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

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4 SUMMARY

5 To preserve genetic diversity in autochtonus breeds it is crucial to keep population healthy and vital. Genetic 6 parameters for backfat thickness and time on test were updated and used in genetic evaluation for field tested 7 pigs in Croatia. Data consisted of 9,406 animals with measurements for production traits recorded from 2000 8 to 2014. The number of animals in pedigree was 10,728. Production traits were modelled using a single trait 9 animal model which included the following fixed class effects: breed, sex, classifier, season, and herd. Weight 10 at the end of the test was included as linear regression in the model for backfat. Direct additive genetic effect, 11 interaction herd-year-season of testing and common litter effect were included as random effects. Variance 12 components were estimated using REML method as implemented in the VCE-6 program. The estimated 13 heritabilities were 0.28±0.03 for backfat thickness and 0.12±0.02 for time on test. Litter effect accounted from

14 15 to 24% of phenotypic variation, while herd-year-season of testing explained additional 24 and 28% of

15 *variability for analysed traits.*

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

17 INTRODUCTION

18 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, 19 Henderson, 1973) has been used as standard procedure for genetic evaluation (Vincek et al., 2004) of 20 production traits used in Croatianpig breeding programme. This approach is predicting the genetic 21 22 potential of the animal based on its own performance and of all phenotyped relatives. Genetic progress 23 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 24 25 measured directly. Those traits are emphasizing the performance traits associated with efficient muscle 26 development. The most important of these are minimum backfat and maximum growth rate. Both 27 traits are of economic importance and because they are also highly heritable, they can be improved by 28 selection. Improvement of these traits through breeding will likely be of use in the form of better feed 29 efficiency, heavier weaning weights and more rapid development of gilts for breeding. The objective 30 of this study was to update genetic parameters for production traits: backfat thickness and time on test 31 (TT) for field tested pigs in Croatia.

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36 MATERIALS AND METHODS

37 Data used for the estimation of genetic parameters and breeding value prediction were collected on

family farms by employees of Croatian Agricultural Agency. Data were taken from database of

39 Croatian Agricultural Agency. Backfatthickness was measured on alive animals at the end of the test

40 with ultrasound (Renco® ultrasound). Data were edited and records were deleted if: a) test date was

41 unknown, b) herd was unknown and c) animals were from different breed than those included in

42 analysis. Additionally, animals were excluded from the analysis if they had less than 75 and more than

43 140 kg and were younger than 120 and older than 360 days at the end of the test. Backfatthickness of

analysed animals was limited within the range from 3.5 to 25 mm. Animals were grouped by herd and

season and groups having less than 3 animals were excluded. Average values for BF and TT are

46 shown in Table 1. As expected, Pietrain has lowest BF (7.06 mm), while Landrace had the greatest

47 value for BF (10.28 mm). Breed with shortest TT was Duroc (180.97 days) and breed with the longest

48 duration of the test was Large White.Correction was made for TT where weight at the end of the

49 testwas set to the 105 kg which represents the average weight of tested gilts in Croatia. Correction was

50 made in a way that average weight of 105 kg is multiplied with number of days in the test for animal

51 divided with real weight of the animal. After data editing, out of total number of data (15,296) for

52 production traits (BF, TT) 9,406 records were used in further analysis.

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

Breed	Backfat thickness				Time on test					
21000	Ν	Mean	Std	Min	Max	 Ν	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

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55 All animals with records and their relatives tracing back for three generations were included in the

56 pedigree file (Table 2). The total number of animals involved in the pedigree was 10,728 and it was

57 tracking back three generations. There were 87.7 % animals with production records (generation 0) in

the pedigree.Siresand dams, parents of those animals, represented additional 9.6 % of the animals.

59 Proportion of animals in the second and third generation decreased (2.5 % and 0.2 %) due to poor

60 structure at the beginning of data collection. Animals were descendants of 1,030 parents in total. Time

span in which data were collected dates animals born from beginning of 2000 and animals tested until

62 end of 2014.

63

64 Table 2. Structure of the pedigree

	Number of generations in pedigree								All	
Item	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	1,030	9.6	268	2.5	24	0.2	10,728	100.0

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66 Choice of the effects in the fixed part of the model was made according to significance of the effect, as 67 well as coefficient of determination (R^2)and degrees of freedom for the model. Random part of the

68 model included effects which are frequently used in the modelaccording to literature review. It

69 consisted of genetic part referred to direct additive genetic effect and environmental effects. The

70 environmental effects were further partitioned to apermanent environmental effect within the parity

71 and contemporary group.

