CHAPTER 3

GENETIC PARAMETER ESTIMATION FOR REPRODUCTIVE TRAITS

3.1 Introduction

The potential for genetic improvement of sow reproductive performance relies on the magnitude of genetic variance and heritabilities of the traits considered for selection, as well as the correlations among them and with other important traits included in the total merit index. Genetic differences between animals are the key factors that will allow breeders to make genetic improvement.

The use of reliable, precise and unbiased genetic parameters such as heritabilities and genetic correlations should be considered as a priority in any breeding program in order to "fine tune" their genetic evaluation procedures. Accurate genetic parameters are essential for the prediction of breeding values and for the prediction of the expected genetic response of selection programmes. It was suggested by Walters (1998) that nucleus breeders should use in their breeding programmes the specific parameters from the herd(s) of origin and recalculate those estimates periodically. Walters' suggestion is based on the fact that changes in genetic parameters can be expected in situations where traits are determined by only a few genes; when generation intervals are shorter; when there is a high selection intensity or high levels of inbreeding (Kinghorn and van der Werf, 2002).

Knowledge of genetic parameters of reproductive traits is essential to estimate accurate breeding values by accounting for all correlations available in a multivariate BLUP analysis. In addition, Roehe and Kennedy (1995) stated that genetic parameters will allow the breeder to combine different traits in selection, to optimise breeding schemes, and to predict genetic response to selection. They suggested that estimates of genetic parameters can be biased by involuntary and directional selection from parity to parity. In order to correct this possible bias, parities 1, 2 and 3 were analysed as separate traits using residual maximum likelihood methods under a tri-variate animal model.

The first objective of this chapter is to estimate heritabilities and genetic correlations across reproductive traits, at different parities for Myora Farms' Large White and Landrace breeds. The second objective is to estimate the genetic correlations among parities in order to test if different parities of the same trait should be treated as repeated records or as separate traits.

3.2 Literature Review

3.2.1 Heritability

A characteristic is not inherited as such. The thing inherited is the ability to respond in a given manner to a given environmental circumstance. "The observed phenotype of an animal is the net result of these inherited potentialities and the environmental circumstances, such as nutrient supply, temperature, diseases, accidents, etc., which it encounters" (Lush, 1948).

A question commonly asked when dealing with quantitative traits is: How much of the existing variation of a trait in a certain population is due to genetic causes and how much to environmental ones? (Lynch and Walsh, 1998). Variance component estimation separating environmental and genetic variances will help us answer this question.

The heritability of a quantitative trait is one of the most important properties. It expresses the proportion of the total variance that is attributable to the average effects of genes, and this is what determines the degree of resemblance between relatives (Falconer, 1981). It is the proportion of superiority of parents in a trait which, on average, is passed on to its offspring. This parameter will allow us to determine the rates at which characters will respond to selection.

It is important to realise that the heritability is a property not only of a character but also of the population and of the environmental circumstances to which the individuals are subjected. Since the value of the heritability depends on the magnitude of all components of variance, a change in any one of these will affect it (Falconer, 1981). Different populations have different genes and/or gene frequencies, giving room for different amounts of genetic variation. Some populations are in more heterogeneous environments, reducing heritability. The same trait in different environments

may actually act as two traits i.e. growth may depend on appetite in one environment and on efficiency in another (Kinghorn, 1992a).

The phenotype (**P**), or performance expressed by an animal, depends on the genotype (**G**) inherited from its parents and the environment (**E**) provided to perform in. This can be expressed in the following formula:

$$\textbf{P} = \textbf{G} + \textbf{E} \qquad\qquad [3\text{-}1]$$

The genotype of an animal can be split further into additive effects i.e. the combined effects of all genes which act additively on the trait of interest, abbreviated to (**A**), plus non-additive effects, due to dominance (**D**) and epistatic (**Ep**) effects.

$$\textbf{G} = \textbf{A} + \left(\textbf{D} + \textbf{Ep}\right) \qquad\qquad [3\text{-}2]$$

Heritability in the broad sense or the *"degree of genetic determination"* is defined as the genotypic value as a proportion of the phenotypic value V_G / V_P. This ratio expresses the extent to which an individual phenotypes' are determined by their genotypes (Falconer, 1981).

Heritability in the narrow sense or *"heritability"* is defined as the breeding value as a proportion of the phenotypic value V_A / V_P. This ratio expresses the extent to which individuals phenotypes are determined by the genes transmitted from their parents (Falconer, 1981). The term heritability was defined by Kinghorn (1992b) as the efficiency of transmission of parental phenotypic superiority to the next generation.

3.2.1.1 Heritability estimates for litter size

Total Number of Piglets Born (TNB)

Heritability estimates reviewed in this study (Table 3-1) were on average 0.11 ± 0.03 for the trait analysed in a repeatability model. The average permanent environmental effect was 0.14 ± 0.06. Average estimates for TNB measured in parity 1, 2 and 3 were 0.10 for each parity based on uni- or multi-variate analyses.

