HERITABILITY AND CORRELATION OF LITTER TRAITS IN PIGS DETERMINED BY REML METHOD

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Abstract: The aim of this study was to determine the heritability coefficients and the correlation between the number of live born piglets (NBA), the number of stillborn piglets (NSB), the number of total born piglets (NTB) and the number of weaned piglets (NW) in the part of population in Swedish Landrace sows in R. Serbia. The results obtained should enable the selection of litter size traits that would be proposed to be included in the selection - breeding program for this breed. The analysis of parameters was carried out on the basis of data on fertility of 4.061 Swedish Landrace sows and their 15.209 litters realized on two pig farms in R. Serbia. There was a genetic relationship between animals among the farms. Components of variance and covariance of observed traits, the share of additive genetic variance component in the phenotypic and correlation of traits at phenotypic and genetic levels, were evaluated using the method of Restricted Maximum Likelihood (REML) using the Multitrait Model (MM). Heritability estimates for the NBA, NSB, NTB and NW amounted to 6.4, 1.6, 6.7 and 1.1%, respectively. Correlation between the NBA and NTB at the phenotypic and genetic level was complete (r_P = 0986, r_G = 0938). Correlation between the NBA and NW at the phenotypic level has not been established, while at the genetic level it was weak. We believe that this is the result of the procedure of equalizing of litters after farrowing. In order to obtain objective genetic parameters for NW this procedure should not be applied in pure breed sows.

Key words: heritability, genetic correlation, phenotypic correlation, litter size, REML method

Introduction

When creating breeding and selection programs and choosing the selection method, mainly the heritability and correlation among traits are considered that are

in the focus of breeders. The correlation between traits of litter size at farrowing and weaning has different strengths and directions, at the phenotypic and at the genetic level.

Litter size traits belong to the group low hereditary traits whose heritability coefficient usually ranges from 10 to 15%. Heritability values for the number of live born piglets in that range are stated by *Radojković et al. (2005b), Holm et al. (2005)* and *Wolf et al. (2005)*. Slightly lower values of heritability of this trait ranging from 0.05 to 0.10 are presented by *Vuković (2003)* and *Luković et al. (2007)*.

Correlation between the number of live and stillborn piglets in the litter was mostly very weak to weak, with a different sign. Genetic correlation between the observed properties in the category of weak positive ($r_G = 0.350$) has been presented by *Vuković (2003)*. Slightly lower value of the observed parameter $r_G = 0.257$ has been established by *Kim (2001)* in the analysis of the correlation of these litter size traits in primiparous sows, whereas the value of the genetic correlation coefficient was in the category of very weak correlation, $r_G = 0.227$, when at the same time the fertility was analyzed in the first three parities. Negative correlation between the analyzed traits, both at the phenotypic and genetic level, has been determined by *Serenius et al. (2004)*. Phenotypic correlation coefficient value was $r_P = - 0.180$, and genetic $r_G = - 0.110$, in the analysis of correlation between the number of live and stillborn piglets in litters of primiparous sows.

Correlation between the number of live born piglets and total born piglets is mainly complete and highly statistically significant (P<0.01). Complete phenotypic correlation between the number of live born piglets and total born piglets in the range of $r_p = 0.922$ to $r_p = 0.929$ have been established by *Radojković et al. (2005a)*. Slightly lower values of phenotype correlations, at the level of a very strong positive correlation $r_P = 0.890$ has been determined by *Serenius et al. (2004)*. Full and positive genetic correlation between these traits of litter size at birth and has also been determined by the following group of authors: *Kim (2001), Vukovic (2003), Serenius et al. (2004)* and *Radojković et al. (2005a)*.

