

Social genetic effects for growth in Landrace pigs with varying group sizes

H.M. Nielsen¹, B. Ask¹, O.F. Christensen², L. Janss², M. Heidaritabar² & P.Madsen²

¹SEGES, Danish Pig Research Center, Axeltorv 2, Copenhagen, Denmark

hmni@seges.dk (Corresponding Author)

²Center for Quantitative Genetics and Genomics, Aarhus University, Denmark

Summary

The aim of this study was to investigate if social genetic effects for average daily gain (ADG) in pigs depend on group size. Records included 119,919 pigs from 13 nucleus Landrace herds in Denmark. Pigs entered the performance test at ~30 kg and were assigned to pens containing between 8 to 15 pigs. Each pen had approximately the same stocking density. A total of 10,803 groups of pigs were included. The ADG from 30 kg to the end of the test (~94 kg) was 1012 g per day. ADG was analysed both separately for each of the eight different group sizes (8 to 15), and on the whole data, including all group sizes. Variance components were first estimated using a classical animal model including the fixed effect of sex, contemporary compartment, along with age and age squared at end of the test as covariates in addition to random effects of animal, group and litter. Thereafter variance components were estimated using a social genetic model, which in addition to the effects included in the classical model, included a social genetic effect. The social genetic variance for the eight different group sizes varied from 4.0 ± 6.1 to 49.8 ± 25 . For the dataset including all group sizes, the social genetic variance was 9.1 ± 2.1 . For all group sizes, except group size 8, T^2 (variance of the total breeding value relative to the phenotypic variance) was higher than the heritability estimated from the classical model. For the total dataset, T^2 from the social model was 0.49 ± 0.01 , whereas the heritability from the classical model was 0.17 ± 0.01 . The direct-social genetic correlations were not significantly different from zero. In conclusion, significant social genetic effects were found for most group sizes. However, we did not find that estimates of social genetic effects for ADG depended on group size in a systematic way.

Keywords: pig, social genetic effects, group size, daily gain

Introduction

Daily gain in pigs has been shown to be a trait affected by social interactions (Bergsma et al., 2013; Chen et al., 2008), where daily gain of a pig depends both on the genes of the pig itself and on the genes of its pen mates. A complicating factor when estimating social genetic effects is that social genetic effects may depend on the number of interacting animals (group size) (Bijma, 2010). In theory, it is assumed that each pig has the same total social genetic effect on its pen mates regardless of group size. Assuming dilution, the social genetic effect of a pig is diluted over group mates such that the effect on each pig is smaller than in small groups (Bijma, 2010; Canario et al., 2010). In practice, pigs are housed in pens of varying group sizes. Therefore, it is important to know whether social genetic effects depend on group size. However, little is known about the relationship between social genetic effects and group size. Therefore, the aim was to investigate whether or not social genetic effects for average daily gain (ADG) depend on group size in a systematic way.

Material and methods

Data

Data were the routinely collected records from boars and gilts entering the performance test in 13 Landrace nucleus herds in the Danish pig breeding program. After weaning, the pigs were housed in weaner units until they weighed approximately 28 kg. They were then moved to finishing pig pens and entered the performance test in sex-specific groups. The performance test for growth ran until the average weight of pigs in a pen reached 94 kg. The pigs were fed *ad libitum* with dry feed during the test. Group sizes at the start of the test varied from 8 to 15 pigs per pen and stocking density was 0.75 m³ to 1.0 m³ per pig at the start of the test. It was not allowed to move pigs between pens when the test had started. ADG for a pig was calculated as the weight at the end of the performance test minus the weight at the start of the performance test divided by the number of days in the test.

The data included 119,919 pigs (Table 1) but only 113,842 pigs had a final weight record. The missing records for individual group sizes varied from 4.4. to 6.4%. ADG varied from 978 to 1,052 g per day. The 13 herds each had from 2 to 4 different group sizes. In total there were 10,803 groups where the number of groups per pen size varied from 316 to 2,299. The pedigree was traced 6 generations back and contained 1,325 sires and 15,155 dams.

