

ESTIMATION OF GENETIC PARAMETERS FOR REPRODUCTIVE TRAITS, PRODUCTION, CARCASS AND MEAT QUALITY TRAITS IN AUSTRALIAN PIGS

S. HERMESCH¹, B. LUXFORD² and H.-U. GRASER¹

¹ Animal Genetics and Breeding Unit *, University of New England, Armidale, NSW, 2351

² Bunge Meat Industries, Corowa, NSW, 2646

SUMMARY

Genetic parameters were estimated for reproduction, production, carcass and meat quality traits using Restricted Maximum Likelihood procedures. Estimates of heritabilities for reproduction traits were low with values from 0.04 to 0.06. Crossfostering will bias estimates of genetic parameters for litter weight at 21 days and should therefore be restricted in a breeding herd when this trait is used in a breeding program. Genetic relationships between reproduction traits and production and carcass traits are favourable with a low to moderate magnitude. Due to the low magnitude of genetic parameters it is not worthwhile in the present situation to incorporate number born alive into a multivariate analysis. However, including litter birth weight and litter weight at 21 days in a multivariate analysis would lead to a more accurate evaluation of these traits.

INTRODUCTION

Multiple trait animal models using best linear unbiased prediction (BLUP) to estimate breeding values have become the standard method for evaluating farm animals. In pig breeding, multiple trait BLUP analyses incorporate growth, carcass and meat quality traits and commonly included traits are average daily gain, feed intake and backfat or lean meat content (Long et al., 1992). Reproduction performance, mostly expressed by litter size (Short, et al., 1994) and more recently by 21 day litter weight (Henzel, 1995), is analysed in single trait evaluations. Future developments in pig breeding will incorporate reproductive traits in multiple trait BLUP analyses (Short, et al. 1994), making good knowledge of genetic and environmental relationships between reproduction, production, carcass and meat quality traits necessary.

The purpose of this paper is to estimate genetic parameters for reproduction traits, including number born alive, litter birth weight and 21 day litter weight, and to analyse their genetic and environmental correlations to average daily gain, daily feed intake, backfat and pH measured 45 minutes after slaughter.

MATERIAL AND METHODS

In cooperation with Bunge Meat Industries, a data set is accumulated to estimate genetic parameters for reproduction, production, carcass and meat quality traits. The data recording and data characterisation for average daily gain (ADG), feed intake (FDINT), backfat (BF) and pH measured 45 minutes after slaughter (pH-45) is given by Hermes et al. (1995). For the analysis of reproduction traits, including number born alive (NBA), litter birth weight (LBW) and litter weight at 21 days (LW21D), data was obtained from three generations of Landrace, Large-White or Duroc sows, that farrowed between 1989 and 1994.

The relevant fixed effects and covariates were derived by using the SAS procedure GLM (SAS, 1991) and are listed in Table 1 for each reproduction trait. The contemporary group year-season was defined in two

* AGBU is a joint institute of NSW Agriculture and the University of New England

month periods. Within the first three days after farrowing piglets were crossfostered and therefore the number of piglets after crossfostering was included as a covariate for litter weight at 21 days.

To analyse the reproduction traits, a repeatability model was fitted. The random part of the model included the animal additive genetic effect, the permanent environmental effect and the residual effect. It was shown with a log likelihood ratio test, that maternal effects were not significant and were therefore not included in the model. The model used for the analysis of reproduction traits was:

$$y = Xb + Zu + Wm + e$$

where y is a vector of observations, b is a vector of fixed effects, u is a vector of additive genetic effects, m is a vector of permanent environmental effects, e is a vector of residual effects and X , Z and W are incidence matrices relating records to the appropriate random or fixed effect. Residual covariances between reproduction traits and average daily gain, feed intake, backfat and pH measured 45 minutes post mortem could not be estimated, since these traits were not recorded on the same animals. The appropriate models for the production, carcass and meat quality traits as well as a further description of the statistical method is given by Hermesch et al. (1995).

Table 1: Fixed effects and covariates included in the model for reproductive traits

Trait	year-season	genetic line	parity	module farrowed	age of litter	no. of piglets after transfostering
NBA	***	***	***	*		
LBW	***	***	***	***		
LW21D	***	***	***		***	***

*** P < 0.1% ; ** P < 1% ; * P < 5%

RESULTS

A data characterisation including the number of sows and the number of litters is presented in Table 1. The fixed effect part of the model explains 5% of the total variation for number born alive whereas the fixed effect model accounts for 50% of the total variation for the trait litter weight at birth. Estimates of heritabilities are low with values from 0.04 to 0.06 for the three reproduction traits. Values for repeatability range from 0.09 for 21 day litter weight to 0.17 for number born alive. The equivalent data characterisation and results from univariate analyses for production, carcass and meat quality traits are presented in Hermesch et al. (1995).

Table 2: Data characterisation, raw phenotypic standard deviations (σ_p), proportion of total variation explained by fixed effect part of model (R^2) and genetic parameters a with standard errors (s.e.) from univariate analysis.

Trait	No. of sows	No. of litters	σ_p	R^2	h^2	s.e.	r
NBA	1799	4357	2.60	0.05	0.06	0.02	0.17
LBW	1787	4006	4.39 kg	0.51	0.04	0.02	0.14
LW21D	1187	1908	11.72 kg	0.26	0.05	0.03	0.09

h^2 : heritability, r : repeatability

Results from bivariate analyses of reproductive traits are presented in Table 3. The relationship between number born alive and litter birth weight is characterised by a low genetic correlation of basically zero and low environmental and phenotypic correlations. The trait 21 day litter weight shows a moderate negative genetic correlation to number born alive and a moderate genetic correlation to litter birth weight. The environmental and phenotypic correlations between litter weight at 21 days and the two reproduction trait measured at birth are low.

