



Estimation of genetic parameters for litter size in pigs from different genetic groups

B. Logar, M. Kovač, Š. Malovrh

University of Ljubljana, Biotechnical Faculty, Department of Animal Science, Domžale, SI-1230 Groblje 3. Slovenia

ABSTRACT

Number of piglets born alive (NBA) and number of piglets born (NB) was analysed. A total of 46,960 litters of Swedish Landrace (SL) Large White (LW), and both F1 sows were included. Records were collected between 1993 and 1998. Animal model and REML procedures were used to estimate genetic and environmental parameters for the first six litters in univariate analyses. Random additive genetic effect and permanent environment effect of the sow were considered. The differences between genotypes were estimated by crossbreeding parameters: additive maternal and additive grand-maternal effect as well as maternal heterosis. Estimates were 0.14 and 0.12 for heritability and 0.20 and 0.18 for repeatability in NB and NBA respectively. The contribution of additive maternal effect to the breed differences (SL-LW) was estimated at 0.10 and 0.26 respectively. The estimated deviation of the F1 from the mid parental value (maternal heterosis effect) was 0.69 and 0.72 for NB and NBA respectively. The additive grand-maternal effect, which expresses the differences between crossbreeds, (SL x LW-LW x SL) was low (0.06 for NB and -0.03 for NBA).

(Keywords: pigs, litter size, variance components, heritability, crossbreeding parameters)

ZUSAMMENFASSUNG

Schätzung von genetischen Parametern für die Wurfgröße beim Schwein aus verschiedenen Zuchtgruppen

B. Logar, M. Kovač, Š. Malovrh

Universität in Ljubljana, Biotechnische Fakultät, Abteilung für Zootechnik, Domžale, SI-1230 Groblje 3. Slowenien

In der vorliegenden Arbeit wurde die Anzahl der geborenen Ferkel (NB) und die Anzahl der lebend geborenen Ferkel (NBA) geschätzt. Insgesamt wurden 46.960 Würfe der Schwedischen Landrassee (SL), Large White (LW) und von beiden die F1 Kreuzungssauen (SL x LW, LW x SL) analysiert. Die Daten stammen aus den Jahren 1993-1998. Für die Schätzung der genetischen- und Umweltparameter für die ersten sechs Würfe in einer univariaten Analyse wurden Tiermodelle und die REML-Methode verwendet. Als zufälliger Effekt wurde additiv der genetischer Effekt und der permanente Umwelteffekt der Sau angenommen. Die Unterschiede zwischen den Genotypen wurden mit Kreuzungsparametern additiv maternalem, additiv grandmaternalem und maternalem Heterosiseffekt geschätzt. Die geschätzte Heritabilität betrug für NB 0.14, für NBA 0.12; und die Wiederholbarkeit 0.20 für NB beziehungsweise 0.18 für NBA. Der Beitrag von additiv maternalem Effekt zum Unterschied zwischen den Rassen (SL-LW)

wurde für NB auf 0.10 und für NBA auf 0.26 geschätzt. Die geschätzte Abweichung bei F1 Sauen vom Elterndurchschnittswert (maternaler Heritabilitätseffekt) betrug für NB 0.69 und für NBA 0.72. Der Beitrag von additiv grandmaternalem Effekt zum Unterschied zwischen den Kreuzungen (SL x LW-LW x SL) wurde auf 0.06 für NB und auf -0.03 für NBA geschätzt.

