

Social Genetic Effects for Litter Size of Sows Housed in Groups during Gestation

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ABSTRACT: Reproductive data (N=7152 sows with 8787 records) were used to estimate breeding values for total litter size under a model fitting both additive and social genetic effects. Pregnancy tested sows which failed to farrow (<1% of records) were allocated trait values of 0. Sows were penned into 1504 groups of between 2 to 10 sows/group during gestation. Seven subsets of data containing a single record per sow were created for re-estimating additive and social breeding values. Variance ratios for social genetic effects (s^2) and non-genetic group effects (g^2) were very low ($s^2 \leq 0.009$ and $g^2 \leq 0.04$) compared to corresponding estimates of heritability ($h^2 \leq 0.21$). Correlations between breeding values across subsets averaged 0.19 and 0.09 for additive and social genetic effects. Therefore, social genetic effects for total litter size were lowly reproducible for sows across different groups. Breeding values from models fitting social genetic effects better described the mean phenotypic performance of groups than did breeding values from additive models without social genetic effects.

Keywords: reproduction; competition; parameters

Introduction

Individual performance for group housed animals can be influenced by competitive interactions amongst animals within the same group. This implies that the accuracy of breeding values will be reduced unless group effects are accounted for, and might favour selection of animals which perform well individually to the detriment of other animals when housed in groups. This phenomenon could reduce observed response to selection. Previous research has demonstrated significant social genetic effects for growth traits in pigs and egg production traits in poultry (see review by Chen et al., 2007). In contrast, there seems to be no evidence of social genetic effects for fat or muscle depth at slaughter age (Bergsma et al, 2007) or pre-weaning growth rates (Bouwman et al., 2010), where competition amongst piglets can also typically be observed.

No research has been conducted to date on the possibility of social effects for reproductive traits of sows. This was of no interest during the period when sows were housed individually during gestation (i.e. until recently). However, newly implemented production systems are based on group housing of sows, where social effects potentially become important. Moreover, studies to date on social effects have not established whether estimates of social genetic effects of individuals are consistent when they can be re-estimated on more than one occasion – for example when sows are remixed into new groups after each farrowing

event. Reproductive performance of group housed sows is often reported to be variable, particularly in the area of unexplained pregnancy loss after the first month of pregnancy (Spooler et al., 2009). The present study was to investigate whether social genetic effects might influence reproductive outcomes for sows housed in groups during gestation, and to establish whether estimates of these effects were correlated between repeated mixing events.

Materials and Methods

Data. Reproductive data were available for nucleus sows recorded at a single location in the USA. Sows were from 9 lines, representing both maternal and terminal breeding goals. Between 2010 and 2013 the gestation pen of each sow was recorded along with reproductive outcomes. Gestation pens were designed to house either 4, 8 or 10 sows (n_{\max}), but often housed up to 2 fewer sows/pen. Therefore, records for individual sows were only retained for analyses if they were present in gestation groups of between 2 to 10 sows (i.e. size n) where $n_{\max}-2 \leq n \leq n_{\max}$ and where all sows in the gestation group had a known reproductive outcome – including failure to farrow. This left N=8787 records in the full data set, containing records from 7152 sows with up to five records/sow (average 1.23 records/sow); 1351 sows had more than one record. Sows with records were progeny of 901 sires and 3764 dams. Seven subsets of data were formed using discrete time intervals, to include only a single record per sow and complete gestation pen groups. Duplicate records/sow necessitated removing some gestation pen groups from data subsets.

The reproductive trait used in this study was total litter size at birth (including mummies) of gestating sows (TB0). Sows which lost their pregnancy after allocation to the gestation pens (0.81% of records) received a trait value of 0 for TB0.

Grouping strategy. Sows were grouped into gestation pens only after a positive pregnancy test, which was conducted around 25-35 days post-mating. Gestation pen groups were formed using mating day, sow line and parity as grouping criteria. First parity and maternal line sows were generally grouped separately to older parity and terminal line sows, respectively. Of the 1504 sow groups, approximately 61% of the pens contained a single parity group of sows. Gestation groups were penned together on one day to avoid multiple mixing events, with few exceptions. Because of variation in gestation length and rebreeding performance, sows were often regrouped between consecutive parities with different sows in different pens, and

were also recorded in pens with different group sizes. However, familiar pen mates from prior groupings could also be present, and sows are generally able to remember previously acquainted sows – at least from the preceding gestation period (Arey, 1999).