Correlation between the number of live born piglets and number of weaned piglets has positive direction, in terms of strength of the correlation it ranges from non-existent to complete, at the phenotypic and genetic level. Thus, *Chen et al. (2003)* report that between these traits there is no phenotypic connection ($r_P = 0.050$) when the data of the number of weaned piglets corrected to number of weaned piglets per litter are analysed, which is the recommended procedure for correction in all cases where the procedure is applied of piglets being moved from litter to litter, in order to equalize the litter sizes. In agreement with previous results are also results obtained by *Radojković et al. (2005a)* in respect to the correlation between observed traits. The authors state that the phenotypic correlation coefficient values were in the range $r_P = 0.071$ and $r_P = 0.048$, when the correlation between the number of live born piglets born and the number of pigs weaned was analysed corrected for the number of piglets weaned in the litter on the basis of

fertility in the first two and first three parities. The highest value of the coefficient of correlation of phenotype and the number of live pigs reared in a very strong class correlation ($r_P = 0.820$) is shown in a study published by *Serernius et al. (2004).*

The highest value of the coefficient of phenotypic correlation of the number of live born and weaned piglets in the class of very strong correlation ($r_p = 0.820$) is presented in a study published by *Serernius et al. (2004).*

The genetic correlation between these traits is generally in the range from strong to complete. Positive genetic correlation of $r_G = 0.726$, $r_G = 0.740$ and $r_G = 0.897$ has been determined by *Čechova and Tvrdon (2002), Vukovic (2003*) and *Radojković et al. (2005a),* respectively. The only exception in respect to the strength of the genetic correlation between these traits is the genetic correlation coefficient determined by *Chen et al. (2003)* where the value of the observed parameter was $r_G = 0.140$, and was the result of correction performed on the number of weaned piglets to number of weaned piglets per litter.

The aim of this study was to determine the heritability coefficients and the correlation between the number of live born piglets (NBA), the number of stillborn piglets (NSB), the number of total born piglets (NTB) and the number of weaned piglets (NW) in the part of population of Swedish Landrace sows which represents the largest population of pigs in R. Serbia. On the basis of these results it would be concluded what combination of litter size traits could be proposed for inclusion in the selection - breeding program for this breed.

Material and methods

For the evaluation of heritability coefficients and phenotypic and genetic correlations, the data on the fertility of sows of Swedish Landrace pigs from two farms in R. Serbia were used. There was a genetic relationship between animals among the farms. On these farms doses of the same boar sire were used for artificial insemination which is the reason for mentioned genetic correlation among animals. 15.209 litters were analysed, that were farrowed by 4.061 sows. The average number of litters per sow was 3.74. Sows originated from 2636 litters, which meant that in average 1.54 animals were chosen per litter. The pedigree file includes information on the origin of three generations. The total number of animals in the pedigree file was 5023. Number of ancestors was 962, while the number of animals with no known origin (base animals) was 808 which are 16.09% of the total number of animals in the pedigree file. From the presented data it can be concluded that the structure of the data was such that it allowed obtaining of reliable results using the REML method. This means that the structure of the frequency distribution of the random effects allowed objective evaluation of components of (co)variance of the observed parameters. The data structure in the

pedigree file provided maximization of the accuracy of evaluation of additive genetic variance component taking into account all available kinship relations between animals and their production results.

Components of variance and covariance of observed traits, the share of additive genetic variance component in the phenotypic, and the correlation between traits at phenotypic and genetic levels, were evaluated using Restricted Maximum Likelihood method (REML -) using Multitrait Model (MM).

The model used for the evaluation of components of (co)variance and calculation of heritability coefficients, genetic and phenotypic correlations for all four traits can be displayed in matrix form as follows:

$$y = X\beta + Z_l l + Z_p p + Z_a a + e$$

where,

y - vector of observations for the analysed traits (NBA, NSB, NTB and NW)

X - matrix of events for the systematic part of the model,

β - vector of unknown parameters for the systematic part of the model,

Z_l – matrix of events of random effect of common environment on the litter in which sows were born (reared),

l - vector of unknown parameters for the effect of common environment on the litter in which sows were born (reared),

Z_p - matrix of events for random effect of permanent environment in sow litters,

p - vector of unknown parameters for the effect of permanent environment in sow litters,

Z_a - matrix of events for direct additive genetic effect of the animal i.e. breeding value,

a - vector of unknown parameters for direct additive genetic effect of the animal i.e. breeding value,

e - vector of random residue.

