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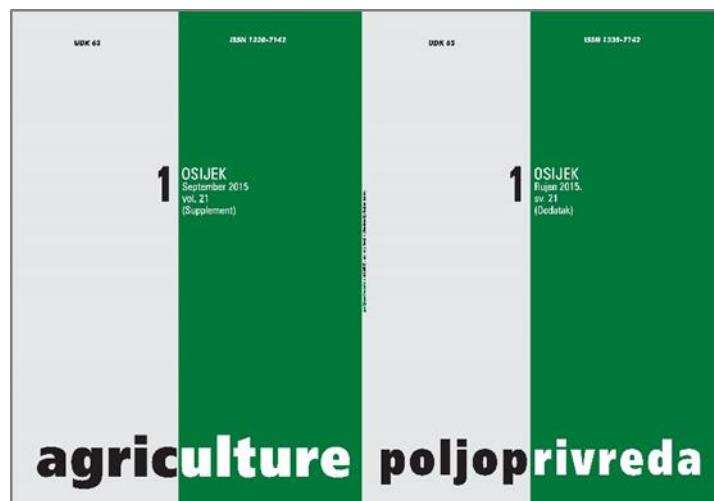
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ESTIMATION OF GENETIC PARAMETERS FOR PRODUCTION TRAITS IN PIG BREEDS IN CROATIA

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SUMMARY

Genetic parameters for backfat thickness and test time were updated and used in genetic evaluation for field tested pigs in Croatia. Data consisted of 9,406 animals with measurements for production traits recorded from 2000 to 2014. The number of animals in pedigree was 10,728. Production traits were modelled using a single trait animal model including the following fixed class effects: breed, sex, classifier, season, and herd. Weight at the end of the test was included as linear regression in the model for backfat. Direct additive genetic effect, interaction herd-year-season of testing and common litter effect were included as random effects. Variance components were estimated using REML method as implemented in the VCE-6 program. The estimated heritabilities were 0.28 ± 0.03 for backfat thickness and 0.12 ± 0.02 for test time. Litter effect accounted from 15 to 24% of phenotypic variation, while herd-year-season of testing explained additional 24 and 28% of variability for analysed traits.

Key-words: genetic parameters, pig, breeding, heritability, genetic trend

INTRODUCTION

Genetic evaluation approaches had huge impact on the efficiency of pork production in the last decades. Since 2005, mixed model methodology known as Best Linear Unbiased Prediction (BLUP, Henderson, 1973) has been used as standard procedure for genetic evaluation (Vincek et al., 2004) of production traits used in Croatian pig breeding programme. This approach predicts the genetic potential of the animal based on its own performance and of all phenotyped relatives. Genetic progress can be achieved for traits that are heritable such as growth rate, backfat thickness (BF) (Ferraz et al., 1993), feed efficiency, muscle thickness and hind leg mass (Hermesch et al., 2000) which can be measured directly. Those traits emphasize the performance traits associated with efficient muscle development. The most important of them are minimum backfat and maximum growth rate. Both traits are of economic importance and since they are also highly heritable, they can be improved by selection. Improvement of these traits through breeding will likely be of use in the form of better feed efficiency, heavier weaning weights and more rapid development of gilts for breeding. The objective of this study was to update genetic parameters for produc-

tion traits: backfat thickness and test time (TT) for field tested pigs in Croatia.

MATERIAL AND METHODS

Data used for the estimation of genetic parameters and breeding value prediction were collected on family farms by Croatian Agricultural Agency employees. Data were taken from database of Croatian Agricultural Agency. Backfat thickness was measured on alive animals at the end of the test with ultrasound (Renco® ultrasound). Data were edited and records were deleted if: a) test date was unknown, b) herd was unknown and c) animals were from different breed than those included in the analysis. Additionally, animals were excluded from the analysis if they had less than 75 and more than 140 kg and were younger than 120 and older than 360 days at the end of the test. Backfat thickness of analysed animals was limited within the range from 3.5 to 25 mm. The animals were grouped by herd and season and groups having less than 3 animals were excluded.

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Average values for BF and TT are shown in Table 1. As expected, Pietrain has lowest BF (7.06 mm), while Landrace had the greatest value for BF (10.28 mm). Breed with the shortest TT was Duroc (180.97 days) and breed with the longest duration of the test was Large White. Correction was made for TT where weight at the end of the test was set to the 105 kg representing the

average weight of the tested gilts in Croatia. Correction was made in a way that average weight of 105 kg is multiplied with number of days in the test for an animal divided with real weight of the animal. After data editing out of total number of data (15,296) for production traits (BF, TT) 9,406 records were used in further analysis.

