

ESTIMATION AND DECOMPOSITION OF GENETIC TRENDS IN A TWO-WAY CROSS USING HUNGARIAN PIG BREEDS

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ABSTRACT

Authors analyzed the estimation and partition of the genetic trends of lean meat percentage and average daily gain of the two-way cross Duroc (Du), Pietrain (Pi) pigs and their cross. The analysis was based on the data collected by the Agricultural Agency of Administration in course of field test between 1998 and 2010 from 68 herds. Total number of animals in the pedigree file was 60926. Genetic parameters and breeding values of average daily gain (ADG) and the lean meat percentage (LMP) were estimated separately by REML and BLUP methods using the VCE6 and PEST software applying a two-trait animal model. For the observed period the authors received a small genetic trend for ADG while it was negligible for LMP. Decomposing these trends to genotypes the highest contributions to the trends were observed for Duroc (ADG) and Pietrain (LMP), respectively.

Key words: pigs / genetic trends / reproduction traits / purebred / crossbred / Hungary

1 INTRODUCTION

In Hungary similarly to other domesticated species in order to maintain the competitiveness of the pig breeding sector it is necessary to continuously improve those traits that are defined in the Breeding Programme. During selection the so called best animals have to be selected to produce the next generation. Generally selection is based on the performance records collected in the course of the various performances (field and station) tests and evaluated by the BLUP procedure (Henderson, 1975) which is the most accepted method for genetic evaluation in most domesticated species (horse, cattle, sheep, pig, rabbit). The first BLUP application in pig breeding was reported almost 30 years ago (Hudson and Kennedy, 1985). As the BLUP procedure predicts the additive genetic value the most straightforward application is accomplished in pure breeding. In the Hungarian pig breeding sector however crossing is widely used. Thus breeding value prediction is conducted using data of both pure-

bred and crossbred pigs. The efficiency of the breeding program is generally evaluated by means of the estimated genetic trends however as noted by García-Cortés *et al.* (2008) this analysis does not allow evaluating each of the single parts of the selection scheme and effectiveness of the different selection decisions (e.g. different sexes, years, breeds, etc).

The objective of the present study was to estimate the contribution of different pig genotypes to the genetic trend of a given two-way cross applied in Hungary.

2 MATERIAL AND METHODS

Analyses were based on the field test data of Pietrain (Pi, 5717), Duroc (Du, 4868), pigs and their cross (Pi x Du, 4728). Data was collected by the Agricultural Agency of Administration (MGSZH) between 1998 and 2010 from 68 herds. Total number of animals in the pedigree file was 60926 (Pi, Du, Pi x Du) and these animals were

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born between 1983 and 2010. 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 ribs (6 cm laterally from the spinal cord) and the loin muscle area between the 3rd and 4th ribs (6 cm laterally from the spinal cord). Using these measurements lean meat percentage (LMP) can be calculated. This trait was used officially in the field test only from 2000 (MGSZH, 2000) but it was collected from 1998. Age (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 (ADG) was also calculated. The regulations of animal housing and feeding conditions are defined in the Hungarian Pig Performance Testing Code (MGSZH, 2009). Descriptive statistics were calculated using SAS 9.1 (SAS Inst. Inc., 2004). Genetic parameters of ADG and LMP were estimated by the REML method using bivariate animal model applying VCE6 (Groeneveld *et al.*, 2008). Breeding values were estimated by BLUP (using the PEST software) (Groeneveld, 1990) with the same model mentioned previously.

The structure of the applied animal model was the following:

$$y = Xb + Za + Wc + e$$

y = vector of observations, b = vector of fixed effects, a = vector of random animal effects, c = vector of common environmental effects, e = vector of random residual effects, X , Z and W are incidence matrices relating records to fixed effects, random animal effects, and common environmental effects, respectively.

In the bivariate model year-month, sex, genotype and herd effects were treated as fixed effects, while additive genetic and common litter effects were considered as random effects. Structure of the used bivariate model is given in Table 1.

Concerning genetic trend decomposition by geno-

Table 1: Structure of the applied animal model

Factor	Type	Level
Year-month	F	157
Sex	F	2
Genotype	F	3
Herd	F	68
Animal	A	60926
Common litter	R	5036

F: fixed effect; A: additive genetic effect; R: random effect

types the applied method was identical to that of Gorjanc *et al.* (2011).

