THE ASSESSMENT OF GENETIC POTENTIAL IN PERFORMANCE TESTED GILTS BY MEANS OF SELECTION INDEXES METHOD

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The objective of this research paper was to make an assessment of breeding value of performance tested gilts of Swedish Landrace and F_1 cross-breds of Swedish Landrace and Great Yorkshire by the method of selection index. The traits on whose basis the breeding value was estimated were: daily liveweight gain, average backfat thickness measured at two sites and carcass meat percentage. These traits were corrected for body mass of 100kg by the method of base indexes and the following average values were determined: corrected daily liveweight gain (KZDP) 408.93g/day, corrected average backfat thickness measured at two sites (KSL) 9.77mm and corrected carcass meat percentage (KPM) 61.08%. Studying the effect of genotype, year and birth season of gilts a statistically significant variation (P>0.05) of these traits provoked by the mentioned factors was not determined while the gilts` sire statistically highly significantly (P<0.001) influenced all studied traits. Heritability coefficients were: h^2= 0.255 for KZDP, h^2= 0.356 for KSL and h^2= 0.349 for KPM. The four selection index equations were constructed among which as the most optimal was chosen the one which includes all three traits (KZDP, KSL and KPM) and whose coefficient of the correlation of selection index and aggregate genotype was $r_{IAG} = 0.594$.

Key words: backfat thickness, liveweight daily gain, meat percentage, heritability, selection index

INTRODUCTION

The assessment of the animal breeding value represents a very delicate procedure by which a greater number of traits, among which some with better and some with poorer values

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should be taken into consideration and on such created basis a conclusion should be reached on what animals should be selected for and what animals should be removed from the further process of breeding. What further hinders this procedure is the fact that manifestation of some traits is hereditary, in greater or lesser degree, so it may happen that animal genetic potential, on which the assessment of breeding value is based, is not regarded in a right way because the impact of the environment factors may be a dominant one. Precisely for these reasons various methods have been used in order to objectively comprehend and select those parent pairs that possess best genetic potential which will be best manifested in given conditions of production. There are different methodological procedures for the assessment of animal breeding value and one of these procedures is the method of selection indexes (PETROVIĆ *et al* 2005).

A method of selection index was applied particularly in pig breeding and in the countries where pig breeding is not at so high a level and where the conditions are still not created for the application of BLAP AM-method on which the assessment of swine breeding value is being based in the countries with developed livestock production (RADOJKOVIĆ *et al* 2012). A practical application of this method is relatively simple because when deriving the equation for the assessment of breeding value it means a simple exchange of determined trait phenotypical values in the animals whose breeding value is being assessed and as a result the animal assessed breeding value expressed in index score is obtained. A main characteristic of this methodological procedure is to compensate for the values of the traits producing, as a final result of the assessments of breeding value, the number of index score on the basis of which the ranking of animals whose breeding value is being evaluated is   performed. The accuracy of selection indexes depends on numerous factors such as trait heritability, true commerical value of the traits, comparative group used as the basis for deriving the index and alike, what can affect the values of partial regression coefficients that are the main factors of the quality of selection index. The greatest accuracy of the animal evaluated breeding value by use of the method of selection indexes is obtained when the effect of the environement factors is reduced to minimum and the value of heritability coefficients of the traits included into index is high (SELLIER *et al* 2000).

The aim of this study stemmed out from the need to evelute genetic potential of the growth rate and carcass quality traits in performance tested gilts of fertile meaty breeds, respecting literature data according to which these traits belong to the mean to high heritability traits group (SAINTILAN *et al* 2012; HOQUE and SUZUKI 2008; IMBOONTA *et al* 2007).

MATERIALS AND METHODS

Data set on the basis of which the analyses were performed and selection indexes constructed has contained the records for 2344 performance tested gilts raised at a pig farm in Serbia. The gilts were of Swedish Landrace race and of F1 generation crossbreds between Great Jorkshire boar and Swedish Landrace sows, born in 4 consecutive years and 4 seasons. They originated from 36 sires with a minimum number of sibs needed for analyses per sire 10, because of the accuracy of calculating genetic parameters, while every sire on average produced 65,11 sibs.

