

Comparison Between Direct and Competitive Models to Investigate Variation of Carcass and Ham Quality Traits in Heavy Pigs

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Summary

Social interactions among animals raised in pens can affect their performance. In this study direct and competitive models were compared to investigate the influence of social genetic effects on variation of carcass weight (CW), carcass lean meat content (LM) and ham round shape (RS) in heavy pigs. Four sequential models including, in addition to sex and slaughter group fixed effects, the random effects of the social group, litter (full-sibs family), direct and social genetic effects of pigs were evaluated. Social group and litter effects accounted for about 4 and 3% of the phenotypic variance, respectively. When social genetic effects were added to model, a small social heritability was estimated for all traits (from 0.3 to 0.7% of the phenotypic variance). A negative correlation between direct and social effects was estimated for LM and RS, reducing the total heritable variance available for selection. Model comparison showed that the best fit was provided by the model including only direct additive genetic effects of pigs. So, this model seems still preferable for the genetic evaluation of the investigated traits.

Key words

social effects, heavy pigs, ham traits

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Aim

Performance of animals raised in groups may be affected by social interactions. The influence of the individual genotype of an animal on the phenotype of its group mates is called social genetic effect (defined also as heritable social effect, associative effect, competitive effect, indirect genetic effect) (Griffing, 1967; Muir, 2005; Bijma et al., 2007a). If present, heritable social effects may increase the total heritable variance (T^2 ; Bergsma et al., 2008) and affect the response to selection (Bijma et al., 2007a; Bijma et al., 2007b). In contrast with classical animal models, competitive models (Arango et al., 2005) incorporate both direct genetic effect (the influence of the individual genotype on the individual phenotype) and social genetic effects. Mixed models incorporating heritable social effects have been applied in light pigs to estimate the influence of social genetic effects on average daily gain (Arango et al., 2005; Chen et al., 2008; Chen et al., 2009; Bowman et al., 2010), backfat and muscle depth (Bergsma et al., 2008; Hsu et al., 2010) and androstenone fat content (Duijvesteijn et al., 2012).

The aim of this study was to compare direct and competitive models to investigate the contribution of social genetic effects on variation of carcass weight, carcass lean meat content and ham round shape in Italian heavy pigs (in contrast to light pigs they are slaughtered at about 160 kg and fed in restricted conditions).

Material and methods

Phenotypic records used in this study were from crossbred Goland heavy pigs. Animals were housed in different physical pens containing from 4 to 7 pigs. Average pen size was 6.1 ± 0.8 and the within-pen average additive relationship was 0.1. Animals were slaughtered at 277 ± 3 days of age and average body weight of 169.7 ± 13.9 kg. Carcass weight (CW) was recorded and carcass lean meat content (LM) was estimated on the basis of backfat fat o'meter measures. A linear scoring system was used by trained experts to attribute a score ranging from 0 (flat thigh) to 4 (marked round shape) for round shape of thighs. Records for all traits were analyzed using the following direct (model 1, 2 and 3) and competitive (model 4) models:

$$\text{Model 1: } \mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e}$$

$$\text{Model 2: } \mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wg} + \mathbf{e}$$

$$\text{Model 3: } \mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wg} + \mathbf{Vl} + \mathbf{e}$$

$$\text{Model 4: } \mathbf{y} = \mathbf{Xb} + \mathbf{Z}_D \mathbf{a}_D + \mathbf{Z}_S \mathbf{a}_S + \mathbf{Wg} + \mathbf{Vl} + \mathbf{e}$$