Table 3: Genetic correlations (r_G) with standard errors (in brackets), environmental correlations (r_E) and phenotypic correlations (r_P) for reproduction traits

TRAIT		LBW		LW21D	
NBA	r_G	0.04	(0.28)	-0.50	(0.23)
	r_E	0.22		-0.01	
	r_P	0.21		-0.04	
LBW	r_G			0.40	(0.32)
	r_E			0.04	
	r_P			0.06	

Average daily gain shows no genetic relationship to number born alive, whereas a higher average daily gain will lead to a slightly lower birth weight and is moderately associated with a higher 21 day litter weight (Table 4). The traits feed intake and backfat show low to moderate favourable genetic correlations to reproduction traits. A somewhat different picture appears for genetic correlations between pH measured 45 minutes after slaughter and the three reproduction traits. A selection for a higher litter size either in number born alive or litter birth weight will lead to a lower pH. However, a higher litter weight at 21 days is strongly associated to a higher pH at 45 minutes after slaughter.

The low environmental correlations between reproduction and the other listed traits show, that environmental effects that are important for reproduction traits do not influence production, carcass and meat quality traits.

Table 4: Genetic correlations (r_G) with standard errors (in brackets), environmental correlations (r_E) and phenotypic correlations (r_P) for reproduction traits, average daily gain, backfat and pH measured at 45 minutes after slaughter.

Trait		ADG		FDINT		BF		pH-45	
NBA	r_G	0.00	(0.07)	-0.04	(0.16)	-0.08	(0.15)	-0.03	(0.22)
	r_E	0.08		0.00		0.00		0.00	
	r_P	0.00		0.00		-0.01		0.00	
LBW	r_G	-0.13	(0.11)	-0.29	(0.18)	-0.22	(0.17)	-0.27	(0.25)
	r_E	0.00		0.00		-0.03		0.00	
	r_P	0.00		-0.03		0.10		-0.02	
LW21D	r_G	0.34	(0.27)	-0.15	(0.21)	-0.09	(0.20)	0.88	(0.07)
	r_E	0.08		0.00		0.00		0.00	
	r_P	0.00		-0.02		-0.02		0.07	

DISCUSSION

The estimates of heritabilities for reproduction traits are at the lower of the range of literatures values (Haley et al., 1988). Using a data set with 20,000 first parity litters Southwood and Kennedy (1990) found an influence of maternal effects on genetic parameters. By fitting a maternal effect estimates of heritabilities increased. This increase is due to a negative relationship between the maternal and the additive genetic effect. The size of this data set (4000 litters) is not sufficient to draw a final conclusion about the influence of maternal effects on reproduction traits. These aspects as well as the low genetic correlation between number born alive and litter birth weight will be subject to a final analysis when the data collection for this project will be completed.

In comparison to number born alive and litter weight at birth, 21 day litter weight is measured after cross-fostering. The environmental effect of crossfostering causes an increase in the environmental variation and therefore a decrease of the heritability for 21 day litter weight. The other two reproduction traits are influenced by different environmental effects which is reflected in the low environmental correlation between number born alive and litter birth weight and 21 day litter weight. These results show that crossfostering might cause a bias in genetic parameters for 21 day litter weight and should therefore be done with caution in a breeding herd when this trait is used in a breeding program.

The estimates of genetic correlations between number born alive and average daily gain, feed intake and backfat are in agreement with Short, et al. (1994) showing that a selection for increased gain, lower backfat and a lower feed intake has either no or a slightly favourable effect on number born alive. The very low genetic correlations of number born alive with these traits indicate that very little is gained for this trait from a multivariate analysis. The situation is somewhat different for litter birth weight and litter weight at 21 days as the genetic correlations are of higher magnitude and a multivariate analysis will lead to a more accurate evaluation of these traits.

The high genetic correlation between litter weight at 21 days and pH measured 45 minutes after slaughter, suggests that a high milk performance of the sow is associated with better meat quality characteristics of the progeny. These results need to be confirmed in a final data analysis which will commence in July 1995 when the data collection for this project will be completed.

ACKNOWLEDGMENT

This work was funded by PIG RESEARCH and DEVELOPMENT CORPORATION under project UNE17P. The Bunge staff are gratefully acknowledged for data collection.

REFERENCES

- HALEY, C.S., AVALOS, E. and SMITH, C. (1988) *Anim. Breed. Abstracts* 56:317
HENZEL, A.L. (1995) *Proc 11th conf. of AAABG*
HERMESCH, S., LUXFORD, B. and GRASER H.-U. (1995) *Proc 11th conf. of AAABG*
LONG, T., BRANDT, H., TIER, B. and FUCHS, W. (1992) *Proc 10th conf. of AAABG* 10. 573
MEYER, K., (1993). "DFREML User Notes V.2.1". AGBU, UNE, Armidale
SAS/STATS (1991), User's Guide" Release 6.03 Edition
SHORT, T.H., WILSON, E.R. and D.G. MCLAREN (1994) *Proc 5th World Conf. of Genetics Applied to Livestock Production* Vol. 17:413
SOUTHWOOD, O.I. and KENNEDY, B.W. (1990) *J. Anim. Sci.* 68:1841