The traits that were analyzed and on the basis of which the gilts breeding value was determined were: corrected daily liveweight gain at the end of test (**KZDP**), corrected average backfat thickness measured at two places at the end of test (**KSL**) and corrected meat percent in carcass at the end of test (**KPM**). Correction of the growth rate and carcass quality traits was

done for the body mass of gilts of 100kg, what is the mass at which the performance test finishes. Respecting the conditions of organisation characteristical for pig production in which the test finishes upon random estimation that the animals have reached the mass of 100kg, what in majority of cases does not correspond to an animal real mass, it was necessary to make corrections for the trait of growth rate in order to create standard conditions for the assessment of breeding value in all animals encompassed by the analysis. For the correction of analysed traits the method of based indexing based on the regression analysis was used.

Statistical processing of data had several phases such as defining a descriptive statistical indicators and measures of variation, then study of variability of traits at phenotypic and genetic level and defining the heritability of these traits. Variability of traits at phenotypic and genetic level and heritability of the same traits and the parameters necessary (variances and covariances) for the construction of selection indexes were calculated by the method of the least squares by application of LSMLMW – HARVEY (1987) and SAS, 9.1.3.(2007) programme packets.

Two mixed models were used on the basis of which the variability and heritability of traits of growth rate and carcass quality in examined gilts were studied:

Model 1: $Y_{ijkl} = \mu + R_i + G_j + S_k + o_{ijkl} + e_{ijkl}$

Where: Y_{ijkl} – is a trait manifestation (KZDP, KZSL,KPM), μ – population general mean, R_i – fixed effect of gilt genotype, G_j – fixed effect of the gilt birth year, S_k – fixed effect of the birth season of gilt, o_{ijkl} – random effect of the gilt`s sire, e_{ijkl} – random effect of non-determined factors.

Model 2: $Y_i = \mu + o_i + e_i$

Where: Y_i – is a trait manifestation (KZDP, KZSL, KPM), μ – population general average, o_i – random effect of gilt`s sire, e_i – random effect of non-determined factors.

Heritability of studied traits has been calculated by the method of inter-class correlation of half-relatives (half-sibs) on sire`s side. Heritability equation may be shown in following way:

$$h^2 = \left(4 \, \sigma_s^2\right) / \left(\sigma_s^2 + \sigma_e^2\right)$$

Where: h^2 – is a heritability coefficient (heritability), σ_s^2 – inter-sires variance, σ_e^2 – intra-sire (error) variance.

Gilt`s breeding performance was estimated by the method of selection index and can be shown by following equation:

$$I = b_1 (X_1 - \bar{X}_1) + b_2 (X_2 - \bar{X}_2) + \ldots + b_n (X_n - \bar{X}_n)$$

Where: I – is a relative breeding performance of the animal estimated by selection index (value of selection index defined for each animal), b_i – partial coeficient of multiplied regression for each trait included in the selection index, $(X_i - \bar{X}_i)$ – difference between individual trait phenotypic value and population average.

For calculating partial regression coeficients (b) following matrices for solving the systems of equations were used:

$$\begin{bmatrix} VarPH(X1) & CovPH(X1X2) & CovPH(X1Xn) \\ CovPH(X1X2) & VarPH(X2) & CovPH(X2Xn) \\ CovPII(XnX1) & CovPII(X2Xn) & VarPII(Xn) \end{bmatrix} * \begin{bmatrix} b1 \\ b2 \\ bn \end{bmatrix} =$$

$$= \begin{bmatrix} \text{VarG(X1)} & \text{CovG(X1X2)} & \text{CovG(X1Xn)} \\ \text{CovG(X1X2)} & \text{VarG(X2)} & \text{CovG(X2Xn)} \\ \text{CovG(XnX1)} & \text{CovG(X2Xn)} & \text{VarG(Xn)} \end{bmatrix} * \begin{bmatrix} \text{v1} \\ \text{v2} \\ \text{vn} \end{bmatrix}$$

This equation yields following expression:

$P * b = G * v$

$b = P^{-1} * G * v$

Where: b – is a vector of the solution of partial regression coefficients for each trait (X), P^{-1}-inverse phenotypical matrix formed of variances and covariances of traits included into selection index, G – genetic matrix formed of variances and covariances of the traits included into selection index, v - vector of relative economic values of the traits included into selection index.