(Schlüsselwörter: Schwein, Wurfgröße, Varianzkomponenten, Heritabilität, Kreuzungsparameter)

INTRODUCTION

In pigs litter size is an important component of sow efficiency, and is therefore one of the objective traits in many selection programmes. *Haley et al.* (1988) suggested that litter size be used in successive parities as repeated measurements. In other words, the litters in different parities would be under the same genetic control, which implies a genetic correlation of one among parities. Many breeding programmes accept this assumption and use a repeatability model for litter size in pigs (*Schaeffer*, 1993; *Alfonso and Noguera*, 1995; *Alfonso et al.*, 1997; *Hofer*, 1998; *Andersen*, 1998; *Tölle et al.*, 1998). *Sadek-Pučnik and Kovač* (1996) obtained high correlations among litter size in the first six parities. The use of two different models to adjust the first litter for age at farrowing and later litters for lactation length was the main reason for not using a simple repeatability model. *Andersen* (1998) showed a way how to handle repeated records with different fixed effects.

The knowledge of genetic parameters for the various traits are the basis for genetic improvement in an advanced breeding programme and for successful selection. In crossbreeding schemes the expression of non-additive genes is even more important. This expression of genes could be evaluated in terms of crossbreeding parameters in the classic crossbreeding model (*Dickerson*, 1969). As has been shown by *Komender and Hoeschele* (1989), the accuracy of crossbreeding estimators can be improved by including genetic relationship between animals in the analysis, for example by an animal model.

The objectives of the research here were: 1) to estimate variance components for litter size in pigs from different genetic groups treating different parities as the same with respect to trait, and 2) to estimate differences between sow genotypes in terms of genetic parameters.

MATERIALS AND METHODS

Litter records from the Nemščak farm were provided by the Slovenian national pig breeding programme for the period between January 1993 and December 1998. Litters from the first to the sixth parity were analysed (*Table 1*). In gilts, age at farrowing (348 ± 31 days) was limited to between 290 and 430 days. The farrowing interval in sows was restricted to between 125 and 250 days. Average litter size was 10.38 for NB and 9.91 for NBA with standard deviation of 2.99 and 2.98 respectively. There were 18,629 Swedish Landrace (SL), 4948 Large White (LW), 21,456 SL x LW (matings of SL females and LW males) and 1927 LW x SL litters. Sows were mated to 312 service boars of five different breeds. The boars with less than ten litters were grouped. Season was created as a year-month-decade interaction and had 217 levels. A total of 17605 animals were included in the pedigree. Among these there were 14,961 sows with litters, 5391 dams and 265 sires, giving at least three generations of ancestors.

Table 1

Number of litters (n), piglets born (NB), and piglets born alive (NBA), previous lactation length and weaning to conception interval (WCI) by number of parities

Parity (1)	n	NB	SD	NBA	SD	Lactation (days) (2)	SD	WCI (days) (3)	SD
1	11882	9.18	2.74	8.76	2.83				
2	9281	10.10	2.81	9.79	2.79	25.42	5.43	24.52	25.63
3	8194	10.87	2.91	10.45	2.88	26.13	4.06	15.19	19.39
4	6936	11.15	2.97	10.62	2.96	26.17	3.78	15.03	19.15
5	5857	11.18	2.99	10.54	2.99	26.01	4.16	14.19	18.51
6	4810	11.02	3.00	10.28	3.00	25.98	4.28	13.86	18.36
Total (4)	46960	10.38	2.99	9.91	2.98	25.91	4.47	17.28	21.37

SD – phenotypic standard deviation (*Phänotypischen Standardabweichungen*)

1. Tabelle: Wurfzahl (n), geborene Ferkel (NB), lebend geborene Ferkel (NBA), Dauer der vorherigen Laktation und Zeitraum zwischen Abferkelung und Trächtigkeit (WCI)

Wurfnr(1), Dauer der vorherigen Laktation(2) und Zeitraum zwischen Abferkelung und Trächtigkeit(3), Gesamt(4)

