

Partition of genetic trend for daily gain by sex in Landrace, Large White, Pietrain, and Duroc pigs

Particija genetskog trenda za dnevni prirast u svinja pasmina landras, veliki jorkšir, pietren i durok

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Abstract

The objective of this study was to analyse the efficiency of genetic improvement of pigs for average daily gain (ADG) in a conventional pig breeding programme in Croatia for Landrace (L), Large White (LW), Pietrain (P), and Duroc (D) breeds. Phenotype data was available for 30,210 L pigs, 11,657 LW pigs, 3,653 P pigs, and 549 D pigs born between 1998 and 2017. Pedigree information contained information about sex of each animal. This information was used to partition genetic trends by sex. Breeding values were estimated using animal model. The estimated genetic trends in L and P breeds were favourable and different from zero at the end of the analysed period. The genetic trend did not show remarkable improvement in analysed period in LW and D breeds. The relative contribution of male animals was 57% in L, 51% in LW, 70% in P, and 50% in D breed. The analyses suggest that breeding activities and selection decisions involving the choice of the animals should be re-evaluated in LW and D breeds.

Keywords: average daily gain, genetic trend, partition, pigs, sex

Sažetak

Cilj rada bio je analizirati učinkovitost selekcije nerastića i nazimica u konvencionalnom uzgojnom programu za svinje pasmina landras, veliki jorkšir, pietren i durok za svojstvo prosječni dnevni prirast. Fenotipski podaci za 30 210 svinja pasmine Landras, 11 657 svinja pasmine veliki jorkšir, 3 653 svinja pasmine pietren i 549 svinja pasmine durok rođenih između 1998. i 2017. Porijeklo je sadržavalo informaciju o spolu svake životinje koja je iskorištena za particiju genetskog trenda prema spolu. Uzgojne vrijednosti procijenjene su modelom životinje. Procijenjeni genetski trendovi u svinja pasmina landras i pietren bili pozitivni prema kraju analiziranog razdoblja. Genetski trendovi nisu pokazali značajan napredak u analiziranom razdoblju u pasmina veliki jorkšir i pietren. Relativni doprinos muških životinja ukupnom genetskom trendu bio je 57% u pasmine landras,

51% u pasmine veliki jorkšir, 70% u pasmine pietren i 50% u pasmine durok. Rezultati analize upućuju na potrebu provjere selekcijskih odluka u pasmina veliki jorkšir i pietren.

Ključne riječi: genetski trend, particija, prosječni dnevni prirast, spol, svinje

Introduction

Genetic improvement of livestock is primarily based on identification of animals with superior genetic value in a population and their use as parents of next generation. In many pig breeding programmes, the standard pedigree-based evaluation, i.e., best linear unbiased prediction (BLUP), (Henderson, 1973; Henderson, 1984) is still the method used for estimation of genetic merit of animals. Application of this method enables comparison of genetic values of animals of different breeds and sexes and from different environments (herds, e.g.). Due to its advantages over other selection methods, BLUP is still method of the choice, as main method for the selection of the pigs or integrated with genomic selection procedures. The application of the animal models within BLUP procedure in pig selection enabled faster genetic improvement, enabling effective selection of animals of both sexes. However, the effect of chosen male animals is normally stronger when genetic improvement is obtained due to higher number of their offspring during life time. Thus, selecting boars might significantly affect the genetic improvement in positive or negative way. The more offspring from a superior boar, the faster the population average for the trait improves. The original sire gets knocked out of the elite group, is culled and replaced by a higher ranked young boar from the now improved general population (Robinson and Burr, 2005).

The success of the selection for desired trait is consequence of selection decisions made. García-Cortés et al. (2008) proposed a simple but powerful method for partition of genetic trends, enabling evaluation of selection policies. This type of analysis allows evaluating each of the single parts of the selection scheme, and the effectiveness of the different selection decisions. This is especially important when genetic improvement is based on imported germplasm, when foreign data is often not available in sufficient amounts or easy to integrate into domestic evaluations, although methodology for such integrations exists (e.g., Vandenplas and Gengler, 2012; Škorput et al., 2015). This method could also be applied to validate selection decisions involving the selection of young boars and gilts for economically important traits. Thus, the application of the method might be helpful for breeding organisations and subjects involved into making selection decisions, enabling more effective and dynamic adoption of breeding programmes.

