Genetic Parameters For Reproductive Traits And Number Of Teats In Pigs

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Introduction

Reproductive traits in pigs were often linked to the ability of sows to deliver as much as possible piglets. Beside, reproductive ability, it is of significant importance weaning ability of sows that among others is related to number of functional teats. Genetic parameters for reproductive traits in pigs were broadly elaborated. The genetic parameters of teat number and its relation to reproductive traits showed various results. Teat number plays a significant role when there are more piglets than teats and the selection on litter size may require improvement of teat number (Hirooka et al., 2001). The present study aimed to evaluate the genetic parameters for main reproductive traits, total number of teats and its relation.

Material and methods

Dataset: The data were obtained from one of the breeding pig farms in Macedonia, where reproductive data was extracted for two genotypes pure breed Large White and F1 crossbreeds of Large White and Landrace sows born from 2003 until 2009. After omitting all illogical information the data consisted of 1598 records for reproductive traits, e.g. number of total born piglets (NTB) and number of born alive (NBA) and 797 records for total number of teats (TNT) that was carefully counted and recorded at age of one month. The information related to genotype, parity, date of farrowing, boar of insemination, age at farrowing, previous lactation length and weaning to conception interval were included for each farrowing. The descriptive statistic of the dataset is presented in Table 1.

Table 1: Descriptive statistics of analyzed traits and covariables used data set

Traits	All	Pure line	Cross line
Reproductive			
Number of records	1598	1103	495
Farrowing age in days (range)	620,13 (1413)	618,37 (1408)	624,06 (1281)
Number of total born (SD)	12,96 (0,090)	12,58 (0,111)	13,82 (0,150)
Number of born alive (SD)	12,12 (0,089)	11,69 (0,108)	13,08 (0,144)
Previous lactation length in days (SD)	25,41 (0,107)	25,31 (0,115)	25,65 (0,238)
Teats			
Number of records	n= 797	n=302	(n =495)
Total number of Teats (SD)	14,10 (0,012)	14,25 (0,029)	14,00 (0,003)

The pedigree data contained all animals with records as well as their ancestors, traced back as far as possible. In total, the pedigree contained 1538 animals. Amongst these, 568 were

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animals with records, 588 were ancestors and 382 animals defined the base population. In the pedigree there were in total 383 sires.

Statistical analyses: The aim of the study was estimate genetic parameters for reproductive traits (NTB and NBA) and TNT as well as correlation between those traits. For the analyses 2 models were used. In the estimation of genetic parameters for the reproductive traits (NTB and NBA) the identical models were used for primiparous ($y_{1ijklmnop}$) and sows ($y_{2ijklmnop}$). The model [1] counted fixed effects for animal genotype (G_i), boar of insemination (B_j) with 54 levels and year-season of farrowing (YSf_k). In each year four seasons were defined with 3 month each starting form Jan. combined with 6 years, forming in total 23 levels. For the effect age of farrowing ($x_{ijklmnop}$), quadratic regression nested within parity grouped in four classes defined as 1st, 2nd, 3rd and 4th and more ($P4_l$) was used. For sows' data estimation ($y_{2ijklmnop}$), fixed part of the model included previous lactation length ($z_{ijklmnop}$) as linear regression and weaning to conception interval (WCL_m) defined as class effect with 3 levels 1-4, 5, and more than 5 days; since 76,7% of the records were in day 4 and 5. Random parts of both models consisted of permanent environmental (pe_{ino}), additive direct animal effect (a_{ino}) and a random residual ($e_{ijklmnop}$).

$$\begin{bmatrix} y_{1ijklmnop} \\ y_{2ijklmnop} \end{bmatrix} = \mu + G_i + B_j + YSf_k + P4_l + b_I\left(x_{ijklmnop} - \overline{x}\right) + b_{II}\left(x_{ijklmnop} - \overline{x}\right)^2 + \\ + \begin{bmatrix} 0 \\ WCL_m + b_I\left(z_{ijklmnop} - \overline{z}\right) \end{bmatrix} + pe_{ino} + a_{ino} + e_{ijklmnop} \qquad [1]$$

