0.04	0.11 ± 0.01
MD	1123.4 ± 171.5	587.3 ± 68.3	0.28 ± 30.2	4099.2 ± 90.1	0.27 ± 0.04	0.11 ± 0.01
PC1	1009.5 ± 173.9	561.0 ± 67.0	**74.1 ± 36.5**	4079.8 ± 88.8	0.25 ± 0.04	0.10 ± 0.01

Abbreviations of estimates: $\hat{\sigma}_A^2$ = additive genetic variance (calculated as 4 times the sire variance component estimate), $\hat{\sigma}_{S\times E}^2$ = sire by environment interaction variance component. Other abbreviations as explained in Table 1.
Note: Significant S×E in bold

There was no or minimal S×E for growth detected using the environmental descriptor based on MD, BF, and DFI, with the interaction terms accounting for 0.01%, 0.3% and 0.8% of the phenotypic variance, respectively. However, there was significant S×E for growth when using the environmental descriptor based on PC1, which accounted for 1.8% of the phenotypic variance.

Although not substantially different, the environmental descriptor based on ADG accounted for even more phenotypic variance at 2.1%. Therefore, the ability to detect S×E for growth rate was greatest using either the environmental descriptor based on ADG or the overall descriptor.

The trait used to quantify the environment is usually based on the same trait that is being modelled. For example, numbers born alive was used to quantify disease environments, in which sow reproductive performance was assessed using numbers born alive (Herrero-Medrano *et al.*, 2015). This was also the case for the environmental descriptor based on ADG used in this current study. While ADG appears to be the driver of PC1, this overall descriptor may appear to be a more objective measure of the environment as it does not solely depend on the trait being modelled. However, use of PC1 does not appear to capture more variation in the environment to increase the ability to detect S×E, and the descriptor based on ADG alone appears sufficient.

Estimates of heritability for ADG were lower using the animal model in the first step of analysis compared to the sire model estimates in the second step of analysis, although they were not appreciably different when taking standard errors into account. Other variance components were stable across models except for estimates of litter effect and residual variances, which were both larger in the sire model. Higher estimates of litter effect in sire models may be attributed to the dam genetic effect being absorbed by the litter component.

The environmental descriptors were partitioned into quintiles to allow for ~ 1,500 pigs classified in each environment. This resulted in 10-17% of sires with progeny across all 5 environments, and 22-25% with progeny in only 1 environment. The ability to detect S×E is greatest when sires are represented across all environments, which can be achieved if the descriptor is partitioned into fewer environments. However, this needs to be balanced out with the need for sufficient differences between environments in order to detect S×E for growth.

CONCLUSIONS

This paper considers CG estimates of alternative production traits as a practical way to quantify the pig environment. The sire interaction model provides a simple method to evaluate the presence of S×E for selection decisions, where estimated breeding values for sires are available across all environments, as well as for specific environments. While a descriptor that encompasses alternative traits may be a more objective measure of the environment, use of the environmental descriptor based on ADG alone may be sufficient to capture most of the phenotypic variability attributed to S×E.

ACKNOWLEDGEMENTS

This study is funded by a Pork CRC postgraduate scholarship and Pork CRC Project 2B-105. Special thanks to Rivalea for making the data available.

REFERENCES

Gilmour A.R., Gogel B.J., Cullis B.R. and Thompson R. (2009) 'ASReml User Guide Release 3.0' VSN International Ltd, Hemel Hempstead, HP1 1ES, UK.

Guy S.Z.Y., Hermesch S. and Thomson P.C. (2015) *Proc. Assoc. Advmt. Anim. Genet.* **21**: 457.

Hermesch S. (2008) *Anim.* **2**: 1178.

Herrero-Medrano J.M., Mathur P.K., ten Napel J., Rashinidi H., Alexandri P. *et al.* (2015*) J. Anim. Sci.* **93**: 1494.

Li L. and Hermesch S. (2016) *J. Anim. Breed. Genet.* **12**: 336.

R Core Team (2016). *R Foundation for Statistical Computing*, Vienna, Austria.

Strandberg E., Brotherstone S., Wall E. and Coffrey M.P. (2009) *J. Dairy Sci.* **92**: 3437.