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Poljoprivreda/Agriculture

ISSN: 1848-8080 (Online)
ISSN: 1330-7142 (Print)

http://dx.doi.org/10.18047/poljo.21.1.sup.19

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Faculty of Agriculture in Osijek, Agricultural Institute Osijek

ISSN 1330-7142
UDK: 639.111.14:636.08
DOI: 10.18047/poljo.21.1.sup.19

THE CONTRIBUTION OF SOCIAL GROUP EFFECT TO VARIATION IN BOARS GROWTH

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Original scientific paper

SUMMARY

The aim of the study was to estimate the contribution of group to phenotypic variance of daily gain on different intervals. The focus was on data structure and differences of variance components estimated with and without effect of the social group. Growth of 806 boars from 443 litters was obtained during the field test in nucleus herd of Pietrain breed. A group was defined as pen mates. Most frequently, the group was formed from 6 and 7 boars. Data sets were prepared with SAS Software, variance components were estimated using VCE-6. The results showed the significant contribution of the group to phenotypic variance of daily gain. Inclusion of the effect of social group reflected in lower heritability and the smaller contribution of common litter environment. Further analysis revealed different contributions of components to phenotypic variance of growth rate on different intervals. The proportion of variation caused by common litter environment was larger on the interval from ±32.0 kg to ±48.8 kg of body weight (22%), compared to interval from ±39.6 kg to ±104.1 kg, explaining 1% of phenotypic variation, that could be the consequence of less defined pretest environment. The social group explained 6% of phenotypic variance for daily gain on interval from ±39.6 kg to ±104.1 kg of body weight, however, the contribution was larger on the interval from ±32.0 kg to ±48.8 kg (23%). The results confirmed the group as an environmental component, causing more variation in daily gain shortly after group formation (±32.0 kg), when a hierarchy is established, and later after its set, the contribution decreases.

Key-words: pigs, genetic evaluation, daily gain, social interaction, group effect

INTRODUCTION

Pigs show several social behaviours such as cooperation, altruism, and aggression. A tendency to establish a social hierarchy often leads to aggressiveness in a group. In limited resources, pigs also compete for food and other limited resources. Traits underlying these behaviours are influenced by interactions between pen mates.

Social environment of an individual is reflected also in its production level and welfare. However, phenotype of an individual is not only affected by its own genes, but also by the genes of pen mates present in individual's social environment (Griffing, 1967; Bijma et al., 2007).

Social environmental effect has biological origin and contributes the heritable variation, in animal breeding known as associative effect or social effect (Griffing, 1967; Muir, 2005; Bijma et al., 2007). Due to its potential for improving performance and animal welfare, models for implementation of social effect in a genetic evaluation were developed. Estimability of social genetic effect depends on effects included in the model, especially on implementation of group effect (Van Vleck and Cassady, 2005; Chen et al., 2008). Bergsma et al. (2008) showed that group effect included as random effect take into account nonheritable social effects to avoid overestimated social genetic variance. Bergsma et al. (2008) also reports covariances among pen mates expressed as genetic variance when pen effects are omitted from the model, due to the relatedness among pen mates. Thus, heritability decreased after inclusion of group effect.

The aim of study was to estimate the contribution of the group to phenotypic variance of daily gain on different intervals. The focus was on data structure and differences in estimates of variance components after including effect of the group.

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MATERIAL AND METHODS

Data of boar's performance was obtained from field test in nucleus herd of Pietrain breed. Performance test and genetic evaluation were conducted in accordance with national breeding program SloHibrid (Kovač and Malovrh, 2012). Boars that finished field test in April 2006 to August 2014, were included in the analysis. Total of 806 boars from 443 litters were considered. The group was defined as the group of pen mates. For the purpose of performance test, 8 pens are available. The surface area of the 6 pens is 7.92 m^2 and 10.06 m^2 of the other two. The group size varied between 2 and 12 individuals, 82% of groups sized of 5 to 8 boars. Preliminary analysis showed no effect of pen size or stocking density on growth and backfat thickness. The majority of groups consisted of boars originated from 3 to 4 litters.

Daily gain (DG) on several intervals up to 100 kg was analyzed (Table 1). Weighing in different stages revealed a large variability of animal's age and weight. Average DG from birth to the beginning of test ranged from 227 to 498 g/day. At the beginning of the test, the oldest boars were more than twice older than the youngest. The differences in the DG from the 1st weighing to the end of test ranged up to 690 g/day. The average relatedness within pen was 0.30, ranged from 0.151 to 0.524. The groups differed also in surface area per animal. On the average, twice as minimal required surface was provided per boars.

