

## Selection for reproduction traits in Hungarian pig breeding in a two-way cross

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The authors analysed reproduction traits in the Hungarian Large White (HLW) and Hungarian Landrace (HL) breeds and their reciprocal crosses ( $F_1$ ) based on the data collected within a field test between 2001 and 2010. The traits were number of piglets born alive (NBA), gestation length (GL), farrowing interval (FI) and age at first insemination (AFI). Genetic parameters were estimated separately for purebreds and crossbreds by the REML method applying two-trait repeatability models for NBA, GL, FI, and two-trait single measurement model for AFI. Records of purebred and crossbred pigs were considered separate traits. The numbers of sows for NBA and GL were 56743-167865, for FI 38541-112059, and for AFI 16083-46143. Total number of animals in the pedigree amounted to 126340. AFI was of moderate heritability with large difference between purebreds and crossbreds: 0.28 for HLW, 0.26 for HL vs. 0.40 for the HLW/HLW $\times$ HL, and 0.41 for the HL/HLW $\times$ HL crosses. Heritability estimates for GL, both in purebreds and crossbreds were moderate: 0.30 for HLW, 0.22 for HL, 0.25 for the HLW/HLW $\times$ HL cross, and 0.25 for the HL/HLW $\times$ HL cross. Heritability coefficients of NBA were low at 0.09, 0.06, 0.07, 0.06, and of FI at 0.06 for all HWL, HL, and their crosses, respectively. Magnitudes of the permanent environment effects ranged between 0.04-0.07 for GL and NBA and were null for FI. Genetic correlation estimates between purebred and crossbred performances were 0.28 and 0.39 for AFI, 0.96 and 0.82 for GL, 0.82 and 0.93 for NBA, as well as 0.65 and 0.33 for FI. Selection of purebred pigs for AFI and FI crossbred performances can be based on the crossbred breeding value whereas selection for NBA and GL can use either breeding value.

**KEYWORDS:** crossbred / pig / purebred / reproduction / variance components

In pig breeding most frequently studied reproduction traits are number of piglets born alive, weaning to service interval and weaning weights measured at different

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weaning ages while age at first insemination, gestation length and farrowing interval are by far less explored traits. Because of the generally low heritabilities [Boesch *et al.* 2000, Täubert and Brandt 2000, Nakavisut *et al.* 2005] these traits are of small genetic gain magnitude. The rate of progress is especially influenced by the fact that the selection of the reproduction traits is based on the purebred performance while the commercial animals are crossbred. Applying combined evaluation of purebreds and crossbreds we can obtain more precise information on the crossbred breeding value of purebred animals [Wei and Van der Werf 1994]. The BLUP procedure developed by Henderson [1975] has been applied in the Hungarian pig breeding for selection decisions since 2008. Although the purebred and crossbred performance records of various crosses are jointly evaluated they are treated as the same trait (considering genotype in the model as a fixed effect). The efficiency of selection performed for the crossbred performance depends on the strength of the relationship between purebred and crossbred breeding values. However, the relationship can only be estimated when crossbred and purebred performances are treated as different traits. Thus, each purebred pig would require its purebred breeding value predicting the performance of the future purebred progeny and a crossbred breeding value predicting the performance of the future crossbred progeny, for every trait.

Our goal was to estimate the possibility of increasing selection efficiency of purebred pigs for pure- and crossbred performances by treating the performances as separate but correlated traits.

## Material 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 a field test conducted between 2001 and 2010. The breeds considered were the Hungarian Large White (HLW), the Hungarian Landrace (HL) and their reciprocal crosses. Numbers of herds were 102, 45, and 80 for HLW, HL, and the crosses, respectively. The numbers of recorded sows for NBA, GL and AFI across the genotypes are presented in Table 1.

**Table 1.** Number of records for each trait and genotype

Item	HLW <sup>1</sup>	HL <sup>2</sup>	F <sub>1</sub> <sup>3</sup>
NBA <sup>4</sup>	167865	56743	163980
GL <sup>5</sup>	167865	56743	163980
FI <sup>6</sup>	112059	38541	110628
AFI <sup>7</sup>	46143	16083	43024

<sup>1</sup>Hungarian Large White; <sup>2</sup>Hungarian Landrace; <sup>3</sup>crossbreds; <sup>4</sup>number of born alive piglets; <sup>5</sup>gestation length; <sup>6</sup>farrowing interval; <sup>7</sup>age at first insemination.