Statistical analyses. The basic model for TB0 accounted for month of mating (32 levels), line (9 levels) and parity group (5 levels) of the sow fitted as systematic effects, with a single random term for the additive genetic effect in data subsets, and an additional random term for permanent environmental effects to account for repeated records in the full data. The extension of the basic model to incorporate social genetic effects included the addition of two random terms; one for the non-genetic group effect and the second for the additive animal social genetic effects. The covariance between direct additive and social genetic effects was not fitted. Homogeneous errors and an equal impact of an individual on their pen mates, independent of pen size, were assumed. Models were fitted using WOMBAT (Meyer, 2007).

Total breeding values (t_i) for individual i in each data subset were calculated as $t_i = a_i + (n-1) \times s_i$, where a_i and s_i are the corresponding additive and social breeding values respectively, and n is the size of the pen the sow was grouped in when the performance was observed. The correlations between additive genetic, social genetic or total breeding values derived from different data subsets were calculated using values for sows with records common across subsets.

Results and Discussion

Parameter Estimates. Fitting a model for social genetic effects significantly ($P < 0.05$) increased the Log Likelihood (LL) in two of the data subsets (Table 1) and in the complete data ($\Delta LL = 3.57$). However, the field data were relatively poorly structured with respect to the total number of records and groups, and relationships amongst sows within groups (Bijma, 2010) to accurately estimate social genetic effects. Moreover, pregnancy was already established prior to grouping sows. Therefore, it seems likely that social interactions would need to be very detrimental to result in significant embryonic or pregnancy loss after Day 35 of pregnancy (Geisert and Schmitt, 2002; Spoolder et al., 2009) to result in a change to TB0.

Characteristics of the distributions of additive (a), social (s) and total (t) breeding values are shown in Table 2, along with the correlations between additive and social breeding values. Variability in social breeding values generally increased with pen size (not presented) providing enough pens and sows in pens of size n were evaluated. Since the effect of t is multiplied by the number of contemporaries an animal has, variability of t was generally greater than variability of a , as is most clearly shown by the increase in interquartile range for t vs a .

Table 1. Estimates of genetic parameters[&] within each data subset (Set) for total born from a social genetic effects model using N records of sows distributed in G groups.

Set	N	G	h^2	s^2	g^2	σ_p^2	ΔLL
1	888	150	0.11	0.000	0.028	12.2	0.82
2	433	81	0.00	0.003	0.040	9.52	1.17
3	1431	258	0.09	0.009	0.000	10.4	3.43
4	1278	217	0.11	0.000	0.000	11.0	0.03
5	1863	329	0.17	0.002	0.000	11.4	0.66
6	1507	250	0.21	0.001	0.027	13.7	2.40
7	1387	219	0.13	0.001	0.000	9.44	0.08

[&]Variances ratios: h^2 : additive genetic; s^2 : social genetic; g^2 : group; σ_p^2 phenotypic variance; ΔLL : change in LogL when adding s and g terms to the basic model.

Table 2. The full and interquartile (in brackets) ranges in additive, social and total breeding values (R_a , R_s , R_t).

Set	R_a	R_s	R_t	r_{as}
1	2.73 (0.35)	V_{neg}	2.73 (0.62)	0.11
2	V_{neg}	0.17 (0.02)	1.08 (0.17)	-0.09
3	2.71 (0.23)	0.52 (0.07)	3.97 (0.79)	0.05
4	3.11 (0.28)	V_{neg}	3.11 (0.62)	-0.15
5	5.20 (0.48)	0.25 (0.27)	5.15 (0.92)	-0.09
6	6.59 (0.54)	0.18 (0.02)	6.51 (1.12)	-0.17
7	3.90 (0.26)	0.09 (0.01)	3.44 (0.61)	-0.06

[&] V_{neg} : negligible variance with range < 0.001 .

The average correlation between additive and social breeding values was -0.05 (range: -0.18 to 0.14), which suggests that to a small extent estimates of favourable genetic merit for litter size under group housing could be associated with concurrent detrimental effects on the performance of pen mates, on average (Table 3). However, the impact of this correlation with respect to historical selection for litter size based on outcomes under individual housing, where the impact of neither aggressive nor submissive tendencies on litter size would be observed, for the current population characteristics is not clear. Moreover, these correlations were not strong, and an estimate of additive merit from the basic model (no social effects) was very highly correlated ($r > 0.97$) with estimates under the extended social effects model. Weaker correlations between additive and social effects might be expected where management strategies (eg see Gonyou and Rioja-Lang, 2014) are used to reduce detrimental interactions between sows at re-grouping and/or at feeding events, as was the case here. It could be speculated that less favourable management might increase the antagonism between additive and social breeding values for litter size.