Any kind of pedigree based mixed model (animal model, sire-maternal grandsire model, ...) is based upon the prior model for breeding values using the recursive system of equation. For animal model the core equation is:

$$a_i = 1/2a_{s(i)} + 1/2a_{d(i)} + w_i \quad (1)$$

where a_i , $a_{s(i)}$, $a_{d(i)}$ are breeding values of individual animal and their parents, respectively, while w_i is individuals' deviation from parent average, i.e., the Mendelian sampling term. For base population members $a_i = w_i$. In matrix notation (1) can be written as:

$$a = Tw, \quad (2)$$

where T describes flow of genes through pedigree (e.g., Henderson, 1976; Woolliams *et al.*, 1999). Equation (2) shows that breeding values are a linear combination of Mendelian sampling terms and that the same equation can be used also for predictors of w , i.e., $\hat{a} = T\hat{w}$.

Garcia-Cortés *et al.* (2008) proposed to define a set of k partitions, such that:

$$P_1 + P_2 + \dots + P_k = I. \quad (3)$$

Using (3) and the fact that $w = T^{-1}a$ they wrote (2) as:

$$\begin{aligned} \hat{a} &= TP_1T^{-1}\hat{a} + \dots + TP_kT^{-1}\hat{a}, \\ &= \hat{a}_1 + \hat{a}_2 + \dots + \hat{a}_k, \end{aligned} \quad (4)$$

where \hat{a}_k is i -th partition of \hat{a} according to the definition of (3). These partitions can be summarized separately to obtain the partitioning of total genetic trend.

Once we have \hat{a} from the routine genetic evaluation, the computation of (4) is very simple and involves only 1) computation of inferred Mendelian sampling terms (\hat{w}) and 2) dropping \hat{w} through pedigree according to (3). We implemented this in the R package part AGV, which eases the computation and presentation of results.

3 RESULTS AND DISCUSSION

Descriptive statistics of the examined traits are provided in Table 2 for each genotype.

The Pietrain pigs showed the highest LMP values on the contrary for ADG the differences between various pig genotypes were small. The estimated variance components for LMP and ADG are presented in Table 3.

The genetic trends for ADG and LMP were calcu-

Table 2: Descriptive statistics of the examined traits

Genotype	Trait	N	Minimum	Maximum	Mean	Std
Pi	LMP	5717	52.70	68.00	61.72	2.10
	ADG.	5717	283.00	774.00	526.61	60.51
	AGE	5717	120.00	295.00	176.15	23.18
Du	LMP	4868	50.00	66.80	58.22	1.87
	ADG.	4868	318.00	756.00	557.02	56.61
	AGE	4868	120.00	285.00	174.80	21.75
Pi × Du	LMP	4728	52.50	66.00	59.74	2.02
	ADG.	4728	317.00	764.00	565.98	67.93
	AGE	4728	120.00	282.00	168.45	21.60

LMP, lean meat percentage %; ADG, average daily gain; AGE, age

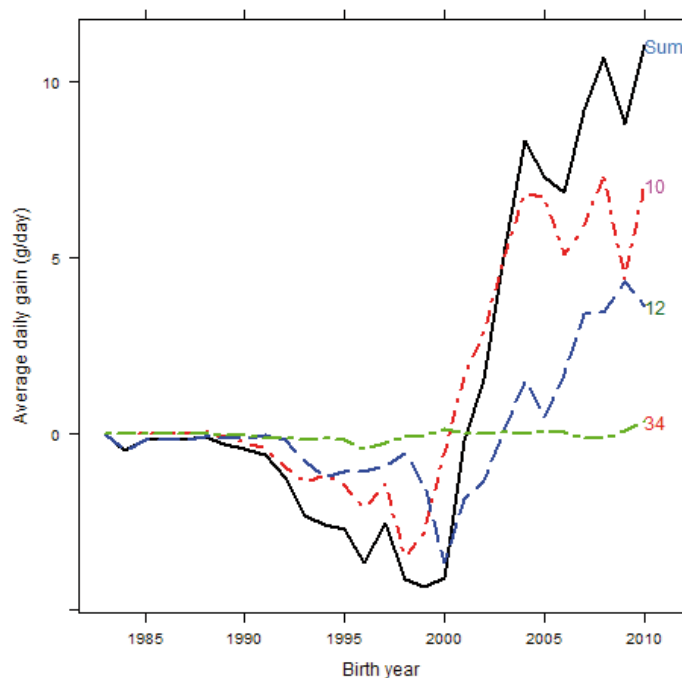
lated using the breeding values of all pigs in the pedigree file. When the whole period was considered the estimated annual trends for ADG and LMP were 0.4 g/day and