The accuracy of estimated breeding value by the method of selection indexes is expressed by the correlation coefficient between selection index and aggregate genotype of each individual. Higher value of this correlation coefficient increases also the accuracy of the assessment of animal breeding value by means of selection index. Aggregate genotype may be explained by following expression:

$$AG = v_1 * h^2_1 * X_1 + v_2 * h^2_2 * X_2 + ... + v_i * h^2_i * X_i$$

Where: AG – is an aggregate genotype, v_i – economic value of the trait (X_i), h^2_i – trait heritability coefficient (X_i), X_i – trait phenotypic value of each individual.

Correlation coefficient of selection index and aggregate genotype which shows the accuracy of selection index is calculated by means of following expression:

$$r_{IAG} = \sigma_I / \sigma_{AG}$$

Where: r_{IAG} – is a correlation coefficient between selection index and aggregate genotype, σ_I – standard deviation of selection index, σ_{AG} – standard deviation of aggregate genotype.

The economic value of the traits included in the selection index was calculated by means of the methodology developed by VUKELIĆ et al. (2004), where economic value of traits is not represented as discount of costs per unit of trait when the trait is increased by one unit, but average values of traits are increased in accordance with the given selection goal which was 10% for each trait. When discount of costs per unit in which the trait is expressed according to set selection goal has been determined, the economic value of traits is obtained by the relation between the cost discount per trait unit included in selection index and primary trait what in this case was the meat percentage in gilts carcasses. Out of this relationship following economic values of the traits were derived:

KPM:	1
KZDP:	0,133
KSL:	6,267

RESULTS AND DISCUSSION

Descriptive statistical indicators of analysed traits of performance tested gilts used for constructing the selection indexes are shown in Table 1.

Table 1. Descriptive statistical indicators of analyzed traits in performance tested gilts

Trait	$\bar{X}$	SD	CV(%)	Min	Max	µ
KZDP (*g*)	408.93	33.26	8.15	293.00	662.00	412.17
KZSL (*mm*)	9.77	2.13	21.8	4.38	19.23	9.60
KPM (*%*)	61.08	3.08	5.04	46.88	70.58	61.16

Corrected daily liveweight gain of 408.93g is considerably lower in relation to the values found in literature. MIJATOVIĆ *et al* (2009) determined corrected daily liveweight gain of 502 g/day, the higher values of daily liveweight gain were also determined by: SZULUC *et al* (2013)**,** VIDOVIĆ *et al* (2012), PETROVIĆ *et al* (2006) and BRKIĆ *et al* (2001). Lower daily liveweight gain in examined gilts in relation to literature data might be explained by restrictive diet in the final phase of trial with the objective to increase the growth of gilts for better reproductive performances, while the body mass remains at the same level (about 130kg) in the moment of the first mating. Average value of KSL of 9.77mm is lower than the value determined by MIJATOVIĆ *et al* (2009), IMBOONTA *et al* (2007) and BRKIĆ *et al* (2001), while carcass meat percentage of 61.08% is relatively high compared with literature data (SZULUC *et al* 2013; MIJATOVIĆ *et al* 2009; BRKIĆ *et al* 2001).

The effects of fixed and random factors and the coefficients of the determination of models which explain the variability of the growth rate trait and carcass quality in performance tested gilts by the method of variance analysis are shown in Table 2.