The highest value of 0.16 was obtained by Johnson et al. (1999) who analysed a selection line selected for 11 generations for ovulation rate and embryonal survival followed by 3 generations of selection for litter size in a Landrace and Large White population. The lowest value of 0.04 was obtained by Alfonso et al. (1997) in a study of two Landrace lines in Spain.

Table 3-1 Summary of literature heritability estimates (h^2) and repeatabilities (r) for number of piglets born in total along with number of records (N)

Reference	N	Breed	h^2	r	h^2 for parity: 1	2	3
(Roehe and Kennedy, 1995)	11,782	Y			0.09	0.14	0.09
(Roehe and Kennedy, 1995)	16,306	LR			0.10	0.09	0.12
(Crump et al., 1997)	5,291	LR	0.12		0.11		
(Alfonso et al., 1997)	15,208	LR[1]	0.07	0.07	0.04	0.06	0.05
(Alfonso et al., 1997)	6,512	LR[2]	0.06	0.09	0.04	0.04	0.10
(Logar et al., 1999)	46,960	LW/LR	0.14	0.20	.	.	.
(Johnson et al., 1999)	2,634	LW/LR[3]	0.16	.			
(Hanenberg et al., 2001)	202,399	LR	0.10	0.19	0.09	0.08	0.12
(Lund et al., 2002)	26,564	LR			0.11		
(Lund et al., 2002)	15,103	Y			0.14		
(Serenius et al., 2003)	6,514	LW	0.11	0.18	0.15	0.13	0.12
(Serenius et al., 2003)	9,154	LR	0.11	0.18	0.14	0.13	0.11
Average	**30,369**		**0.11**	**0.15**	**0.10**	**0.10**	**0.10**
Std Deviation	**60,484**		**0.03**	**0.06**	**0.04**	**0.04**	**0.03**

Breeds abbreviations: LW=Large White; LR=Landrace; Y=Yorkshire;
[1] AI population; [2] Natural Mating population; [3] LW and LR Composite

Number of Piglets Born Alive (NBA)

Estimates reviewed in this study (Table 3-2) were on average 0.10 for parities 1, 2 and 3 and 0.11 ± 0.05 when all parities were considered in a repeatability model. Estimates ranged between 0.02 and 0.27. These average estimates are in agreement with previous reviews made by Hermesch (1996) and Rothschild and Bidanel (1998). Hermesch (1996) found average estimates of 0.07 for the repeated records, 0.10, 0.11 and 0.10 for average estimates for parities 1, 2 and 3 respectively. Rothschild and Bidanel (1998) found a mean heritability of 0.09 for 96 studies ranging from 0 to 0.66.

Table 3-2 Summary of literature heritability estimates (h^2) and repeatabilities (r) for number of piglets born alive along with number of records (N)

Reference	N	Breed	h^2	r	h^2 for parity: 1	2	3
(Ferraz and Johnson , 1993)	893	LR	0.11	.	.	.	.
(Ferraz and Johnson , 1993)	517	LW	0.10	.	.	.	.
(Irgang et al., 1994)	5,799	LR	.	.	0.15	0.21	0.02
(Irgang et al., 1994)	4,561	LW	.	.	0.09	0.15	0.18
(Irgang et al., 1994)	1,817	DU	.	.	0.15	0.11	0.10
(Rydhmer et al., 1994)	4,068	Y	.	.	0.13	0.12	.
(Kerr and Cameron, 1995)	1,220	LW	.	.	0.06	.	.
(Roehe and Kennedy, 1995)	11,782	Y	.	.	0.07	0.11	0.09
(Roehe and Kennedy, 1995)	16,306	LR			0.09	0.10	0.12
(Tholen et al., 1996)	3,942	Synthetic	.	.	0.12	0.13	0.16
(Tholen et al., 1996)	6,050	LW/LR	.	.	0.10	0.11	0.09
(Alfonso et al., 1997)	15,208	LR[1]	0.06	0.07	0.04	0.05	0.05
(Alfonso et al., 1997)	6,512	LR[2]	0.05	0.09	0.06	0.05	0.09
(Crump et al., 1997)	5,291	LR	0.09	0.19	0.11	.	.
(Duc et al., 1998)	10,526	LW	.	.	0.06	0.09	0.10
(Täubert et al., 1998)	54,816	Ger	.	.	0.07	0.08	0.10
(Johnson et al., 1999)	2,634	LW/LR[3]	0.17	.	.	.	.
(Logar et al., 1999)	46,960	LW/LR[4]	0.12	0.18	.	.	.
(Kaufmann et al., 2000)	1,928	LW	0.22	0.06	.	.	.
(Bizelis et al., 2000)	1,540	LR	0.25	0.30	0.27	.	.
(Bizelis et al., 2000)	367	LW	0.13	0.24	0.15	.	.
(Hermesch et al., 2000b)	13,064	LW/LR	.	.	0.08	0.09	0.08
(Hanenberg et al., 2001)	58,194	LR	.	.	0.06	0.04	0.08
(Bozzi et al., 2002)	1,192	CS	0.05	.	.	.	.
(Noguera et al., 2002)	66,620	LR	.	.	0.06	0.07	0.09
(Robinson and Quinton, 2002)	43,415	Y	0.10	.	.	.	.
(Robinson and Quinton, 2002)	24,729	LR	0.10	.	.	.	.
(Chen et al., 2003)	251,296	Y	0.10	0.17	.	.	.
(Chen et al., 2003)	75,262	DU	0.09	0.17	.	.	.
(Chen et al., 2003)	83,332	H	0.08	0.14	.	.	.
(Chen et al., 2003)	53,234	LR	0.08	0.15	.	.	.
(Nguyen et al., 2003)	993	LW	0.07	.	.	.	.
(Hamann et al., 2004)	48,577	LR	0.11*	0.14*	0.15	.	.
(Hamann et al., 2004)	23,003	PI	0.09*	0.25*	0.15	.	.
(Holm et al., 2004)	6,718	LR	.	.	0.07	.	.
Average	**26,776.2**		**0.11**	**0.17**	**0.10**	**0.10**	**0.10**
Standard Deviation	**45,517.0**		**0.05**	**0.07**	**0.05**	**0.04**	**0.04**