For TNT estimation Model [2], genotype (G_i) as a fixed effect, additive direct animal effect (a_{ij}) and a random residual (e_{ijk}) were included in the model.

$$y_{ijk} = \mu + G_i + a_{ij} + e_{ijk} \qquad [2]$$

Before the final construction of the model several single traits models were run exploiting REML approach. Random regression with Legendre polynomials were also tested up to second level but did not converge successfully. Finally, the three traits analyses were carried out using the software package VCE version 6.0 (Groeneveld et al., 2008).

Results and discussion

Estimations were taken with care since limited number of animals with sufficient data was available. Nevertheless, the results of genetic parameters estimates and are shown in Table 2. Reproductive traits represented had low heritability with estimates of h^2=0,01±0,00 for NTB and h^2=0,02±0,01 for NBA. Common environment estimates for those treats were close to zero. Low heritability values are reported by other authors, too (Duc et al., 1998; Hanenberg et al., 2001; Lukovic, 2004). Low estimates can occur due to unfavorable data structure, and complexness of the model used. On the other hand the heritability estimated for TNT was high (h^2=0,29±0,02), and in accordance to other findings (Fernandez et al., 2004). Those results are not in compliance with Zhang et al. (2000) who suggest very high heritability estimates for number of teats in both sexes (from h^2=0.53 to h^2=0.43). On contrary, in previous estimations done by Vukovic et al. (2007) on other data set reported h^2=0.16±0.02

for TNT. Generally teat number is considered to be moderately heritable with heritability of about 0,3 according Canadian swine national system for recording conformation traits (2001), however this source of information is reporting relatively high values of heritability of number of traits from some investigations before 1981.

Table 2: Estimated variances heritability and common environment.

Traits	σ^2_a	σ^2_{pe}	σ^2_e	$h^2 \pm$ SE	$c^2 \pm$ SE
NTB	0,112	0,002	0,988	0,01±0,00	0,00±0,00
NBA	0,205	0,072	0,969	0,02±0,00	0,01±0,01
TNT	0,035	---	0,086	0,29±0,02	---

Phenotypic correlation between reproductive traits and TNT (Table 3) were zero, while direct additive genetic correlations were low r_g=0,12±0,09 between NTB and TNT, and r_g=0,14±0,11 between NBA and TNT. However, the phenotypic correlation between reproductive traits was r_p=0,88±0,11 despite complete genetic correlation (r_g=0,99±0,05). Different genetic correlation between reproductive traits and TNT was reported, e.g. Pumfrey et al. (1980) moderate negative, Skjervold (1963), moderate positive. The estimated values for TNT and reproductive traits in our analyses has to be proved in other research based on larger data set.

Table 3: Estimation of correlations$^{\alpha}$.

Traits	NTB	NBA	TNT
NTB	---	0,99±0,05	0,12±0,09
NBA	0,88±0,11	---	0,14±0,11
TNT	0,00±0,09	0,00±0,22	---

$^{\alpha}$ Phenotypic and genetic correlations below and above the diagonal, respectively.

Conclusion

The main objective of this study was reporting of our preliminary results from estimation of genetic parameters for reproductive traits and total number of teats in sows. Heritability values estimated for total born piglets (NTB) and number of born alive (NBA) were close to zero, due to limited data used in the evaluation. However, with additional data in genetic evaluation for litter size traits one should expect heritability values around of h^2=0,10 resulting with improvement of those traits in selection programs. For total number of teats (TNT) moderate heritability was estimated h^2=0,29±0,02. The genetic correlations of reproductive traits with TNT were r_g=0,12±0,09 and r_g=0,14±0,11 with NTB and NBA. The results suggest that TNT has solid base for selection and should be considered into breeding programs for increasing productive capacity of sows.

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