The model for the analysis of litter size traits at farrowing (NBA, NSB, NTB) the following systematic effects were included: farm, parity, season, litter genotype, duration of the previous weaning to conception interval, linear effect of duration of previous lactation and square regression effect of age of the sow at farrowing nested within the parity. Model that analyses the litter size at weaning (NW) included the following systematic effects: farm, parity, season, litter genotype, number of weaned piglets per litter after equalization (cross-fostering) and square regression effect of age of sow at farrowing nested within parity.

To determine the phenotypic and genetic (co)variances of the analysed traits and to determine the percentage share of the additive genetic variance component in the phenotypic, using REML method, we used the software package "VCE-5" (*Kovač et al., 2002*).

Results and Discussion

Table 1 shows the established heritability coefficients of analysed traits and phenotypic and genetic correlations between them.

Table 1. Heritability (at diagonal), genetic (below diagonal) and phenotypic (above diagonal) correlation coefficients of litter traits

Trait	NBA[1]	NSB	NTB	NW
NBA	**0.064** ± 0.008	- 0.100[**2]	0.938[**]	0.042[ns]
NSB	0.164[**] ± 0.104	**0.016** ± 0.003	0.250[**]	- 0.046[ns]
NTB	0.986[**] ± 0.008	0.326[**] ± 0.057	**0.067** ± 0.008	0.025[ns]
NW	0.312[**] ± 0.145	0.187[**] ± 0.185	0.331[**] ± 0.187	**0.011** ± 0.003

[1] - NBA (number of born alive piglets), NSB (number of still born piglets), NTB (number of total born piglets), NW (number of weaned piglets)
[2] - probability: * - $p<0.05$; ** - $p<0.01$; ns - $p>0.05$

Heredity of NBA and NTB was low and almost identical. This result was expected because these two traits feature full correlation at the phenotypic and the genetic level as confirmed by the results (r_p = 0.938 and r_G = 0.986). Similar heritability coefficient values for the NBA are presented by *Kim (2001), Vuković (2003)* and *Luković et al. (2007)* Higher heritability values for the NBA are presented by *Radojković et al. (2005b)*, *Holm et al. (2005)*, *Wolf et al. (2005), Abell et al. (2012)* and *Popovac et al. (2012)*. Heritability of TNB is consistent with the results that are stated by Kim (2001) and Imboonta et al. (2007), while Čechova and Tvrdon (2002), Vukovic (2003), Radojkovic et al. (2005b) and Popovac et al. (2012) have been established higher values.

Full and positive genetic correlation between NBA and TNB, which is consistent with this research, have been established by the following group of authors: *Kim (2001)*, *Vuković (2003)*, *Serenius et al. (2004*) and *Radojković et al. (2005a)*.

Heredity of NSB was very low, and the same results have been obtained by *Vuković (2003)*, *Serenius et al. (2004*) and *Radojković et al. (2005b)*.

Phenotypic correlation between the NSB and NBA was negative but at the lower limit of very weak, which is consistent with the result presented by *Serenius et al. (2004)* and *Popovac et al. (2012)*. Phenotypic correlation coefficient between the NSB and NTB was positive, which is understandable because the increased number of stillborn piglets also increases the number of total born piglets, and on the verge of a very weak and weak correlation. A similar result was obtained by *Kim (2001)*. At the genetic level, correlations between NSB on one side and NBA and TNB on the other were positive and in the class of very weak and weak which is consistent with the results obtained by *Kim (2001)* and *Vuković (2003)*.

