Original Article

Use of Different Models for Estimation of Genetic Parameters and Genetic Trends of Performance Test Traits of Gilts

Dragomir Lukač

Abstract

The aims of this research were to compare estimates of variance components using different animal models and to determine the most suitable mixed model for estimating genetic parameters and genetic trends for traits in performance test of gilts of different breeds using REML. A total of 73129 gilts of four genotypes in the period of 2009 to 2013 were included in the analyses. Four mixed models were constructed. Information criterion of Akaike (AIC) and Bayesian information criterion (BIC) were used to suggest which model is an adequate model for evaluation of genetics parameters. With the introduction of certain factors in the models, reduction in components of variance and heritability in all studied traits was observed. Heritability traits in four genotypes and models were at medium to high degree of heritability. The resulting genetic trends were different between the models and the coefficients of determination (R^2) were relatively high. Average gain and meat percentage were established positive (favourable) or negative (unfavourable) genetic trends in all models, while back fat thickness and lateral back fat thickness in all models were established to have positive (unfavourable) genetic trends. Based on the obtained results in this study, it is concluded that it is necessary to include mixed models in the estimation of breeding values in order to eliminate their influence, which significantly affects the variation of important traits for selection. In addition, with the inclusion of a greater number of parameters in mixed models, the models become more accurate and provide more accurate assessment of genetic and breeding value.

Keywords: genetics parameters, genetics trend, gilts, performance test, restricted maximum likelihood

University of Novi Sad, Faculty of Agriculture, Department of Animal Science, Trg Dositeja Obradovića 8, 21000 Novi Sad, Serbia
***Correspondence**: dragomir.lukac@stocarstvo.edu.rs*

Introduction

The most popular pig breeds in Serbia are Landrace and Yorkshire for maternal lines and their hybrids. The use of breeds and purebred lines in efficient crossbreeding programs depends on the availability of improved genotypes to achieve good results. For this reason, the selection and evaluation of breeds and purebred lines that are to be used are important steps for the success of any animal breeding program. Recent industrial need for genetic evaluation of pigs for selection is increasing with global trends for seed stock pig patient. Under field conditions, the replacement of sows by gilts accounts for about 40-55% annually (Stalder et al., 2005; Engblom et al., 2007). Without a quality breeding stock that will be used in further reproduction and parents of the next generation it is not possible to achieve genetic improvement in swine production. According to most authors (Nowachowicz et al., 2012; Chen et al., 2002), each genetic improvement in the performance that occurs in the population is a result of the mating of animals that have achieved significant results in performance test and have good breading values. For this reason, special attention must be paid to the breeding and selection of gilts on the farms.

Good selection of gilts with knowledge of their genetic parameters which are obtained by certain mathematical and statistical methods can be used to achieve genetic progress and improve desired traits. Therefore, accurate estimates of genetic parameters for these traits are essential for estimating breeding values and optimizing prediction of genetic response to selection (Buczynski et al., 2001; Imboonta et al., 2007).

Restricted maximum likelihood (REML) under an animal model for estimating variance and covariance components has become the method of choice for genetic parameter estimation in animal breeding because of its desirable statistical properties (Saton et al., 2002; Ronnegrad et al., 2010). The use of REML under an animal model for estimation of genetic variances and covariance allows separation of genetic effects from random environmental and other nuisance effects, and can be easily extended to estimation of other effects. However, the accuracy of estimating variance components is dependent on the data structure of the population and the model used (Clement et al., 2001; Meyer, 2007). For this reason, the objectives of this research were to compare estimates of variance components using different animal models to determine whether simpler models produce estimates similar to those produced by more complex alternatives, and to determine the most suitable mixed model for estimating genetic parameters and genetic trends for traits in performance test of different breeds of gilts using REML.

Materials and Methods

Animals at performance test: For quantitative-genetic analysis, results of the performance traits of tested gilts from 48 farms in Serbia in the period of 2009 to 2013 were used. A total of 73129 gilts of four different genotypes; pure Landrace (20979 gilts), pure Yorkshire (14746 gilts), hybrid $F_{1(YxL)}$ (24945 gilts) and hybrid $F_{1(LxY)}$ (12459 gilts); were used in this study. On all farms, the gilts were housed in groups from 8 to 12 animals with floor area of 0.7-1.0 m^2 per gilt. Thickness of fat and meat percentage were measured with ultrasound machines Krautkrämer S22 and Piglog 105, which met the standards relating to the value of the coefficient of determination ($R^2>0.64$) and the residual standard deviation (SDR<2.50).

Analyzed traits: The analyses presented here are related to four performance test traits: average gain (AG), meat percentage (MP), back fat thickness (BFT1), and lateral back fat thickness (BFT2). Weights recorded at the start and at the end of test were used to calculate AG in kg. Thickness of fat in the loin area (BFT1) was measured by ultrasound between 3-4 ribs back, 7 cm lateral from the middle line, while the lateral back fat thickness (BFT2) was measured at the lumbar between 3 and 4 lumbar vertebrae, the last lumbar vertebra, 7 cm lateral from the back middle line. The meat percentage was measured in the dorsal part between ribs 3 and 4, 7 cm lateral to the back line.