Table 1. Descriptive statistics

Variable		N	$\bar{x}$	σ	min	max
At the beginning of test	Weight (kg)	806	32.0	3.9	21.5	45.0
	Age (days)	806	83.5	7.1	48	109
At 1st weighing	Weight (kg)	806	39.6	4.7	26.0	56.0
	Age (days)	806	97.6	7.0	77.0	123.0
At 2nd weighing	Weight (kg)	806	48.8	5.7	35.0	69.0
	Age (days)	806	111.6	7.1	91	138
End of the test	Weight	806	104.1	9.6	80.0	136.0
	Age (days)	806	182.2	10.7	147.0	222.0
	Backfat (mm)	793	8.0	1.3	4.7	12.3
Daily gain (g/day)	Birth to the beginning of test	806	361.5	42.3	227	498
	Beginning to 2nd weighing	806	602.0	129.2	74	1222
	From 1st weighing to end	806	765.7	110.3	439	1129
	From birth to end	806	571.8	59.6	385.0	768.4
Average group relatedness		133	0.304	0.078	0.151	0.524
Surface area (m^2/animal)		806	1.41	/	0.7	4.0

N –number of observations; σ – standard deviation; $\bar{x}$ - mean; min – minimum; max – maximum

Two datasets were prepared. **Dataset 1** consisted of performance data at the end of the field test (weight and backfat thickness at the last two weighing). DG from birth to the end of test and backfat (BF) was analyzed. Fixed part of the statistical model included season as month-year interaction, model for BF consisted of effect of weight at BF measured as covariate. Common litter, direct additive genetic, permanent environment were treated as random effects. Permanent environment effect was used due to repeated measures of an animal.

(Co)variance components were estimated with two-trait repeatability model (eq. 1). Models were used (written in matrix notation):

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Z}_c\mathbf{c} + \mathbf{Z}_a\mathbf{a} + \mathbf{Z}_p\mathbf{p} + \mathbf{e} \quad (1)$$

where **y** is the vector of observations. Unknown parameters for fixed effects are presented in vector **β** with incidence matrix **X.** Vectors **c, a** and **p** with incidence matrix $\mathbf{Z_c}$, $\mathbf{Z_a}$ and $\mathbf{Z_p}$ present common litter effect, direct additive genetic effect, permanent environment effect, respectively, **e** is vector of residual. To estimate the contribution of group to phenotypic variance, the group was added as random effect (equation 2).

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Z}_c\mathbf{c} + \mathbf{Z}_a\mathbf{a} + \mathbf{Z}_g\mathbf{g} + \mathbf{Z}_p\mathbf{p} + \mathbf{e} \quad (2)$$

where **g** is a vector of random group effect and $\mathbf{Z_g}$ incidence matrix. It was assumed that random effects and residual follow normal distribution:

$$\mathbf{c} \sim N\left(\mathbf{0}, \mathbf{I}_c\sigma_c^2\right),\ \mathbf{a} \sim N\left(\mathbf{0}, \mathbf{A}\sigma_A^2\right),\ \mathbf{g} \sim N\left(\mathbf{0}, \mathbf{I}_g\sigma_g^2\right),$$
$$\mathbf{p} \sim N\left(\mathbf{0}, \mathbf{I}_p\sigma_p^2\right),\quad e \sim N\left(\mathbf{0}, \mathbf{I}_e\sigma_e^2\right) \quad (3)$$

where $\mathbf{I_c}$, $\mathbf{I_g}$, $\mathbf{I_p}$, $\mathbf{I_e}$ are identity matrices of the appropriate dimensions, and **A** is a relationship matrix.

Dataset 2 was used to obtain the contribution of the social group to phenotypic variance of DG on different intervals. Following traits were analyzed: daily gain (DG_1) from the beginning of the test (±32.0 kg) to 2nd weighing (±48.8 kg), daily gain (DG_2) from 1st weighing (±39.6) to the test end (±104.1 kg) and BF thickness at the last weighing. Permanent environment effect was omitted from the model 1 and 2 (equation 1, 2) as one measure for an animal was observed. Three-trait model was used.

Fixed part of model was developed with SAS 9.3 (SAS Inst. Inc., 2011). Covariance components were estimated by the residual likelihood method (REML) using statistical package VCE-6 (Groeneveld et al., 2010).

RESULTS AND DISCUSSION

Heritability estimates for DG (dataset 1) from the first model 1 was 61% (Table 1), being higher than the heritability, usually estimated in commercial breeding farms (Clutter and Brascamp, 1998). The common litter environment contributed 14% and permanent environment accounted for 5% of phenotypic variance. Heritability for BF was 55%, which is in line with the literature (Clutter and Brascamp, 1998), larger contribution of unexplained variance could be the result of feeding *ad libitum*. After including group effect in the model for DG (15% variance), heritability dropped from 61% to 55% for DG, and common litter variance from 14% to 8%, indicating a partial additive genetic effect due to relatedness between pen mates (Bergsma et al., 2008). The group did not cause the variation in BF.