The aim of the paper was to partition genetic trend for average daily gain (ADG) by sexes in four pure breeds and to evaluate effectiveness of breeding activities involving selection of young boars and gilts.

Materials and methods

Data for average ADG were available for 46,211 pigs from field test of young boars and gilts within Croatian breeding programme. Data records were provided by Croatian Agricultural Agency. Following breeds and crossbreeds were included in the study: Landrace (L), Large White (LW), Duroc (D), Pietrain (P) (Table 1). After data checking for illogical values 46,069 data records remained in the analysis (Table 1).

Table 1. Descriptive statistics for average daily gain

Breed	N (males)	N (females)	N	Mean	Standard deviation
Landrace	4,524	25,686	30,210	520.87	69.53
Large White	1,187	10,470	11,657	504.32	58.21
Pietrain	1,663	1,990	3,653	517.37	73.29
Duroc	146	403	549	570.93	75.26
Total	7,520	38,549	46,069	517	67.87

A pedigree was available with 31,136 L, 15,141 LW, 5,054 P, and 1,141 D and animals including information about the sex of animals (Table 2). The completeness of pedigree was different within breeds. The lowest proportion of ancestors within pedigree was in L breed (2%) while the highest proportion of ancestors was found in D breed (48%). The highest proportion of base animals was found in D (35%), while the lowest number of base animals was observed in P breed (4%). Differences were also observed in number of animals per sires: the lowest number of animals per sire was found in P breed, while LW had the highest proportion of animals per sire.

Table 2. Pedigree structure within breeds

Breed	Total number of evaluated animals	No. of animals with records	No. of ancestors	No. of base animals	No. of sires	No. of animals per sire
L	31,136	30,210	926	1,938	1,559	17.18
LW	15,141	11,657	3,484	925	678	22.33
P	5,054	3,653	1,401	205	176	6.48
D	1,141	549	592	399	513	9.85

ADG was analysed by the standard pedigree based linear mixed model, where y_i is the vector of observations for the i -th trait, the fixed effects were herd-year-month of test and sex (\mathbf{b}_i) and random effects were common litter environment (\mathbf{w}_i) and additive genetic effect \mathbf{a}_i with the corresponding incidence matrices \mathbf{X}_i , $\mathbf{Z}_{w,i}$, and $\mathbf{Z}_{a,i}$.

Residual maximum likelihood method implemented in VCE 6 software (Groeneveld et al., 2008) was applied to estimate variance and covariance components. Breeding values were estimated using the same model as for variance components. Genetic trends for ADG were estimated using the breeding values of all pigs in the pedigree file for each breed separately. Breeding values, and therefore the genetic trends were expressed in units of estimated additive genetic variance specific for each breed to facilitate comparisons.

Breeding values ($\hat{\mathbf{a}}$) were decomposed by the sex, i.e., contribution of the selection of sires and the contribution of the selection of dams within breeding programme. For animal model the core equation is:

$$a_i = 1/2 a_{s(i)} + 1/2 a_{d(i)} + w_i \quad (1)$$

where a_i , $a_{s(i)}$, $a_{d(i)}$ are breeding values of individual animal and their parents, respectively, while w_i is individuals' deviation from parent average, i.e., the Mendelian sampling term. For base population members $a_i = w_i$. In matrix notation (1) can be written as:

$$\mathbf{a} = \mathbf{T} * \mathbf{w} \quad (2)$$

where \mathbf{T} describes flow of genes through pedigree (e.g., Henderson, 1973; Woolliams et al., 1999). Equation (2) shows that breeding values are a linear combination of Mendelian sampling terms and that the same equation can be used also for predictors of \mathbf{w} , i.e.,

$$\hat{\mathbf{a}} = \mathbf{T} * \hat{\mathbf{w}} \quad (3)$$

García-Cortés et al. (2008) proposed to define a set of k partitions, such that:

$$\mathbf{P}_1 + \mathbf{P}_2 + \mathbf{P}_3 + \dots + \mathbf{P}_k = \mathbf{I} \quad (4)$$