Models and statistical analyses: Significance of fixed effects and their inclusion in the models were determined for each trait using the GLM procedures in software package Statistica 10. In order to examine the influence of season, the year was divided into three seasons: Season I (November, December, January and February); Season II (March, April, September and October); Season III (May, June, July and August). For estimation of genetic parameters in models, the data have been defined random, fixed and regression effects (Table 1). In all constructed models, influence of animals was included as random effects, while effects of farm, year, season and breed in the models were included as fixed effects. Duration of performance test of gilts and their ages at the end of the test were included in the models as fixed effects, no matter to a linear effect on the analyzed traits.

Table 1 Significance of fixed, regression and random effects included in model for analysis of traits in performance test

Traits	Fixed effects			Regression effects		Random effects
	Farm	**Year**	**Season**	**Test duration**	**Final body weight**	**Animal**
AG, g	**	**	**	**	**	✓
BFT1, mm	**	**	**	**	**	✓
BFT2, mm	**	**	**	**	**	✓
MP, %	**	**	**	**	**	✓

AG = average gain, BFT1 = back fat thickness, BFT2 = back fat thickness lateral, MP = meat percentage, ** $p<0.01$

To estimate genetic parameters for each genotype, four different models were constructed:

$$Y_{ijklm} = \mu + A_i + F_j + Y_k + S_l + \mathrm{e}_{ijklm} \quad \text{(M1)}$$
$$Y_{ijklm} = \mu + A_i + F_j + Y_k + S_l + b_1(X - \bar{X}) + \mathrm{e}_{ijklm} \quad \text{(M2)}$$
$$Y_{ijklm} = \mu + A_i + F_j + Y_k + S_l + b_2(X - \bar{X}) + \mathrm{e}_{ijklm} \quad \text{(M3)}$$
$$Y_{ijklm} = \mu + A_i + F_j + Y_k + S_l + b_1(X - \bar{X}) + b_2(X - \bar{X}) + \mathrm{e}_{ijklm} \quad \text{(M4)}$$

where $\boldsymbol{Y_{ijklm}}$= phenotypic values of traits, $\boldsymbol{\mu}$ = average mean, $\boldsymbol{A_i}$= random effects of animal, $\boldsymbol{F_j}$= fixed effects of farm, $\boldsymbol{Y_k}$ = fixed effects of year, $\boldsymbol{S_l}$= fixed effects of season, $\boldsymbol{b_1}$ = regression coefficient of performance test duration, $\boldsymbol{b_2}$ = regression coefficient of body weight at the end of the test, and $\boldsymbol{e_{ijklm}}$ = random error.

Genetics parameters, including variance components and ratios, were estimated using the restricted maximum likelihood (REML) procedure based on an animal model using the Wombat program (Meyer, 2007) with multivariate analyses. The model can be represented in matrix terms by

$$\mathbf{y = Xb + Za + e}$$

where **y** is the vector of observations, ***X*** is the incidence matrix of fixed effects, **b** is the vector of fixed effects, ***Z*** is the incidence matrix of random effects, **a** is the vector of random effects, and ***e*** is the vector of residuals.
The model has the following assumptions

$$E\begin{pmatrix} y \\ a \\ e \end{pmatrix} = \begin{pmatrix} X\beta \\ 0 \\ 0 \end{pmatrix} \text{ and } V\begin{pmatrix} a \\ e \end{pmatrix} = \begin{pmatrix} A \otimes G & 0 \\ 0 & I_n \otimes R \end{pmatrix}$$

where **G** is the additive (co) variance matrix, **A** is the numerator relationship matrix, **R** is the residual variance matrix, $\mathbf{I_n}$ is the identity matrix with the order given by the number of animals (**n**) , and $\otimes$ is the Kronecker product between matrices.

Comparison criteria: Information criteria of Akaike and Bayesian information criteria tests were used in the comparison of models. In both tests, the most accurate model was the one which had the highest negative AIC and BIC values. e.g. according to these two tests we could select the model which fitted better to data structures. The values of the Akaike Information Criteria (AIC) and Bayesian Information Criteria (BIC) were obtained as follows:

$$\mathrm{AIC} = -2 \log (\mathrm{ML}_k) + 2p_k$$
$$\mathrm{BIC} = -2 \log (\mathrm{ML}_k) + p_k \log (n)$$

where $\boldsymbol{ML_k}$ = Maximum Log Likelihood for model k, $\mathbf{p_k}$ = number parameter for model *k*, and **n** = number of observation in model *k*.

Genetics trend: The genetic trends for the direct additive genetic values were calculated by regression of average predicted breeding values obtained from software Wombat of animal traits per testing year.