Table 3: Variance and covariance components for average daily gain (ADG) and lean mean percentage (LMP)

	V_A	Cov_A	V_C	Cov_C	V_E	Cov_E
ADG	672	-1.47	952	-1.26	1095	1.48
LMP	0.52		0.61		0.27	

V_A , additive genetic variance; Cov_A additive genetic covariance; V_C random litter variance; Cov_C random litter covariance; V_E residual variance; Cov_E residual covariance

–0.004%, respectively. Restricting the trend calculation to purebreds Duroc pigs showed an annual progress of 0.62 g/day and –0.02% for ADG and LMP, respectively. For the Pietrain breed these values were 0.26 g/day and 0.013%. However when only the period between 2000 and 2010 was considered these trends were 1.32 g/day and –0.002%, respectively. Concerning purebreds Duroc had an annual progress of 0.84 g/day and –0.05% for ADG and LMP, while for Pietrain pigs annual genetic trends of 1.42 g/day and 0.048% were received for the ADG and LMP, respectively. The observed values were very similar to the reported values of Csató *et al.* (1994) and Radnóczy *et al.* (2009) for Hungarian Large White

**Figure 1:** Partitioning of the genetic trend by genotype for average daily gain (g/day) (10, Duroc; 12, Pietrain; 34, Pietrain × Duroc)

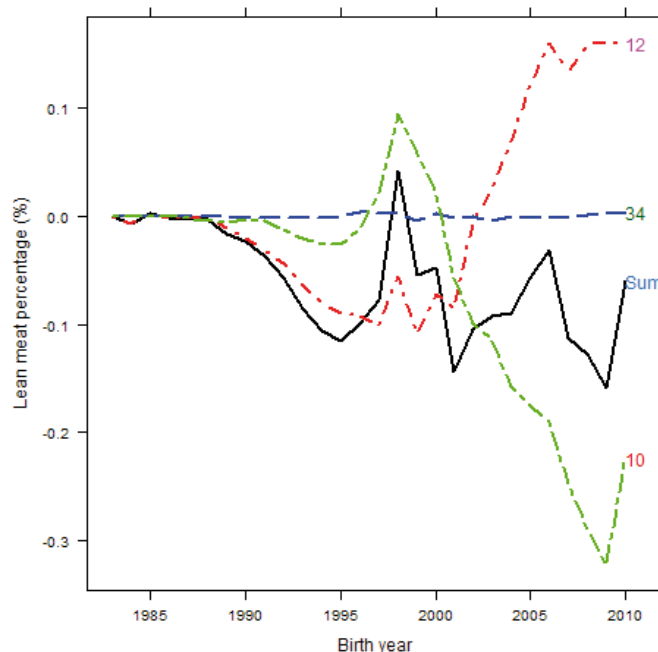


Figure 2: Partitioning of the genetic trend by genotype for lean meat percentage (%) (10, Duroc; 12, Pietrain; 34, Pietrain \times Duroc)

and Hungarian Landrace populations. Concerning LMP Radnóczy *et al.* (2009) noted that preceding their evaluated period (2004–2009) the trait was substantially improved which can explain the lack of the observed progress. On the contrary for LMP Wolf *et al.* (2001) reported higher annual genetic trends (0.29%). Other authors Ten Napel and Johnson (1997) reported substantial annual trend for ADG (5.1 g/day) also greatly exceeding our results. However, the BLUP index became the basis of selection only since 2008 thus the increase of the genetic trends can be expected.

Decomposing the estimated genetic trends of ADG and LMP according to the various genotypes (Duroc, Pietrain and their cross) can be viewed in Fig. 1 and 2.

Although the obtained genetic trends were small for both traits it can be seen that the genetic progress was different in the various pig genotypes. In ADG the highest performance was shown by Duroc compared to the other genotypes. On the contrary as expected for LMP the Pietrain pigs had the largest contribution to the annual trends.

4 CONCLUSIONS

The observed small genetic progress obtained in both traits is probably the result of the fact that the selection is based on the BLUP procedure only from 2008.

The increase of the trends is expected in the future. By the decomposition of the trend by the various genotypes makes it possible to evaluate the progress in detail in the specific two-way cross and its use can be advocated for all crossing construction.

5 ACKNOWLEDGEMENT

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