

# Pig Growth is Affected by Social Genetic Effects and Social Litter Effects that Depend on Group Size

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## Introduction

Social genetic variation in average daily gain was found in pigs in recent studies (Arango, J., I. Misztal, S. Tsuruta, et al. 2005; Bergsma, R., E. Kanis, E. F. Knol, et al. 2008; Chen, C. Y., S. D. Kachman, R. K. Johnson, et al. 2008; Chen, C.Y., Johnson, R.K., Newman, S., et al. 2009). We formulated two hypothesis: a/ apart from genetic influences, the litter environment may partly shape social effects; b/ group size may affect the magnitude of social effects which may be smaller in larger groups because the influences of pigs on the growth of their group members are distributed (diluted) over more recipients than in smaller groups. Our objectives were to estimate the genetic parameters for growth with social litter effects and social genetic effects, accounting or not for the impact of group size on social effects.

## Material and methods

**Animals and data.** Quality Genetics (S-244 82 Kävlinge) provided data from the Yorkshire Swedish purebred population. They were collected between May 2003 and October 2007. Ten conventional nucleus herds based on loose-housing systems were involved. Piglets were kept isolated with their litter mates until weaning at approximately 5 wk of age. In some herds, the piglets remained in the same pen until 10 wks of age, but in some herds the piglets were at weaning moved from the farrowing pens to growing pens. During the fattening period, a total of 5 to 15 animals of the same gender (female or castrated male) were raised per pen and they were fed at a high feeding intensity, *ad libitum* if dry fed. The individual weight was measured at the end of the fattening period (interval 80-130 kg). We analysed the average daily gain over the lifespan (ADG) calculated as follow:  $ADG = weight / (date\ of\ weighing - date\ of\ birth)$ . Information on growth of 43,332 pigs born from 4,005 dams and 424 sires corresponding to 6,461 litters was available.

**Statistical analyses.** Pig growth was analyzed with the REML procedure of the ASReML software (Gilmour, A.R., Gogel, B.J., Cullis, B.R. et al. 2006). The pedigree included 55,982 animals. The models were compared according to likelihood with use of chi-square statistics.

**Classical social models.** The model included a vector for the following fixed effects: number of groupmates (10 levels), sex (castrate male or female), and a herd-year-season effect (152 levels), and age and age<sup>2</sup> at weighing as covariates. The random effects will be described in the model for analysis of ADG, here below:

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$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zb}_D + \mathbf{Zs}_S + \mathbf{Wc} + \mathbf{Vg} + \mathbf{Ul} + \mathbf{Tpe} + \mathbf{Qk} + \mathbf{e}$$

where  $\mathbf{y}$  is the observation for ADG ;  $\mathbf{X}$ ,  $\mathbf{Z}$ ,  $\mathbf{W}$ ,  $\mathbf{V}$ ,  $\mathbf{U}$ ,  $\mathbf{T}$ ,  $\mathbf{Q}$  are incidence matrices;  $\mathbf{b}$  is a vector for fixed effects,  $\mathbf{a}_D$  is a vector of random direct genetic effects and  $\mathbf{a}_S$  indicates social genetic effects of the groupmates of the pig producing the record, with

$$\text{Var} \begin{bmatrix} \mathbf{a}_D \\ \mathbf{a}_S \end{bmatrix} = \begin{bmatrix} \sigma_{A_D}^2 & \sigma_{A_D A_S} \\ \sigma_{A_D A_S} & \sigma_{A_S}^2 \end{bmatrix} \otimes \mathbf{A}, \text{ where } \mathbf{A} \text{ is the relationship matrix. The vector } \mathbf{c} \text{ is a}$$

vector of random pen effects with  $\mathbf{c} \sim N(0, \mathbf{I}\sigma_c^2)$ ;  $\mathbf{g}$  a vector of random group effects with  $\mathbf{g} \sim N(0, \mathbf{I}\sigma_g^2)$ ;  $\mathbf{l}$  a vector of random litter effect with  $\mathbf{l} \sim N(0, \mathbf{I}\sigma_l^2)$ ;  $\mathbf{pe}$  a vector of random permanent effect provided by the dam with  $\mathbf{pe} \sim N(0, \mathbf{I}\sigma_{pe}^2)$ ;  $\mathbf{k}$  a vector of random social litter effects with  $\mathbf{k} \sim N(0, \mathbf{I}\sigma_k^2)$ ; and  $\mathbf{e}$  is a vector for residuals with  $\mathbf{e} \sim N(0, \mathbf{I}\sigma_e^2)$ . The social litter effects in  $\mathbf{k}$  take into account that offspring born in the same litter may have similar non-genetic social effects on ADG of their group members.

