

The mixed model equation used in the repeatability models can be written in matrix notation as:

$$\mathbf{Y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{u} + \mathbf{W}\mathbf{c} + \mathbf{e} \quad [3-7]$$

where \mathbf{Y} represents the vector of observations of different parities, \mathbf{b} represents the vector of the fixed effects, \mathbf{u} represents a vector of additive genetic effects $\sim (0, \mathbf{A}\sigma_a^2)$; \mathbf{c} is the vector of random permanent non-genetic effects $\sim (0, \mathbf{I}_c\sigma_c^2)$; and \mathbf{e} represents a vector of residual effects $\sim (0, \mathbf{I}_e\sigma_e^2)$. \mathbf{X} , \mathbf{Z} and \mathbf{W} are known incidence matrices and \mathbf{I}_c and \mathbf{I}_e are identity matrices.

The variance covariance structure of random effects of the repeatability animal model was:

$$\mathbf{V} \begin{bmatrix} \mathbf{u} \\ \mathbf{p} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{A}\sigma_a^2 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{I}_c\sigma_c^2 & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{I}_e\sigma_e^2 \end{bmatrix} \quad [3-8]$$

where σ_a^2 is the direct additive genetic variance and σ_c^2 is the variance due to permanent environmental effects and σ_e^2 is the residual variances.

Bi-variate model

Genetic and phenotypic correlations across traits and within parities 1, 2 and 3 were estimated using a bi-variate animal model.

The mixed model equations used in the bi-variate analyses can be written in matrix notation as:

$$\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_2 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_2 \end{bmatrix} \begin{bmatrix} \mathbf{u}_1 \\ \mathbf{u}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix} \quad [3-9]$$

where \mathbf{y}_1 and \mathbf{y}_2 represents the vector of observations of different parities, \mathbf{b}_1 and \mathbf{b}_2 represents the vector of the fixed effects, \mathbf{u}_1 and \mathbf{u}_2 represents a vector of additive genetic effects $\sim (0, \mathbf{A}\sigma_a^2)$ and \mathbf{e}_1 and \mathbf{e}_2 represents a vector of residual effects $\sim (0, \mathbf{I}\sigma_e^2)$. The matrix \mathbf{X}_1 is the incidence matrix for the fixed effects of trait one and \mathbf{X}_2 is the incidence matrix for the fixed effects of trait two; the \mathbf{Z}_1 and \mathbf{Z}_2 matrixes are the incidence matrix relating observations on trait one and two to animals; \mathbf{A} is the additive genetic relationship matrix and \mathbf{I} is the identity matrix.

The variance covariance structure of random effects of the bi-variate animal model was:

$$V \begin{bmatrix} u_1 \\ u_2 \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} A\sigma_{a1}^2 & A\sigma_{a12} & 0 & 0 \\ A\sigma_{a21} & A\sigma_{a2}^2 & 0 & 0 \\ 0 & 0 & I\sigma_{e1}^2 & I\sigma_{e12} \\ 0 & 0 & I\sigma_{e21} & I\sigma_{e2}^2 \end{bmatrix} \quad [3-10]$$

where σ_{a1}^2 and σ_{a2}^2 are direct additive genetic variances, and σ_{e1}^2 and σ_{e2}^2 are the residual variances for traits 1 and 2 respectively; σ_{a12} is the direct genetic covariance between traits 1 and 2, and σ_{e12} their residual covariance.

Genetic parameters were analysed using restricted maximum likelihood (REML) method with an average information algorithm as implemented in the ASREML software (Gilmour et al., 2002).

3.3.2.2 Fixed Effects

Fixed effects were tested using PROC GLM in SAS (SAS Institute Inc, 1990). Significance levels are presented for fixed effects included in **b** in equation [3-7] in Table 3-12 and for fixed effects included in **b**_{1,2,3} in equations [3-5] and [3-9] in Table 3-13.

Farrowing season (FS) was defined as a three month period: summer (December to February), autumn (March to June), winter (July to August) and spring (September to November).

Litter breed (LB) had two levels: purebred and crossbred.

Farrowing day (FD) was defined as the day of the week when the litter was born (Monday to Sunday).

Mating Type (MAT) had two levels: natural mating or artificial insemination, depending on the type of mating used for that litter.

Parity (PAR) was included in the repeatability models.

Age at Farrowing (AF) was fitted as linear covariable (in days) in the models analysing individual parities.

Age Group (AGp) was fitted as a class in the repeatability models, nested within parity. It had 50 classes including the age at farrowing in days starting at 296 days with classes of 30 days.

All possible interactions were tested and later excluded from the models due to being non significant ($P > 0.05$).

