Genetic Parameters of Growth Traits from a Joint Evaluation of Purebred and Crossbred Pigs

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Summary

Authors analyzed average daily gain and lean meat percentage of the Pietrain (Pi), Duroc (Du) and their cross (PixDu); Pietrain (Pi) and Hampshire (Ha) and the cross (PixHa) using the national database for the period of 1997-2010. The heritability estimates for average daily gain (0.20±0.02, 0.24±0.02, 0.25±0.03, 0.37±0.06, 0.37±0.02 for Pi, Du, PixDu, Ha, PixHa, respectively); and lean meat percentage (0.17±0.02, 0.15±0.02, 0.13±0.02, 0.22±0.06, 0.20±0.02 for Pi, Du, PixDu, Ha, PixHa, respectively) were low. Genetic correlation between the purebreds and the crossbreds ranged from moderately high to high for average daily gain (0.93±0.15, 0.85±0.12, 0.56±0.14, 0.75±0.12) and from moderate to moderately high for lean meat percentage (0.65±0.16, 0.56±0.16, -0.38±0.17, 0.48±0.20) for Pi – PixDu, Du – PixDu, Ha – PixHa, Pi – PixHa, respectively. Based on the results the selection of the purebred parents for crossbred pigs can be based on the performance of their purebred breeding values of average daily gain. On the contrary for lean meat percentage the crossbred breeding values of the purebred pigs can also be used to select the best purebred pigs for crossing.

Key words

pig, genetic correlation, daily gain, lean meat percent, purebred, crossbred
Introduction

The genetic parameter estimates of some traits provide relevant information for the breeders to choose the proper breeding method. If the heritability of a trait is high, the variability of this trait in the population is basically due to genetic factors. In this case pure breeding is to be employed that exploits primarily the additive genetic variance. In case of low $h^2$ the pure breeding is less efficient and progeny test is needed that however lengthens the generation interval. For traits with low heritability crossbreeding methods can be applied exploiting also the non additive genetic factors. Any crossbreeding method is successful only if the populations to be crossed are homogeneous, differ significantly in allele frequency and the magnitude of the dominance is high. There is no any direct information about allele frequencies or about magnitude of the dominance. However Wei and van der Werf (1994), Baumung et al. (1997) showed that the magnitude of the dominance can be estimated indirectly. Analysing together the performance of the purebreds and that of the crossbreds (related to the purebreds), the genetic correlation between the purebred and crossbred performance refers to the magnitude of the dominance. The lower the estimated genetic correlation the larger is the dominance, indicating efficient crossbreeding. The objective of our analysis was to estimate genetic correlation between the purebred and crossbred performance for growth traits of pig genotypes that are generally used as paternal partners in crossings.

Materials and methods

The analysis was based on the data collected by the National Institute for Agricultural Quality Control (presently Agricultural Agency of Administration) in the course of field test conducted between 1997-2010. The analyzed breeds were the Pietrain (Pi), Duroc (Du) and their cross (Pi x Du), and Hampshire (Ha) and its cross with Pietrain (PixHa) (Table 1). The total number of animals in the pedigree file for the (PixHa) and (Pi x Du) genotypes was 42004 and 60926, respectively.

In the field test ultrasonic (SONOMARK 100) fat depth measurements were taken from boars and gilts between 80 and 110 kg between the 3rd and 4th lumbar vertebrae (8 cm laterally from the spinal cord), between the 3rd and 4th rib (6 cm laterally from the spinal cord) and the loin muscle area between the 3rd and 4th rib (6 cm laterally from the spinal cord). Using these measurements lean meat percentage can be calculated. Age and body weight (with an accuracy of 1 kg) of the animals were recorded at the same time from which their average daily gain was also calculated. The regulations of animal housing and feeding conditions are defined in the Hungarian Pig Performance Testing Code (MGSZH, 2009). Basic descriptive statistics were calculated applying SAS (SAS Inst. Inc., Cary, NC) (Table 2).

Genetic parameters of average daily gain and the lean meat percentage were estimated separately by REML method using the PEST (Groeneveld, 1990) (only for data coding) and VCE5 softwares (Kovac and Groeneveld, 2003) applying two-trait animal models. Average daily gain and lean meat percentage records of the purebred and crossbred pigs were considered as separate traits. Altogether two runs were performed. The structure of the animal model was the following:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 \\ 0 \\ X_2 \\ 0 \end{bmatrix} \begin{bmatrix} b_1 \\ 0 \end{bmatrix} + \begin{bmatrix} Z_1 \\ Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} W_1 \\ W_2 \end{bmatrix} \begin{bmatrix} c_1 \\ c_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

where $y_i = \text{vector of observations for the } i^{th} \text{ trait}$, $b_i = \text{vector of fixed effect for the } i^{th} \text{ trait}$, $a_i = \text{vector of random animal effects for the } i^{th} \text{ trait}$, $c_i = \text{vector of common litter effects for the } i^{th} \text{ trait}$, and $X_i$, $Z_i$ and $W_i$ are incidence matrices relating records of the $i^{th}$ trait to fixed effects, random animal effects and random common litter effects, respectively.

