

# Estimation of Genetic Parameters for Meat Quality and its Composite Traits

István NAGY <sup>1</sup>(✉)

Zoltán CSÖRNYEI <sup>2</sup>

Henrietta Nagyné KISZLINGER <sup>1</sup>

János FARKAS <sup>1</sup>

## Summary

Meat quality score and its composite traits of the Hungarian Large White pigs were analyzed using the national station test database for the period of 1994-2005. The distribution of the meat quality score was substantially different from the normal distribution and the average score of the population was close to the possible maximum. Based on the results the traits can hardly be improved by selection.

Analysing separately the composite parameters of the meat quality score ( $\text{pH}_1$ ,  $\text{pH}_2$ , colour, organoleptic evaluation) the highest heritability estimates were estimated for meat colour and  $\text{pH}_2$  ( $0.38 \pm 0.01$ ;  $0.35 \pm 0.01$ , respectively). The lowest heritability was estimated for the organoleptic evaluation ( $0.15 \pm 0.01$ ), on the other hand this composite trait showed the highest genetic correlation with the meat quality score ( $0.72 \pm 0.01$ ), which is unfavourable. Based on the results the meat quality traits should be restricted to meat colour and  $\text{pH}_2$ .

## Key words

pig, meat quality, genetic parameters, environmental factors

<sup>1</sup> University of Kaposvár, 40 Guba S. str., H-7400 Kaposvár, Hungary

✉ e-mail: [nagy.istvan@ke.hu](mailto:nagy.istvan@ke.hu)

<sup>2</sup> Agricultural Agency of Administration, 24 Keleti K. str., H-1024 Budapest, Hungary

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## Introduction

During the last decades the consumers showed preference towards the so called lean meats. Fulfilling this requirement is not easy in pig breeding as a 70 kg carcass can contain about 30% fat. Besides environmental factors like restricted feeding genetic improvement also contributes to the fulfilment of the consumers' demands. Among the selection criteria traits lean meat percentage has a high importance. The heritability of this trait is moderate (Nagy et al., 2008) but it can be estimated on live animals. Because of its economic importance the Hungarian pig populations were intensively selected for this trait during the last years and their performance subsequently substantially improved. However it has to be noted that according to several authors (Groeneveld et al., 1996; Garreau et al. 1998, Csató et al., 2002; Nagy et al., 2008) the lean meat percentage is negatively correlated with meat quality (with meat quality score). Therefore, the improvement of lean meat percentage may result in the lowered meat quality. Similarly to lean meat percentage meat quality is also considered as an economically important trait and generally included in most pig breeding programs. In Hungary the meat quality is described by the meat quality score (MGSZH, 2009) which is defined by several composite parameters (pH, meat colour and organoleptic evaluation) (Table 1). Depending on the recorded values for the composite traits the meat quality score can be varied between 2 (1, 1, 0) and 10 (4, 3, 3) (Table 1) as the sum of the scores of the composite traits. It has to be noted that according to Groeneveld et al. (1996) the composition of meat quality score is not optimal. The scoring system (MGSZH, 2009) (Table 1) treats the characteristics of the two pH values as identical [normal, pale soft exudative (PSE), dark firm dry (DFD)] that means that after measuring a normal pH<sub>1</sub> it is impossible to detect a pH<sub>2</sub> falling into the PSE interval. If this were true, measuring two successive pH values is pointless. It is also unclear what score is defined for the 5.9–6.1 pH<sub>2</sub> intervals.

In connection with above mentioned discrepancies the objective of this study was to analyze in detail the statistical characteristics of the meat quality score and its composite traits (as defined by the Hungarian pig breeding sector). Our second objective was to estimate the genetic parameters of meat quality scores and their composite traits. Based on the results it will be possible to determine if the present system used for describing meat quality (in the Hungarian pig breeding sector) is efficient enough to be used for genetic selection.

## 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 station test conducted between 1994–2005. The analyzed breed was the Hungarian Large White. The animals with records (Table 2) originated from eight stations and were reared in 9047 litters. The total number of animals in the pedigree file was 31260. At the end of station test pigs were slaughtered after reaching the live weight of 105±2 kg. Then meat quality parameters were determined using the left half of carcass. The pH values were measured in the *musculus longissimus dorsi* between the 13th and 14th vertebrae with a precision of 0.1. The first and second pH measurements were recorded within 45 minutes (pH<sub>1</sub>) and 24 hours (pH<sub>2</sub>) after the slaughter,

respectively. Meat colour measurements (using Optostar device) and organoleptic evaluations were done 24 hours after slaughter at the same body region as described for the pH measurements. The regulations of animal transport, housing and feeding conditions are defined by the Hungarian Pig Performance Testing Code (MGSZH, 2009). Appropriate scores of pH<sub>1</sub>, pH<sub>2</sub>, and meat colour were calculated from composite traits' recordings according to Table 1. Basic descriptive statistics were calculated applying SAS (SAS Inst. Inc., Cary, NC). Genetic parameters of pH<sub>1</sub>, pH<sub>2</sub>, meat colour, organoleptic evaluation and meat quality score were estimated by REML method using VCE5 software (Kovac and Groeneveld, 2003) applying a multi-trait animal model. The structure of the animal model was the following:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{a} + \mathbf{W}\mathbf{c} + \mathbf{e}$$

$\mathbf{y}$  = vector of observations,  $\mathbf{b}$  = vector of fixed effects,  $\mathbf{a}$  = vector of random animal effects,  $\mathbf{c}$  = vector of common environmental (random litter) effects,  $\mathbf{e}$  = vector of random residual effects,  $\mathbf{X}$ ,  $\mathbf{Z}$  and  $\mathbf{W}$  are incidence matrices relating records to fixed, random animal and random litter effects, respectively.