Table 3-12 Fixed effects for reproductive traits in parities 2 to 10 (2+) and total variation explained by these effects (R^2)

Trait	R^2	Breed	Fixed effects				
			FS	LB	FD	PAR(AGp)	MAT
TNB ₂₊	0.11	LW	***	***	***	***	*
	0.11	LR	***	NS	***	***	NS
NBA ₂₊	0.08	LW	***	***	***	***	
	0.08	LR	***	NS	***	***	
GL ₂₊	0.35	LW	***		***	**	
	0.31	LR	***		***	NS	
NWea ₂₊	0.10	LW	***			***	
	0.13	LR	***			***	
AvBW ₂₊	0.10	LW	***	***		***	
	0.10	LR	***	NS		***	
Av21dW ₂₊	0.11	LW	***			NS	
	0.13	LR	***			*	

*** $P < 0.1\%$; ** $P < 1\%$; * $P < 5\%$; NS not significant however included in the model.

FS= Farrowing season; LB=Litter breed; FD=Farrowing day; PAR(AGp)=Age Group nested within parity; MAT=Mating type

Table 3-13 Fixed effects for reproductive traits in parities 1 to 3 and total variation explained by these effects (R^2)

Trait	R^2	Breed	Classes				Covariables
			FS	LB	FD	MAT	AF
TNB ₁	0.04	LW	***				***
	0.07	LR	***			**	
TNB ₂	0.07	LW	**	**	***		***
	0.08	LR	**	NS	***		***
TNB ₃	0.07	LW	*	***	***		
	0.07	LR	***	*	***		
NBA ₁	0.03	LW	*				
	0.06	LR	***			***	
NBA ₂	0.06	LW	**	***	***		***
	0.08	LR	***	NS	***		**
NBA ₃	0.07	LW	NS	***	***		
	0.07	LR	**	NS	***		
GL ₁	0.07	LW	***		**		
	0.07	LR	***		*		
GL ₂	0.29	LW	***		***		**
	0.20	LR	**		***		NS
GL ₃	0.38	LW	***		***		
	0.33	LR	***		***		
NWea ₁	0.14	LW	***				
	0.17	LR	***				
NWea ₂	0.10	LW	***				
	0.14	LR	***				
NWea ₃	0.08	LW	***				
	0.10	LR	***				
AvBW ₁	0.05	LW	***				
	0.06	LR	***				
AvBW ₂	0.05	LW	NS	***			
	0.07	LR	***	NS			
AvBW ₃	0.08	LW	***	***			
	0.05	LR	*	NS			
Av21dW ₁	0.06	LW	***				
	0.17	LR	***				
Av21dW ₂	0.21	LW	***				*
	0.12	LR	***				***
Av21dW ₃	0.15	LW	***				
	0.11	LR	***				

*** $P < 0.1\%$; ** $P < 1\%$; * $P < 5\%$; NS not significant however included in the model.

FS= Farrowing season; LB=Litter breed; FD=Farrowing day; MAT=Mating type; AF=Age at farrowing;

3.3.2.3 Random Effects

The only random effect used in the analyses for traits recorded in one parity was the additive direct genetic effect of the sow. An additional permanent environmental effect of the sow was included when analysing repeated records over different parities. Service sire effect was considered and later excluded from the model because the estimates were really small and in all cases were smaller than their standard errors, and thus not significant. Small service sire effects were fitted by Chen et al. (2003), See et al. (1993) and Serenius et al. (2003), however the majority of studies did not include this effect. Maternal genetic effects and common family environmental effects were not included in the analyses; preliminary univariate analyses showed that these random effects were not significant ($P < 0.05$). This approach is in agreement with other authors i.e.: Alfonso et al., 1997; Chen et al., 2003; Crump et al. 1997; Hermes et al., 2001a; Roehe and Kennedy, 1995.

3.4 Results and Discussion

3.4.1 Heritabilities

The heritability estimates and variance components for reproductive traits of LW and LR sows are presented in Tables 3-14 to 3-19.

3.4.1.1 Estimates for litter size

Total Number of Piglets Born (TNB)

Heritability estimates for the trait TNB ranged from 0.10 to 0.23. The repeated records estimates were 0.10 for LR and 0.18 for LW. Individual parity estimates were 0.16, 0.18 and 0.23 for LW and 0.17, 0.10 and 0.16 for LR respectively for parities 1, 2 and 3.

Estimates obtained from a repeatability model for the LR breed (Table 3-14) were slightly lower than the average estimate found in the literature review (see Table 3-1). In contrast, the estimates

from the repeatability model for LW breed were higher than the average estimate from the literature.

Table 3-14 Number of records, parity, heritability (h^2), standard error (s.e.), repeatability (r) and variance components of total number born (TNB) for Large White (LW) and Landrace (LR) sows

TNB	Parity	Records	h^2	s.e.	R	s.e.	σ_C^2	σ_A^2	σ_E^2	σ_P^2
LW	1	2,657	0.16	0.03	-	-	-	1.34	6.83	8.17
	2	2,276	0.18	0.04	-	-	-	1.82	8.23	10.05
	3	1,868	0.23	0.04	-	-	-	2.43	7.97	10.40
	2+	8,374	0.18	0.02	0.29	0.01	1.12	1.87	7.39	10.38
LR	1	1,752	0.17	0.04	-	-	-	1.23	5.64	6.87
	2	1,458	0.10	0.04	-	-	-	0.78	7.23	8.01
	3	1,241	0.16	0.05	-	-	-	1.35	6.94	8.29
	2+	5,541	0.10	0.02	0.18	0.02	0.72	0.88	7.03	8.63

