

GENETIC PARAMETERS FOR LITTER SIZE IN BLACK SLAVONIAN PIGS WITH EACH PARITY TREATED AS A DIFFERENT TRAIT

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ABSTRACT

The objective of this study was to estimate genetic parameters for litter size in Black Slavonian pigs using a multiple trait model with each parity treated as a different trait. A total of 4733 litter records from the first to the sixth parity from sows that farrowed between January 1998 and December 2010 were included in the analysis. Estimates of additive genetic variance with a multiple trait model were in the range from 0.05 to 0.48 across parities, and heritabilities were estimated in the range between 0.03 and 0.21. Estimates of phenotypic correlations were much lower than those of genetic correlations. Due to the unexpected changes of variances with a parity, the best option for genetic evaluation of litter size could be the use of repeatability model. With increasing number of data and with proper data structure alternative, modelling of litter size of Black Slavonian pig using multiple trait model could be taken into consideration.

Key words: pigs / genetic parameters / litter size / local breed / multiple trait model

1 INTRODUCTION

Black Slavonian pig is a Croatian autochthonous breed developed at the end of the 19th century. Due to the introduction of modern breeds Black Slavonian breed became less and less used up to the point of facing extinction in the middle of 1990s when the number of animals was reduced to only 60 sows and five boars (Uremović *et al.*, 2000). Since the year 1996 population of Black Slavonian pigs started to increase, primarily due to the state subsidies and the efforts of individual pig breeders. During this period animal performance database for reproduction traits of Black Slavonian pigs was established to provide information for management and selection. Namely, litter size of Black Slavonian pigs is lower than in modern pig breeds, on average six to seven piglets born alive (Senčić *et al.*, 2001). In the last few years, population of Black Slavonian pigs increased to more than 900 sows and 120 boars (Croatian Agricultural Agency, 2013), which opens a possibility to renew breeding programme for this local breed and to determine genetic parameters

for litter size as one of the most important traits in pig breeding.

Knowledge of genetic parameters for litter size in pigs is necessary to estimate accurate breeding values, to optimize breeding schemes, and to predict response to selection (Roehe and Kennedy, 1995). There are several approaches regarding the method for genetic evaluation of litter size. They mainly depend on genetic correlations between litter size in subsequent parities, size of data set, capacity of computing etc. Multiple trait analysis supposes subsequent observations to be different traits. Estimates of genetic correlations between litter sizes in different parities are often lower than one (Alfonso *et al.*, 1994; Irgang *et al.*, 1994), especially between the first and later parities (Serenius *et al.*, 2003). The low correlations between parities indicate that different genes are responsible for litter size in different parities. Therefore, multiple trait analysis is preferred in such situation in order to increase the efficiency of selection. The objective of this study was to estimate genetic parameters for litter size of Black Slavonian pigs using a multiple trait model.

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2 MATERIAL AND METHODS

Data for this study were obtained from the Croatian Agricultural Agency. Litter records from the first to the sixth parity from sows that farrowed between January

Table 1: Basic statistics for the number of piglets born alive by parity

Parity	No. of records	Min	Max	Mean	SD
1	1,446	1	16	5.77	1.69
2	1,075	1	13	6.29	1.69
3	831	1	15	6.23	1.74
4	569	1	14	6.42	1.85
5	455	1	11	6.18	1.58
6	357	1	13	6.23	1.70
Total	4,733	1	16	6.12	1.72

1998 and December 2010 were included in the analysis. Litter size was presented as the number of piglets born alive (NBA). Beside the identification number of a sow and NBA, individual record consisted of the following variables: breeding organisation (eight regions), parity (1–6), service boar, and farrowing season (month-year interaction). All months with less than five records were joined to next closest month, while boars with less than five litters were joined in one group separately by region. After data editing, there were 132 seasons, and 164 service boars, and a total of 4733 litter records (Table 1).

Litter records were obtained from 1649 animals with 2.9 litters per animal (Table 2). The number of animals with complete records of all six parities was 272 which comprised 16% of the observed population. The pedigree file was prepared for three generations and included 1862 triplets of animal, sire and dam with 179 sires and 581 dams.

Preliminary analysis using the repeatability model showed that following fixed effects should be included in the statistical model for NBA: farrowing season as year-month interaction, service boar, and parity. The multiple trait (MT) analysis was performed in way that litter records by parity were treated as different traits resulting in the six-trait model (1), which implies that the model

Table 2: Data and pedigree structure

Item	Data	Item	Pedigree
No. of litters	4,733	No. of sires	179
No. of animals	1,649	No. of dams	581
Litters per animal	2.9	No. of animals per sire	11.3
No. of animals with all 6 parities	272	No. of animals per dam	3.5

consisted only of additive genetic effect as a random effect. The appropriate MT model was:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_a\mathbf{a} + \mathbf{e}, \quad (1)$$

with the following covariance structure (2):

$$\text{var} \begin{bmatrix} \mathbf{a} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{A} \otimes \mathbf{G}_0 & 0 \\ 0 & \sum_i \mathbf{R}_{0i} \end{bmatrix}, \quad (2)$$

where \mathbf{G}_0 is a matrix of additive genetic covariances for NBA between parities and \mathbf{R}_{0i} is a diagonal matrix of parity class specific residual variances for animal i . Residuals within and between animals were assumed independent. Estimation of the covariance components with MT models was based on the Residual Maximum Likelihood method using the VCE-5 software package (Kovač *et al.*, 2002).