72 The model [1] that best fit BF and TT [2] was determined with fixed effects as follows: breed (B_i),sex

- 73 (S_j) , classifier (C_k) , season (M_l) , and herd effect (O_m) . Additionally, weight at end of test
- 74 $(x_{ijklmno})$, nested within breed was included in the model [1] as a covariable.
- 75

76 $y_{ijklmno} = \mu + B_i + S_j + C_k + M_l + O_m + b_{1i}(x_{ijklmno} - \bar{x}) + h_n + l_i + a_{io} + b_{1i}(x_{ijklmno} - \bar{x}) + h_n + h_i +$

77 $e_{ijklmno}[1]$

78 $y_{ijklmno} = \mu + B_i + S_j + C_k + M_l + O_m + h_n + l_i + a_{io} + e_{ijklmno}[2]$

79 Random part was same in both models. It consisted of contemporary group defined as interaction of

80 herd-year-season of testing (h_n) , common litter environmental effect (l_i) referred to permanent

81 environmental effect within the parity and direct additive genetic effect (a_{io}).

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

85 RESULTS AND DISSCUSION

- 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.

89

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

Model		Trait	
110401	Backfat	Time on test	
\mathbb{R}^2	0.53	0.33	
DF for model	195	191	
σ_{e}	2.87	544.07	
В	< 0.0001	<0.0001	
S	< 0.0001	<0.0001	
С	<0.0001	<0.0001	
М	<0.0001	<0.0001	
0	< 0.0001	<0.0001	

91 values of fixed effects

92 R^2 - coefficient of determination, DF for model- degrees of freedom for model, σ_e -standard deviation for residual, B- breed

93 effect S- sex effect C- classifier effect M- season effect O- herd effect

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95 Estimated genetic parameters for BF and TT are shown in Table 4. Additive genetic variance for BF

96 and TT was in the range of estimations observed for BF and TT in analysis of family farms (Škorput,

97 2013). Additive genetic variance for BF was higher compare to estimates of Malovrh and Kovač

98 (1999) for German Landrace (0.23 mm²) and Large White (0.25 mm²), but lower than Swedish

99 Landrace (0.38 mm²). Estimated heritability was 28 % for BF and 12% for TT. Vincek et al. (2004)

reported similar heritability estimates that were 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

102 White, Pietrain and their crosses. Malovrh and Kovač (1999) obtained heritability from 0.11 to 0.35

103 for BF of gilts and from 0.23 to 0.40 for boars estimated for Swedish landrace, Large White, and

104 German Landrace on big farms in Slovenia. However, heritability in this paper was lower in

105 comparison to estimated heritabilities by Škorput (2013), where the same breeds were used. Time span

106 of analysed animals in Škorput (2013) was from 1998 to 2008.

Table 4. Covariance component estimates ±standard errorfor backfat thickness and time on test at
 family farms

_	Trait	Va	V_1	V _{hys}	Ve	h^2	12	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

109BF*- backfatthickness; TT- time on test; V₁- variance of common litter environment; V_a- additive genetic variance; V_{hys}-110variance of herd-year-seasoninteraction; V_e- residual variance, l²- ratio for common litter, h²- heritability, hys²- ratio for herd-
year-seasoninteraction, e²- ratio for residual

112 Heritability estimated by Imboonta et al. (2007) for BF and TT was higher than in our analysis

113 (0.61±0.02 BF and 0.38±0.02 for average daily gain which can be compared to TT). For analysis they

114 used Landrace sows from Thailand which came from one nucleus herd. This can explain better

115 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
- 117 0.23 and 0.55) compare to 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
- 120 pig carcass (Imboonta et al. 2007). However, correlation between selection for production traits and
- 121 decreased reproductive performance has been reported. Production traits are necessary to combine in
- selection programme.
- 123 Interaction herd-year-season of testing explained 23 % of phenotypic variance in BF and higher
- 124 proportion (28 %) for TT. Common litter effect explained 15 % of total phenotypic variance for BF,
- whereas for TT common litter variance obtained 24 % of phenotypic variance. Malovrh and Kovač
- 126 (1999) reported common litter variance for BF to be lower in smaller breeds for Slovenian Swedish
- 127 Landrace, Large White, and German Landrace. In their case, common litter variance explained 14 %
- 128 of phenotypic variance, which was similar to our findings. On contrary, common litter variance
- explained higher proportion of phenotypic variance (23 % for BF) in the study of Škorput (2013).
- 130 Similar proportion of common litter variance (26 %) was obtained for TT. Interaction of herd-year-
- season of testing accounted 23 % of total variance for BF and 28 % for TT.
- 132 Genetic trends of BV for BF and TT were calculated as the linearregression of the average annual
- 133 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
- 136 oscillation afterwards. Grey barsin both genetic trends represent number of animals tested per year and
- 137 reduction of animals tested was obvious.
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141 CONCLUSION

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

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