σ_C^2 = perm. environm. variance; σ_A^2 = additive genetic variance; σ_E^2 = environmental variance; σ_P^2 = phenotypic variance

Phenotypic variance (σ_P^2) was consistently smaller in the first parity in both breeds, and subsequently increased with parity, indicating that first parity gilts are more uniform at their TNB performance, in both breeds. In addition, environmental variance (σ_E^2) was higher in parity two for both breeds. Additive genetic variance (σ_A^2) increased with parity for the Large White breed and was smaller in parity two for the Landrace breed. In addition (σ_A^2) in parity 3 for Large White sows was notably higher than in previous parities.

Number Born Alive (NBA)

Heritability estimates for NBA ranged from 0.11 up to 0.23. The repeated records estimates were 0.11 for LR and 0.16 for LW. Individual parity estimates were 0.18, 0.17 and 0.19 for LW and 0.16, 0.11 and 0.23 for LR respectively for parities 1, 2 and 3. Estimates observed in this study (Table 3-15) for the Large White breed are slightly higher than the average estimate found in the review of the literature (Table 3-2).

Table 3-15 Number of records, parity, heritability (h^2), standard error (s.e.), repeatability (r) and variance components of number born alive (NBA) for Large White (LW) and Landrace (LR) sows

NBA	Parity	Records	h^2	s.e.	r	s.e.	σ_C^2	σ_A^2	σ_E^2	σ_P^2
LW	1	2,657	0.18	0.03	-	-	-	1.31	6.11	7.42
	2	2,276	0.17	0.04	-	-	-	1.52	7.37	8.89
	3	1,868	0.19	0.04	-	-	-	1.56	6.82	8.38
	2+	8,374	0.16	0.02	0.25	0.01	0.75	1.37	6.42	8.54
LR	1	1,752	0.16	0.04	-	-	-	0.99	5.31	6.30
	2	1,458	0.11	0.04	-	-	-	0.79	6.42	7.21
	3	1,241	0.23	0.05	-	-	-	1.62	5.52	7.14
	2+	5,541	0.11	0.02	0.15	0.02	0.36	0.78	6.29	7.43

σ_C^2 = perm. environm. variance; σ_A^2 = additive genetic variance; σ_E^2 = environmental variance; σ_P^2 = phenotypic variance

The heritability estimate obtained for the repeatability model for the LW breed was similar to the result obtained by Johnson et al. (1999) where they analysed the response in litter traits to 14 generations of selection to increase litter size (0.17). The variance components of that study ($\sigma_A^2 = 1.37$, $\sigma_E^2 = 6.89$ and $\sigma_P^2 = 8.26$) were very similar to the ones presented in Table 3-15 for the LW breed, although the environmental variance was slightly lower in comparison to this study. Estimates from the repeatability model for the LR breed were in agreement with the average estimate observed in the summary of literature estimates presented in Table 3-2.

Similar to TNB, phenotypic variances (σ_P^2) were consistently smaller for the first parity in both breeds, and were higher for the second parity as a result of a higher environmental variance (σ_E^2) in both breeds. Additive genetic variance (σ_A^2) increased with parity for the Large White breed similarly to what occurred in other studies (Roehe and Kennedy, 1995; Tholen et al., 1996) and was considerably smaller in parity two for the Landrace breed.

Number of Piglets Weaned (NWea)

Low heritability estimates of 0.04 (LW) and 0.01 (LR) were obtained for the repeatability model for NWea (Table 3-16). The results obtained for the first three parities in the LR breed were similar (0.01), whereas the estimates for LW sows in parities 1, 2 and 3 were 0.05, 0.07 and 0.05 respectively. Estimates for the repeated records from LW breed are in agreement with the average estimate presented in Table 3-3. In contrast, the LR breed had estimates with very low additive variances and heritability estimates non-significantly different from 0 ($P>0.05$).

The trait NWea is strongly influenced by non-genetic factors such as cross-fostering practices. This means that not necessarily the biological mother has the maternal effect on a given piglet's survival, since the maternal effect for the piglet is the environmental effect of the sow that nurses it (Lund et al., 2002). This makes the definition and relevance of the trait Number of Piglets Weaned a challenge. Rothschild and Bidanel (1998) presented a review of 42 studies and reported a mean heritability for number of piglets weaned of 0.07 with a range between 0 and 1.0. This broad range included different definitions of the trait as well as different management practices which make the comparison between studies very difficult.

