GENETIC PARAMETERS FOR PIGLET MORTALITY, WITHIN LITTER VARIATION OF BIRTH WEIGHT, LITTER SIZE AND LITTER BIRTH WEIGHT

S. Hermesch¹, B.G. Luxford² and H. -U. Graser¹

¹Animal Genetics and Breeding Unit^{*}, University of New England, Armidale, NSW 2351 ²Bunge Meat Industries, Corowa, NSW 2646

SUMMARY

Genetic parameters were estimated for litter traits from 2297 litters of 1767 sows from three maternal lines of a commercial breeding herd. Heritability estimates were 0.05 and 0.06 for total number of piglets born (NBT) and number of piglets that died per litter (NDIED). Heritabilities were higher for total litter weight (TLWB: 0.16), average piglet weight per litter (APWB: 0.31) and the harmonic mean (HMPWB: 0.28). Selection to reduce within litter variation is achievable given the heritability of 0.11 for coefficient of within litter variation (CVPWB). Litter size (NBT) was positively correlated with TLWB (rg: 0.54) and NDIED (rg: 0.76), but had no significant genetic relationships with the other traits. Litter mortality was negatively correlated (rg: -0.46) with APWB and HMPWB. HMPWB is genetically the same trait as APWB and does not provide additional information. The alternative description of within-litter variation (CVPWB) had no significant genetic correlation with other litter traits and provides little opportunity for genetic improvement of litter mortality. Instead, APWB should be considered in selection programs in addition to litter size to improve piglet weights and piglet survival.

Keywords: Pigs, genetic parameters, litter mortality, litter size, litter weight.

INTRODUCTION

A major goal of improving reproductive performance of the sow is to increase the number of piglets weaned. In order to achieve this goal breeding programs have primarily focussed on improving litter size. However, the number of piglets weaned depends not only on the number of piglets born but also on the piglet's viability. A review of selection experiments showed that the proportion of piglets born dead increases with selection for litter size (Blasco *et al.* 1995). In addition, Le Dividich (1999) described the weight of the piglet at birth and the within-litter variation of piglet weights at birth as major causes for perinatal mortality. Previous research has shown that the average piglet weight at birth is genetically unfavourably correlated with litter size (Tholen *et al.* 1996; Hermesch *et al.* 2000). However, information about genetic relationships between within-litter variation, pre-weaning piglet mortality and further reproductive performance of the sow is limited since the required data is not recorded routinely in breeding herds. The aim of this paper is to present estimates of genetic parameters for litter size, litter birth weight, average piglet weight at birth, within-litter variation of piglet birth weight and piglet mortality recorded in a commercial nucleus herd.

MATERIAL AND METHODS

Individual piglet weights at birth were recorded for 2297 litters of 1767 sows from three maternal

^{*} AGBU is a joint institute of NSW Agriculture and The University of New England

Proc. Assoc. Advmt. Anim. Breed. Genet. Vol 14

lines over a time period of two years at Bunge Meat Industries. These sows with litter records were from 237 sires and 1196 sows. The pedigree included four generations with 486 sires and 2463 dams in total. Every piglet of each litter, including stillbirths, was individually weighed within 12 hours of birth. These piglet records were used to derive the litter traits of the sow, including number of piglets born in total (NBT), total litter birth weight (TLWB) and average piglet weight at birth (APWB). Mortality rate of each litter (NDIED) was described as the number of recorded piglets dying per litter within 30 days of birth and included the number of stillbirths per litter. The within-litter variation was defined by the coefficient of variation of individual piglet weights within a litter (CVPWB) and the harmonic mean of the piglet weights. The harmonic mean (HMPWB) is defined as the reciprocal of the arithmetic mean of reciprocals

$$HMPWB = n \bigg/ \sum_{i=1}^{n} \frac{1}{x_i}$$

where n is the number of observations (x_i).

The fixed effect model for each trait was derived using the SAS procedure GLM (SAS 1988). Month of farrowing, line and parity of the sow were significant effects for all traits analysed. The interaction of line by parity was significant for APWB and HMPWB. An alternative fixed effect model fitting litter size (NBT) as a linear covariable was applied to CVPWB. Variance components were estimated using ASREML (Gilmour *et al.* 1999) applying an animal model with the permanent environment of the sow fitted as an additional random effect to take repeated records into account.