The variance-covariance matrices for the random additive genetic, random common litter and residual effects were:

$$\text{var}[a] = G \otimes A, \text{ with } G = \begin{bmatrix} \sigma^2_a \\ \sigma^2_a \\ \sigma^2_{a2} \end{bmatrix}$$

$$\text{var}[c] = W \otimes I, \text{ with } W = \begin{bmatrix} \sigma^2_c \\ \sigma^2_c \\ \sigma^2_{c2} \end{bmatrix}$$

$$\text{var}[e] = R \otimes I, \text{ with } R = \begin{bmatrix} \sigma^2_e \\ \sigma^2_e \\ \sigma^2_{e2} \end{bmatrix}$$

where $A$ is the numerator relationship matrix among the animals, $I$ is an identity matrix, $\sigma^2_a$, $\sigma^2_c$, and $\sigma^2_e$ are additive genetic variance, common litter variance and residual variance for trait $i$, $\sigma_{aj}$, $\sigma_{cj}$ and $\sigma_{ej}$ are corresponding additive genetic, common litter and residual covariances between traits $i$ and $j$.

In the model year-month, sex, herd effects were treated as fixed effects, while additive genetic and litter effects were considered as random effects.

Results and discussion

In Table 2 the descriptive statistics for the genotypes are presented. The animals showed large variability for both traits possibly because of the wide weight interval of the evaluated pigs. Viewing the genotype means the highest lean meat percentage was observed for the purebred Pietrain pigs while Pietrain x Hampshire pigs had the largest average daily gain.

Estimated heritabilities for the field test traits are presented in Table 3. Both traits show low heritability and are in agreement with literature (Lutaaya et al., 2001; Zumbach et al., 2007; Habier et al., 2009). However, it has to be noted that the low heritability of lean meat percentage might also be the result of imprecise ultrasound scanning and substantially higher heritability values for this trait were reported for purebred pig populations (Sonesson et al., 1998; 0.41; Knapp et al., 1997; 0.40-0.53). In our study the heritability of the purebred and crossbred populations did not
show tendential differences. Contrary to our results Brandt and Täubert (1998) found that two crossbred lines showed higher heritability estimates than purebreds and one possible explanation for that results could be that the higher degree of heterozygotes in crossbreds could increase the additive genetic variance. Similar results were reported by Merks and Hanenberg (1988).

Estimated random litter effects (common environment effect of the sow) are given in Table 4. The relative importance of this effect was higher for the average daily gain. The estimated values exceeded that of the additive genetic effects similarly to the results of Nagy et al. (2008). This finding is interesting as common litter effect is related to the environment during suckling and its magnitude should decrease with the increasing age. On the contrary, Brandt and Täubert (1998) reported low values (0.09-0.17). For the trait lean meat percentage the values are higher than the estimates of Nagy et al. (2008) for Hungarian Large White and Hungarian Landrace.

The genetic correlation coefficients between the purebred genotypes and their crosses are presented in Table 5. For average daily gain the estimates ranged between moderately high to high in accordance with findings of other authors (Brandt and Täubert, 1998; Wolf et al., 2002; Stamer et al., 2007). These results suggest that for this trait the crossbred information will not cause major changes and selection of the purebred pigs can be based on the purebred breeding values. Nevertheless estimates of present study for lean meat percentage were low to moderate, contrary to Wolf et al. (2002) and Stamer et al. (2007) who reported from high correlations (0.97 and 0.99, respectively). In our study a negative correlation between Ha and Pi x Ha (-0.38) was found that should be treated with caution.

### Conclusions

Based on the results it can be concluded that average daily gain and lean meat percentage did not show the same characteristics. Genetic correlations were quite high for average daily gain between purebred and crossbred pigs thus for purebred pigs use of the purebred breeding values are satisfactory. On the con-
trary for lean meat percentage (where the genetic correlations between purebreds and crossbreds were substantially lower) the crossbred breeding values of the purebred pigs can also be used to select the best purebred pigs for crossing.

References