Breeds abbreviations: LW=Large White; LR=Landrace; DU=Duroc; H=Hampshire; PI=Pietrain; CS=Cinta Senese; Y=Yorkshire; Ger=German sows;
[1] AI population; [2] Natural Mating population; [3] LW and LR Composite; [4] LW and LR Crosses;
* Includes parities 2-10

The highest heritability estimate (0.27) was obtained by Bizelis et al. (2000) in a study made in Greece using 1,540 records of a 1st parity Danish Landrace population. A high estimate of 0.17 was also obtained by Johnson et al. (1999) in Nebraska. The French study by Kaufmann et al. (2000) reported a heritability of 0.22 and attributed this high value to the homogeneity of the environment (management, feeding) under which animals were kept.

The lowest value (0.02) was obtained in a Brazilian study made by Irgang et al. (1994) using 3,287 records of a 3rd parity Landrace population in southern Brazil. Alfonso et al. (1997) reported from two Spanish Landrace populations, heritabilities of 0.05 and 0.06 for repeated records estimates.

Studies made in Australia included Hermesch et al. (2000b) and Tholen et al. (1996). Hermesch et al. (2000b) reported heritability estimates of 0.08 ± 0.02 for NBA at parity 1, 0.09 ± 0.02 at parity 2 and 0.08 ± 0.02 at parity 3 in a study made at Bunge Meat Industries from 1992 till 1995 using Landrace and Large White breeds. Tholen et al. (1996) reported heritability estimates of 0.12 ± 0.03, 0.13 ± 0.03 and 0.16 ± 0.04 for parities 1,2 and 3 respectively analysing 3,943 records of an Australian Synthetic LW/LR line.

Number of Piglets Weaned (NWea)

Average estimates for heritability of the trait NWea were 0.05 ± 0.03, being 0.10 ± 0.04, 0.12 ± 0.05 and 0.14 ± 0.11 for parities 1, 2 and 3 respectively (Table 3-3). Rothschild and Bidanel (1998) presented a review of 42 studies and reported a mean heritability for number of piglets weaned of 0.07.

The trait NWea is influenced by management practices such as cross-fostering and is defined in various ways across studies (i.e. including piglets fostered on, and not including piglets fostered off; including only piglets born in the litter; etc.). Due to this influence and different trait definitions it is difficult to compare estimates across studies. The low heritability of the trait also corroborates this high influence of non-genetic factors in this trait.

Table 3-3 Summary of literature heritability estimates (h^2) and repeatabilities (r) for number of piglets weaned along with number of records (N)

Reference	N	Breed	h^2	h^2 for parity: 1	2	3
(Chen et al., 2003)	251,296	Y	0.04	.	.	.
(Chen et al., 2003)	75,262	DU	0.06	.	.	.
(Chen et al., 2003)	83,332	H	0.03	.	.	.
(Chen et al., 2003)	53,234	LR	0.02	.	.	.
(Johnson et al., 1999)	2,634	LW/LR[3]	0.08	.	.	.
(Irgang et al., 1994)	5,799	LR	.	0.15	0.17	0.03
(Irgang et al., 1994)	4,561	LW	.	0.08	0.17	0.18
(Irgang et al., 1994)	1,817	DU	.	0.14	0.11	0.06
(Roehe and Kennedy, 1995)	11,782	Y	.	0.07	0.07	0.11
(Roehe and Kennedy, 1995)	16,306	LR	.	0.07	0.08	0.06
(Kerr and Cameron, 1995)	1,220	LW	0.08	.	.	.
Average	**50,602**		**0.05**	**0.10**	**0.12**	**0.09**
Std Deviation	**77,068.2**		**0.03**	**0.04**	**0.05**	**0.06**