Of all the sires and dams 10.5% and 9.6% of the boars and 14% and 20.6% of the sows had both purebred and crossbred progeny for HWL and HL, respectively. The purebred and crossbred pigs were kept partly in the same herds which means that environmental connectedness (43% for HLW/HLWxHL and 12% for HL/HLxHLW) existed between purebreds and crosses. Parity ranged between 1 and 17. The studied traits were age at first insemination (AFI), number of piglets born alive (NBA), gestation length (GL), and farrowing interval (FI). The data was divided in two subsets, each of them contained records of one purebred genotype and that of the adequate cross. The purebred and crossbred performances were considered separate traits. Variance components were estimated separately by the REML method using the VCE6 package [Groeneveld *et al.* 2008] with a two-trait animal models. Records were set to missing when not observed within the following intervals: 105-125 days for GL, 139-290 days for FI and 150-450 days for AFI. Altogether 8 runs were performed. The repeatability model for NBA, GL, FI was:

$$\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_2 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_2 \end{bmatrix} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{W}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{W}_2 \end{bmatrix} \begin{bmatrix} \mathbf{pe}_1 \\ \mathbf{pe}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix}$$

where:

$y_i$  – vector of observations for the  $i^{\text{th}}$  trait;

$b_i$  – vector of fixed effects for the  $i^{\text{th}}$  trait;

$a_i$  – vector of random animal effects for the  $i^{\text{th}}$  trait;

$pe_i$  – vector of random permanent environment effects for the  $i^{\text{th}}$  trait;

$X_i$ ,  $Z_i$  and  $W_i$  – are incidence matrices linking records of the  $i^{\text{th}}$  trait with adequate effects.

The model for AFI was the same as the model for the other traits except for the random permanent environment effect.

The (co)variance structures for the random additive genetic, permanent environment and residual effects were:

$$\text{Var}[\mathbf{a}] = \begin{bmatrix} \sigma_{a_1}^2 & \sigma_{a_1 a_2} \\ \sigma_{a_2 a_1} & \sigma_{a_2}^2 \end{bmatrix} \otimes \mathbf{A}, \quad \text{Var}[\mathbf{pe}] = \begin{bmatrix} \sigma_{pe_1}^2 & \sigma_{pe_1 pe_2} \\ \sigma_{pe_2 pe_1} & \sigma_{pe_2}^2 \end{bmatrix} \otimes \mathbf{I}$$

where:

$\mathbf{A}$  – the numerator relationship matrix among the animals;

$\mathbf{I}$  – an identity matrix;

$\sigma_{a_1}^2$ ,  $\sigma_{pe_1}^2$  and  $\sigma_{e_1}^2$  – additive genetic, permanent environment and residual variances for trait  $i$ ;

$\sigma_{a_1 a_2}$  and  $\sigma_{pe_1 pe_2}$  – corresponding additive genetic and permanent environment covariances between traits.

Total number of animals in the pedigree was 126340. The effects fitted in the models are summarized in Table 2.

**Table 2.** Effects fitted in the models for each trait

Effect	Type	NBA <sup>1</sup>	GL <sup>2</sup>	FI <sup>3</sup>	AFI <sup>4</sup>
Parity	fixed	x	x	x	-
Year-month of farrowing	fixed	x	x	x	-
Herd	fixed	x	x	x	x
Year-month of insemination	fixed	-	-	-	x
Permanent environment	random	x	x	x	-
Animal	random	x	x	x	x

<sup>1</sup>number of piglets born alive; <sup>2</sup>gestation length; <sup>3</sup>farrowing interval; <sup>4</sup>age at first insemination.

## Results and discussion

Descriptive statistics are shown in Table 3. The highest variability was found for NBA. However, the minimum and maximum values of AFI, GL and FI were constrained so the averages were similar in all the genotypes except of AFI where differences were still found in favour of the purebred HL. Crossbred pigs were not superior to the purebreds in any of the traits.

**Table 3.** Descriptive statistics for the genotypes for the traits recorded

Item	Trait	Minimum	Maximum	Mean	SD
HLW <sup>5</sup>	AFI <sup>1</sup> (days)	154	450	279	46
	GL <sup>2</sup> (days)	105	125	115	2
	NBA <sup>3</sup>	1	25	10.3	2.6
	FI <sup>4</sup> (days)	140	289	166	27
HL <sup>6</sup>	AFI (days)	155	450	254	43
	GL (days)	105	125	117	2
	NBA	1	22	10.5	2.6
	FI (days)	140	289	161	24
F <sub>1</sub> <sup>7</sup>	AFI (days)	153	450	268	44
	GL (days)	105	125	116	2
	NBA	1	24	10.4	2.4
	FI (days)	140	289	162	24

<sup>1</sup>age at first insemination; <sup>2</sup>gestation length; <sup>3</sup>number of piglets born alive; <sup>4</sup>farrowing interval; <sup>5</sup>Hungarian Large White; <sup>6</sup>Hungarian Landrace; <sup>7</sup>pooled crossbreds.