Results

Phenotypic parameters: Table 2 shows the mean value and standard deviation (SD) of the testing traits of gilts of different genotypes. The average number of days needed to reach the body weight at the end of the test of about 111 kg was higher in the gilts of pure breeds than the hybrid gilts, 5 days and 14 days, respectively, while daily gain was higher in the hybrid gilts. The hybrid $F_{1(LxY)}$ generation gilts had lower thickness of the back (BFT1) and lateral (BFT2) fat, and a higher percentage of meat (MP) compared to the other three genotypes of gilts estimated by ultrasound scanner on the final day of the test.

Table 2 Means and SD of testing traits in performance test

Traits	Yorkshire		Landrace		$F_{1(YxL)}$		$F_{1(LxY)}$	
	Means	**SD**	**Means**	**SD**	**Means**	**SD**	**Means**	**SD**
AET, days	200	24	200	23	195	25	186	27
AG, g	534.28	64.16	525.85	57.04	547.65	72.63	578.19	80.90
BFT1, mm	15.56	4.78	15.06	4.62	15.52	4.67	13.99	4.26
BFT2, mm	15.10	5.04	15.07	4.68	15.45	4.81	13.56	4.44
MP, %	57.35	4.18	56.47	4.10	56.59	4.10	57.89	3.64
FBW, kg	111.00	12.00	108.00	13.00	110.00	13.00	111.00	11.00

AET = age at the end of the test, AG = average gain, BFT1 = back fat thickness, BFT2 = back fat thickness lateral, MP = meat percentage, FBW = final body weight

Comparison and evaluation of models: Log likelihoods, AIC and BIC for the four models are shown in Table 3. According to Table 3, the increasing number of parameters for the effects resulted in the higher negative Log L, AIC and BIC values, which contributed to the more accurate assessment of the investigated traits. In our models, Akaike information criterion (AIC) and Bayesian information criterion (BIC) values were lowest in model 4 (M4), which included all fixed and regression effects in all breeds, suggesting that this model would be the most adequate model for our data. In contrast, model 1 (M1), which included only fixed effects, had the largest AIC and BIC values, suggesting that this model is not an adequate model for genetics parameters evaluation.

Genetic parameters: Residual, direct additive genetic and phenotypic variance components, residual and direct heritability with standard errors for the traits of the performance test of gilts obtained on the basis of four models designed for Yorkshire gilts are shown in Table 4, for Landrace gilts in Table 5, the hybrid gilts $F_{1(YxL)}$ in Table 6 and the hybrid gilts $F_{1(LxY)}$ in Table 7.

From Table 4 it can be seen that all traits from the performance test of Yorkshire breed obtained medium to high degree of heritability. It may also be noted that with the inclusion of certain factors in the model the reduction in components of variance and heritability for all the observed traits occurred. Thus, the maximum value of variance components and heritability was recorded in model 1 (M1), which involved fixed factors of farm, year and season, and the lowest value in model 4 (M4), which, in addition to the fixed factors from model 1, included the regression effects of age and body weight at the end of the test. Using different models that were constructed on the basis of the different components of fixed factors, different values of heritability were obtained. Direct heritability for AG traits differed between the models and ranged from 0.097 for model 4 to 0.935 for model 3, for MP from 0.315 for model 4 to 0.401 for model 1, for BFT1 from 0.372 for model 2 and 4 to 0.427 for model 1, and for BFT2 from 0.312 for model 4 to 0.375 for model 1.

Table 3 Comparison and evaluation of AM based on Log Likelihood function (Log L), Akaike Information Criterion (AIC) and Schwarz Bayesian Information Criterion (BIC)

Breeds	Models	Log L	AIC	BIC
Yorkshire	M1	-165274.372	-165304.372	-165442.443
	M2	-145998.239	-146028.239	-146166.173
	M3	-121727.271	-121747.271	-121837.035
	M4	-103003.417	-103023.417	-103113.089
Landrace	M1	-230746.663	-230776.663	-230920.039
	M2	-204169.400	-204199.400	-204342.680
	M3	-171699.965	-171719.965	-171813.281
	M4	-139379.963	-139399.963	-139493.214
$F_{1(YxL)}$	M1	-273092.905	-273122.905	-273268.884
	M2	-242792.458	-242822.458	-242968.352
	M3	-202915.949	-202935.949	-203031.005
	M4	-164586.193	-164606.193	-164701.192
$F_{1(LxY)}$	M1	-127622.215	-127652.215	-127787.752
	M2	-113393.048	-113423.048	-113558.419
	M3	-91270.465	-91290.465	-91378.532
	M4	-76617.875	-76637.875	-76725.830

Table 4 Variance and heritability for traits of performance test of Yorkshire gilts