where \mathbf{y} is the vector of observations; \mathbf{b} is a vector of fixed effects (sex and slaughter group) with incidence matrix \mathbf{X} ; \mathbf{a} (\mathbf{a}_D) is a vector of direct additive genetic effect with incidence matrix \mathbf{Z} (\mathbf{Z}_D); \mathbf{a}_S is a vector of social additive genetic effects with incidence matrix \mathbf{Z}_S ; \mathbf{g} is the vector for social group effect (the pen where individual is raised) with incidence matrix \mathbf{W} and $\mathbf{g} \sim N(0, \mathbf{I} \sigma_g^2)$; \mathbf{l} is the vector for random litter (the full-sibs family of individual) effect with incidence matrix \mathbf{V} and $\mathbf{l} \sim N(0, \mathbf{I} \sigma_l^2)$, and \mathbf{e} is the vector of residuals with $\mathbf{e} \sim N(0, \mathbf{I} \sigma_e^2)$. Vectors \mathbf{a}_D and \mathbf{a}_S have a multivariate normal distribution

($MVN \sim (0, \mathbf{C} \otimes \mathbf{A})$), where $\mathbf{C} = \begin{bmatrix} \sigma_d^2 & \sigma_{ds} \\ \sigma_{ds} & \sigma_s^2 \end{bmatrix}$, \mathbf{A} is the numerator relationship matrix calculated using 11 generations and \otimes denotes the Kronecker product.

Estimates of genetic parameters were obtained by the EM-REML method using BLUPF90 family of programs (Misztal et al., 2008). Akaike Information Criterion (AIC) (Akaike, 1974) was used to evaluate model fitting and to compare different models.

Result and discussion

Descriptive statistics for investigated traits are summarized in Table 1. Number of phenotypic records available was 9,871 for CW, 4,191 for LM and 9,362 for RS. The amount of social groups was 1,645, 703 and 1,556 respectively. The number was larger than the minimum number suggested by Bijma (2010) to be able to estimate social genetic effects.

Table 1. Number of pigs, litters, social and slaughter groups and descriptive statistics for carcass weight (CW), lean meat content (LM) and ham round shape score (RS) ¹

	Traits		
	CW (kg)	LM (%)	RS
N. of pigs	9,871	4,191	9,362
N. of litters	1,839	850	1,787
N. of social groups	1,645	703	1,556
N. of slaughter groups	146	66	142
Mean	135.1	49.6	1.8
SD	10.9	2.7	0.9
P1	109.4	42.8	0
P99	161.6	56.2	4

¹ P1: 1st percentile; P99: 99th percentile

Genetic parameters calculated for the four models are presented in Table 2. Direct heritability (h^2_d) for CW was 0.42, for LM was 0.39 and for RS was 0.37 (model 1). When social groups were included in the model (model 2), h^2_d exhibited slight changes. Social group effect (g^2) accounted for 6, 5, and 2% of the total phenotypic variance (σ_p^2) for CW, LM and RS, respectively. The AIC for model 2 was smaller than AIC for model 1, so the inclusion of social groups as random effect in the model provided a better fit to the data.

When litter effect (l^2) was considered (model 3), h^2_d decreased for all traits, as g^2 for CW. The drop in group variance due to the introduction of litter was however slight and regarded only CW, suggesting that a possible confounding between the effects of litter and social group is trivial. Litter effect accounted for 1.4 to 4.6% of σ_p^2 . Comparison between AIC for model 2 and model 3 suggested a better fit when litter effect was accounted for in the model.

Inclusion of social genetic effects (model 4) decreased h^2_d by 0.02 for CW and RS and by 0.01 for LM, that is possibly due to a partitioning of the additive variance in direct and social components. Only for CW, and consistently with other studies (Arango et al., 2005; Bowman et al., 2010; Hsu et al., 2010), g^2 decreased. This finding suggests that some confounding between social group and heritable social effects might have occurred (Cantet and Cappa, 2008). Social heritability (h^2_s) for CW was 0.007, for LM was 0.004 and for RS was 0.003. That means that social ge-

Table 2. Parameters estimates and Akaike Information Criterion (AIC) for the four models ^{1,2}