Covariance components were obtained by Restricted Maximum Likelihood (REML, Peterson and Thompson, 1971) using the Powell algorithm in PeRun (Kovač, 1992). The evaluation with the best set of covariance components was performed by means of PEST (Groeneveld and Kovač, 1990). The statistical model included crossbreeding parameters, age at first farrowing for gilts, lactation length and weaning to conception interval for sows, service boar (B_j), parity (P_i), and season of insemination (S_k) as fixed effects. The random part of the model consisted of permanent environment of the sow (p_i) and additive genetic effect (a_i). Age at first farrowing (x_{1kl}) was adjusted by quadratic regression, while lactation (x_{2ikl}) and weaning to conception interval (x_{3ikl}) was fitted as linear regression. The following repeatability model was used:

$$y_{ijkl} = P_i + B_j + S_k + b_1 x_{1kl} + b_2 x_{1kl}^2 + b_3 x_{2ikl} + b_4 x_{3ikl} + \alpha_m x_{4l} + \delta_m x_{5l} + \alpha_{gm} x_{6l} + p_i + a_i + e_{ijkl}$$

The crossbreeding parameters accommodated maternal additive effect (α_m), maternal heterosis effect (δ_m) and additive grand-maternal effect (α_{gm}). All of these were fitted as linear regression in order to obtain differences between genotypes straight from the model, as suggested by Dickerson (1969). The genotype class was replaced by the coefficients used as independent variables x_{4l} , x_{5l} and x_{6l} given in Table 2.

In order to describe covariance structure, the model was rewritten in matrix form:

$$y = X\beta + Za + Wp + e$$

where y stood for the observation vector, β for the vector of fixed effects, a for the vector of animal genetic effect, p for the vector of permanent environmental effects, and e for the vector of residuals. Matrices X , Z , W are corresponding incidence matrices.

Expectations and covariance matrices of random variables are described in the following equations:

$$E \begin{bmatrix} \mathbf{y} \\ \mathbf{a} \\ \mathbf{p} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{X}\boldsymbol{\beta} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix} \quad \text{and} \quad V \begin{bmatrix} \mathbf{a} \\ \mathbf{p} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{A}\sigma_a^2 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{I}\sigma_p^2 & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma_e^2 \end{bmatrix}$$

where A is a genetic relationship matrix; I is an identity matrix; σ_a^2 , σ_p^2 , σ_e^2 additive genetic, permanent environment and residual variances, respectively; cov(a,e') and cov(a,p') are equal to zero.

Table 2

The coefficients for additive maternal (α_m), maternal heterosis (δ_m) and additive grand-maternal (α_{gm}) effects

Genotype (1)	Crossbreeding parameter(2)		
	Additive maternal (α_m)	Maternal heterosis (δ_m)	Additive grand-maternal (α_{gm})
Swedish Landrace	1	0	1
SL x LW	0.5	1	1
LW x SL	0.5	1	0
Large White	0	0	0

SL - Swedish Landrace, LW - Large White, F1 - SL x LW or LW x SL (breed of dam given first.) (*Erste Mutterrasse*.)

2. Tabelle: Koeffizienten für additiv maternale Effekte (α_m), maternale Heterosis (δ_m) und additive grandmaternale Effekte (α_{gm})

Genotyp(1), Kreuzungsparameter(2)

RESULTS AND DISCUSSION

Estimates of genetic, environmental and phenotypic parameters are presented in Table 3. Total phenotypic, permanent environmental and residual variances proved larger for NBA than for NB. The estimate of h^2 was 0.14 for NB and 0.12 for NBA. The estimates are close to the values reported by See et al. (1993), Crump et al. (1997) and Southwood and Kennedy (1990). In addition, Haley et al. (1988) reviewed heritabilities from many sources and concluded in summary that about 10% of variation in litter size was heritable. Heritability estimates were higher for NB than for NBA. The same conclusion was reached by Roehle and Kennedy (1995), Kisner et al. (1996), Mercer and Crump (1994) and Crump et al. (1997). Permanent environment effect explained 6% of phenotypic variation. The repeatability estimates (0.20 and 0.18) were close to the values reported by Mercer and Crump (1994) but larger than those reported by Kisner et al. (1996).