Heritability coefficient for NW was very low. Close values of this parameter have been determined by *Kim (2001),* who in his research also applied the equalization effect (cross-fostering) when calculating the heritability of the trait. In

the case when a sow breeds not only her piglets in the litter, in the assessment of the genetic variability of NW practically only sow maternal ability is evaluated, as well as her ability to raise certain number of piglets after equalization (cross-fostering). Totally objective evaluation of heritability of this trait is obtained only when mixing of piglets between litters is not implemented. More reviews of the heritability for this trait in the range from 5 to 10% are presented in the research by *Čechova and Tvrdon (2002)*, *Chen et al. (2003)*, *Vuković (2003)*, *Serenius et al. (2004)*, *Radojković et al. (2005b)* and *Popovac et al. (2012)*.

Phenotypic correlation between NBA and NTB, on one side and NW on the other, has not been established, which is also a consequence of equalization (cross-fostering) and this is consistent with the results presented by *Chen et al. (2003)* and *Radojković et al. (2005b)*. The genetic correlation between these traits was in the class of weak and below the values presented by *Čechova and Tvrdon (2002)*, *Vuković (2003)* and *Radojković et al. (2005a)*, while only in the research presented by *Chen et al. (2003)* the value of this parameter was lower.

Conclusion

The presented results clearly show the low heritability of fertility traits. However, in addition to pronounced phenotypic variability of these traits, it is still enough to make a systematic selection of pigs for these traits possible. NBA trait is of the greatest importance for pig breeders because the litter size at farrowing is precondition for success in all other phases of pork production. It is fully connected with the trait NTB, so that inclusion of these traits in the breeding program would not be justified. Correlation between NBA and NW at the genetic level determined in this study was weak but positive, which would actually allow independent selection for these two traits. Recommendation would be to avoid cross-fostering of litters of pure breed sows on selection farms, in order to objectively evaluate the genetic parameters for NW which would provide greater selection effects. For the ultimate choice of litter size traits that would be included in the breeding - selection program for the Swedish Landrace breed, it would be necessary to conduct research on a larger part of the population with respect to the previous recommendation. At this point, the choice would be NBA because of all the conclusions presented.

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Naslednost i povezanost osobina veličine legla svinja utvrđena REML metodom

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Rezime

Cilj istraživanja bio je da se utvrde koeficijenti naslednosti i povezanosti između broja živorođene prasadi (NBA), broja mrtvorođene prasadi (NSB), broja ukupnorođene prasadi (NTB) i broja odgajene prasadi (NW) u delu populacije krmača rase švedski landras u R. Srbiji. Dobijeni rezultati treba da omoguće izbor osobina veličine legla koje bi bile predložene za uključivanje u selekcijsko - odgajivački program za ovu rasu.

Ocena analiziranih parametara sprovedena je na osnovu podataka o plodnosti 4061 krmača rase švedski landras i njihovih 15209 legala ostvarenih na dve farme svinja u R. Srbiji između kojih postoji genetska povezanost među životinjama. Komponente varijanse i kovarijanse posmatranih osobina, udeo aditivne genetske komponente varijanse u fenotipskoj i povezanost osobina na fenotipskom i genetskom nivou ocenjene su metodom ograničene najveće verovatnoće (REML - Restricted Maximum Likelihood) primenom višeosobinskog modela (MM - Multitrait Model).

Heritabiliteti za NBA, NSB, NTB i NW su iznosili 6.4, 1.6, 6.7 i 1.1 %, respectively. Povezanost NBA i NTB na fenotipskom i na genetskom nivou je bila potpuna (r_P = 0.986, r_G = 0.938). Povezanost NBA i NW na fenotipskom nivou nije utvrđena, dok je na genetskom bila slaba. Smatramo da je to posledica postupka ujednačavanja legala posle prašenja. Radi dobijanja objektivnih genetskih parametara za NW ovaj postupak ne treba primenjivati kod čistorasnih krmača.

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