$\mathbf{Z}_D$  and  $\mathbf{Z}_S$  are incidence matrices for the direct and social genetic effects. The phenotypic variance was calculated as follow:  $\sigma_p^2 = \sigma_{A_D}^2 + \sigma_c^2 + \sigma_g^2 + \sigma_l^2 + \sigma_{pe}^2 + (\bar{n} - 1)\sigma_{A_S}^2 + \sigma_e^2$  where  $\bar{n}$  denotes the mean group size of the population. The total genetic variance available for response to selection,  $\sigma_{TBV}^2$ , was calculated as follow:

$$\sigma_{TBV}^2 = \sigma_{A_D}^2 + 2(\bar{n} - 1)\sigma_{A_D, A_S} + (\bar{n} - 1)^2 \sigma_{A_S}^2.$$

**Models with dilution of social effects with group size.** According to the equation for  $\sigma_{TBV}^2$ , total genetic variance increases with group size. It can be hypothesized, however, that an individual's social effect on each group member becomes smaller in larger groups, because it is distributed over more recipients. We refer to this phenomenon as dilution of social effects in larger groups. As a consequence,  $\sigma_{A_S}^2$  would decrease with group size, and ignoring such dilution would cause overestimation of  $\sigma_{TBV}^2$  in large groups. The same applies to the social litter effect. We tested the existence of such relation between  $\sigma_{A_S}^2$  and  $\bar{n}$  or/and  $\sigma_k^2$  and  $\bar{n}$  by analyzing data subsets with different  $\bar{n}$  (we incremented group sizes by 1 from 5-10 pigs to 10-15 pigs).

As a more sophisticated approach, we modeled dilution by scaling social effects depending on group size, using  $A_{S,i}(n) = \left(\frac{\bar{n} - 1}{n - 1}\right)^d A_{S,i}$ , where  $d$  is the degree of dilution and  $n$  is group size. A  $d = 0$  indicates that the social effect of a genotype is independent of group size, so that there is no dilution and  $\sigma_{TBV}^2$  increases with group size. A  $d = 1$  indicates that the social effect is proportional to  $1/(n-1)$ , so that dilution is complete, and  $\sigma_{TBV}^2$  has the same value for all group sizes. Moreover, the  $\bar{n} - 1$ -term causes the estimate of  $\sigma_{A_S}^2$  to apply to the

mean group size. Dilution was applied to both social genetic effects ( $d_{As}$ ) and social litter effects ( $d_k$ ). The dilution of social effects when group size increases was estimated by varying  $d$  from 0 to 1 in steps of 0.1, taking the  $d$ -value giving the maximum likelihood as best estimate. Heterogeneous residual variances according to group size were set in order to subdivide the data set in 11 subpopulations of independent residual variance.

## Results and discussion

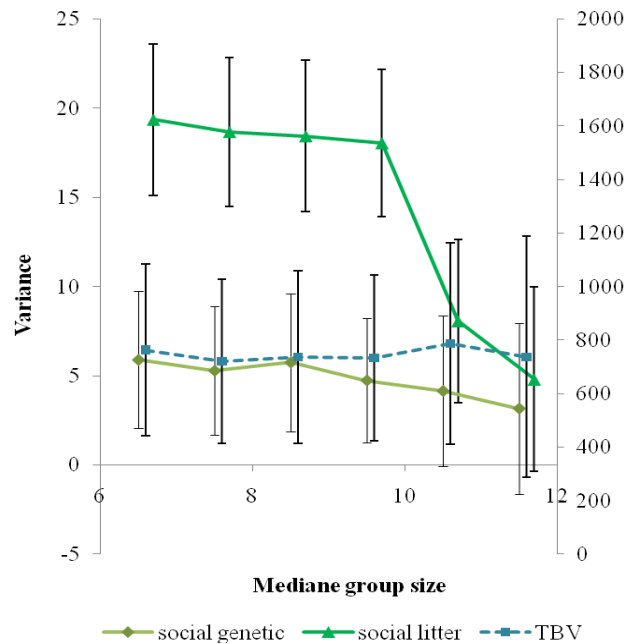
Pigs were weighed at 161 d of age (SD 13). ADG averaged 629 g/d (SD 83). At weighing, group size averaged 8.5 pigs/group and groups were created with mixing of pigs from 4 to 5 litters (SD 1.7). The fixed effects were significant and the addition of the random effects one by one in the model always improved the data fitting ( $p < 0.01$ ). The estimates for variance components of ADG are given in Table 1.