Traits	Model	V_e	V_a	V_p	h_e^2	SEh_e^2	h^2	SEh^2
AG, g	M1	527.95	1809.41	2337.37	0.226	0.024	0.774	0.024
	M2	694.20	520.03	1214.24	0.572	0.025	0.428	0.025
	M3	137.05	1980.68	2117.74	0.065	0.023	0.935	0.023
	M4	108.303	11.67	119.981	0.903	0.016	0.097	0.016
MP, %	M1	8.77	5.87	14.65	0.599	0.024	0.401	0.024
	M2	8.69	5.63	14.32	0.607	0.024	0.393	0.024
	M3	7.78	4.17	11.95	0.651	0.023	0.349	0.023
	M4	8.02	3.69	11.72	0.685	0.023	0.315	0.023
BFT1, mm	M1	7.73	5.76	13.50	0.573	0.024	0.427	0.024
	M2	7.93	4.70	12.64	0.628	0.024	0.372	0.024
	M3	7.15	4.64	11.80	0.606	0.024	0.394	0.024
	M4	7.23	4.35	11.59	0.624	0.024	0.376	0.024
BFT2, mm	M1	8.45	5.07	13.53	0.625	0.024	0.375	0.024
	M2	7.87	3.70	11.57	0.680	0.023	0.320	0.023
	M3	7.74	4.06	11.81	0.656	0.023	0.344	0.023
	M4	8.72	3.95	12.67	0.688	0.023	0.312	0.023

V_e = residual variance, V_a = additive genetic variance, V_p = phenotypic variance, h_e^2 = heritability of residual variance, h^2 = heritability, SEh^2 = standard error of heritability

From Table 5 it can be seen that all the traits from the performance test of Landrace gilts obtained with models showed medium to high degree of heritability. The inclusion of some factors in the models gradually reduced residual, additive genetic and phenotypic variance and different values of heritability were obtained. However, model 1 (M1) showed the highest heritability estimates for all the observed traits. Direct heritability for AG traits differed between models and ranged from 0.170 for model 4 to 0.804 for model 3, for MP from 0.248 for model 3 to 0.480 for model 1, for BFT1 from 0.276 for model 3 to 0.522 for model 1, and for BFT2 from 0.299 for model 3 to 0.565 for model 1.

From Table 6 it can be seen that all the traits from the performance test of hybrid gilts $F_{1(YxL)}$

obtained with models also showed medium to high heritability. Similar to the previous two breeds, it can also be noted that with the inclusion of some factors in the models the reduction in residual, additive genetic and phenotypic variance occurred. Thus, the maximum value of the components of variance was obtained within model 1 (M1), which involved fixed factors of farm, year and season, and the lowest value was within model 4 (M4), which, in addition to the fixed factors from model 1, involved the regression effects of age and body weight at the end of the test. Direct heritability for AG traits differed between models and ranged from 0.343 for model 4 to 0.880 for model 3, for MP from 0.273 for model 3 to 0.523 from model 1 and 4, for BFT1 from 0.302 for model 3 to 0.583 for model 1, and for BFT2 from 0.316 for model 3 to 0.575 for model 1.

Table 5 Variance and heritability for traits of performance test of Landrace gilts

Traits	Model	V_e	V_a	V_p	h_e^2	SEh_e^2	h^2	SEh^2
AG, g	M1	388.63	1437.63	1826.26	0.213	0.019	0.787	0.019
	M2	432.62	765.02	1197.65	0.361	0.021	0.639	0.021
	M3	320.02	1314.40	1634.42	0.196	0.020	0.804	0.020
	M4	56.84	11.6524	68.50	0.830	0.014	0.170	0.014
MP, %	M1	7.86	7.26	15.13	0.520	0.020	0.480	0.020
	M2	7.83	6.93	14.77	0.530	0.020	0.470	0.020
	M3	9.50	3.13	12.64	0.752	0.019	0.248	0.019
	M4	6.78	5.89	12.68	0.535	0.020	0.465	0.020
BFT1, mm	M1	6.88	7.51	14.40	0.478	0.020	0.522	0.020
	M2	6.97	6.87	13.84	0.503	0.021	0.497	0.021
	M3	8.76	3.34	12.11	0.724	0.019	0.276	0.019
	M4	6.34	5.76	12.11	0.524	0.020	0.476	0.020
BFT2, mm	M1	6.30	8.18	14.48	0.435	0.020	0.565	0.020
	M2	6.41	7.65	14.06	0.456	0.020	0.544	0.020
	M3	8.63	3.67	12.31	0.701	0.019	0.299	0.019
	M4	5.83	6.44	12.28	0.475	0.020	0.525	0.020

V_e = residual variance, V_a = additive genetic variance, V_p = phenotypic variance, h_e^2 = heritability of residual variance,
h^2 = heritability, SEh^2 = standard error of heritability

Table 6 Variance and heritability for traits of performance test of $F_{1(YxL)}$ gilts