Expected values of  $\mathbf{a}$  and  $\mathbf{e}$  were  $E(\mathbf{a}) = E(\mathbf{c}) = E(\mathbf{e}) = 0$ . The variance-covariance structure assumed to be  $V(\mathbf{a}) = \mathbf{A}\sigma^2_a$ ,  $V(\mathbf{c}) = \mathbf{I}\sigma^2_c$ ,  $V(\mathbf{e}) = \mathbf{I}\sigma^2_e$ , and  $\text{cov}(\mathbf{a}, \mathbf{e}) = \text{Cov}(\mathbf{e}, \mathbf{a}) = 0$ , where  $\mathbf{A}$  is the numerator relationship matrix. Also  $\text{cov}(\mathbf{y}, \mathbf{a}) = \mathbf{ZA}\mathbf{I}\sigma^2_a$ .

In the model year-month, sex, station effects were treated as fixed effects, while additive genetic effect and litter effect were considered as random effects. Using the (co)variance components the breeding values of the considered traits (BLUP) and the estimates of influencing the environmental factors (BLUE) were obtained applying the PEST software (Groeneveld, 1990) based on the same multi-trait animal model as described previously.

## Results and discussion

Based on the descriptive statistics of the examined traits (Table 2) the meat quality score and its composite traits' mean almost reach the possible maximum with considerable skewness. For meat quality score 71% of all cases had a maximum score of 10. For the organoleptic evaluation the population reached 96% of the maximum score. These results indicate that the selection limit has almost been reached and the population cannot be further improved by selection. However, the calculated mean scores for pH<sub>1</sub> and pH<sub>2</sub> were not identical contrary to the official expectation (Table 1). Only for the 60% of all cases showed identical scores for the successive pH measurements. The scores of the pH<sub>1</sub> measurements exceeded that of the pH<sub>2</sub> in 26% of the cases while for 14% of the cases the pH<sub>2</sub> measurements had higher scores than that of the pH<sub>1</sub> recordings. Based on these results the scoring system of the pH measurements shown in Table 1 should be changed.

The estimated genetic parameters of the analyzed traits are provided in Table 3. It can be seen that the heritability estimates of the pH<sub>2</sub> and meat colour were higher compared to the heritability of the meat quality score (table 3) therefore it would be more efficient to select on these composite traits directly to obtain larger selection response. Somewhat lower heritabilities were found for pH<sub>1</sub> (0.15±0.05) and pH<sub>2</sub> (0.21±0.03) by de Vries et al. (1994) for the Yorkshire breed. Even lower heritabilities were reported by Hermesch et al. (2000) for the same traits

**Table 1.** Definition of the scores for meat quality parameters

Character	pH-value			Colour		Organoleptic evaluation	
	pH <sub>1</sub>	pH <sub>2</sub>	Score	Value	Score	Character	Score
PSE	≤5.6	≤5.4	1	<59	1	(Highly) pale soft exudative	(0)
	5.7	5.6	2				1
Normal	5.8-6.2	5.7-5.8	4	60-76	3	Pink, good water holding capacity	3
DFD	6.3≤	6.2≤	3	76<	2	Dark firm dry	2

**Table 2.** Descriptive statistics of the examined traits

Trait	N	Min	Max	Mean	Standard deviation
pH <sub>1</sub>	17399	1	4	3.71	0.65
pH <sub>2</sub>	17399	1	4	3.55	0.78
Meat colour (Optostar value)	17399	1	3	2.77	0.61
Organoleptic evaluation	17399	1	3	2.88	0.42
Meat quality score	17399	3	10	9.35	1.28

(0.15±0.04; 0.14±0.04) noting that possible genetic progress is limited. Concerning meat colour our results exceeded that of other studies (Hovenier et al., 1992; de Vries et al., 1994; Knapp et al., 1997; Garreau et al., 1998) where the estimated heritability for meat colour ranged between 0.19 and 0.29. In the present study the organoleptic evaluation had the lowest heritability. The estimated genetic parameters had small standard errors, therefore the analyzed data provided enough information. The magnitude of the random litter effects was small for all traits thus the common environmental effect shared by the fullsibs until weaning did not influence these traits. For the random litter effect an opposite tendency was found compared to the heritability estimates as Hovenier et al. (1992) reported higher values (0.17±0.02, 0.21±0.02) than reported here.