Table 1. Average backfat thickness and testing age for analysed breeds

Breed	Backfat thickness					Time on test				
	N	Mean	Std	Min	Max	N	Mean	Std	Min	Max
Large White	736	10.19	2.59	4.95	20.68	736	202.50	42.77	120.00	362.00
Landrace	6,782	10.28	2.25	4.95	23.98	6,782	182.21	26.56	119.00	365.00
Duroc	306	9.86	2.38	5.28	19.36	306	180.97	30.08	126.00	356.00
Pietren	1,582	7.06	1.17	4.29	13.31	1,582	187.60	22.66	128.00	305.00
Total	9,406	9.72	2.45	4.29	23.98	9,406	184.66	28.25	119.00	365.00

All animals with records and their relatives tracing back for three generations were included in the pedigree file (Table 2). The total number of animals involved in the pedigree was 10,728 and it was tracking back three generations. There were 87.7% animals with production records (generation 0) in the pedigree. Sires and dams, parents of those animals, represented additional 9.6%

of the animals. Proportion of animals in the second and third generation decreased (2.5% and 0.2%) due to poor structure at the beginning of data collection. Animals were descendants of 1,030 parents in total. Time span in which data were collected relates to the animals born from beginning of 2,000 and animals tested until end of 2014.

Table 2. Structure of the pedigree

Item	Number of generations in pedigree								All	
	0		1		2		3			
	n	%	n	%	n	%	N	%	n	%
Male	3,566	33.2	374	3.5	171	1.6	17	0.2	4,128	38.5
Female	5,840	54.4	656	6.1	97	0.9	7	0.1	6,600	61.5
All	9,406	87.7	1030	9.6	268	2.5	24	0.2	10,728	100.0

Choice of the effects in the fixed part of the model was made by the effect significance, as well as coefficient of determination (R^2) and degrees of freedom for the model. Random part of the model included effects frequently used in the model according to literature review. It consisted of genetic part referred to direct additive genetic effect and environmental effects. The environmental effects

were further partitioned to a permanent environmental effect within the parity and contemporary group.

The model [1] that best fit BF and TT [2] was determined with fixed effects as follows: breed (B_i), sex (S_j), classifier (C_k), season (M_l), and herd effect (O_m). Additionally, weight at end of test ($x_{ijklmno}$), nested within breed was included in the model [1] as a covariable.

$$y_{ijklmno} = \mu + B_i + S_j + C_k + M_l + O_m + b_{1i}(x_{ijklmno} - \bar{x}) + h_n + l_i + a_{io} + e_{ijklmno} \quad [1]$$

$$y_{ijklmno} = \mu + B_i + S_j + C_k + M_l + O_m + h_n + l_i + a_{io} + e_{ijklmno} \quad [2]$$

Random part was same in both models. It consisted of contemporary group defined as interaction of herd-year-season of testing (h_n), common litter environmental effect (l_i) referred to permanent environmental effect within the parity, direct additive genetic effect (a_{io}) and residual error ($e_{ijklmno}$).

The GLM procedure (SAS Inst. Inc., 2001) based on Least Square Method was used to define the fixed part of the model. Covariance components were estimated by Residual Maximum Likelihood method as implemented in the VCE 6 (Kovač et al., 2002) software.

RESULTS AND DISCUSSION

The proportion of variation accounted for fixed part of the model for BF was 53.21%. On the other hand, fixed part of the model for TT explained lower proportion of variation (33.25%). All listed effects in the model were significant ($p < 0.0001$) as shown in Table 3.

Table 3. Coefficients of determination, degrees of freedom (DF), standard deviation for residual (σ_e), p-values of fixed effects

Model	Trait	
	Backfat	Test time
R ²	0.53	0.33
DF for model	195	191
σ_e	2.87	544.07
B	<0.0001	<0.0001
S	<0.0001	<0.0001
C	<0.0001	<0.0001
M	<0.0001	<0.0001
O	<0.0001	<0.0001

R²- coefficient of determination, DF for model- degrees of freedom for model, σ_e - standard deviation for residual, B - breed effect; S - sex effect; C - classifier effect; M - season effect; O - herd effect

Table 4. Covariance component estimates \pm standard error for backfat thickness and test time at family farms

Trait	V _a	V _l	V _{hys}	V _e	h ²	l ²	hys ²	e ²
BF*	0.80±0.08	0.69±0.04	0.69±0.06	0.97±0.05	0.28±0.03	0.15±0.01	0.23±0.02	0.33±0.02
TT	56.58±10.53	134.64±7.48	134.64±8.00	172.93±7.43	0.12±0.02	0.24±0.01	0.28±0.01	0.36±0.02

BF*- backfat thickness; TT- time on test; V_a- additive genetic variance; V_l- variance of common litter environment; V_{hys}- variance of herd-year-season interaction; V_e- residual variance, h²- heritability; l²- ratio for common litter, hys²- ratio for herd-year-season interaction, e²- ratio for residual

Heritability estimated by Imboonta et al. (2007) for BF and TT was higher than in our analysis (0.61±0.02 for BF and 0.38±0.02 for TT). For the analysis they used Landrace sows from Thailand coming from one nucleus herd. This can explain better connectivity of their data. Similar to previously compared studies, Bidanel et al. (1994) estimated higher heritability for TT and BF in Large White and French Landrace populations (0.25, 0.45 and 0.23 and 0.55) compared to the current study. Generally, heritability estimated on field test data are lower in comparison to data collected in stations (Peškovičová et al., 2002). Selection practices have shortened TT and together with this improved the average daily gain, BF thickness and other traits of pig carcass (Imboonta et al. 2007). However, correlation between selection for production traits and decreased reproductive performance has been reported. Production traits are necessary to combine in selection programme.