### Heritability and repeatability

**Age at first insemination.** Heritabilities and magnitudes of permanent environmental effects are presented in Table 4. AFI was moderately heritable showing large difference between purebreds and crossbreds (0.28 and 0.26 vs. 0.40 and 0.41). In the literature we did not find separate values for purebred and crossbred pigs but Hanenberg *et al.* [2001] reported  $h^2$  of 0.318 for Dutch Landrace sows which is in accordance

**Table 4.** Heritability coefficients ( $h^2$ ) and permanent environment component proportion of the phenotypic variance (PE) across traits and genotypes (*standard errors in parentheses*)

Genotype	Trait	$h^2$	PE
HLW <sup>5</sup>	AFI <sup>1</sup>	0.28 (0.00)	-
HL <sup>6</sup>		0.26 (0.00)	-
HLWxHL		0.40 (0.00)	-
HLxHLW		0.41 (0.00)	-
HLW	GL <sup>2</sup>	0.30 (0.01)	0.06 (0.00)
HL		0.22 (0.01)	0.04 (0.01)
HLWxHL		0.25 (0.01)	0.07 (0.01)
HLxHLW		0.25 (0.01)	0.07 (0.01)
HLW	NBA <sup>3</sup>	0.09 (0.00)	0.06 (0.00)
HL		0.06 (0.01)	0.06 (0.01)
HLWxHL		0.07 (0.00)	0.06 (0.00)
HLxHLW		0.06 (0.00)	0.06 (0.00)
HLW	FI <sup>4</sup>	0.06 (0.00)	0.00 (0.00)
HL		0.06 (0.01)	0.00 (0.00)
HLWxHL		0.06 (0.00)	0.00 (0.00)
HLxHLW		0.06 (0.00)	0.00 (0.00)

<sup>1</sup>age at first insemination; <sup>2</sup>gestation length; <sup>3</sup>number of piglets born alive; <sup>4</sup>farrowing interval; <sup>5</sup>Hungarian Large White; <sup>6</sup>Hungarian Landrace.

with our findings. Holm *et al.* [2005] estimated 0.31 for Norwegian Landrace pigs. Kumari and Rao [2010] made their experiment on Large White Yorkshire crossbred pigs and obtained a value of 0.16. The low estimate of this author can probably be explained by a small size (255) of the dataset.

**Gestation length.** Estimates of the heritability coefficients for GL in both pure- and crossbred pigs were of moderate magnitude (0.22-0.30). Farkas *et al.* [2007] analyzing data of HLW and HL pigs found very similar estimates (0.26 and 0.18, respectively). Nakavisut *et al.* [2005] obtained somewhat lower coefficients – 0.12 and 0.18 for pure- and crossbreds, respectively. In accordance with the previous authors Kumari and Rao [2010] estimated heritability at 0.18 for crossbred pigs while Hanenberg *et al.* [2001] reported heritability of 0.28 for purebred Dutch Landrace.

The magnitude of permanent environment component for GL can be considered low. Farkas *et al.* [2007] estimated permanent effects of similar magnitude (0.09) for both pure- and crossbred genotypes. Nakavisut *et al.* [2005] found twice as high value for crossbreds (0.18).

**Number of piglets born alive.** Heritability for NBA was one of the lowest amongst the studied traits with the  $h^2$  estimates of 0.06-0.09, thus indicating the importance of the environment in moulding of this trait. NBA is a broadly investigated trait. We found numerous papers of other authors reporting similar results. Farkas *et al.* [2007] studied the same genotypes and their estimates, 0.07 for HLW and 0.07 for LR, were

in agreement with our results. Fischer *et al.* [1999] obtained in Large White and its cross with Landrace heritability coefficients of 0.015-0.098 and 0.033-0.133 for purebred and crossbred pigs, using a repeatability model. Täubert and Brandt [2000] also studied Large White and Landrace pigs, as well as their crosses, and reported results very close to those of ours. Ehlers *et al.* [2005] found coefficients of 0.15 for both pure- and crossbreds while Nakavisut *et al.* [2005] reported  $h^2$  of 0.1 and 0.05 for purebred and crossbred sows. Lowest heritability (0.02) reported Boesch *et al.* [2000] for the outbreds of the Large White and Landrace populations.