The estimated genetic correlation coefficients among the examined traits justify our supposition that the two consecutive pH measurements although relatively strongly correlated cannot be treated as repetitions of the same trait. This result was in accordance with the findings of Bidanel et al. (1994) and de Vries et al. (1994) who estimated genetic correlation coefficients 0.49±0.29 and 0.41±0.06, respectively. Therefore, it is not advised to describe these two traits with only one score as it is done in Hungary. Both pH measurements had positive but low genetic correlation coefficients with meat colour. Contrary to our estimates Hovenier et al. (1992) estimated moderately high (0.71±0.09) genetic correlation between pH<sub>2</sub> and meat colour. Moderately strong genetic correlation was found between meat colour and the organoleptic evaluation and between meat colour and meat quality score. In this study strong genetic correlation was only found between the organoleptic score and meat quality score. This last finding is not favourable because it suggests that the overall meat quality is mostly connected to a subjective score rather than to other traits measured objectively (pH and meat colour).

Using the estimated (co)variance components the breeding values were predicted for all traits (BLUP) and the magnitude of the environmental factors were also estimated (BLUE) (Table 5). Sex had only a slight effect on the examined traits. Sex effect

**Table 3.** Genetic parameters of the examined traits (±standard errors)

Trait	$h^2/\sigma^2_a$	$c^2/\sigma^2_c$
pH <sub>1</sub>	0.25±0.009; 0.008	0.08±0.006; 0.003
pH <sub>2</sub>	0.35±0.006; 0.006	0.07±0.005; 0.001
Meat colour (Optostar value)	0.38±0.008; 9.09	0.12±0.005; 2.95
Organoleptic evaluation	0.15±0.006; 0.27	0.06±0.004; 0.10
Meat quality score	0.25±0.007; 0.22	0.04±0.005; 0.04

<sup>1</sup> $\sigma^2_a$ , additive genetic variance; <sup>2</sup> $\sigma^2_c$ , common environmental variance

**Table 4.** Estimated genetic correlation coefficients among the examined traits (±standard errors)

Traits	Genetic correlation coefficients
pH <sub>1</sub> - pH <sub>2</sub>	0.68±0.011
pH <sub>1</sub> - Meat colour (Optostar value)	0.19±0.027
pH <sub>1</sub> - Organoleptic evaluation	-0.23±0.036
pH <sub>1</sub> - Meat quality score	-0.11±0.036
pH <sub>2</sub> - Meat colour (Optostar value)	0.36±0.021
pH <sub>2</sub> - Organoleptic evaluation	-0.05±0.025
pH <sub>2</sub> - Meat quality score	0.22±0.023
Meat colour (Optostar value) - Organoleptic evaluation	0.49±0.006
Meat colour (Optostar value) - Meat quality score	0.46±0.011
Organoleptic evaluation - Meat quality score	0.72±0.009

**Table 5.** The maximum magnitude of the environmental factors expressed as % of the examined traits' mean

Trait	Year-month	Sex	Station
pH <sub>1</sub>	5.6%	0.10%	9.3%
pH <sub>2</sub>	4.3%	0.05%	2.1%
Meat colour (Optostar value)	21.0%	0.09%	22.3%
Organoleptic evaluation	24.3%	0.13%	21.9%
Meat quality score	30.7%	0.15%	18.8%

on pH<sub>2</sub> was also analyzed by D'Souza et al. (2002) and they also reported relatively small differences between sexes noting that the female pigs had lower ultimate muscle pH. On the contrary to sex effects we found that year-month and station effects were substantial especially for meat colour, organoleptic evaluation, and meat quality score. It can be concluded that the presently used scoring system is substantially affected by the environmental factors.

Concerning selection meat quality can be treated and calculated as an index from the composite traits. For instance in France it is computed from the ultimate pH, reflectance and water loss of semi membranosus muscle (Garreau et al., 1998). The meat quality index has been included in breeding goals for 20 years in France (Lebret, 2004) and has not deteriorated over this period (eg. the intramuscular fat content has not decreased). However meat quality could be improved by selecting separately for composite traits keeping in mind that the values above or below the optimal range are both undesirable. Canalising selection would be possibly a good choice as it keeps the mean of the selected trait stable while the variance is decreased (Mulder et al., 2008).

### Conclusions

If Hungary would like to keep the scoring system to describe meat quality it would be advantageous to replace the scores with the sum of population mean and breeding values of the composite traits thus the environmental effects would be removed. Yet even in this case it could be considered to remove from the meat quality score the organoleptic evaluation.

When meat quality can be expressed differently as meat quality score then it would be advisable to select the pigs for those composite traits that are having the highest heritability estimates (pH<sub>2</sub> and meat colour).

The meat quality could be described using pH<sub>2</sub> and meat colour. As the population mean is located in the optimal range for both traits the estimated breeding values could be used to select those animals that are not far away from the mean. The farther is the breeding value from the zero the lower is the genetic merit. This way the efficiency of the selection could be improved compared to the conventional meat quality score where most animals obtain maximum score that makes efficient selection impossible.

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