Traits	Model	V_e	V_a	V_p	h_e^2	SEh_e^2	h^2	SEh^2
AG, g	M1	409.95	1672.06	2082.02	0.197	0.017	0.803	0.017
	M2	422.95	1103.02	1525.98	0.277	0.018	0.723	0.018
	M3	196.17	1443.93	1640.10	0.120	0.018	0.880	0.018
	M4	47.90	25.00	72.91	0.657	0.017	0.343	0.017
MP, %	M1	7.13	7.83	14.96	0.477	0.019	0.523	0.019
	M2	7.09	7.51	14.61	0.486	0.019	0.514	0.019
	M3	9.08	3.40	12.49	0.727	0.016	0.273	0.016
	M4	6.00	6.59	12.59	0.477	0.019	0.523	0.019
BFT1, mm	M1	6.05	8.48	14.53	0.417	0.019	0.583	0.019
	M2	6.12	8.00	14.13	0.434	0.019	0.566	0.019
	M3	8.67	3.75	12.42	0.698	0.016	0.302	0.016
	M4	5.96	6.46	12.43	0.480	0.019	0.520	0.019
BFT2, mm	M1	6.06	8.19	14.25	0.425	0.018	0.575	0.018
	M2	6.10	7.84	13.95	0.438	0.019	0.562	0.019
	M3	8.64	3.99	12.63	0.684	0.017	0.316	0.017
	M4	5.86	6.52	12.39	0.473	0.019	0.527	0.019

V_e = residual variance, V_a = additive genetic variance, V_p = phenotypic variance, h_e^2 = heritability of residual variance,
h^2 = heritability, SEh^2 = standard error of heritability

From Table 7 it can be seen that all the traits from the performance test of hybrid gilts $F_{1(LxY)}$ obtained with models showed exclusively high degree of heritability, which was different from the other genotypes of gilts. However, similar to the previous analysis it can also be noted that with the inclusion of some factors in the models the reduction in residual, additive genetic and phenotypic variance occurred. Using different models that were constructed based on different components of fixed factors, different values of heritability were obtained. Direct heritability for AG traits differed between models and ranged from 0.235 for model 4 to 0.997 for model 3, for MP from 0.622 for model 4 to 0.640 from model 1, for BFT1 from 0.666 for model 1 to 0.686 for model 3, and for BFT2 from 0.638 for model 1 to 0.657 for model 4.

Genetic trends: The estimates of the genetic trends for the direct additive genetic effects and coefficients of determination (R^2) are shown in Table 8. The obtained genetic trends differed between the models and the coefficients of determination R^2 were relatively high. The largest positive (favourable) genetic trend for AG was established within model 1 (M1) and the lowest genetic trend was obtained within model 4 (M4) in all genotypes of gilts. Genetic trend for the AG ranged from -0.04 to 8.35 in the Yorkshire gilts, from 0.17 to 5.45 in the Landrace gilts, from 0.08 to 2.37 in the $F_{1(YxL)}$ gilts and from 0.12 to 2.88 g day/year in the $F_{1(LxY)}$ gilts.

For the MP in all models, negative (unfavourable) genetic trend for all genotypes was established. Therefore, the largest negative genetic trend was obtained within model 4 (M4) and the lowest negative genetic trend was obtained within model 1 (M1). The genetic trend for MP ranged from -0.13 to -0.35 in the Yorkshire gilts, from -0.33 to -0.48 in the Landrace gilts, from -0.30 to -0.44 in the $F_{1(YxL)}$ gilts and from -0.01 to -0.19%/year in the $F_{1(LxY)}$ gilts. For BFT1 and BFT2 in all models, positive (unfavourable) genetic trend for all genotypes was established, with the largest positive genetic trend obtained within model 2 (M2). The genetic trend for BFT1 ranged from 0.44 to 0.16 at Yorkshire, from 0.71 to 0.57 at Landrace, from 0.63 to 0.46 in the $F_{1(YxL)}$ and from 0.29 to 0.21 mm/year in the $F_{1(LxY)}$, while the genetic trend for BFT2 ranged from 0.44 to 0.17 in the Yorkshire gilts, from 0.64 to 0.45 in the Landrace gilts, from 0.56 to 0.44 in the F $_{1(YxL)}$ gilts and from 0.23 to 0.15 mm/year in the $F_{1(LxY)}$ gilts.

Table 7 Variance and heritability for traits of performance test of $F_{1(LxY)}$ gilts

Traits	Model	V_e	V_a	V_p	h_e^2	SEh_e^2	h^2	SEh^2
AG, g	M1	544.59	1399.30	1943.89	0.280	0.026	0.720	0.026
	M2	505.36	945.87	1451.24	0.348	0.026	0.652	0.026
	M3	3.68	1058.44	1062.13	0.003	0.022	0.997	0.022
	M4	54.17	16.67	70.84	0.765	0.021	0.235	0.021
MP, %	M1	4.45	7.92	12.37	0.360	0.027	0.640	0.027
	M2	4.26	7.64	11.90	0.358	0.027	0.642	0.027
	M3	3.49	6.05	9.54	0.366	0.027	0.634	0.027
	M4	3.50	5.87	9.38	0.374	0.028	0.626	0.028
BFT1, mm	M1	3.45	6.90	10.36	0.334	0.026	0.666	0.026
	M2	3.22	6.71	9.93	0.324	0.027	0.676	0.027
	M3	2.90	6.34	9.24	0.314	0.027	0.686	0.027
	M4	2.90	6.22	9.12	0.318	0.027	0.682	0.027
BFT2, mm	M1	3.71	6.53	10.24	0.362	0.027	0.638	0.027
	M2	3.53	6.37	9.91	0.356	0.027	0.644	0.027
	M3	3.25	6.13	9.38	0.346	0.027	0.654	0.027
	M4	3.19	6.11	9.30	0.343	0.027	0.657	0.027