Table 1. Number of animals, groups, herds and average daily gain for group sizes 8 to 15 and in total. Group size is the number of animals in the pen at start of the test

Group size	No. of animals	No. of groups	No. of herds	Average daily gain
8	18,392	2,299	5	1037.8
9	7,848	872	2	978.2
10	6,740	674	5	1044.2
11	24,739	2,249	6	1009.8
12	25,428	2,119	6	998.5
13	4,108	316	3	1052.4
14	20,244	1,446	6	1011.4
15	12,420	828	5	998.5
Total	119,919	10,803	13	1012.1

Statistical analysis

The data was analysed using both an animal model without social genetic effects (classical model) and an animal model with social genetic effects (social model) using the DMU software (Madsen and Jensen, 2013). The classical model was:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_D \mathbf{a}_D + \mathbf{Z}_L \mathbf{l} + \mathbf{Z}_G \mathbf{g} + \mathbf{e} \quad (1)$$

where \mathbf{y} is a vector with ADG, \mathbf{X} is a design, \mathbf{b} is a vector with fixed effect including covariates for age of the pig and age squared, sex and compartment, which is nested within farm and group size, \mathbf{a}_D , \mathbf{l} , \mathbf{g} , \mathbf{e} are vectors with random direct additive genetic effects, random litter effects, random group/pen effects, and residuals. \mathbf{X} , \mathbf{Z}_D , \mathbf{Z}_L , and \mathbf{Z}_G are incidence matrices. The social genetic model was:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_D \mathbf{a}_D + \mathbf{Z}_S \mathbf{a}_S + \mathbf{Z}_L \mathbf{l} + \mathbf{Z}_G \mathbf{g} + \mathbf{e} \quad (2)$$

where \mathbf{a}_S is a vector of random social additive genetic effects and \mathbf{Z}_S is the associated incidence matrix. The remaining parameters were as described above. The total heritable variance was estimated as: $T^2 = \sigma_{IBV}^2 / \sigma_P^2$, with total heritable variance (σ_{IBV}^2) being: $\sigma_{A_D}^2 + 2(n-1)\sigma_{A_{DS}} + (n-1)^2\sigma_{A_S}^2$, and the phenotypic variance (σ_P^2): $\sigma_{A_D}^2 + (n-1)\sigma_{A_S}^2 + (n-1)r[2\sigma_{A_{DS}} + (n-2)\sigma_{A_S}^2] + \sigma_{GROUP}^2 + \sigma_{LITTER}^2 + \sigma_E^2$. Where $\sigma_{A_D}^2$ = direct additive genetic variance; $\sigma_{A_S}^2$ = social genetic variance; $\sigma_{A_{DS}}$ = direct-social genetic covariance; n = number of pigs in the pen at start of test, σ_{GROUP}^2 = group/pen variance, σ_{LITTER}^2 = litter variance, σ_E^2 = residual variance, and r = average genetic relationship within each group. (Co) variance components for ADG were estimated both for each group size and across all group sizes using the whole dataset. The log-likelihood from the classical model was compared with the log-likelihood from the social genetic model to test whether the full model (social model) could be reduced to the classical model.

Results and discussion

Significant social genetic effects for ADG were found for all group sizes except group size 8. The social genetic variance varied from 4.0 for group size 8 to 49.8 for group size 13 (Table 2). The social genetic variance estimated across the whole dataset was 9.1. The genetic covariance between direct and social genetic effects was negative for group sizes 9 and 15, and for the whole data set. However, these correlations all had high standard errors.

Table 2. Variance components from a social genetic model and heritabilities from a classical model for different group sizes (GS).