The average correlation of breeding values across data subsets was 0.19 (range: -0.42 to 0.42) for additive effects compared to 0.09 (range: -0.15 to 0.46) for social genetic effects. The expected correlation between breeding values estimated from different data subsets under the same model can be shown to be approximately $a_1 \times a_2 \times rg_{12}$ under certain assumptions, where a_1 and a_2 are the average accuracies of EBVs from each model and rg_{12} is the genetic correlation (Calo et al., (1973); Notter and Diaz (1993)). Therefore, the correlation between additive breeding values

could be approximated as $0.4 \times 0.4 \times 1 = 0.16$ for TB0, similar to the observed average across subsets. The positive correlation of 0.09 for social genetic effects, which would be estimated with even lower accuracy, therefore implies a high genetic correlation between repeated expressions for social genetic effects, but this cannot be calculated directly. A sow's interaction with other sows might alter with changing group dynamics, reducing the underlying correlation, but the low correlation may also simply reflect a very low accuracy of estimation.

Table 3. Pearson correlations between additive×additive (above diagonal) or social×social (below diagonal) breeding values across data subsets (Set).

Set	1	2	3	4	5	6	7
1		0.06	0.24	0.19	0.12	-0.42	0.42
2	-0.03		0.21	0.13	0.16	0.28	0.07
3	-0.11	0.23		0.40	0.32	0.15	0.01
4	-0.15	-0.03	0.05		0.32	0.21	0.25
5	0.11	0.06	0.05	0.00		0.41	0.23
6	0.35	0.01	0.23	0.06	0.46		0.19
7	-0.15	-0.11	0.06	0.41	0.04	0.29	

Predicted group performance. Mean performance and the standard deviation in TB0 for each of 1504 groups of sows was calculated, along with means for additive (M_a and M_{as}), social (M_s) and total breeding values (M_t), where M_a and M_{as} reflect additive breeding values predicted from either an additive model or a model fitting both additive and social genetic effects. Mean total born was fitted as the dependent variable in a GLM fitting line group (LG: maternal vs terminal) and parity groups (PG: 6 levels) as the starting point. Means of breeding values were added to this base model to evaluate their individual or joint contribution towards explaining observed means and standard deviations in total born.

Line group and parity group combined explained 21% of the variation in mean total born (Table 4). The R^2 was improved to 54% through knowledge of estimated genetic merit of the group; this was slightly lower (51%) when additive breeding values were obtained from a competitive effects model. Social breeding values alone improved R^2 from 21% to 32%. However, the highest R^2 for mean performance was obtained from fitting M_t or $M_{as}+M_s$ (which are essentially equivalent) as explanatory variables. Therefore, group outcomes were more accurately predicted using EBVs from social genetic models than they were from additive models. All variables explained <10% of the variation in TB0 of individual sows within group.

Table 4. Variation explained ($R^2 \times 100$) in the mean or SD of TB0 (M_{TB0} , SD_{TB0}) calculated for N=1504 sow groups from fitting* alternative explanatory variables

Trait	LG+PG*	M_a	M_{as}	M_s	$M_{as}+M_s$	M_t
M_{TB0}	21	54	51	32	57	57
SD_{TB0}	6.1	9.3	8.9	6.2	9.1	9.2

*All models fit line and parity group (LG+PG); M_a and M_{as} : mean additive breeding values from additive only or additive+social models; M_s : mean social breeding values; M_t : mean total breeding values.

Conclusion

Results suggest that social genetic effects might influence the reproductive performance of group housed sows, and that social genetic effects are (albeit lowly) correlated across grouping events. Accounting for the effect of individual interactions on reproductive outcomes improved the accuracy of predicting the mean performance of sows grouped together during gestation, implying better model fit despite limited statistical evidence for improved fit of a more parameterized model. However, the very low heritability of social genetic effects indicates low accuracy of estimation. Larger data sets are required to more accurately establish the correlations between repeated expressions of social effects for reproductive traits, since sows will be re-grouped regularly throughout their productive lifetime. Alternatively, earlier in life estimates of social genetic effects from growth or feed intake data might also be informative proxies for identifying the social merit of sows housed in groups prior to selection. This possibility should be evaluated.

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