For breed abbreviations see Table 3-2

3.2.1.2 Heritability estimates for litter weight traits

Average Piglet Weight at Birth (AvBW) & Litter Weight at Birth (LBW)

Average estimates for the heritability of repeated records of birth weight were 0.28 ± 0.13 for AvBW and 0.17 ± 0.10 for LBW. Roehe (1999) suggested that LBW was shown to have a low estimate of heritability caused by inflation of residual variance due to the variation in litter size and low additive genetic variance mainly due to functional combination of litter size and individual birth weight. His study was based on pure- and crossbred performances, and thus, non-additive genetic effects such as dominance may be influencing his estimates.

Studies that previously summarised literature estimates of heritabilities for piglet birth weight included Rothschild and Bidanel (1998) who reported a mean heritability for litter birth weight of 0.29 with a range between 0 and 0.66 and a more recent review made by Ryhdmer (2000) who presented a mean heritability for average piglet birth weight of 0.4 with a range of 0.1 and 0.6.

Table 3-4 Summary of literature heritability estimates (h^2) and repeatabilities (r) for Average Piglet Birth Weight and Litter Birth Weight along with number of records (N)

Reference	N	Breed	h^2	r	h^2 for parity: 1	2	3
Average Piglet Birth Weight							
(Tholen et al., 1996)	3,942	Synthetic			0.30	0.28	0.35
(Tholen et al., 1996)	6,050	LW/LR			0.15	0.11	0.14
(Hermesch et al., 2000b)	7,454	LW/LR			0.15	0.16	0.15
(Crump et al., 1997)	5,291	LR	0.21	.	0.22		
(Crump et al., 1997)	5,291	LR	0.21	0.28			
(Roehe, 1999)	14,950	Pb Xb	0.43				
Average	**7,163**		**0.28**	**0.28**	**0.21**	**0.18**	**0.21**
Std Deviation	**3,984**		**0.13**	**-**	**0.07**	**0.09**	**0.12**
Litter Birth Weight							
(Johnson et al., 1999)	2,634	LW/LR[3]	0.32				
(Hermesch et al., 2000b)	7,624	LW/LR			0.08	0.22	0.20
(Crump et al., 1997)	5,291	LR	0.15	.	0.11		
(Crump et al., 1997)	5,291	LR	0.13	0.22			
(Roehe, 1999)	14,950	Pb Xb	0.08				
Average	**7,158**		**0.17**	**0.22**	**0.10**	**0.22**	**0.20**
Std Deviation	**4,700**		**0.10**	**-**	**0.02**	**-**	**-**

For breed abbreviations see Table 3-2; Pb Xb = pure- and crossbred lines

Average Piglet Weight at 21 days (Av21dW)

The mean heritability estimates for Av21dW was 0.08 ± 0.01 for repeated records. Previous review of the literature found an average heritability estimate for the trait litter weight at 21 days adjusted by the number of piglets weighed of 0.17 ranging from 0.07 to 0.38 out of 15 studies (Rothschild and Bidanel, 1998). Chen at al. (2003) analysed the trait litter weight at 21 days adjusted for the number of piglets after transferring (cross-fostering) in four different breeds from the National Swine Registry Swine Testing and Genetic Evaluation System (STAGES) and found similar results across all breeds. More than 50% of the litters of these studies were cross-fostered and this could be the reason for such low heritability estimates.

Table 3-5 Summary of literature heritability estimates (h^2) and repeatabilities (r) for Average Piglet Weight at 21 days along with number of records (N)

Reference	N	Breed	h^2	r	h^2 for parity: 1	2	3
(Chen et al., 2003)	251,296	Y	0.08				
(Chen et al., 2003)	75,262	DU	0.07				
(Chen et al., 2003)	83,332	Ham	0.08				
(Chen et al., 2003)	53,234	LR	0.09				
(Kaufmann et al., 2000)	1,928	LW	0.08				
(Tholen et al., 1996)	3,942	Synthetic			0.17	0.12	0.23
(Hermesch et al., 2000b)	1,111	LW/LR			0.07		
Average	**93,010**		**0.08**		**0.12**	**0.12**	**0.23**
Std Deviation	**93,996**		**0.01**		**0.07**	**-**	**-**

For breed abbreviations see Table 3-2

3.2.1.3 Gestation Length

Average heritability estimates from three studies found in the literature are presented in Table 3-6. These estimates found ranged from 0.20 up to 0.29 with an average of 0.23 ± 0.04 from the studies with repeated records and an average of 0.24 from those studies with only parity 1 records.