Interaction herd-year-season of testing explained 23% of phenotypic variance in BF and higher proportion (28%) for TT. Common litter effect explained 15% of total

Estimated genetic parameters for BF and TT are shown in Table 4. Additive genetic variance for BF and TT was in the range of estimations observed for BF and TT in analysis of family farms (Škorput, 2013). Additive genetic variance for BF was higher compared to estimates of Malovrh and Kovač (1999) for German Landrace (0.23 mm²) and Large White (0.25 mm²), but lower than Swedish Landrace (0.38 mm²). Estimated heritability was 28% for BF and 12% for TT. Vincek et al. (2004) reported similar heritability estimates being in the interval from 0.02 to 0.29 for BF and from 0.04 and 0.20 for TT based on data from three Croatian farms for Swedish and Dutch Landrace, Large White, Pietrain and their crosses. Malovrh and Kovač (1999) obtained heritability from 0.11 to 0.35 for BF of gilts and from 0.23 to 0.40 for boars estimated for Swedish Landrace, Large White, and German Landrace on big farms in Slovenia. However, heritability in this paper was lower in comparison to estimated heritabilities by Škorput (2013), where the same breeds were used. Time span of analysed animals in Škorput (2013) was from 1998 to 2008.

phenotypic variance for BF, whereas for TT common litter variance obtained 24% of phenotypic variance. Malovrh and Kovač (1999) reported common litter variance for BF to be lower in smaller breeds for Slovenian Swedish Landrace, Large White, and German Landrace. In their case, common litter variance explained 14% of phenotypic variance, being similar to our findings. On the contrary, common litter variance explained higher proportion of phenotypic variance (23% for BF) in the study of Škorput (2013). Similar proportion of common litter variance (26%) was obtained for TT.

Genetic trends of BV for BF and TT were calculated as the linear regression of the average annual predicted breeding values on the birth year (Figure 1). For each trait, genetic trend was shown for all animals. Genetic trend for BF was positive until 2009, with small drop in 2010 and stagnation thereafter. Genetic trend for TT was positive with peak in 2006 and then drop until 2011 and oscillation afterwards. Grey bars in both genetic trends represent number of animals tested per year and reduction of animals tested was obvious.

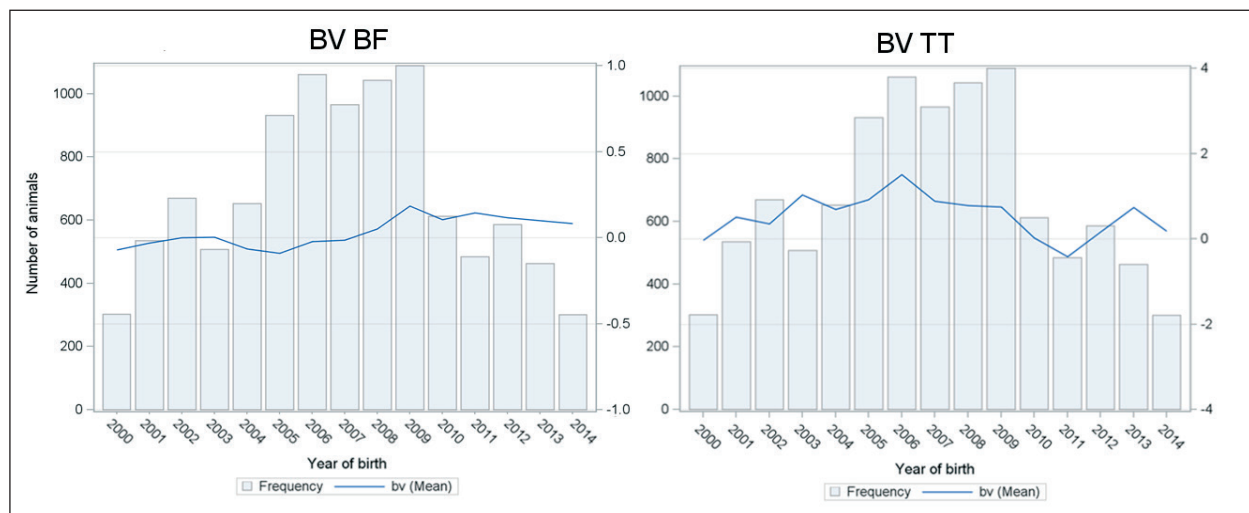


Figure 1. Genetic trends for backfat and time on test with number of animals per year

CONCLUSION

Data structure affected the estimation of genetic parameters and prediction of breeding values. Heritability estimates for BF (0.28) and for TT (0.12) were lower compared to literature estimates for those traits due to specific data structure and low connectivity between the farms. Future perspective for genetic evaluation of pigs included in National pig breeding programme is to include additional production trait measures and estimate breeding values for fertility traits.

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