3 RESULTS AND DISCUSSION

Additive genetic and phenotypic correlations for NBA among the first six parities were presented in Table 3. Phenotypic correlations between different parities were generally low (less than 0.40), in particular between the

Table 3: Estimates of phenotypic (above diagonal) and additive genetic correlations (below diagonal)

	Parity					
Parity	1	2	3	4	5	6
1		0.12	0.03	0.12	0.08	0.03
2	0.74		0.38	0.39	0.11	0.17
3	0.20	0.80		0.25	0.04	0.18
4	0.88	0.96	0.63		0.15	0.12
5	0.90	0.42	0.16	0.09		0.00
6	0.40	0.91	0.96	0.01	0.05	

first and other parities (less than 0.13) and between any parity and the last two (the fifth and sixth) parities. The highest phenotypic correlations were between the second, third, and fourth parity. Genetic correlations between the adjacent parities were higher and ranged between 0.01 and 0.96. The highest values were observed among the pairs of the first four subsequent parities and remarkably lower for last two parities. Pattern of the decrease of genetic correlation along the distance between parities was not smooth, due to the oscillations for some pairs of parities. Low

Table 4: Estimates of variance components and ratios of phenotypic variance with standard errors for NBA

Parity	σ^2_{ph}	σ^2_a	σ^2_e	h^2	e^2
1	2.05	0.05 ± 0.02	1.99 ± 0.03	0.03 ± 0.01	0.97 ± 0.01
2	2.35	0.48 ± 0.05	1.87 ± 0.05	0.20 ± 0.03	0.79 ± 0.03
3	2.15	0.46 ± 0.07	1.69 ± 0.06	0.21 ± 0.05	0.78 ± 0.05
4	1.98	0.34 ± 0.05	1.64 ± 0.06	0.17 ± 0.05	0.82 ± 0.05
5	1.60	0.14 ± 0.07	1.45 ± 0.07	0.09 ± 0.06	0.90 ± 0.06
6	1.59	0.07 ± 0.03	1.51 ± 0.06	0.04 ± 0.03	0.95 ± 0.03

σ^2_{ph} —phenotypic variance; σ^2_a —additive genetic variance; σ^2_e —residual error variance; h^2 —heritability; e^2 —ratio of residual error variance

genetic correlations between litter size in different parities indicates that phenotype records from different parities should be treated as different traits (Irgang *et al.*, 1994; Roehe and Kennedy, 1995). Direct additive genetic correlations obtained with MT analysis for six traits are lower than in Hanenberg *et al.* (2001), who reported an increase from 0.79 between the first and the second parity to 0.96 between the fifth and the sixth parity. Considerably lower values of additive genetic correlations between the pairs of the last three parities in this study suggest the potential issue with the data structure to apply the MT model.

Estimates of variance components and ratios of phenotypic variance by parities are presented in Table 4. Total phenotypic variance, as a sum of all variance components by parities, ranged between 1.59 and 2.35, with the increasing values up to the third parity and decreasing values afterwards. Direct additive genetic variances ranged between 0.06 in the first parity and 0.48 in the third parity with heritabilities between 0.03 in the first parity and 0.21 in the third parity. Heritability estimates from the second to the fourth parity using the MT model were substantially higher than the generally accepted average of 0.10. In some studies heritabilities obtained with the MT model were generally smaller than those calculated with the repeatability model (Alfonso *et al.*, 1997). Small additive genetic variances and consequently low heritabilities were found in this study in the first and the last parity. Lower heritability estimated in the first parity with the MT model is in line with the study of Roehe and Kennedy (1995). Exceptionally high estimates of heritabilities in higher parities were found by Kovač and Sadek-Pučnik (1997), and they explained them as a consequence of numerical problems.

4 CONCLUSIONS

For estimation of genetic parameters of litter size in pigs different methods can be used. With the assumption of unit genetic correlations between parities and constant

variance along parities the repeatability model is the model of choice. In the situation when genetic correlations between parities are lower, a multiple trait model is suggested. However, sufficient data with proper structure is needed to apply multiple trait model and if this requirement is not met as is often the case with less numerous local pig breeds, the best option is to use the repeatability model.

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