Using (4) and the fact that $\mathbf{w} = \mathbf{T}^{-1} * \mathbf{a}$ they wrote (3) as:

$$\begin{aligned} \hat{\mathbf{a}} &= \mathbf{T} * \mathbf{P}_1 * \mathbf{T}^{-1} * \hat{\mathbf{a}} + \dots + \mathbf{T} * \mathbf{P}_k * \mathbf{T}^{-1} * \hat{\mathbf{a}} \\ &= \hat{\mathbf{a}}_1 + \hat{\mathbf{a}}_2 + \hat{\mathbf{a}}_k, \end{aligned} \quad (5)$$

where $\hat{\mathbf{a}}_i$ are partitions of $\hat{\mathbf{a}}$ according to the definition of (4). These partitions can be summarized separately to obtain the partitioning of total genetic trend. After obtaining $\hat{\mathbf{a}}$ from the routine genetic evaluation, the computation of (3) involves only computation of inferred Mendelian sampling terms ($\hat{\mathbf{w}}$) and dropping $\hat{\mathbf{w}}$ through pedigree according to (2). This was implemented this in the R package partAGV, which eases the computation and presentation of results. Finally, average relative contribution of each sex to the total genetic trend was evaluated by summarizing partitions divided by the estimates of the total genetic trend.

Results and discussion

Genetic parameters

Components of the variance were obtained for every breed in the analysis (Table 3). Estimation of genetic parameters showed that values of the heritability (h^2) were moderate. The highest h^2 was found in P breed, while the lowest values were observed in D breed. Numerous studies provided variance components for growth rate in pigs. Hoque and Suzuki (2008) provided estimates of genetic parameters for daily gain on the population of L and D with values of h^2 of 0.38 and 0.47, respectively. Similar results were obtained for the same trait in L and D breeds by Gjerlaug et al. (2012) with values of h^2 for daily gain of 0.41 and 0.42. Kiszlinger et al. (2011) found lower heritability (0.2) for daily gain than obtained in this study for P breed. Krupa and Wolf (2013) found relatively low heritability of ADG for LW breed of 0.2.

Table 3. Variance components and ratios to phenotypic variance for daily gain

Breed	$V_l \pm SE$	$V_a \pm SE$	$V_e \pm SE$	$V_{ph} \pm SE$
Landrace	712.77±22.22	1,021.01±0.02	667.84±0.01	2,401.62
Large White	474.29±28.19	586.09±55.73	860.31±33.76	1,920.71
Pietrain	896.1±79.5	1,190.03±139	488.926±73.06	2,575.06
Duroc	1,554.82±335.06	588.53±586.14	834.78±301.39	2,978.14
	$l^2 \pm SE$	$h^2 \pm SE$	$e^2 \pm SE$	
Landrace	0.3±0.09	0.43±0.02	0.28±0.01	
Large White	0.25±0.01	0.3±0.03	0.45±0.02	
Pietrain	0.35±0.03	0.46±0.04	0.2±0.03	
Duroc	0.52±0.09	0.2±0.19	0.28±0.11	

V_l -variance of common litter environmental effect; V_a -direct additive genetic variance; h^2 -heritability; V_e -residual error variance

Partition of genetic trends for daily gain

Overall genetic trend for ADG in L breed was favourable and was increasing until 2015 (Figure 1). After 2015 genetic trend started to decrease. This decrease might be consequence of lower number of tested animals in recent years within breeding programme. Testing small number of animals brings a risk of unfavourable selection decisions and reduces the choice of superior animals. In such situation, genetic improvement is dependent on small number of tested animals and import of foreign germplasm. Possibility of unfavourable selection decisions then increases, especially when new boars are introduced into population.