Table 3-16 Number of records, parity, heritability (h^2), standard error (s.e.), repeatability (r) and variance components of number of piglets weaned (NWea) for Large White (LW) and Landrace (LR)

NWea	Parity	Records	h^2	s.e.	r	s.e.	σ_C^2	σ_A^2	σ_E^2	σ_P^2
LW	1	1,109	0.05	.02	-	-	-	0.74	13.88	14.62
	2	979	0.07	.03	-	-	-	0.94	12.63	13.57
	3	870	0.05	.03	-	-	-	0.80	13.95	14.75
	2+	4,221	0.04	.01	0.08	0.01	0.56	0.58	13.69	14.83
LR	1	913	0.01	.01	-	-	-	0.12	15.21	15.33
	2	811	0.01	.01	-	-	-	0.10	13.02	13.12
	3	706	0.01	.01	-	-	-	0.11	13.26	13.37
	2+	3,241	0.01	.01	0.05	0.01	0.65	0.07	13.57	14.29

σ_C^2 = perm. environm. variance; σ_A^2 = additive genetic variance; σ_E^2 = environmental variance; σ_P^2 = phenotypic variance

3.4.1.2 Estimates for Average Piglet Weights

Average Piglet Birth Weight (AvBW)

Estimates for the heritability of AvBW ranged from 0.28 to 0.50. Repeated records estimates were 0.28 for the LR breed and 0.31 for the LW breed. Estimates for parities 1, 2 and 3 were 0.35, 0.34 and 0.41 for the LW breed and 0.50, 0.32 and 0.33 for the LR breed (Table 3-17).

The values obtained in this study are in line with the average estimate obtained in the summary of the literature estimates presented in Table 3-4 for the repeated records and slightly higher than the average of the individual parities estimates. The latter were similar to those obtained in an Australian study made by Tholen et al. (1996) using 9,590 records of a Landrace x Large White synthetic breed recorded during 1983-1995. Heritability estimates were slightly lower than the average estimate obtained by Lotta Rydhmer (2000) in her review (0.40).

Table 3-17 Number of records, parity, heritability (h^2), standard error (s.e.), repeatability (r) and variance components of average piglet birth weight (AvBW) for Large White (LW) and Landrace (LR)

AVBW	Parity	Records	h^2	s.e.	r	s.e.	σ_C^2	σ_A^2	σ_E^2	σ_P^2
LW	1	1,109	0.35	0.06	-	-	-	0.02	0.04	0.06
	2	979	0.34	0.06	-	-	-	0.02	0.05	0.07
	3	870	0.41	0.07	-	-	-	0.02	0.04	0.06
	2+	4,221	0.31	0.04	0.42	0.02	0.01	0.02	0.04	0.07
LR	1	913	0.50	0.08	-	-	-	0.03	0.03	0.06
	2	811	0.32	0.07	-	-	-	0.02	0.05	0.07
	3	706	0.33	0.07	-	-	-	0.02	0.04	0.06
	2+	3,241	0.28	0.04	0.38	0.02	0.01	0.02	0.04	0.07

σ_C^2 = perm. environm. variance; σ_A^2 = additive genetic variance; σ_E^2 = environmental variance; σ_P^2 = phenotypic variance

The heritability estimates of AvBW of LR sows in parity one had a larger additive variance (σ_A^2) and a smaller environmental variance (σ_E^2) than the other estimates and hence had a higher heritability.

Average Piglet Weight at 21 days (Av21dW)

Average piglet weight at 21 days recorded in parities 2 till 10 has a moderate heritability for LW (0.12) and LR (0.16) sows (Table 3-18). In LW, heritabilities decreased from 0.23 in the first parity to 0.09 in the third parity. Estimates did not differ significantly between parities (0.18 to 0.19) in LR.

Table 3-18 Number of records, parity, heritability (h^2), standard error (s.e.), repeatability (r) and variance components of average piglet weight at 21 days (Av21dW) for Large White (LW) and Landrace (LR)

AV21dW	Parity	Records	h^2	s.e.	r	s.e.	σ_C^2	σ_A^2	σ_E^2	σ_P^2
LW	1	1,109	0.23	0.04	-	-	-	0.15	0.53	0.68
	2	979	0.16	0.04	-	-	-	0.11	0.59	0.70
	3	870	0.09	0.04	-	-	-	0.06	0.60	0.66
	2+	4,221	0.12	0.02	0.21	0.01	0.07	0.08	0.56	0.71
LR	1	913	0.17	0.05	-	-	-	0.10	0.46	0.56
	2	811	0.19	0.05	-	-	-	0.10	0.43	0.53
	3	706	0.19	0.06	-	-	-	0.09	0.38	0.47
	2+	3,241	0.16	0.03	0.23	0.02	0.04	0.08	0.38	0.50

σ_C^2 =perm. environm. variance; σ_A^2 =additive genetic variance; σ_E^2 =environmental variance; σ_P^2 =phenotypic variance

Environmental variances (σ_E^2) for parities 1 to 3 increased from 0.53 to 0.60 for the LW breed and decreased from 0.46 to 0.38 for the LR breed.

The heritability estimates were slightly higher than the average of 0.10 presented in a review of nine studies by Hermes (1996). They were also higher than the average estimate (0.08) found in

the summary of the literature estimates in Table 3-15 for repeated records. In contrast, they were lower than the average estimates reviewed by Rotschild and Bidanel (1998) where they showed an average estimate of 0.17 after reviewing 15 studies.