Parameter	Traits											
	Carcass weight (kg)				Lean meat content (%)				Ham round shape score			
	M1	M2	M3	M4	M1	M2	M3	M4	M1	M2	M3	M4
h^2_d	0.42	0.41	0.36	0.34	0.39	0.40	0.34	0.34	0.37	0.37	0.36	0.34
h^2_s	~	~	~	0.007	~	~	~	0.004	~	~	~	0.003
T^2	~	~	~	0.52	~	~	~	0.22	~	~	~	0.30
r_{ds}	~	~	~	0.004	~	~	~	-0.598	~	~	~	-0.435
g^2	~	0.06	0.05	~	0.05	~	0.05	0.06	0.02	~	0.06	0.03
l^2	~	~	0.05	~	~	~	0.04	0.04	~	~	0.04	0.02
AIC	84,780	84,710	84,675	92,400	22,384	22,358	22,353	26,048	29,931	29,922	29,916	37,324

¹M1: model 1 included the fixed effects of sex and slaughter group and direct genetic effect of animals; M2: model 2 included social group as random effect in addition to M1; M3: model 3 included litter as random effect in addition to M2; M4: model 4 included social genetic effects as random effect in addition to M3.

² h^2_d : direct heritability = σ^2_d / σ^2_p ; h^2_s : social heritability = σ^2_s / σ^2_p ; T^2 : total heritable variance = $\sigma^2_{TBV} / \sigma^2_p$; g^2 : group effect = σ^2_g / σ^2_p ; l^2 : litter effect = σ^2_l / σ^2_p ; σ^2_{TBV} : variance of total breeding value (sum of individual's direct breeding value and its social breeding value multiplied by number of group mates); σ^2_p : phenotypic variance $\sigma^2_p = \sigma^2_d + \sigma^2_e$ for M1, $\sigma^2_p = \sigma^2_d + \sigma^2_g + \sigma^2_e$ for M2, $\sigma^2_p = \sigma^2_d + \sigma^2_g + \sigma^2_l + \sigma^2_e$ for M3, $\sigma^2_p = \sigma^2_d + (n-1)r[2\sigma_{ds} + (n-2)\sigma^2_s] + (n-1)\sigma^2_s + \sigma^2_g + \sigma^2_l + \sigma^2_e$ for M4, where σ^2_d : direct genetic variance, σ_{ds} : genetic covariance between direct and social effects, σ^2_s : social genetic variance, σ^2_g : social group variance, σ^2_l : litter variance, σ^2_e : residual variance, n: average group size, r: within pen average additive relationship; r_{ds} : correlation coefficient between direct and social genetic effects = $\sigma_{ds} / (\sigma^2_d \sigma^2_s)^{0.5}$. A tilde (~) indicates that genetic parameter was not calculated.

netic effects accounted only for 0.3 to 0.7 % of σ^2_p , negligible in terms of response to selection. It could be due to small average group size. The correlation between direct and social genetic effects was positive for CW, suggesting that individuals with positive direct effect for this trait exerted, on average, positive social effects on CW of their group mates. The total heritable variation (T^2) therefore resulted greater than h^2_d . In contrast, the correlation between direct and social genetic components was negative for LM and RS. Individuals with positive direct breeding value for LM and RS had on average negative social effects on the phenotype of their group mates. This heritable competition decreases the total heritable variation (Bijma et al., 2007a) and hence may decrease the response to selection for LM and RS. Comparison between AIC for direct models and the competitive model revealed that the model without social genetic effects provided the best fit to our data and seems preferable for the genetic evaluation of the investigated traits.

Conclusions

The contribution of social genetic effects to carcass weight, carcass lean meat content and ham round shape variation was investigated for the first time in heavy pigs. The social genetic variance estimated for all traits was small. The potential of LM and RS to respond to selection may be reduced as a consequence of the negative influence of animals with positive direct breeding value for these traits on phenotypes of their group mates. Model comparison revealed that the direct model including social group, litter and direct genetic effects in addition to sex and slaughter group as fixed effects gave a better fit to our data when compared to a competitive model. Since contribution of social genetic effects in heavy pigs might be different under other conditions (e.g. group size, average relatedness within social group or feeding strategy) further researches are recommended.

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