Table 3

Estimates of phenotypic
(σ^2), error (σ_e^2), permanent environment (σ_p^2), additive genetic (σ_a^2) variance,
repeatability, relative contribution of the permanent environment effect of sow (p^2)
and heritability (h^2) for the traits NB and NBA

Trait (4)	Variance components (1)				Repeatability (2)	Ratio (3)	
	σ^2	σ_e^2	σ_p^2	σ_a^2	r	p^2	h^2
NB	8.0114	6.4451	0.4573	1.1090	0.20	0.057	0.138
NBA	8.0877	6.5996	0.4994	0.9887	0.18	0.062	0.122

3. Tabelle: Phänotypische Varianz (σ^2), Restvarianz (σ_e^2), zufällige permanente Umweltvarianz (σ_p^2), Wiederholbarkeit, permanenter Umweltanteil (p^2) und Heritabilität (h^2) für geborene und lebend geborene Ferkel

Komponenten der Varianz(1), Wiederholbarkeit(2), Verhältnis(3), Eigenschaften (4)

In the crossbred sows litter size was about 0.7 piglets higher than in the pure-bred sows. SL gilts were on average 11 days younger than LW gilts at first farrowing. The difference between the two F1 genotypes was seven days, the SL gilts falling between the two extremes from this aspect (Table 4). The shortest weaning to conception interval was recorded in the LW. Previous lactation length did not differ greatly between the genotypes.

Table 4

Number of litters (n), number of piglets born (NB), number of piglets born alive
(NBA), previous lactation length, weaning to conception interval (WCI)
and first farrowing age

Genotype(3)	n	NB	NBA	Gilts(1)		Sows(2)
				Age (days)(4)	Lactation (days)(5)	WCI (days)(6)
Swedish Landrace (SL)	18629	9.96	9.53	346	25.57	18.82
SL ¹ x LW	21456	10.84	10.33	349	26.20	16.33
LW x SL	1927	10.58	10.21	342	25.76	16.36
Large White (LW)	4948	9.92	9.39	357	25.88	16.21
Total (7)	46960	10.38	9.91	348	25.91	17.28

¹Breed of dam (Mutterrasse)

4. Tabelle: Wurfzahl (n), geborene Ferkel (NB), lebend geborene Ferkel (NBA), Alter beim 1. Wurf, Dauer der vorherigen Laktation und Zeitraum zwischen Abferkelung und Trächtigkeit (WCI)

Jungsauen(1), Sauen(2), Genotyp(3), Alter beim 1. Wurf in Tagen(4), Dauer der vorherigen Laktation(5), Zeitraum zwischen Abferkelung und Trächtigkeit(6), Gesamt(7)

For the interval observed litter size increased with age of gilts at first farrowing. The regression coefficients were similar for both traits. The results were comparable with *Sadek* (1994), from another nucleus herd in Slovenia. Furthermore, the effect of previous lactation length was smaller (0.026) than expected. *Kovač et al.* (1984) and *Sadek* (1994) excluded records with short lactation (under 18 days) and obtained regression coefficients more than twice as high (0.057 and 0.065). As records with short lactation were included in this study the regression line did not give the best fit to the records with longer lactation. With this in mind the authors suggested that litters in which lactation was short should not be included in genetic evaluation. The third independent variable, the weaning to conception interval, was found to have little effect on litter size (0.008 per day for NB or 0.007 for NBA).

The estimates of crossbreeding parameters included in the analyses are shown in *Table 5*. The additive maternal effect showed that Swedish Landrace sows had 0.091 more piglets per litter at birth than Large White sows. A larger difference (0.36) was observed with respect to piglets born alive. Contrary phenotypic differences between pure-breds were smaller for both traits. The main cause of this may lie in different age at first farrowing. SL gilts were younger at farrowing, and thus smaller litters were expected. In addition, LW sows produced more stillborn piglets, resulting in a sizeable difference between the sows of these two breeds.