3.4.1.3 Estimates of Gestation Length (GL)

Heritability estimates for GL decreased, from 0.46 to 0.37 (LW) and from 0.46 to 0.31 (LR) in the first to third parity (Table 3-19) due to a decrease in the additive variance. The estimates for the repeated records were 0.44 and 0.49 for the LW and LR breeds. These results were higher than the estimates shown in the review of the literature shown in Table 3-6.

Table 3-19 Number of records, parity, heritability (h^2), standard error (s.e.), repeatability (r) and variance components of gestation length (GL) for Large White (LW) and Landrace (LR)

GL	Parity	Records	h^2	s.e.	r	s.e.	σ_C^2	σ_A^2	σ_E^2	σ_P^2
LW	1	2,654	0.46	0.04	-	-	-	0.84	1.00	1.84
	2	2,275	0.40	0.04	-	-	-	0.57	0.85	1.42
	3	1,867	0.37	0.04	-	-	-	0.45	0.77	1.22
	2+	8,367	0.44	0.03	0.53	0.01	0.18	0.86	0.91	1.95
LR	1	1,751	0.46	0.05	-	-	-	0.91	1.06	1.97
	2	1,455	0.44	0.05	-	-	-	0.76	0.95	1.71
	3	1,240	0.31	0.05	-	-	-	0.43	0.95	1.38
	2+	5,532	0.49	0.04	0.53	0.02	0.09	1.00	0.95	2.04

3.4.2 Genetic Correlations

3.4.2.1 Correlations across traits and within parities

Estimates of genetic and phenotypic correlations for reproductive traits of the sow are presented in Table 3-20 and Table 3-21 for LW and LR breeds respectively. Estimates of genetic correlations between litter size traits at birth (TNB and NBA) ranged from 0.94 to 0.99 among parities and

breeds in agreement with previous studies (Nguyen et al., 2003; Roehe and Kennedy, 1995). TNB and NBA can be treated as the same trait.

Table 3-20 Genetic correlations (above diagonal) and Phenotypic correlations (below diagonal) with standard errors, across reproductive traits within parities 1, 2 and 3 for Large White sows

Trait	Parity	NBA	TNB	NWea	GL	AvBW	AvWW
NBA	1		0.97 ± 0.02	-0.23 ± 0.22	0.17 ± 0.12	-0.61 ± 0.10	-0.36 ± 0.14
	2		0.98 ± 0.01	-0.96 ± 0.24	0.12 ± 0.14	-0.64 ± 0.11	-0.72 ± 0.17
	3		0.99 ± 0.01	0.01 ± 0.28	-0.18 ± 0.13	-0.59 ± 0.13	-0.92 ± 0.19
TNB	1	0.91 ± 0.003		-0.22 ± 0.23	0.20 ± 0.12	-0.60 ± 0.10	-0.35 ± 0.14
	2	0.94 ± 0.002		-0.83 ± 0.24	0.17 ± 0.13	-0.61 ± 0.11	-0.61 ± 0.17
	3	0.91 ± 0.004		-0.13 ± 0.26	-0.08 ± 0.12	-0.43 ± 0.13	-0.83 ± 0.20
NWea	1	0.01 ± 0.02	-0.02 ± 0.02		-0.31 ± 0.18	0.35 ± 0.22	0.17 ± 0.24
	2	-0.02 ± 0.02	-0.02 ± 0.02		-0.14 ± 0.16	0.33 ± 0.23	0.59 ± 0.33
	3	0.02 ± 0.02	0.01 ± 0.02		-0.19 ± 0.20	0.37 ± 0.25	0.58 ± 0.45
GL	1	-0.12 ± 0.02	-0.11 ± 0.02	-0.03 ± 0.02		-0.08 ± 0.12	0.06 ± 0.11
	2	-0.16 ± 0.02	-0.14 ± 0.02	-0.01 ± 0.02		-0.03 ± 0.13	-0.12 ± 0.14
	3	-0.16 ± 0.03	-0.13 ± 0.03	-0.03 ± 0.02		-0.23 ± 0.14	0.05 ± 0.22
AvBW	1	-0.57 ± 0.02	-0.59 ± 0.02	0.11 ± 0.03	0.10 ± 0.02		0.63 ± 0.12
	2	-0.60 ± 0.02	-0.59 ± 0.02	0.04 ± 0.03	0.11 ± 0.03		0.44 ± 0.18
	3	-0.58 ± 0.02	-0.57 ± 0.02	0.05 ± 0.03	0.16 ± 0.03		0.78 ± 0.26
AvWW	1	-0.16 ± 0.02	-0.16 ± 0.02	-0.24 ± 0.03	0.10 ± 0.02	0.36 ± 0.03	
	2	-0.16 ± 0.02	-0.16 ± 0.02	-0.33 ± 0.03	0.07 ± 0.03	0.35 ± 0.03	
	3	-0.16 ± 0.03	-0.18 ± 0.03	-0.23 ± 0.03	0.13 ± 0.03	0.31 ± 0.04	

Moderate to high negative genetic correlations were found between litter size traits (TNB and NBA) and AvBW (-0.54 to -0.83) among parities and breeds showing a higher antagonistic relationship than previous studies (Hermesch et al., 2000b; Nguyen et al., 2003; Tholen et al., 1996). These results indicate that selection for litter size will result in lighter piglets in average at birth. Myora's outstanding performance in litter size, higher than the highest value published for any Australian piggery by Australian Pork Limited annual report 2003 (APL, 2003), may have contributed to these high correlations.