Table 3-6 Summary of literature heritability estimates (h^2) and repeatabilities (r) for Gestation Length along with number of records (N)

Reference	N	Breed	h^2	r	h^2 for parity: 1	2	3
(Hanenberg et al., 2001)	58,194	LR	0.29	0.35	0.25	0.26	0.24
(Crump et al., 1997)	5,291	LR	0.20	.	0.22		
(Crump et al., 1997)	5,291	LR	0.20	0.29			
(Nguyen et al., 2003)	?	LW	0.24				
Average	**22,925**		**0.23**	**0.32**	**0.24**	**0.26**	**0.24**
Std Deviation	**30,544**		**0.04**	**0.04**	**0.02**	**-**	**-**

For breed abbreviations see Table 3-2

3.2.2 Correlations between reproductive traits

The relationship between the observed performances of two metric characters is the phenotypic correlation or correlation of phenotypic values. The phenotypic correlation (r_P) has been described as:

$$r_p = \frac{\mathbf{Cov}\left(\mathbf{P_x}, \mathbf{P_y}\right)}{\sigma_{Px}\ \sigma_{Py}} \qquad [3\text{-}3]$$

Where Cov (Px, Py) is the covariance between the phenotypes of trait x and trait y and σ_{Px} and σ_{Py} are the standard deviations of the phenotypes of trait x and y respectively.

Two metric characters are correlated at the genetic level mainly due to pleiotropism; however gametic phase disequilibrium is also a possible cause of correlation especially in populations derived from crosses between divergent strains.

Pleiotropism is the property of a gene whereby it affects two or more characters, so that if the gene is segregating it causes simultaneous variation in the characters it affects. The degree of correlation arising from pleiotropism expresses the extent to which two characters are influenced by the same genes (Falconer, 1981).

The genetic correlation between two metric characters quantifies the direction and strength of the association between breeding values of those traits. The genetic correlation (r_G) has been described as:

$$r_G = \frac{\mathbf{Cov}\left(\mathbf{A_x}, \mathbf{A_y}\right)}{\sigma_{Ax}\ \sigma_{Ay}} \qquad [3\text{-}4]$$

Where Cov (Ax, Ay) is the covariance between the true breeding values of trait x and trait y and σ_{Ax} and σ_{Ay} are the genetic standard deviations of trait x and y respectively.

3.2.2.1 Genetic and Phenotypic correlations across traits

Number of piglets born alive (NBA) has a high genetic correlation with TNB as reported by Nguyen et al, (2003) (0.88 and 0.90 in Mong Cai and Large White sows) and Roehe and Kennedy (1995) (0.92, 0.93, 0.91 for Yorkshire sows and 0.92, 0.94 and 0.93 for Landrace sows in parities 1, 2 and 3 respectively).

A positive correlation between NBA and NWea is shown in Table 3-7 ranging from 0.07 (Chen et al., 2003) up to 0.83 (Roehe and Kennedy, 1995). In contrast, Johnson et al. (1999) presented a negative correlation (-0.18) between Number of foetuses at 50 days of gestation (positively correlated with NBA 0.61) and NWea after cross-fostering in a study in Nebraska where they analysed the response in litter traits after 14 generations of selection to increase litter size.

A single negative estimate (-0.27) was found in the literature for the genetic correlation between NBA and GL from a study with Large White sows in southern Vietnam (Nguyen et al., 2003).

A negative genetic correlation was found between NBA and AvBW in several studies ranging from -0.11 in southern Vietnam (Nguyen et al., 2003) down to -0.53 in an Australian study (Hermesch et al., 2000b). A clear difference exists for the genetic correlations of NBA and Av21dW between two Australian studies (Hermesch et al., 2000b; Tholen et al., 1996) and an American study made in several breeds (Chen et al., 2003). The Australian studies showed moderate negative correlations (-0.27 and -0.35) while the American showed low positive correlations (0.14, 0.10, 0.13 and 0.15). The authors of the later study suggested that this discrepancy was caused by a high influence of cross-fostering in their study (more than 50% of the litters were cross-fostered).

The genetic correlation between AvBW in parities 1, 2 and 3 with the Av21dW in parity 1 was reported by Hermesch et al. (2000b). They reported a negative correlation between $AvBW_1$ and $Av21dW_1$ of -0.11 ± 0.29 and a positive genetic correlation between $AvBW_2$ and $Av21dW_1$ (0.42 ± 0.27) as well as $AvBW_3$ and $Av21dW_1$ (0.48 ± 0.32).