RESULTS

The traits NBT and NDIED were characterised by a low coefficient of variation and low heritabilities of 0.06 and 0.05 (Table 1). Among the litter traits analysed, APWB and the similar trait HMPWB had the largest heritability estimates of 0.31 and 0.28. Selection for a reduced within-litter variation is possible given the heritability estimates of 0.11 for CVPWB. Including NBT as a linear covariable in the model (CVPWB-A) resulted in an increase of the coefficient of determination from 0.07 to 0.19 but had no significant effect on the heritability estimate. There was no variation due to the permanent environment of the sow for CVPWB. In contrast, other litter traits had estimates of the permanent environment of the sow as a proportion of the phenotypic variance in the range of 0.05 to 0.14.

Table 1. Coefficient of determination (\mathbb{R}^2), heritabilities (h^2) and permanent environment of the sow (pe_{sow}) as a proportion of the phenotypic variance (σ_p^2) for litter traits of the sow

Trait		Ν	\mathbf{R}^2	h ²	se*1	pe _{sow}	se	σ_{p}^{2}
NBT		2281	0.06	0.06	0.03	0.11	0.05	7.88
NDIED		2297	0.05	0.05	0.03	0.05	0.05	3.27
TLWB	kg	2278	0.17	0.16	0.04	0.14	0.05	14.1
APWB	kg	2281	0.16	0.31	0.05	0.14	0.05	0.05539
HMPWB	kg	2281	0.13	0.28	0.05	0.11	0.05	0.06089
CVPWB	%	2278	0.07	0.11	0.03	0.00	-	37.8
CVPWB-A* ²	%	2278	0.19	0.12	0.03	0.00	-	32.9

^{*1} standard error; *² adjusted for NBT

Proc. Assoc. Advmt. Anim. Breed. Genet. Vol 14

Litter size was genetically highly correlated with NDIED (0.76 ± 20) and TLWB (0.54 ± 0.15) but had no significant genetic relationship with further litter traits included in this study (Table 2). The unfavourable negative phenotypic correlation between NBT and APWB was mainly based on the permanent environment of the sow (-0.60 ± 03). Litter mortality (NDIED) had a genetic correlation of -0.46 ± 0.20 with APWB and HMPWB. Genetic correlations between these two traits (APWB and HMPWB) and further reproductive traits were similar supporting the genetic correlation of unity between them. Piglet weights at birth as described by APWB and HMPWB had a negative genetic relationship with within-litter variation. The harmonic mean takes within litter variation into account and the genetic correlation with CVPWB was slightly stronger for HMPWB (-0.36 ± 0.14) in comparison with APWB (-0.27 ± 0.15). Adjustment of CVPWB for NBT did not allow estimation of the genetic correlation between CVPWB-A and NBT. Genetic correlations with NDIED and TLWB were reduced to -0.08 ± 32 and -0.51 ± 11 . The different fixed effect model had no influence on genetic correlations between CVPWB and average piglet weight traits.

Table 2. Genetic and phenotypic correlations (x 100) (1st and 2nd row above diagonal) and correlations of permanent environment of the sow and temporary environment (1st and 2nd row below diagonal) along with standard errors (x 100, in brackets) for litter traits of the sow

Trait	NBT		NDIED		TL	TLWB		APWB		HMPWB		CVPWB	
NBT			76	(20)	54	(15)	-17	(20)	-18	(20)	22	(26)	
			50	(01)	82	(01)	-47	(02)	-49	(02)	36	(02)	
NDIED	56	(33)			14	(27)	-46	(20)	-46	(20)	05	(33)	
	48	(03)			25	(02)	-43	(02)	-46	(02)	22	(02)	
TLWB	68	(14)	-18	(45)			73	(11)	71	(12)	-08	(18)	
	89	(01)	32	(04)			08	(02)	05	(02)	14	(02)	
APWB	-35	(26)	-55	(32)	38	(26)			99	(-)*	-26	(12)	
	-60	(03)	-47	(03)	-21	(04)			99	(-)*	-47	(02)	
HMPWB	-40	(30)	-58	(35)	44	(35)	99	(-)*			-32	(13)	
	-60	(02)	-48	(04)	-23	(04)	99	(-)*			-56	(02)	
CVPWB	-		-		-		-		-				
	39	(03)	23	(03)	21	(03)	-55	(02)	-67	(02)			