Estimates of genetic correlations between NBA and Av21dW were moderately to highly antagonistic for Large White, increasing with parity (-0.36, -0.72 and -0.92). Similar genetic relationships were found between TNB and Av21dW with estimates of -0.35, -0.61 and -0.83. In Landrace sows, this correlation was lower (-0.25, -0.05 and -0.09). Similar relationships were found between TNB and Av21dW being the estimates -0.17, -0.11 and -0.07. These estimates were consistent with those reported by Hermes et al. (2000b) and Tholen et al. (1996) in two Australian studies and had opposite signs of those reported by Chen et al. (2003) in an American study with 50% of cross-fostering across litters. Such a high level of cross-fostering can be causing this difference with other studies. The different levels of performance in litter size between breeds at Myora Farm, higher for LW sows, and in Av21dW, higher for LR sows, may be responsible for the differences across breeds for these correlations.

The genetic correlation between NBA and NWea in the Large White breed was negative for parities one (-0.23) and two (-0.96). In contrast, parity three had a genetic correlation of 0.01 between these two traits. These results are indicating that Large White sows with larger litters at farrowing don't have the genetic potential to wean more piglets. In other study, Johnson et al. (1999) found a negative genetic correlation between NWea and the number of live fetuses at 50 days of gestation, which had a positive genetic correlation with NBA, in a population selected over 14 generations for increased ovulation rate and litter size as well as subject to cross-fostering. The authors concluded that the lighter weight at birth of piglets from big litters at birth were responsible for this correlation. All previous studies reported positive correlations between NBA and NWea (Bizelis et al., 2000; Chen et al., 2003; Nguyen et al., 2003; Roehe and Kennedy, 1995; Tholen et al., 1996). The lack of additive variance in the trait NWea in the LR breed caused the standard errors for genetic correlations of this trait to be very high and in many cases the estimates were out of the parameter space, hence the correlations obtained in this case can be misleading. In addition, in cases with very low heritabilities (0.01) the definition of the genetic correlation is difficult because the denominator is tending to 0 which often results in very high positive or negative correlations depending on the sign of the covariance estimate.

The genetic correlation between NBA and GL ranged from 0.17, 0.12 and -0.18 in LW sows and -0.03, 0.05 and -0.16 in LR sows. The results of parity three are in line with the correlation reported

by (Nguyen et al., 2003) among all parities in an Australian LW population. High standard errors were obtained for these estimates.

Average birth weight was positively correlated with NWea among parities 1, 2 and 3 for LW sows (0.35 0.33 and 0.37) similar to results obtained by Nguyen et al. (2003). A high positive genetic correlation was found between AvBW and Av21dW for both breeds. Estimates were 0.63, 0.44 and 0.78 for Large White and 0.46, 0.51 and 0.69 for Landrace. Selection for higher average piglet weights at birth will lead to heavier piglets in average at 21 days post farrowing in both breeds and in Large White, sows will wean more piglets as well.

Number of piglets weaned was positively correlated with Av21dW (0.17, 0.59 and 0.58) among parities in LW sows.

Table 3-21 Genetic (above diagonal) and Phenotypic correlations (below diagonal) with standard errors across reproductive traits within parities 1, 2 and 3 for Landrace sows

Trait	Parity	NBA	TNB	NWea	GL	AvBW	AvWW
NBA	1		0.95 ± 0.03	-0.34 ± 0.87	-0.03 ± 0.15	-0.72 ± 0.11	-0.25 ± 0.20
	2		0.94 ± 0.05	-0.99 ± 0.00	0.05 ± 0.24	-0.83 ± 0.18	-0.05 ± 0.28
	3		0.99 ± 0.02	-0.91 ± 1.13	-0.16 ± 0.16	-0.54 ± 0.15	-0.09 ± 0.21
TNB	1	0.91 ± 0.004		-0.44 ± 0.86	-0.12 ± 0.14	-0.70 ± 0.11	-0.17 ± 0.20
	2	0.93 ± 0.004		-0.99 ± 0.00	0.12 ± 0.24	-0.94 ± 0.17	-0.11 ± 0.28
	3	0.89 ± 0.006		-0.64 ± 1.27	0.17 ± 0.23	-0.58 ± 0.16	-0.07 ± 0.24
NWea	1	0.02 ± 0.02	0.01 ± 0.02		0.13 ± 0.55	0.98 ± 1.10	0.70 ± 1.46
	2	-0.004 ± 0.03	-0.01 ± 0.03		-0.16 ± 0.66	0.16 ± 0.80	1.00 ± 3.06
	3	-0.02 ± 0.03	-0.02 ± 0.03		-0.39 ± 1.34	1.18 ± 2.73	-0.02 ± 0.88
GL	1	-0.14 ± 0.03	-0.15 ± 0.03	-0.06 ± 0.03		-0.18 ± 0.12	0.11 ± 0.14
	2	-0.17 ± 0.03	-0.14 ± 0.03	-0.02 ± 0.03		0.02 ± 0.17	0.24 ± 0.15
	3	-0.18 ± 0.03	-0.12 ± 0.03	-0.02 ± 0.03		0.08 ± 0.20	0.21 ± 0.21
AvBW	1	-0.50 ± 0.03	-0.49 ± 0.03	0.05 ± 0.03	0.06 ± 0.04		0.46 ± 0.14
	2	-0.57 ± 0.02	-0.58 ± 0.02	0.05 ± 0.04	0.11 ± 0.04		0.51 ± 0.17
	3	-0.56 ± 0.03	-0.53 ± 0.03	0.03 ± 0.04	0.10 ± 0.04		0.69 ± 0.14
AvWW	1	-0.14 ± 0.03	-0.14 ± 0.03	-0.21 ± 0.04	0.12 ± 0.03	0.41 ± 0.03	
	2	-0.10 ± 0.03	-0.11 ± 0.03	-0.32 ± 0.04	0.10 ± 0.03	0.38 ± 0.03	
	3	-0.14 ± 0.03	-0.13 ± 0.03	-0.54 ± 0.03	0.16 ± 0.03	0.41 ± 0.04	