GS	Parameter								T^2	h^2_a
	$\sigma_{A_D}^2$	$\sigma_{A_S}^2$	$r_{A_{DS}}$	σ_{GROUP}^2	σ_{LITTER}^2	σ_E^2	σ_{IBV}^2			
8	2903	4.0±6.1	0.02±0.32	771	588	6151	3115	0.30±0.02	0.28±0.01	
9	1703	25.2±12.6	-0.16±0.19	503	619	5226	2789	0.33±0.04	0.21±0.01	
10	2797	34.8±23	0.25±0.24	716	855	8499	7049	0.51±0.05	0.20±0.01	
11	2634	24.0±8.2	0.04±0.14	1077	826	7661	5217	0.41±0.02	0.21±0.01	
12	2539	15.0±7.0	0.16±0.16	960	751	6417	5044	0.31±0.02	0.24±0.01	
13	1534	49.8±25	0.12±0.25	557	542	6754	9475	0.84±0.08	0.23±0.01	
14	2169	13.7±6.3	0.003±0.12	862	726	6811	4501	0.45±0.02	0.15±0.01	
15	2122	23.9±10.2	-0.10±0.18	867	719	7895	6173	0.40±0.03	0.20±0.01	
All	2700	9.1±2.3	-0.05±0.09	1005	694	6815	3524	0.49±0.01	0.17±0.01	

^aheritability estimated from the classical model

The heritability of ADG estimated using the classical model varied from 0.15 to 0.28 for the eight different group sizes (Table 2). T^2 , which was estimated using the social model and which reflect the total heritable variance relative to the phenotypic variance, varied from 0.30 to 0.84, which are in the range found by other authors (Bergsma et al., 2013; Canario et al., 2010, Chen et al., 2008). Except for group size 8, T^2 was significantly higher than the heritability estimated from the classical model supporting the presence of social genetic effects. Across the whole data set, the heritability from the classical model was 0.17, whereas T^2 was 0.49. Except for group size 8, the likelihood ratio test for comparing the classical

model with the social model indicated that the social models fitted better than the classical models ($P \leq 0.05$).

In this study we estimated social genetic effect separately for each group size. Most previous studies analysed data with a fixed group size or ignored dilution (Chen et al., 2008; Bergsma et al., 2013). Canario et al. (2010) however, found a significantly better fit for a model including a dilution effect in a data set with group sizes from 5 to 15. They however looked at the trait ADG from birth to slaughter. At least 250-500 groups are needed to accurately estimate social genetic parameters (Bijma, 2013). Even though we had a large amount of data we did not find any clear pattern indicating that social genetic effects depends on group size in a systematic way. One reason may be that the fact that pigs leaving the pen was unaccounted for. Censoring may be a problem since sick or dead animals may be the most informative animals (Bunter et al., 2015). Another complicating factor is that the data were obtained from different breeding herds, which may use different strategies for mixing the pigs before they enter the performance test. This is a problem because the phenotypic social effects of a pig is linked to how related the pig is to the recipient (Bijma, 2013). Early-life social effects in pigs may also affect the growth of their group mates later in life because pigs with the same experiences in early life develop similar social skills (Canario et al., 2017). Such effects may have affected our estimates.

Conclusion

We found significant social genetic variances for ADG for most group sizes analysed. However, we did not find any clear indications that social genetic effects for ADG depend on group size in a systematic way. Differences between herds may have affected our estimates.

List of References

- Bijma, P. (2010).** Multilevel selection 4: Modelling the relationship of indirect genetic effects and group size. *Genetics*. 186:1029-1031.
- Bijma P. (2013). The quantitative genetics of indirect genetic effects: a selective review of modelling issues. *Heredity*. 1-9.
- Bunter *et al.* (2015). Social genetic effects influence reproductive performance of group-housed sows. *J. Anim. Sci.* 93:3783-3793.
- Canario *et al.* (2017). The early-life environment of a pig shapes the phenotypes of its social partners in adulthood. *Heredity*. 1-8.
- Bergsma *et al.* (2013). Genetic correlations between lactation performance and growing-finishing traits in pigs. *J. Anim. Sci.* 91:3601-3611.
- Canario *et al.* (2010). Pig growth is affected by SGE and social litter effects that depend on group size. In 9th World Congress on Genetics Applied to Livestock Production (Giessen: German Society for Animal Science), 87.
- Chen *et al.* (2008). Estimation of genetic parameters for average daily gain using models with competition effects. *J. Anim. Sci.* 86: 2525-2530.
- Madsen P, Jensen, J: A User's Guide to DMU. A package for analyzing multivariate mixed models. University of Aarhus, Research Centre Foulum, Denmark, November 2013.