Table 3-7 Summary of literature estimates of genetic (above diagonal) and phenotypic correlations (below diagonal) across reproductive traits

Reference	Breed	NBA	NWea	GL	AvBW	21dLW
Number Born Alive (NBA)						
(Chen et al., 2003)	Y		0.19			0.14
(Chen et al., 2003)	DU		0.07			0.10
(Chen et al., 2003)	Ham		0.20			0.13
(Chen et al., 2003)	LR		0.14			0.15
(Bizelis et al., 2000)	LW		0.70			
(Bizelis et al., 2000)	LR		0.46			
(Tholen et al., 1996)	Synth				-0.43	-0.27
(Tholen et al., 1996)	LW/LR				-0.45	
(Roehe and Kennedy, 1995)	Y		0.63			
(Roehe and Kennedy, 1995)	LR		0.83			
(Hermesch et al., 2000b)	LW/LR				-0.53	-0.35
(Nguyen et al., 2003)	LW		0.43	-0.27	-0.11	
Number Weaned (NWea)						
(Chen et al., 2003)	Y	0.06				0.75
(Chen et al., 2003)	DU	0.02				0.65
(Chen et al., 2003)	Ham	0.06				0.71
(Chen et al., 2003)	LR	0.05				0.73
(Bizelis et al., 2000)	LW	0.67				
(Bizelis et al., 2000)	LR	0.89				
(Roehe and Kennedy, 1995)	Y	0.59				
(Roehe and Kennedy, 1995)	LR	0.55				
(Nguyen et al., 2003)		0.32		0.34	0.27	
Gestation Length (GL)						
(Nguyen et al., 2003)	LW	-0.09	0.05		0.08	
Average Piglet Birth Weight (AvBW)						
(Tholen et al., 1996)	Synth	-0.22				
(Tholen et al., 1996)	LW/LR	-0.28				
(Hermesch et al., 2000b)	LW/LR	-0.28				
(Nguyen et al., 2003)		-0.11	-0.01	-0.01		
Litter Weight at 21 days (21dLW)						
(Chen et al., 2003)	Y	0.06	0.80			
(Chen et al., 2003)	DU	0.03	0.77			
(Chen et al., 2003)	Ham	0.04	0.79			
(Chen et al., 2003)	LR	0.07	0.78			
(Tholen et al., 1996)	Synth	-0.04				
(Hermesch et al., 2000b)	LW/LR	-0.01				

For breed abbreviations see Table 3-2

3.2.2.2 Genetic and Phenotypic correlations within traits and among parities

The correlations among parities 1 to 3 for the trait TNB was reported by Alfonso et al. (1997) where they described the genetic correlation between parities 1-2 to be 0.90 and 0.95 and 1-3 to be 0.93 and 0.53 for two different populations. For parities 2-3 the genetic correlation was 0.89 and 0.83. Hanenberg et al. (2001) reported a genetic correlation for TNB of 0.83, 0.74 and 0.90 for parities 1-2, 1-3 and 2-3 respectively.

Hermesch et al. (2000b) reported genetic correlations among parities 1 to 3 for the trait AvBW. The estimates were 0.79, 0.58 and 078 between parities 1-2, 1-3 and 2-3 respectively. In addition Tholen et al. (1996) reported genetic correlations of 0.85, 0.59 and 0.73 for the same parities combinations.

Estimates of the genetic correlations of the trait NWea were reported by Roehe and Kennedy (1995) between parities. Two populations were used for the analyses and the estimates were: 0.81, 0.88 and 0.69 for Landrace sows and 0.17, 0.34 and 0.59 for Yorkshire sows between parities 1-2, 1-3 and 2-3 respectively.

Hanenberg et al. (2001) presented a genetic correlation for GL in parities 1-2, 1-3 and 2-3 of 0.95, 0.94 and 0.98 respectively.

Average estimates of genetic correlations (Table 3-8) among parities for the trait NBA were 0.69 ± 0.17 between parities 1-2, 0.75 ± 0.18 between parities 1-3 and 0.92 ± 0.10 between parities 2-3. Parity 1 has the lowest genetic correlation with other parities, while parities 2 and 3 are similar genetically.

Table 3-8 Summary of literature estimates of genetic (above diagonal) and phenotypic correlations (below diagonal) among parities 1, 2 and 3 of NBA