3.4.2.2 Correlations within traits and among parities

In order to test if different parities should be treated as separate traits, records from different parities within each reproductive trait were analysed separately assuming they are separate traits. A genetic correlation among parities of 1 will assume that the same trait recorded in different parities is genetically the same trait.

Genetic correlation among parities 1, 2 and 3 for NBA in LW sows were significantly ($P < 0.1$) different from 1 (0.83) between parities 1 and 2 as well as 1 and 3 (0.84). In LR sows, this correlation was significantly different ($P < 0.1$) from 1 between parities 1 and 2 (0.75) as well as between parities 2 and 3 (0.70). For the trait TNB, LW sows had a genetic correlation significantly different from unity ($P < 0.1$) for parities 1 and 2 (0.81), as well as 1 and 3 (0.83). There was no significant difference ($P < 0.1$) from unity in genetic correlations for TNB of LR sows due to the size of the standard errors.

Average piglet weight at birth in LW sows had a genetic correlation significantly different ($P < 0.05$) from unity (0.82) between parities 1 and 3, and a non significant differences ($P > 0.1$) between parities 1 and 2 (1.02), as well as for parities 2 and 3 (0.99). In contrast, none of the genetic correlations for AvBW in LR sows were different from unity. Genetic correlations for Av21dW were significantly ($P < 0.1$) different from unity between parities 1 and 2 (0.80) in LW sows and between parities 2 and 3 (0.61) in LR sows ($P < 0.05$).

Several correlations in Table 3-22 had results out of the parameter space i.e. NBA_2 and NBA_3 1.07 ± 0.07 . This was due to the need of setting these correlations without constraints in ASREML (Gilmour et al. 2002) for making them converge.

Table 3-22 Genetic correlations (above diagonal) and Phenotypic correlations (below diagonal) with standard errors within reproductive traits among parities 1, 2 and 3 for Large White and Landrace sows

	Parity	Large White			Landrace		
		1	2	3	1	2	3
NBA	1		0.83 ± 0.10	0.84 ± 0.11		0.97 ± 0.16	0.75 ± 0.15
	2	0.21 ± 0.02		1.07 ± 0.07	0.16 ± 0.03		0.70 ± 0.18
	3	0.22 ± 0.02	0.30 ± 0.02		0.17 ± 0.03	0.16 ± 0.03	
TNB	1		0.81 ± 0.10	0.83 ± 0.10		0.89 ± 0.18	0.82 ± 0.16
	2	0.22 ± 0.02		1.01 ± 0.06	0.17 ± 0.03		0.80 ± 0.20
	3	0.23 ± 0.02	0.33 ± 0.02		0.20 ± 0.03	0.21 ± 0.03	
NWea	1		0.89 ± 0.27	0.00 ± 0.35		-0.59 ± 0.0	0.99 ± 0.0
	2	-0.01 ± 0.02		0.72 ± 0.32	0.06 ± 0.03		-0.48 ± 0.0
	3	0.02 ± 0.02	0.09 ± 0.02		0.03 ± 0.03	0.03 ± 0.03	
AvBW	1		1.02 ± 0.06	0.82 ± 0.09		1.02 ± 0.05	1.00 ± 0.08
	2	0.38 ± 0.03		0.99 ± 0.06	0.42 ± 0.04		1.01 ± 0.09
	3	0.41 ± 0.04	0.44 ± 0.03		0.37 ± 0.04	0.43 ± 0.04	
Av21dW	1		0.80 ± 0.12	0.84 ± 0.20		0.89 ± 0.15	0.61 ± 0.20
	2	0.20 ± 0.03		1.16 ± 0.17	0.21 ± 0.03		0.84 ± 0.15
	3	0.13 ± 0.03	0.21 ± 0.03		0.19 ± 0.04	0.25 ± 0.03	
GL	1		0.94 ± 0.03	0.92 ± 0.04		0.98 ± 0.03	1.00 ± 0.04
	2	0.50 ± 0.02		0.97 ± 0.03	0.52 ± 0.02		1.01 ± 0.04
	3	0.46 ± 0.02	0.50 ± 0.02		0.44 ± 0.03	0.48 ± 0.03	