Table 2. Tables of the variance analysis for the traits of growth rate and carcass quality in performance tested gilts (P>0.05-n.s.; P<0.001-***)

Traits	Effects				R^2
	Genotype	Year of birth	Season of birth	Sire	
KZDP	n.s.	n.s.	n.s.	***	0.464
KSL	n.s.	n.s.	n.s.	***	0.317
KPM	n.s.	n.s.	n.s.	***	0.315

Gilts genotype, year and season of birth did not have any significant effect (P>0.05) on any of the tested traits, while the gilt`s sire displayed a statistically high significant effect (P<0.001) on all tested traits of growth rate and carcass quality. The results are not in compliance with the results of GOGIĆ *et al* (2012), who determined a significant effect of gilt genotype on daily liveweight gain and backfat thickness. The same group of authors determined a statistically significant effect of gilt`s sire on these traits. Statistically significant effect of the gilt`s year of birth on daily liveweight gain and backfat thickness was determined in the study of RADOVIĆ *et al* (2012), but the same authors did not confirm a significant effect of genotype on corrected daily liveweight gain (KZDP), backfat thickness and carcass meat percentage at the end of the trial. A significant effect of gilt`s sire on daily liveweight gain was established by VIDOVIĆ *et al*

(2012). The absence of the effect of the environment factor on tested traits contributes to the quality of constructed selection indexes because this method of the assessment of breeding performance does not take into account the effects of external factors.

Heritability and variances of the traits of liveweight gain and carcass quality are shown in Table 3.

Table 3. Heritability, error of heritability-$h^2 \pm se$ and variance (inter-sire variance-σ_s^2; intra-sire variance - σ_e^2; additive variance- σ_A^2; phenotypic variance - σ_P^2.)

Traits	σ_s^2	σ_e^2	$h^2 \pm se$	σ_A^2	σ_P^2
KZDP	70.6655	1038.6491	0.255±0.070	282.6624	1109.3146
KZSL	0.4039	4.1359	0.356±0.090	1.6154	4.5398
KPM	0.8311	8.7055	0.349±0.089	3.3242	9.5366

Heritability value for KZDP of $h^2 = 0.255$ is the same as the value determined by NGUYEN and MCPHEE (2004), while higher heritability of this trait which ranged in the interval of $h^2 = 0.270$ to $h^2 = 0.470$ was found in the studies by: SAINTILAN *et al* (2012), SZYNDER-NEDZA *et al* (2010), HOQUE and SUZUKY (2008)*,* IMBOONTA *et al* (2007), and VUKOVIĆ *et al* (2007). Gilts low heritability of KZDP of $h^2 = 0,140$ at the end of test determined by means of REML method was found in the studies by: MALOVRH and KOVAČ (1999) ranking this trait into the group of low heritability traits. The values of the heritability coefficients for KSL and KPM of $h^2 = 0.356$ and $h^2 = 0.349$, respectively, put these traits into the group of mean heritability traits, while BRKIĆ *et al* (2001) determined a high heritability of these traits. URANKAR *et al* (2012) and IMBOONTA *et al* (2007) determined a mean heritability of these traits in their studies.

On the basis of analyse determined parametres a few selection indexes have been constructed in which, on the basis of the value of correlation coefficents of selection indices and aggregate genotype on one hand, and selection strategy on the other, the best equation in selection index for breeding value estimation in performance tested gilts was chosen. Table 4 shows the equations in selection indices and the correlation coefficient of index and aggregate genotype (r_{IAG}).

Table 4. Selection indices equations and coefficients of correlation - r_{IAG} of selection index and aggregate genotype

Selection index-SI	r_{IAG}
$SI_1 = -0.622^a (x_1 - 61.08) - 0.851^b (x_2 - 9.77) + 0.029^c (x_3 - 408.93)$	0.594
$SI_2 = -0.086^a (x_1 - 61.08) - 1.608^b (x_2 - 9.77)$	0.596
$SI_3 = 0.314^a (x_1 - 61.08) + 0.032^c (x_3 - 408.93)$	0.517
$SI_4 = 2.222^b (x_2 - 9.77) + 0.034^c (x_3 - 408.93)$	0.590

[a] – values of partial regression coefficients for KPM, [b] – values of partial regression coefficients for KSL, [c] – values of partial regression coefficients for KZDP, x_i – traits phenotypic values of each individual.

The accuracy of constructed selection indices measured by the coefficients of correlation r_{IAG} ranged in the interval of $r_{IAG} = 0.517$ in the index 3, to $r_{IAG} = 0.596$ in the index 2. The approximate values of correlation coefficients of different indices allow for the possibility to choose the selection indexes which include a greater number of traits of equal importance in

the trials with undiminished accuracy of estimated breeding performance in individuals. In line with all this the most optimal selection index for estimation of gilts breeding value in fertile swine breeds and their cross-breds, the SI_1, which includes three traits, namely KPM, KSL and KZDP, was chosen.