V_e = residual variance, V_a = additive genetic variance, V_p = phenotypic variance, h_e^2 = heritability of residual variance, h^2 = heritability, SEh^2 = standard error of heritability

Table 8 Genetic trends ($\hat{b}$) coeficients of determination (R^2) and probability values (P) for direct genetics effect

Traits	Models	Yorkshire			Landrace			$F_{1(YxL)}$			$F_{1(LxY)}$		
		($\hat{b}$)	R^2	P	($\hat{b}$)	R^2	P	($\hat{b}$)	R^2	P	($\hat{b}$)	R^2	P
AG, g	M1	8.35	0.87	**	5.45	0.61	ns	2.37	0.36	ns	2.88	0.34	ns
	M2	6.47	0.76	**	2.67	0.71	ns	1.33	0.26	ns	2.77	0.43	ns
	M3	5.79	0.89	**	3.76	0.42	ns	1.55	0.21	ns	1.02	0.10	ns
	M4	-0.04	0.01	ns	0.17	0.31	ns	0.08	0.08	ns	0.12	0.04	ns
MP, %	M1	-0.13	0.66	ns	-0.40	0.63	ns	-0.30	0.79	**	-0.01	0.00	ns
	M2	-0.13	0.63	ns	-0.33	0.49	ns	-0.43	0.56	ns	-0.03	0.01	ns
	M3	-0.31	0.92	*	-0.39	0.63	ns	-0.34	0.78	**	-0.17	0.24	ns
	M4	-0.35	0.95	*	-0.48	0.70	ns	-0.44	0.77	**	-0.19	0.28	ns
BFT1, mm	M1	0.44	0.64	ns	0.61	0.78	**	0.53	0.83	**	0.28	0.58	ns
	M2	0.39	0.95	*	0.71	0.88	**	0.63	0.70	ns	0.29	0.53	ns
	M3	0.16	0.88	*	0.57	0.72	ns	0.48	0.89	**	0.21	0.45	ns
	M4	0.20	0.92	*	0.59	0.77	**	0.46	0.87	**	0.22	0.47	ns
BFT2, mm	M1	0.36	0.77	**	0.52	0.93	*	0.55	0.77	**	0.21	0.15	ns
	M2	0.44	0.70	ns	0.64	0.93	*	0.56	0.78	**	0.23	0.16	ns
	M3	0.17	0.38	ns	0.46	0.78	**	0.44	0.86	**	0.15	0.09	ns
	M4	0.25	0.54	ns	0.45	0.91	**	0.51	0.80	**	0.18	0.12	ns

AG = average gain, BFT1 = back fat thickness, BFT2 = back fat thickness lateral, MP = meat percentage, * $p<0.01$, ** $p<0.05$, ns = not significant

The regression equations for AG (M1, M2, M3) in the Yorkshire gilts were statistically significant ($p<0.05$), while in the other genotypes and models statistically significant ($p>0.05$) differences were not present. Highly statistically significant regression equations ($p<0.01$) for MP were obtained for the Yorkshire gilts (M3, M4) and statistically significant regression equations ($p<0.05$) for the hybrid gilts $F_{1(YxL)}$

(M1, M3, M4). The regression equations for BFT1 in the Yorkshire gilts (M2, M3, M4) were highly statistically significant ($p<0.01$), while in the Landrace gilts (M1, M2, M4) and hybrid gilts $F_{1(YxL)}$ (M1, M3, M4) were statistically significant ($p>0.05$). For BFT2 in the Landrace gilts (M1, M2) highly significant ($p<0.01$) regression equations were established, while in the Yorkshire (M1), Landrace (M3, M4) and hybrid gilts $F_{1(YxL)}$ significant regression equations ($p<0.05$) were established.

Discussion

The obtained average values of the performance traits of the tested gilts were lower than the genetic potential of the genotypes in other countries. However, phenotypic traits variability is large enough for the proper selection of positive variants which can increase the average value of the analyzed traits and genetic improvement in the future. Similar to our results, many other researchers have found significant differences in the characteristics and variability of performance test of gilts between different genotypes. Popovac et al. (2014) recorded average daily gain of 408.93 g, average back fat thickness of 9.77 mm with percentage of meat in carcass of 61.08% in Landrace gilts and hybrid gilts $F_{1(LxY)}$. Szyndler-Nedza et al. (2010) conducted a performance test which lasted from 150 to 210 days in Yorkshire gilts and recorded at the end of the test body weight of 104.7 kg, daily gain of 630 g, percentage of meat in carcass of 62.3% and thickness of back fat of 9.1 mm. Eckert and Žak (2010) studied nucleus farms in Poland with Yorkshire gilts and determined back fat thickness of 9.77 mm, percentage of meat of 61.08% and life daily gain of 447.7 g. Szulc et al. (2013) determined daily gain of 655.23 g, back fat thickness of 11.96 mm and percentage of meat in carcass of 58.08% in Yorkshire gilts. Kawecka et al. (2009) had gilts of synthetic Polish lines and at the end of the performance test of 180 days recorded life gain of 572 g, daily gain in the assay of 701 g, average fat thickness of 10.5 mm and percentage of meat in carcass of 58.7%.