As expected, litter size increased in crossbred sows. Maternal heterosis effect was estimated at 0.69 for NB and 0.72 for NBA (*Table 5*), which was twice as large as the difference between pure-breds. This was in agreement with values (from 0.6 to 0.7) summarised by *Rothschild* and *Bidanel* (1998).

In order to estimate the difference between the F1 crossbreeds, additive genetic effect of the grand-maternal breed was included in the analysis. The differences between the two crosses were negligible for NB (0.064) and for NBA (-0.025). Therefore, crosses may be used interchangeably with the expectation of almost the same litter size at birth in both crossbreeding schemes, the only difference expected being due to smaller litters in pure-bred LW. However, there was some evidence that LW and LW x SL sows might also lose more piglets during lactation. Due to cross-fostering this suspicion could not be proved from regular litter recording.

Table 5

Estimates of crossbreeding parameters

Crossbreeding parameter(1)	Piglets born(2)	Piglets born alive(3)
Additive maternal (α_m)	0.091	0.36
Maternal heterosis (δ_m)	0.69	0.72
Additive grand-maternal (α_{gm})	0.064	-0.025

5. Tabelle: Schätzung der Kreuzungsparameter

Kreuzungsparameter(1), Anzahl der geborenen Ferkel(2), Anzahl der lebend geborenen Ferkel(3)

Because of the high genetic correlation between NB and NBA (0.95) there are no reasons for using both traits for selection on litter size (*Tölle et al.*, 1998). Even higher

correlation (0.97) was obtained in analysis of Logar (1998, unpublished results). The number of live-born piglets accounts for losses during farrowing. In addition, *Johnson et al.* (1999) justified lower NBA values with an undesirable genetic relationship between litter size during gestation and numbers of stillborn and mummified piglets. *Haley et al.* (1988) purposed that number of piglets weaned should be used even further. However, this would require that cross-fostering in the nucleus be stopped.

CONCLUSIONS

Litter size records were analysed using the REML method and a univariate repeatability model.

- Additive maternal crossbreeding parameter estimates were 0.091 and 0.36 piglets for NB and NBA, respectively.
- Estimated maternal heterosis was 0.7 piglets in both traits.
- Estimates for additive grand-maternal effect were negligible.
- The model used in this analysis could be used for genetic evaluation of litter size, with small corrections.
- The NBA could be more suitable in comparison with NB.

ACKNOWLEDGEMENTS

The authors acknowledge the Nemščak farm in Slovenia for providing data for this study.

REFERENCES

- Andersen, S. (1998). The national Danish pig breeding program. V: International workshop Introduction of BLUP animal model in pigs, Praga-Uhrineves, 1998-09-03/05. 9.
- Alfonso, L., Noguera, J.L. (1995). Choice of genetic model for evaluating litter size in pigs. In: Book of Abstracts of the 46th Annual meeting of the EAAP, Praga, 1995-09-04/07. Wageningen, Wageningen Pers, 59.
- Alfonso, L., Noguera, J.L., Babot, D., Estany, J. (1997). Estimation of genetic parameters for litter size at different parities in pigs. *Livestock Production Science*, 47. 149-156.
- Crump, R.E., Haley, C.S., Thompson, R., Mercer, J. (1997). Individual animal model estimates of genetic parameters for reproduction of Landrace pigs performance tested in a commercial nucleus herd. *Animal Science*, 65. 285-290.
- Dickerson, G.E. (1969). Experimental approaches in utilising breed resources. *Animal Breeding Abstracts*, 37. 191-202.
- Groeneveld, E., Kovač, M. (1990). A generalized computing procedure for setting up and solving mixed linear models. *Journal of Dairy Science*, 73. 513-531.
- Haley, C.S., Avalos, E., Smith, C. (1988). Selection for litter size in the pig. *Animal Breeding Abstracts*, 56. 317-332.
- Hofer, A. (1998). Genetic evaluation in the Swiss national breeding program. In: International workshop Introduction of BLUP animal model in pigs, Praga-Uhrineves, 1998-09-03/05. 6.