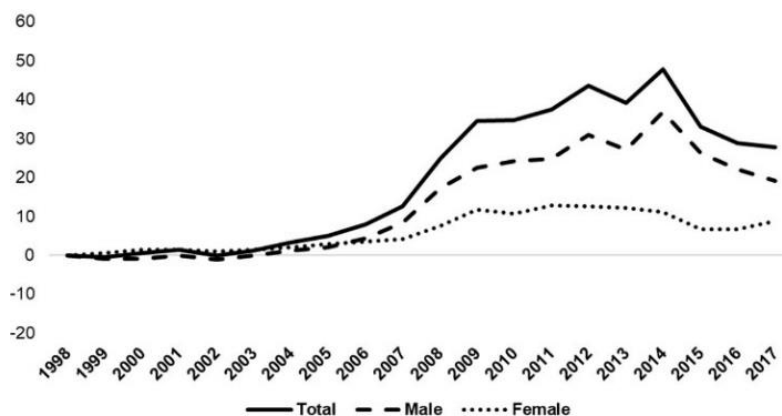


Figure 1. Partition of genetic trend for daily gain by sex in Landrace breed

Analysis of relative contributions showed that average contribution of selected males was 57% to a total genetic trend, while the relative contribution of dams was 43%. The selection intensity in the breeding programme for young boars and gilts is the same: 15% of the animals with the highest rank according to index is chosen for nucleus herds. Normally, the phenotypic expression is higher for young boars, which results in higher breeding values for young boars.

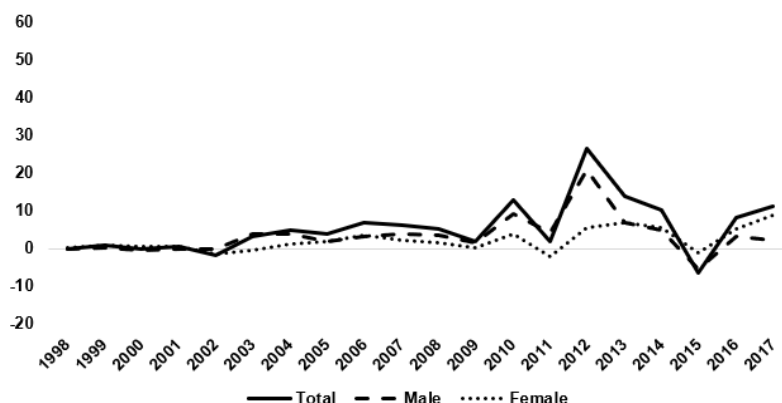


Figure 2. Partition of genetic trend for daily gain by sex in Large White breed

The genetic trend for daily gain in LW breed was unfavourable and no significant increase in analysed trait is observed in analysed period (Figure 2). After 2012 there is strong decrease in the genetic trend of analysed trait. The analysis of the relative contribution of male and female contribution to a total genetic trend shows that in 2012 contribution of the boars was 79% and strong decrease in the genetic trend can be attributed to a choice of a boars with lower genetic values. Such scenario is described by Robinson and Burr (2005). Moreover, the lack of the positive and favorable genetic trend was also induced by the low genetic and total phenotypic variance for ADG in LW breed. By the application of the method for partition of genetic trends, it is possible to conduct further analysis of genetic trend for LW breed

and to detect error in selection, such as time (year) when selection was conducted and to identify animals which contributed to the genetic trend in negative way.