* se could not be estimated

DISCUSSION

Litter size has been analysed before in Australian studies and the heritability estimate found in this study was slightly lower than estimates presented previously (Tholen *et al.* 1996; Hermesch *et al.* 2000). However, the quantity of the data used in this study is limited and differences were not significant. Litter mortality was described as the number of piglets dying per litter. In comparison, other studies have often used the proportion of piglets surviving to describe litter mortality. Despite these differences in trait definitions the heritability estimate of 0.05 for NDIED equals the mean heritability estimate for litter survival of 16 studies reviewed by Rothschild and Bidanel (1998). Heritability estimates for litter weight traits (TLWB and APWB) correspond well to previous studies (Tholen *et al.* 1996; Hermesch *et al.* 2000).

Proc. Assoc. Advmt. Anim. Breed. Genet. Vol 14

The permanent environment of the sow explained no variation for CVPWB and additional analyses were carried out treating CVPWB as a different trait in the first parity and later parities. These analyses showed that the heritability estimate for CVPWB was higher in the first parity (0.22 ± 0.08) than in later parities (0.08 ± 0.05). The proportion of variation in CVPWB that was explained by the permanent environment of the sow was 0.03 ± 0.07 when only later parities were considered. In addition, this trait was genetically a different trait in the first parity in comparison to later parities ($rg: 0.35\pm0.26$) and might better be considered in a bivariate analysis. Overall, the phenotypic relationship between uniform litter weights and litter mortality as described by Le Dividich (1999) was also observed in this study but was due to an environmental correlation rather than a genetic relationship indicating limited use of this trait for genetic improvement of litter mortality.

A summary of selection experiments for litter size showed that the increase in number born dead represented up to half of the total increase in litter size (Blasco *et al.* 1995). This genetic relationship is confirmed in this study. However, the strong genetic correlation of 0.79 between NBT and NDIED may partly be due to the trait definition of NDIED. The average piglet weight at birth (APWB) is the second trait with a significant genetic relationship with NDIED. The unfavourable genetic correlation between NBT and APWB was lower in this study than previously reported (Tholen *et al.* 1996; Hermesch *et al.* 2000). Average piglet weight at birth has a moderate heritability and should be considered in breeding programs to avoid further increase in litter mortality rates as a result of selection for increased litter size.

ACKNOWLEDGEMENT

The Pig Research and Development Corporation provided funding for this project (UNE23P). Diligent data recording by Trina Adams and Leigh McKenzie at Bunge Meat Industries is greatly appreciated.

REFERENCES

Blasco, A., Bidanel, J.P. and Haley, C.S. (1995) In "The neonatal pig. Development and survival". p 17, editor M.A Varley, CAB International, Wallingford.

Gilmour, A.R., Cullis, B.R., Welham, S.J. and Thompson, R. (1999) "NSW Agriculture Biometric Bulletin No. 3. ASREML Reference Manual". NSW Agriculture, Orange, NSW, Australia

Hermesch, S., Luxford, B.G. and Graser, H.-U. (2000) Livest. Prod. Sci. 65: 261.

Le Dividich, J. (1999) In "Manipulating Pig Production Vol VII". p. 135, editor P.D. Cranwell, Australasian Pig Science Association, Adelaide.

Rothschild, M.F. and Bidanel, J.P. (1998) In "The genetics of the pig". p 313 editor M.F. Rothschild and A. Ruvinsky, CAB International, Wallingford.

SAS/STATS (1988) "User's Guide" Release 6.03 Edition., SAS Institute Inc.

Tholen, E., Bunter, K.L., Hermesch, S. and Graser, H. - U. (1996) Austr. J. Agric. Res. 47: 1275.