Comparing the values of correlation coefficients of selection index and aggregate genotype with the research conducted by BRKIĆ (2002) in which he constructed selection indexes for the growth rate and carcass quality traits in performance tested gilts of fertile breeds and their cross-breds where the correlation coefficients were in the range of $r_{IAG} = 0.329$ to $r_{IAG} = 0.821$, it can be observed that the values of the coefficients obtained in this research are somewhere towards the mean values obtained by the mentioned author. Also the author determined that the greatest accuracy had a selection index which includes five following traits: age at the end of test, daily liveweight gain, two values of backfat thickness and carcass meat percentage. KRALIK *et al* (2007) report that the assessment of breeding value in fertile breed boars at the end of test is determined by the method of selection indexes which include the traits such as daily liveweight gain, backfat thickness and feed conversion. Selection index devised by SUZUKI *et al* (2005) for gilts and boars of the Duroc population in Japan includes the traits such as daily liveweight gain, backfat thickness, meat percentage and content of intramuscular fat.

Observing the traits on whose basis the breeding value is estimated not only in gilts but in the boars of fertile meaty and exceptionally meaty breeds as well, it can be concluded that a primary place in the assessment of swine breeding value goes to the daily liveweight gain and backfat thickness, regardless of whether the assessment was performed by means of selection index or by some other methodological procedure. What certainly favours this methodological procedure in relation to some others is its possibility to be used when there is no enough information on the origin, and that the construction of selection index is relatively fast and simple what are essential factors which influence the assessment of animal breeding performance when the pig production in Serbia and in the region is in question.

CONCLUSION

On the basis of all said it can be concluded that gilt`s genotype, year and season of birth did not statistically significantly affected KZDP, KSL and KPM while the gilt`s sire displayed statistically highly significant effect on all tested traits.

Heritability coefficients for KZDP, KSL and KPM were in the interval of $h^2 = 0.255$ to $h^2 = 0.356$ ranking these traits in the group of mean heritability traits.

Four selection indexes have been constructed among which as the most optimal one for the assessment of breeding value has been chosen the one which includes all three tested traits (KZDP, KSL and KPM). The accuracy of this chosen selection index estimated by the index correlation coefficient and aggregate genotype was $r_{IAG} = 0.594$.

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PROCENA GENETSKOG POTENCIJALA PERFORMANS TESTIRANIH NAZIMICA METODOM SELEKCIJSKIH INDEKSA

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Izvod

Cilj rada bio je da se proceni priplodana vrednost performans testiranih nazimica rase švedski landras i F_1 meleza švedskog landrasa i velikog jorkšira metodom selekcijskog indeksa. Osobine na osnovu kojih je procenjena priplodna vrednost grla su: životni dnevni prirast, prosečna debljine leđne slanine izmerena na dva mesta i procenat mesa u trupu. Ove osobine su korigovane na telesnu masu od 100kg, metodom baznih indeksa i utvrđne sledeće vrednosti: korigovani životni dnevni prirast (KZDP) 408.93g/dan, korigovana prosečna debljine leđne slanine izmerena na dva mesta (KSL) 9.77mm i korigovani procenat mesa u trupu (KPM) 61.08%. Ispitujući uticaj genotipa, godine i sezone rođenja nazimica nije ustanovljeno statistički značajno variranje (P>0.05) ovih osobina izazvano navedenim faktorima, dok je otac nazimice statistički visoko značajno (P<0.001) uticao na sve ispitivane osobine. Koeficijenti heritabiliteta su iznosili: h^2= 0.255 za KZDP, h^2= 0.356 za KSL i h^2=0.349 za KPM. Konstruisane su četiri jednačine selekcijskih indeksa od kojih je kao najoptimalnija izabrana ona koja uključuje sve tri osobine (KZDP, KSL I KPM) i čiji je koeficijent korelacije selekcijskog indeksa i agregatnog genotipa iznosio r_{IAG} = 0.594.