- Johnson, R.K., Nielsen, M.N., Casey, D.S. (1999). Response in ovulation rate, embryo survival, and litter traits in swine to 14 generation of selection to increase litter size. *Journal of animal science*, 77. 541-557.
- Kisner, V., Brandt, H., Glodek, P., Moellers, B. (1996). Die Analyse von Sauenaufzuchtleistungen in der Versuchsstation Relliehausen zur Entwicklung von Kriterien der Wurfqualität. 3. Mitteilung: Schätzung genetischer Parameter für Wurfleistung und Kriterien der Wurfqualität. *Archiv für Tierzucht*, 39. 143-152.
- Kovač, M., Šalehar, A., Krašovic, M. (1984). Parametri reprodukcijskega ciklusa svinj na slovenskih farmah prašičev. 3. Laktacija. In: Poročilo RP, Ljubljana, BF, VTOZD za živinorejo, 253-246.
- Kovač, M. (1992). Derivative free methods in covariance components estimation. PhD thesis. Urbana, University of Illinois, 147.
- Komender, P., Hoeschele, I. (1989). Use of mixed-model methodology to improve estimation of crossbreeding parameters. *Livestock Production Science*, 21. 101-113.
- Mercer, J.T., Crump, R.E. (1994). Genetic parameter estimates for reproduction traits in purebred Landrace pigs. In: *Proceedings of the 5th World Congress on Genetics Applied to Livestock Production*, Guelph, 1994-08-07, 12. Guelph, Organising Committee of the 5th WCGALP, 15. 489-495.
- Peterson, H.D., Thompson, R. (1971). Recovery of inter-block information when block size are unequal. *Biometrika*, 58. 545-554.
- Roehe, R., Kennedy, B.W. (1995). Estimation of genetic parameters for litter size in Canadian Yorkshire and Landrace swine with each parity of farrowing treated as a different trait. *Journal of animal science*, 73. 2959-2970.
- Rothschild, M.J., Bidanel, J.P. (1998). Biology and genetics of reproduction. V. The genetics of the pig (ed. Ruvinsky, M. J., Rothschild, A.). Oxon, CAB International, 313-343.
- Sadek, K. (1994). Napoved plemenske vrednosti za velikost gnezda pri prašičih. *Diplomska naloga*. Domžale, BF, Oddelek za zootehniko, 51.
- Sadek-Pučnik, K., Kovač, M. (1996). Genetic parameters for litter size in successive parities in pigs. In: 47th Annual meeting of the EAAP, Lillehammer, 1996-08-25/29, 6.
- Schaeffer, L.R. (1993). Within-herd evaluation of sow reproductive traits. *Canadian Journal of Animal Science*, 73. 223-230.
- See, M. T., Mabry, J. W., Bertrand, J. K. (1993). Restricted maximum likelihood estimation of variance components from field data for number of pigs born alive. *Journal of animal science*, 71. 2905-2909.
- Southwood, O.I., Kennedy, B.W. (1990). Estimation of direct and maternal genetic variance for litter size in Canadian Yorkshire and Landrace swine using an animal model. *Journal of Animal Science*, 68. 1841-1847.
- Tölle, von K.H., Tholen, E., Trappmann, W., Stork, F.J. (1998). Möglichkeiten der Zuchtwertschätzung für Reproduktionsmerkmale beim Schwein am Beispiel eines Schweinezüchtverbandes. *Züchtungskunde*, 70. 351-361.

Corresponding author (*Adresse*):

Betka Logar

University of Ljubljana, Biotechnical Faculty

SI-1230 Domžale, Groblje 3. Slovenia

Universität Ljubljana, Biotechnische Fakultät

SI-1230 Domžale, Groblje 3. Slowenien

Tel.: 386-61-717-800, Fax: 386-61-721-005

e-mail: betka@mrcina.bfro.uni-lj.si