The magnitude of the permanent environment component was low (0.06) also for this trait in all the genotypes. Our findings were in agreement with the results of other teams. Fischer *et al.* [1999] estimated the environment component ratio at 0.032, 0.042, and 0.099, 0.100 for purebreds and crossbreds, respectively, while Nakavisut *et al.* [2005] obtained much higher estimates – 0.19 for purebred and 0.32 for crossbred sows.

**Farrowing interval.** As in the case of NBA the heritability of FI appeared low ( $h^2=0.06$ ) across the genotypes. In the available literature we could not find simultaneous information about genetic determination of the performance of purebreds and crossbreds for FI. The purebred performance was studied by Tholen *et al.* [1996] and they obtained  $h^2=0.1$  for the first two farrowings. On the other hand, Kumari and Rao [2010] studied crossbred performance and received the same result. Serenius *et al.* [2003] studied FI of purebred pigs, using a repeatability model as well, and they estimated heritability coefficients of 0.4 for both Large White and Landrace sows. The results of Oh *et al.* [2006], who analyzed the performance of Duroc, Landrace and Yorkshire dams, were similar to the current estimates ( $h^2=0.07$ ).

The magnitude of permanent environment effect for farrowing interval was null in our study but Boesch *et al.* [2000] arrived at higher values of 0.08 and 0.11 for purebred, and 0.04 and 0.05 for crossbred sows. Serenius *et al.* [2003] obtained  $h^2=0.04$  and 0.05 for Large White and Landrace. Neto *et al.* [2009] reported  $h^2=0.5$ -0.7 in Dalland sows, whereas Oh *et al.* [2006] obtained  $h^2=0.3$ .

#### Genetic correlations

The research hypothesis of the present study was that the genetic correlations between the purebred and crossbred performances deviate from 1.0. Based on the reports of other authors (e.g. Wei and van der Werf 1994, Baumung *et al.* 1997, Lutaaya *et al.* 2001) several reasons for lower genetic correlation between pure- and crossbred genetic performances can exist. The gene frequencies influencing the traits can be different between the purebred populations. Genetic correlations also tended to be lower if the traits are affected by non-additive effects (dominance and epistasis). Besides, non-genetic factors like different management of purebreds and crossbreds can further affect the correlations due to genotype x environment interactions.

**Age at first insemination.** Estimates of genetic correlations are presented in table 5. Correlation between pure- and crossbred populations can be considered very low

in both datasets (0.28 and 0.39). According to the Hungarian Agricultural Agency of Administration there are no substantial differences among the environmental conditions provided to the purebred and crossbred pigs when they are kept at different herds. Hence, the departure of the genetic correlation from unity may be explained by one of the genetic factors mentioned above. Estimates of other authors in the literature were not found. Low correlation suggests advantage of using the crossbred breeding value for selection.

**Gestation length.** We found much higher correlations of 0.96 and 0.82 for this trait than those reported by Nakavisut *et al.* [2005] – 0.52 – who explained the moderate genetic correlation by interaction or dominance effects. In our study the crossbred breeding value is not expected to provide more information about the performance to be realized in the next generation.

**Number of born alive.** Correlation between purebred and crossbred performances was significant at 0.82 and 0.93, which agreed with the estimates of Täubert and Brandt [2000] – 0.81-0.99 – who studied the first three litters in Large White, Landrace, and their cross. Boesch *et al.* [2000] reported medium to high correlations (0.49-0.81). Fischer *et al.* [1999] found medium correlation as well (0.52-0.71) where the lower value was estimated using a model without permanent environmental effect. The lowest correlation (0.37) was published by Nakavisut *et al.* [2005]. Purebred breeding value can be used in the selection of purebred pigs for crossing.

**Farrowing interval.** In the HLW – HLWxHL dataset we found a two times higher correlation coefficient (0.65) than in the HL – HLxHLW one (0.33). Lutaaya *et al.* [2001] studied a crossbred model for production traits in swine and also found larger correlation between one of the purebred lines and the crossbreds. They interpret this as a line complementarity. In our paper it would mean that the HLW genotype contributes more to farrowing interval than the HL genotype. For this trait no other literature information was available to compare our findings with.

Based on the genetic correlations between purebred and crossbred pigs for GL and for NBA usage of the crossbred breeding values in selection is not necessary as the two types of evaluation are equivalent. We found, however, lower correlations for AFI and for FI which suggest that the application of the purebred breeding values in selection could improperly predict the crossbred performance. Wei and van der Werf (1994) suggested that if the correlation between purebred and crossbred performance is less than 0.8 it is worth combining the purebred selection with the crossbred one. They found that the combined crossbred-purebred selection would bring more genetic progress for most reproduction traits than purebred selection alone. Therefore breeders should also consider the crossbred breeding value in the selection.

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