Reference	Breed	NBA1	NBA2	NBA3
NBA1				
(Roehe and Kennedy, 1995)	Y		0.49	0.98
(Roehe and Kennedy, 1995)	LR		0.92	0.92
(Tholen et al., 1996)	Synthetic		0.74	0.74
(Tholen et al., 1996)	LW/LR		0.56	0.57
(Alfonso et al., 1997)	LR		0.92	0.91
(Alfonso et al., 1997)	LR		0.87	0.47
(Duc et al., 1998)	MC		0.55	0.87
(Duc et al., 1998)	LW		0.44	0.84
(Täubert et al., 1998)	LW		0.61	0.51
(Täubert et al., 1998)	LR		0.77	0.88
(Hermesch et al., 2000b)	LW/LR		0.62	0.61
(Hanenberg et al., 2001)	LR		0.83	0.74
NBA2				
(Roehe and Kennedy, 1995)	Y	0.12		0.66
(Roehe and Kennedy, 1995)	LR	0.07		0.99
(Tholen et al., 1996)	Synthetic	0.17		1.00
(Tholen et al., 1996)	LW/LR	0.17		1.00
(Alfonso et al., 1997)	LR	0.14		1.00
(Alfonso et al., 1997)	LR	0.12		0.83
(Duc et al., 1998)	MC	0.14		0.97
(Duc et al., 1998)	LW	0.12		0.87
(Täubert et al., 1998)	LW	-		0.99
(Täubert et al., 1998)	LR	-		0.88
(Hermesch et al., 2000b)	LW/LR	0.11		0.95
(Hanenberg et al., 2001)	LR	0.04		0.90
NBA3				
(Roehe and Kennedy, 1995)	Y	0.06	0.14	
(Roehe and Kennedy, 1995)	LR	0.06	0.07	
(Tholen et al., 1996)	Synthetic	0.19	0.23	
(Tholen et al., 1996)	LW/LR	0.14	0.22	
(Alfonso et al., 1997)	LR	0.11	0.12	
(Alfonso et al., 1997)	LR	0.13	0.13	
(Duc et al., 1998)	MC	0.12	0.15	
(Duc et al., 1998)	LW	0.13	0.18	
(Hermesch et al., 2000b)	LW/LR	0.09	0.12	
(Hanenberg et al., 2001)	LR	0.10	0.07	

For breed abbreviations see Table 3-2; MC=Vietnamese Mong Cai

3.3 Materials and Methods

3.3.1 Description of the data

Reproductive performance data were obtained from purebred Landrace (LR) and Large White (LW) sows at the nucleus and multiplier herds from Myora Farm. Records of litters from the first to tenth parity born between January 1995 and May 2004 were analysed.

Several limits were imposed to the dataset, which are presented in Table 3-9. Only litters from purebred LW and LR sows mated to purebred LW or LR boars were kept in the dataset. Sows that did not have their first litter after the 1st of January 1995 and before the 1st of May 2004 were deleted with all their subsequent litters. The age of farrowing was limited for the first three litters as described in Table 3-9. Every litter that did not fit in the range of limits imposed was excluded from the analysis. The limits imposed to the reproductive traits were implemented in order to avoid errors in the data collection and to exclude sows with reproductive problems.

Table 3-9 Limits implemented to edit the dataset used for estimating genetic parameters

	Limits	
	Units	**Limits imposed**
Age at farrowing -Parity 1	days	280-560
Age at farrowing -Parity 2	days	420-700
Age at farrowing -Parity 3	days	560-860
Reproductive Traits		
Numbers Born Alive **NBA**	piglets	2-22
Total Numbers Born **TNB**	piglets	4-24
Numbers Born Dead **NBD**	piglets	0-10
Numbers Weaned **NWea**	piglets	0-14
Gestation Length **GL**	days	111-120
Average Birth Weight **AvBW**	kg	0.5-3
Average Piglet Weight at 21day **Av21dW**	kg	4.0-8.6

The dataset, after editing, contained 18,324 litters with 11,031 litters from 2,724 Large White sows and 7,293 litters from 1,780 Landrace sows. The number of litters, sows, service sires, dams and sires were presented in Table 3-10 for the two breeds and for each farrowing year.

Table 3-10 Number of litters, sows, service sires, dams and sires, for each breed among farrowing year

Farrowing year	Breed	Litters	Sows	Service Sires	Dams	Sires
1995	LW	513	345	71	162	45
	LR	264	173	59	94	31
1996	LW	1,050	610	97	271	64
	LR	471	275	91	136	47
1997	LW	1,256	707	89	323	90
	LR	599	341	80	174	72
1998	LW	1,340	737	79	343	103
	LR	744	404	78	215	87
1999	LW	1,343	737	82	354	103
	LR	762	404	79	224	85
2000	LW	1,264	723	72	325	96
	LR	830	451	72	249	86
2001	LW	1,326	716	71	325	80
	LR	926	499	65	270	77
2002	LW	1,323	761	76	357	84
	LR	1,014	584	70	285	78
2003	LW	1,209	642	78	319	80
	LR	1,234	632	90	271	76
2004	LW	407	407	63	224	63
	LR	449	449	68	215	66
95 to 04	**LW**	**11,031**	**2,724**	**417**	**963**	**220**
	LR	**7,293**	**1,780**	**419**	**672**	**193**

LW=Large White; LR=Landrace

The number of litters sorted by the parity of the sow is presented in Table 3-11. The percentage of sows culled (CR%) from one parity to the next are also shown. A total of 6,801 Large White and 4,451 Landrace records were obtained when sows older than the 3rd parity were ignored.