Large White sows had a genetic correlation significantly different from 1 ($P < 0.05$) for the trait GL between parities 1 and 2 (0.94) and between parities 1 and 3 (0.92). In addition, genetic correlations for GL recorded in LR were not significantly ($P < 0.05$) different from one.

Several authors (Alfonso et al., 1997; Bizelis et al., 2000; Crump et al., 1997; Serenius et al., 2003) prefer to treat different parities as repeated measurements of a trait, assuming a genetic correlation of 1 among parities, implementing a repeatability model. On the other hand a number of authors (Hanenberg et al., 2001; Hermes et al., 2000a; Irgang et al., 1994; Noguera et al., 2002; Roehe, 1999; Roehe and Kennedy, 1995; Rydhmer et al., 1994; Serenius et al., 2003; Taubert et al., 1998; Tholen et al., 1996) prefer to treat at least parity one as a different trait assuming that the genes that

regulate the expression of a trait at parity one are not necessarily doing the same influencing subsequent parities.

3.5 Discussion and Conclusions

Knowledge of heritability and genetic correlations is essential in order to estimate reliable breeding values by accounting for all relationships between traits in a multivariate BLUP analysis.

The breeding goal of most piggeries worldwide is to enhance the number of piglets weaned per sow per year. The importance of litter size at birth in pig improvement programs has increased at the same time as the economic weight of backfat thickness and, to a lesser extent, of feed conversion ratio have decreased (Perez-Enciso and Bidanel, 1997). The number of piglets born or born alive per litter is still the only reproduction trait used in most breeding programmes (Rydhmer, 2000) despite the fact that the number of piglets weaned is the main goal. Therefore, piggeries that have been selecting over a number of years for litter size and have reached a point where the number of piglets weaned is not increasing as expected, should include other traits in their breeding program to enhance the number of piglets weaned.

The heritability estimates found in this study for litter size in the Large White breed are higher than the mean estimate presented in the review of the literature on Table 3-2. However, these estimates are in line with the heritabilities reported by Johnson et al. (1999) in a study where they evaluated the responses in litter traits to 14 generations of selection to increase litter size. The Large White breed at Myora Farm had an average performance for NBA of more than 12 piglets over the last 10 years. This level of performance in litter size for the LW breed, slightly higher than the one reported by Johnson et al. (1999), is based on more than 12 years of selection using BLUP EBVs in order to enhance the prolificacy of this particular breed.

Acknowledging the fact that there is a negative correlation between NBA and NWea as shown in this study, and that the only reproductive trait included in the breeding programs of most piggeries is litter size (Rydhmer, 2000), it should be a priority to assure that the selection decisions take this antagonism into consideration. An increase in litter size will decrease the average piglet birth

weight as shown in this study, leading to an increase in pre-weaning mortality (Hermesch et al., 2001b; Knol et al., 2002). Therefore, the inclusion of average birth weight as a trait in the selection criteria is recommended in agreement with Rydhmer et al. (1994) and Hermesch et al. (2001b). The procedure of weighing litters within 12 hours after farrowing for recording birth weight, before any cross-fostering is done makes the trait AvBW more reliable than litter weight recorded 3 weeks after farrowing which is influenced by cross-fostering.

Roehe and Kalm (2000) showed that the single most important risk factor that affects pre-weaning mortality is the piglet's individual birth weight. However this trait is very labour intensive to record. Litter birth weight is commonly recorded and can be adjusted by the number of piglets weighed for being used as potential selection criteria. This adjustment of litter weight at birth for litter size is necessary, because its estimates are more in line with their expectations and not influenced by variation in litter size (Roehe, 1999).

The antagonistic correlation between NBA and AvBW as well as the positive correlation between NWea with AvBW and Av21dW reinforces the need for including AvBW in the selection criteria. The emphasis placed on NBA and AvBW in the \$Index should be done cautiously in order not to over-emphasize birth weight traits and unintentionally decrease litter size by selecting heavier piglets from smaller litters.

Estimates of genetic parameters can be biased by involuntary and directional selection from parity to parity (Roehe and Kennedy, 1995). In order to account for this possible source of bias, reproductive traits of the sow recorded in parities one to three were treated as separate traits. The results obtained in this study indicate that the hypothesis of genetic homogeneity between reproductive traits in different parities could be rejected for the Large White population. At least parity one should be treated as a separate trait for the traits NBA, TNB, AvBW, AvWW and GL considering them different traits genetically.

The genetic parameters obtained in this study indicate that there are opportunities for improving reproductive performance of the sow by selecting on more than litter size.