The knowledge of phenotypic and genetic parameters provides us information about trait changes that have occurred due to the effect of different genetic and paragenetic factors. The inclusion of a large number of paragenetic factors in the models results in more precise estimates of genetic parameters and breeding values, as confirmed in this study. Many authors (Yang, 2005; Burnham and Anderson, 2004; Maniatis et al., 2013) who studied different models concluded that the inclusion of as many parameters as possible in the model led to the reduction in AIC and BIC values, therefore the models were more accurate and provided more precise estimates of parameters, but their inclusion in the model depended on the availability of the data collected.

According to the given tables, the heritability of performance test traits obtained in different genotypes within different models ranges from medium to high heritability, and according to Wolf and Wolfova (2012), the involvement in the selection program will contribute significant genetic progress of these traits and the application of statistical and mathematical methods will enable accurate identification of genetically superior animals. The inclusion of certain factors in the models caused the cost reduction in components of variance and heritability in all the studied traits. The lowest value of heritability for AG was shown in model 4 (M4) with the regression influences of age and body weight at the end of the test, while model 3 (M3) with the regression effect of body weight at the end of the test showed the highest heritability for all genotypes of gilts. For MP, BFT1 and BFT2 lowest heritability estimates were shown by model 3 (M3) in the Landrace and hybrid $F_{1(YxL)}$ gilts, model 4 (M4) in the Yorkshire and model 1 (M1) without regression influence in the hybrid $F_{1(LxY)}$ gilts; while the highest heritability estimates were obtained by model 1 (M1) in the Yorkshire, Landrace and hybrid $F_{1(YxL)}$ gilts and model 3 and 4 in the hybrid $F_{1(LxY)}$ gilts.

The values of heritability obtained by the models designed for MP, BFT1 and BFT2 were relatively low, while for the AG significant variability between individual heritability models for all gilt breeds was observed. The relatively low heritability and high variability can be explained by the large phenotypic variability characteristics and the influence of different systematic factors that lead to high variance of the environment causing the proportion of additive gene to change. This especially occurs in AG and it is thus necessary to include in the models the length of the performance test and body weight at the end of the test. For this reason it is necessary to include larger number of environmental factors into models for genetic evaluation of these traits.

Slightly lower values of heritability in relation to AG was determined by Szynder-Nędza et al. (2010) in Yorkshire (0.29) and Landrace (0.39) gilts, Hoque and Suzuky (2008) in Landrace (0.47), Imboonta (2007) in Landrace (0.38), Popovac et al. (2014) in Landrace and $F_{1(LxY)}$ (0.25), Gilbert et al. (2007) in Yorkshire (0.35), and Nguyen and McPhee (2005) in Yorkshire (0.19). Similar and high heritability values for BFT1 and BFT2 were recorded by Tänavots et al. (2002) in Landrace (0.77), Yorkshire (0.60), $F_{1(LxY)}$ (0.55) and $F_{1(YxL)}$ (0.79); Cai et al. (2008) in Yorkshire (0.63); Imboonta et al. (2007) in Landrace (0.61); and Hoque and Suzuki (2008) in Landrace (0.54); while slightly lower heritability was recorded by Popovac et al. (2014) in Landrace and $F_{1(LxY)}$ (0.35), and Zumbach et al. (2007) in $F_{1(YxL)}$ (0.38). Heritability for meat percentage ranged from 0.49-0.73 in the research of Tänavots et al. (2002), 0.57 in Cai et al. (2008), 0.13 in Serenius et al. (2004), and 0.40 in Nguyen and McPhee (2005).

The resulting genetic trends differed between the model and the coefficients of determination R^2 were relatively high. The introduction of larger number of models had the aim to analyze which of these models matched, and which of them should be chosen and suggested as most acceptable. It is believed that the more accurate the model takes into account the more statistical impact, with the higher coefficient of determination R^2.

The study of Nguyen and McPhee (2005) in lines of gilts selected for high growth in the test achieved annual genetic trend of 8.73 g/day/year, whereas the results of the Torres et al. (2005) the genetic trend for gilts was -1.19 g/day/year, and in the boars was -0.29 g/day/year.