Table 2. Ratios for variance components (bold) and corresponding correlations between traits (italic) with standard errors estimated with both models in dataset 1

Variance component	Model 1		Model 2	
	Daily gain	BF	Daily gain	BF
Common litter environment	**0.14**±0.04	*-0.14±0.34* **0.04**±0.04	**0.08**±0.03	*0.25±0.61* **0.02**±0.03
Direct additive genetic effect	**0.61**±0.08	*-0.01±0.15* **0.55**±0.10	**0.55**±0.09	*-0.04±0.15* **0.53**±0.09
Group effect	/	/ /	**0.15**±0.02	*-0.79±0.30* **0.05**±0.03
Permanent environment	**0.05**±0.06	*-0.29±0.61* **0.14**±0.08	**0.05**±0.05	*-0.15±0.57* **0.13**±0.07
Residual	**0.20**±0.02	*-0.33±0.06* **0.28**±0.02	**0.18**±0.01	*-0.33±0.06* **0.27**±0.02

Daily gain - from the birth to the test end (±104.1 kg); BF- backfat thickness

Results of dataset 2 revealed varied contributions of variance components for DG on different intervals of body weight (dataset 2; Table 3). Heritability for DG was low (8%) on the interval from ±32.0 kg to ±48.8 kg of body weight and high (82%) on interval from ±39.6 kg to ±104.1 kg, indicating the majority of variation originated from genetic differences among tested animals. Low heritability in the first interval and correlation of breeding values for DG in these two intervals (0.57) revealed that selection in early stages could not be performed. The proportion of variation caused by common litter environment was 36% in the interval from ±32.0 kg to ±48.8 kg of body weight, and accounted 4% in the interval ±39.6 kg to ±104.1 kg. Substantial proportion in the first interval could be explained by varied lactation length and less defined pretest environment.

The results from model 2 revealed the significant variance for the group effect (Table 3). The group effect contributed 6% of phenotypic variation of DG on the interval from ±39.6 kg to ±104.1 kg whereas the contribution was larger in the interval from ±32.0 kg to ±48.8 kg (23%). Bergsma *et al*. (2008) reported group contributed 27% of phenotypic variance in DG from ±27.0 kg to finishing. Our results revealed group causing more variation in DG shortly after group formation (±32.0 kg), when a hierarchy is established, and later after its set, the contribution decreases.

Table 3. Ratios for variance components (bold) and corresponding correlations between traits (italic) with standard errors estimated with both models in dataset 2

Variance component	Model 1			Model 2		
	DG_1	DG_2	BF	DG_1	DG_2	BF
Common litter environment	**0.36**±0.05	*0.18±0.31* **0.04**±0.03	*0.40±0.34* *-0.20±0.78* **0.05**±0.05	**0.22**±0.05	*0.58±0.43* **0.01**±0.02	*0.44±0.32* *-0.47±0.57* **0.05**±0.04
Direct additive genetic effect	**0.08**±0.05	*0.57±0.35* **0.82**±0.08	*0.03±0.34* *0.03±0.14* **0.63**±0.10	**0.05**±0.03	*0.67±0.34* **0.76**±0.06	*-0.16±0.39* *0.06±0.14* **0.61**±0.07
Group effect	/	/ / /	/ / /	**0.23**±0.05	*-0.19±0.27* **0.06**±0.03	*0.66±0.87* *0.61±0.94* **0.00**±0.00
Residual	**0.56**±0.05	*-0.07±0.20* **0.15**±0.08	*-0.10±0.13* *0.12±0.27* **0.32**±0.10	**0.49**±0.05	*-0.06±0.16* **0.17**±0.08	*-0.06±0.11* *0.05±0.21* **0.33**±0.07

DG_1 – daily gain from the beginning of the test (±32.0 kg) to 2nd weighing (±48.8 kg); DG_2 -from 1st weighing (±39.6 kg) to the test end (±104.1 kg); BF- backfat thickness

CONCLUSION

Contributions of components to phenotypic variance of DG and BF were estimated. Heritability for DG was low on the first interval (±32.0 kg to ±48.8 kg) and high on the interval ±39.6 kg to ±104 kg. It indicates that selection in early stages could not be performed. The proportion of variance caused by common litter environment was larger on the interval from ±32.0 kg to ±48.8 kg of body weight (22%), compared to interval from ±39.6 kg to ±104.1 kg, explaining 1% of phenotypic variation. The group explained 6% of phenotypic variance of daily gain on interval from ±39.6 kg to ±104 kg of body weight. However, the contribution was larger on the interval from ±32.0 kg to ±48.8 kg (23%). The group effect caused more variation in DG shortly after group formation (±32.0 kg), when a hierarchy is established, and later after its set, the contribution decreases.

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(Received on 11 May 2015; accepted on 6 July 2015)