Table 3-11 Number of records (N); Culling rate between one parity and the previous one (CR%) for each parity and breed.

Breed	Large White		Landrace	
Parities	N	CR %	N	CR %
1st	2,657	-	1,752	-
2nd	2,276	14.3	1,458	16.8
3rd	1,868	17.9	1,241	14.9
4th	1,478	20.9	966	22.2
5th	1,056	28.6	692	28.4
6th	748	29.2	517	25.3
7th	467	37.6	333	35.6
8th	259	44.5	183	45.1
9th	148	42.9	104	43.2
10th	74	50.0	47	54.8
1st to 10th	11,031		7,293	

It is clearly observed in Table 3-11 how the absolute numbers of sows decreased for higher parities showing a higher proportion of culled sows in each parity group.

3.3.2 Statistical Analyses

3.3.2.1 Models used for Analysis

An individual animal model was used in order to allow information on all known relationships between animals to be incorporated in the analysis.

Tri-variate model

Heritabilities, phenotypic and genetic correlations were estimated for each reproductive trait for parities 1, 2 and 3 using a tri-variate animal model considering each parity as a separate trait.

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

$$\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \\ \mathbf{y}_3 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & 0 & 0 \\ 0 & \mathbf{X}_2 & 0 \\ 0 & 0 & \mathbf{X}_3 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \\ \mathbf{b}_3 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_1 & 0 & 0 \\ 0 & \mathbf{Z}_2 & 0 \\ 0 & 0 & \mathbf{Z}_3 \end{bmatrix} \begin{bmatrix} \mathbf{u}_1 \\ \mathbf{u}_2 \\ \mathbf{u}_3 \end{bmatrix} + \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \\ \mathbf{e}_3 \end{bmatrix} \qquad [3\text{-}5]$$

where $\mathbf{y}_1$, $\mathbf{y}_2$ and $\mathbf{y}_3$ represents the vector of observations of parities one, two and three respectively, $\mathbf{b}_1$, $\mathbf{b}_2$ and $\mathbf{b}_3$ represent the vector of fixed effects, $\mathbf{u}_1$, $\mathbf{u}_2$ and $\mathbf{u}_3$ represent vectors of additive genetic effects $\sim (0, \mathbf{A}\sigma^2_a)$ and $\mathbf{e}_1$, $\mathbf{e}_2$ and $\mathbf{e}_3$ represent vectors of residual effects $\sim (0, \mathbf{I}\sigma^2_e)$. The matrix $\mathbf{X}_1$ is the incidence matrix for the fixed effects of parity one, the $\mathbf{X}_2$ matrix is the incidence matrix for the fixed effects of parity two and the $\mathbf{X}_3$ matrix is the incidence matrix for the fixed effects of parity three; the $\mathbf{Z}_1$ $\mathbf{Z}_2$ and $\mathbf{Z}_3$ matrices are the incidence matrices relating observations on parity one, two and three 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 tri-variate animal model is:

$$V \begin{bmatrix} \mathbf{u}_1 \\ \mathbf{u}_2 \\ \mathbf{u}_3 \\ \mathbf{e}_1 \\ \mathbf{e}_2 \\ \mathbf{e}_3 \end{bmatrix} = \begin{bmatrix} \mathbf{A}\sigma^2_{a1} & \mathbf{A}\sigma_{a12} & \mathbf{A}\sigma_{a13} & 0 & 0 & 0 \\ \mathbf{A}\sigma_{a21} & \mathbf{A}\sigma^2_{a2} & \mathbf{A}\sigma_{a23} & 0 & 0 & 0 \\ \mathbf{A}\sigma_{a31} & \mathbf{A}\sigma_{a32} & \mathbf{A}\sigma^2_{a3} & 0 & 0 & 0 \\ 0 & 0 & 0 & \mathbf{I}\sigma^2_{e1} & \mathbf{I}\sigma_{e12} & \mathbf{I}\sigma_{e13} \\ 0 & 0 & 0 & \mathbf{I}\sigma_{e21} & \mathbf{I}\sigma^2_{e2} & \mathbf{I}\sigma_{e23} \\ 0 & 0 & 0 & \mathbf{I}\sigma_{e31} & \mathbf{I}\sigma_{e32} & \mathbf{I}\sigma^2_{e3} \end{bmatrix} \qquad [3\text{-}6]$$

where σ^2_{a1}, σ^2_{a2} and σ^2_{a3} are direct additive genetic variances, and σ^2_{e1}, σ^2_{e2} and σ^2_{e3} are the residual variances for trait one, two and three respectively; σ_{a12} is the direct genetic covariance between traits one and two, and σ_{e12} their residual covariance.

Repeatability model

Heritabilities, phenotypic and genetic correlations were estimated for each reproductive trait for parities 2 till 10 using a repeatability animal model considering different parities as a repeated record of the same trait.