**Table 1. Estimates of variance components for ADG in Swedish Yorkshire population**

Model	$\sigma_{Ad}^2$	$\sigma_{As}^2$	$\sigma_{Ad,As}$	$\sigma_k^2$	$\sigma_{TBV}^2$	$\hat{T}^2$	$r_{Ad,As}$	$d_{As}$	$d_k$	Log L
1	590 67 <sup>b</sup>	12 2	6 8	NF <sup>c</sup>	1332 184	0.27 0.04	0.07 0.10	NF	NF	-203 006
2	596 67	4 1	-5 7	16 2	752 142	0.16 0.03	-0.10 0.15	NF	NF	-202 309
3	596 67	12 2	5 9	13 2	1342 192	0.28 0.04	0.06 0.10	1	NF	-202 272
4 <sup>a</sup>	600 67	9 2	-2 8	16 2	1079 170	0.23 0.04	-0.02 0.11	1	1	-202 250
5	602 67	NF	NF	19 2	602 67	0.08 0.01		NF	1	-202 274

<sup>a</sup> Model 4 best fits the data; <sup>b</sup> SE on the 2<sup>nd</sup> line; <sup>c</sup> NF: not fitted

Including both social genetic and social litter effects improved fitting of the data, and the estimate of  $T^2$  decreased clearly when fitting social litter effects (Model 2 vs. 1). Without social litter effects, the social variance would have been overestimated (Chen, C. Y., S. D. Kachman, R. K. Johnson, et al. 2008). The genetic correlation between direct and social effects was not significant but dilution effects due to group size on social genetic and social litter effects were detected. The social genetic effects for ADG were not significant from 10.5 pigs / pen upwards (Figure 1), which coincides rather well with the limit set at 12 pigs to enhance a change in behavior strategy within the pen (Andersen, I.L., Naevdal, E., Bakken, M., et al. 2004). A full dilution ( $\hat{d} = 1$ ) was detected on both social genetic effects and social litter effects. Conversely, Arango, J., I. Misztal, S. Tsuruta, et al. (2005) found no dilution in their population. Here, scaling applied on both social genetic and litter effects led to the best fitting. Considering both dilutions successively led to an increase and a decrease of the social genetic variance and of the direct-social genetic covariance, resulting in a final estimate for  $T^2$  of 0.23. The difference between  $\sigma_{Ad}^2$  and  $\sigma_{TBV}^2$  revealed that social effects contributed 44% of the heritable variation in ADG (Model 4). Genetic social effects remained significant when dilution on the social litter variance was accounted for (Model 5 vs. 4;  $p < 0.001$ ).



**Figure 1: Estimates of social variances (1<sup>st</sup> axis) and variance of TBV (2<sup>nd</sup> axis) for ADG obtained with data sets of different range of group size and use of Model 2.**

## Conclusion

A further step in the comprehensive modeling of growth was reached. New explicative effects were considered in the social model (compared to Bergsma, R., E. Kanis, E. F. Knol, et al. 2008; Chen, C.Y., Johnson, R.K., Newman, S., et al. 2009). We observed that social composition of fattening groups influence growth: both social genetic and social litter effects were of importance to avoid bias in estimates of genetic variance. We showed that group size affects social heritable variance, in agreement with Bijma, P., W. M. Muir, and van Arendonk, J. A. M. (2007) and Harfield and Wilson (2007). Moreover, we showed that in larger groups, the social genetic and social litter effects decrease proportionally to group size, likely because fewer interactions occur between pigs.

## References

- Andersen, I.L., Naevdal, E., Bakken, M., et al. (2004). *Anim. Behav.* 68:965-975.  
 Arango, J., I. Misztal, S. Tsuruta, et al. (2005). *J. Anim. Sci.* 83:1241–1246.  
 Bergsma, R., E. Kanis, E. F. Knol, et al. (2008). *Genetics* 178:1559–1570.  
 Bijma, P., W. M. Muir, and van Arendonk, J. A. M. (2007). *Genetics* 175:277–288.  
 Chen, C. Y., S. D. Kachman, R. K. Johnson, et al. (2008). *J. Anim. Sci.* 86:2525-2530.  
 Chen, C.Y., Johnson, R.K., Newman, S., et al. (2009). *J. Anim. Sci.* 87:844-849.  
 Gilmour, A.R., Gogel, B.J., Cullis, B.R. et al. (2006). ASREML Release 2.0.  
 Harfield, J.D., and Wilson, A.J. (2007). *Genetics.* 177:667-668.