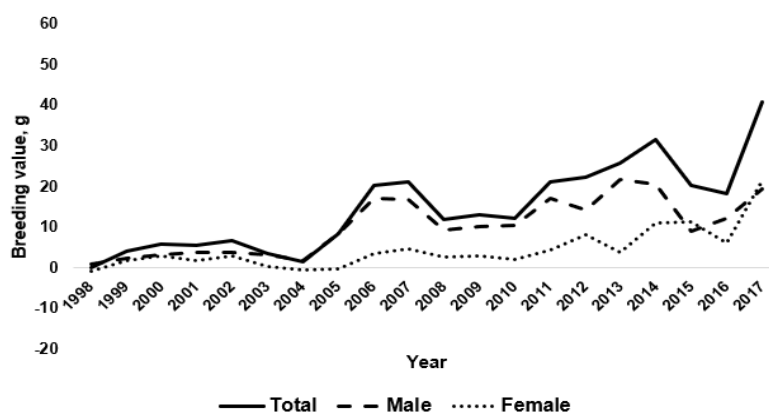


Figure 3. Partition of genetic trend for daily gain by sex in Pietrain breed

Favourable genetic trend for daily gain was observed in Pietrain breed. The increase is remarkable from 2005, which can be linked to the period of introducing BLUP in pig breeding in Croatia (Vincek et al., 2004). The contribution of sire partition is strong (Table 4) and sires are carriers of genetic improvement. Favourable genetic trend is also observed in dam partition, resulting in positive total genetic trend. Positive selection results for ADG might be also attributed to high additive genetic variance for P breed. In particular breeding programme Pietrain is used as terminal sire line. Terminal (paternal) lines are selected in nucleus herds and then multiplied to compose parental stock used by pork producers to produce crossbred commercial pigs (Dekkers, 2007). Thus, genetic improvement should result in more efficient production of fatteners as the final product of pigs in breeding programme.

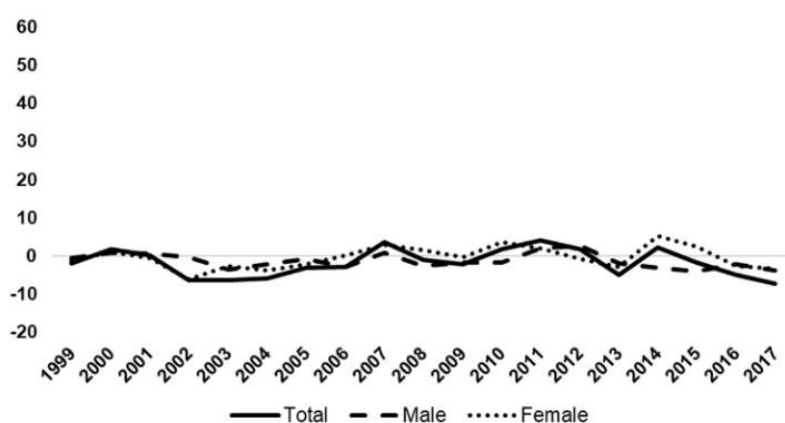


Figure 4. Partition of genetic trend for daily gain by sex in Duroc breed

There was no improvement in genetic trend when D breed was considered. Average contributions of the male and female component were equal in the analysed period.

This is due to small number of animals with records and unfavourable pedigree structure. Moreover, poor selection effects might be attributed to low genetic variability in this breed. However, the total phenotypic variance observed in D breed was high, implying the strong effect of environmental effects. In order to improve genetic gain in D breed, it is necessary to enlarge an amount of information from tested animals and to improve quality of the testing procedure and pedigree. Also, it should be considered that tested animals of D breed already had a higher phenotypic expression of the analysed trait than the other tested breeds, and further genetic improvement becomes more demanding.

Table 4. Average contributions (%) to genetic trend by sex

Breed	Male	Female
Landrace	57	43
Large White	51	49
Pietrain	70	30
Duroc	50	50

Other studies dealing with decomposition of the genetic trends by source of variation in pigs, including sex of the selected animals are scarce. A few studies included decomposition of the genetic trends by breeds (Nagy et al., 2012) or origin (Škorput et al., 2015). Torres Filho et al. (2005) summarized breeding values according to sex in LW breed, where authors noticed significantly higher estimates of genetic trend in males compared to females in the analyzed pedigree.

To improve genetic potential in breeds where genetic trends in analysed periods are unfavourable, revision of selection decisions is needed. Introduction of germplasm with high genetic values is highly recommended to make further genetic progress. In LW and D partition of the boars did not show significant improvement. This is especially visible in D breed, where sire partition contributed with average of 50%, but did not show improvement in genetic values for daily gain. The average contribution of the sire component in LW breed was also lower than in breeds that showed favourable genetic trends. Further partitions of genetic trends can be used to pinpoint, which breeding activities need most attention, such as contribution of different breeders and insemination centres.

Conclusion

The application of the method for the partition of the genetic trends for analysed trait could help in defining selection decisions which contribute to the direction and the magnitude of the genetic trend. Genetic trends for L and P breed were positive and favourable during analysed period. On the contrary, genetic trends for LW and D breeds did not show positive and favourable trend in the analysed period. In L and P

breed the contribution of the selected males was stronger than the contribution of the selected females. In LW and D breed there was almost equal contribution of males and females selected. Further analysis is recommended in order to re-evaluate selection decisions and to improve genetic trends in analysed trait.

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