In the study Chen et al. (2002) the estimated genetic trend for fat thickness was -0.45 and -0.31 mm/year in Yorkshire and Landrace gilts. Michalska et al. (2006) showed significant changes in the performance test of gilts over a period of 10 years with decrease in the average age at the end of the test from 190 to 171 days, increase in body weight at the end of the test from 94.7 kg to 100.3 kg, decrease in back fat thickness from 14.4 mm to 10.3 mm, and increase in percentage of meat from 54 to 58%, and that the daily gains achieved in the test was about 578 g. In the research of Dube et al. (2011) in South Africa during the period of 1990 to 2008 decrease in back fat thickness from 14 to 11 mm was observed as well as increase in average daily gain from 890 to 1000 g and percentage of meat from 66.5 to 69.5% in Yorkshire and Landrace gilts in performance test. According to Kennedy et al. (1996), in Canada by the use of intensive selection for a period of 17 years reduction in back fat thickness of 3.5 mm or 26% of the average thickness was recorded since 17 days of age up to 100 kg, or 9% from the mean value.

It has long been known that the phenotypic variability of traits in addition to hereditary affects numerous abiotic factors. The action complicates accurate assessment of genetic parameters and breeding value or additive genetic value. Therefore, it is necessary to include mixed models to estimate the breeding values in order to eliminate the influence, which significantly affects the variation of important traits for selection. In addition, the inclusion of a greater number of parameters in mixed models makes models more accurate and provides a more accurate assessment of genetic and breeding value as demonstrated in this study.

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บทคัดย่อ

การใช้แบบจำลองต่างกันเพื่อประเมินค่าพารามิเตอร์ทางพันธุกรรมและแนวโน้มทางพันธุกรรมต่อการแสดงออกของลักษณะสายพันธุ์ของสุกรสาว

Dragomir Lukač

วัตถุประสงค์ของการวิจัยนี้เพื่อเปรียบเทียบค่าประเมินขององค์ประกอบความแปรปรวนจากแบบจำลองสัตว์ที่แตกต่างกัน และกำหนดแบบจำลองผสมที่มีความเหมาะสมที่สุดสำหรับการประเมินค่าพารามิเตอร์ทางพันธุกรรมและแนวโน้มทางพันธุกรรมต่อลักษณะสายพันธุ์ในการทดสอบการแสดงออกของสุกรสาวสายพันธุ์ต่างกันโดยใช้ REML ทำการวิเคราะห์สุกรสาวสี่จีโนไทป์จำนวนทั้งหมด 73,129 ตัว ระหว่างปี 2009 ถึง 2013 ทำการสร้างแบบจำลองผสมสี่แบบ และใช้เกณฑ์จาก Akaike information criterion (AIC) และ Bayesian information criterion (BIC) เพื่อตัดสินแบบจำลองที่เหมาะสมที่สุดสำหรับประเมินค่าพารามิเตอร์ทางพันธุกรรม ด้วยปัจจัยที่แน่นอนในแบบจำลองจึงสังเกตการลดลงขององค์ประกอบความแปรปรวนและอัตราพันธุกรรมของทุกลักษณะสายพันธุ์ที่ทำการศึกษา อัตราพันธุกรรมของลักษณะสายพันธุ์ใน 4 จีโนไทป์ และแบบจำลองอยู่ในอัตราระดับกลางถึงสูง ผลของแนวโน้มทางพันธุกรรมที่ได้นี้แตกต่างกันระหว่างแบบจำลองและสัมประสิทธิ์การตัดสินใจมีค่าสูงเมื่อเปรียบเทียบกัน ค่าเฉลี่ยร้อยละของน้ำหนักและเนื้อถูกกำหนดเป็นแนวโน้มพันธุกรรมบวก (น่าพอใจ) หรือลบ (ไม่น่าพอใจ) ในทุกแบบจำลอง ในขณะที่ความหนาของไขมันสันหลังและความ หนาของไขมันสันหลังด้านข้างในทุกแบบจำลองถูกกำหนดเป็นแนวโน้มพันธุกรรมบวก (ไม่น่าพอใจ) จากผลการทดลองที่ได้ในการศึกษาครั้งนี้ สรุปว่ามีความจำเป็นต้องรวมแบบจำลองผสมในการประเมินค่าการผสมพันธุ์เพื่อตัดผลกระทบเหล่านั้นออกไป ซึ่งมีผลกระทบอย่างมีนัยสำคัญต่อการเปลี่ยนแปลงลักษณะสายพันธุ์ที่สำคัญสำหรับการคัดเลือก นอกจากนี้เมื่อรวมพารามิเตอร์จำนวนมากขึ้นในแบบจำลองผสม ทำให้แบบจำลองมีความถูกต้องมากขึ้นและทำให้เพิ่มความถูกต้องในการประเมินค่าสายพันธุ์และการผสมพันธุ์

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University of Novi Sad, Faculty of Agriculture, Department of Animal Science, Trg Dositeja Obradovića 8, 21000 Novi Sad, Serbia

***ผู้รับผิดชอบบทความ** *E-mail: dragomir.lukac@stocarstvo.edu.rs*