Nuñez, P., Negro, S., Casellas, J., Varona, L., Ibáñez-Escriche, N. (2026) Quantifying social genetic variance for feed efficiency in pigs, *Proceedings 13th World Congress on Genetics Applied to Livestock Production* 23925: https://doi.org/10.31274/wcgalp.23925
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Quantifying social genetic variance for feed efficiency in pigs

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Introduction

In groups of growing pigs, access to the feed supply may be a source of stress and induce aggression. Social interactions within group-housed pigs are a very important component for pig well-being, influencing feeding behaviour and productivity. As a result, applying classical animal models to socially affected traits may lead to suboptimal or even antagonistic selection responses (Muir, 2005; Muir and Schinckel, 2002). This can occur because animals that perform better in a classical scenario may have a strong social genetic effect that negatively influences contemporary mates (Ellen *et al.,* 2014). For instance, animals with genetic predispositions for high survival rates may also exhibit elevated levels of aggressiveness and competitive behaviour, which may potentially influence welfare in future generations (Muir and Cheng, 2004).

Social models allow a separation between direct additive effects and indirect social genetic effects. Under these models, the phenotype of individual *i* is not only affected by its own genes, but also by the genes of their contemporary animals (Griffing, 1967, Bijma *et al.,* 2007). Social models allow to estimate the true breeding value (TBV) which is calculated as $TBV_i = DBV_i + (n-1)\ SBV_i$, being DBV the direct breeding value and SBV the social breeding value, and n-1 reflects the number of contemporary mates. A large list of studies has included social effects to capture an extra source of genetic variability (Bergsma *et al.,* 2008; Herrera-Cáceres *et al.*, 2019; Leite *et al.*, 2023; Nielsen *et al.,* 2018). In general, studies including social effects considered that all the pen mates contribute equally. This may create a problem of identifiability between the social genetic effect and the pen effect (Cantet and Cappa, 2008). In this regard, previous studies have proposed methods to introduce intensities of interactions based on the Euclidean distance between means of feeding behavior traits (Ragab *et al.*, 2019) or total time fighting captured by visual observations (Angarita *et al*., 2020). Ragab *et al.* (2019) showed an improvement in model fit and changes in ranking when this model was applied. On the other hand, Angarita *et al.* (2020) found that the model including intensities allowed a better estimation of social effects. However, the latter created intensities based on visual observations to account for the time each couple of animals spent fighting is an extremely laborious work that requires high amount of time. In this study, we aimed to create a simple measure of social intensity based on the frequency of displacements between animals, which can be easily obtained from the reports from automatic feeders.

Materials & Methods

Animals and databases. The database used in this study belonged to a unique nucleus of selection of Iberian pigs from IngaFood S.A. (Extremadura, Spain). Animals were fed using automatic feeders (Nedap, Groenlo, the Netherlands). The database comprises phenotypes of feed conversion rate (FCR) from 1,195 animals with a complete automatic feeder report, including 1,776,299 visits spanned from August 2021 to September 2025. The animals were randomly mixed and raised in pens with an average of 12.4 ± 2.06 pigs per pen (with a mean pen density of 1.1 m^2 per animal). The maximum number of litter mates sharing the same pen was four. Only visits up to 180 days of age were considered. The animals entered the testing

period with an initial weight of 31.4 ± 8.4 kg and an age of 104 ± 15 days and finished with 80.4 ± 12.0 kg at 180 days of age. The number of days with records was 85.5 ± 15.1. Pedigree information included 2,304 individual-sire-dam entries containing the 1,195 tested animals and their ancestors, with a maximum of 5 generations. The median of the genetic relationship between pigs was 0.085.

Statistical analyses. Three different models were performed to estimate variance components of FCR: (1) a traditional additive genetic model (GM), (2) a classical social model with a binary incidence matrix (SBM), and (3) a social model with continuous interaction intensities (SCIM). The SBM assumed equal interaction among contemporaneous animals using a binary social incidence matrix. The SCIM incorporated continuous interaction intensities derived from automatic feeder data, quantified as the frequency of displacements between pairs of animals. Displacements were defined as feeder visits in which the interval between consecutive animals was less than 60 seconds together with a reduction in feed intake of the displaced animal. The reduction was considered when feed consumption was lower than the median of a 5-days-slicing window. In SCIM, the value of intensity exerted from animal *j* on *i* ($\mathbf{Z}s[i \leftarrow j]$) was calculated as the number of times that *j* displaced *i* divided by the total number of times that *i* was displaced. Initial frequency values had a range from 0 to 0.46, with a median of 0.07. These values were then standardized in a way that the mean of each line was 1, making these results comparable with those from SBM. All the unknown parameters were estimated with BLUPF90+ family programs (Aguilar *et al.,* 2018). The social group additive variance (σ^2_{spen}) was obtained as $(n-1)\sigma^2_s$ in SBM and SCIM, where *n* is the mean number of animals per pen. Then, the relationship between $\sigma^2_{spen}/\sigma^2_{Phe}$ was calculated. Alternatively, we calculated this proportion including covariances $[(\sigma^2_{spen}+\sigma_{ds_pen})/\sigma^2_{Phe}]$, which represents a percentage that social effects add to the genetic variance. The term σ_{ds_pen} was calculated as $r(n-1)[(n-2)\sigma^2_s+2\sigma_{ds}]$ in the SBM and SCIM.

Results & Discussion

Phenotypic mean for FCR was 3.94 ± 0.56, which is according to this specific breed (Nuñez *et al*., 2025). Preliminary results of variance components estimations are shown in Table 1. No relevant differences between AIC were found from the different models, which ranged between 1,396 and 1,401. The GM and SCIM estimated a moderate direct heritability (h^2_d) for FCR (0.15±0.04), being slightly higher in SBM (0.19±0.05). The SBM showed a reduction of pen variance and an increase in direct additive variance. In this regard, additive and pen variance were similar between GM and SCIM. The SBM yielded a higher proportion $\sigma^2_{spen}/\sigma^2_{Phe}$ (0.13±0.04) compared with SCIM (0.06±0.01) which is mainly due to the lower values for σ^2_s and σ_{ds}. When the relation $(\sigma^2_{spen}+\sigma_{ds_pen})/\sigma^2_{Phe}$ was computed (not shown in Table 1), SBM also yielded higher proportion (0.30±0.09) compared with SCIM (0.10±0.05). Correlation between additive and social effects was positive in both social models, being very high in SBM (0.71±0.19) and moderate in SCIM (0.35±0.18). The high correlation between additive and social values in SBM likely suggests a confounding between these effects, which may be improved using models SCIM due to better identifiability. In this regard, Ragab *et al.* (2019) reported better predictive performance with models including intensities compared with a SBM. This is likely due to a more realistic model compared with SBM where an equal level of interaction is assumed, and may solve a classical problem of collinearity between pen and social effects, as reported by Cantet and Cappa (2008). However, these analyses were performed with limited data and more information from more animals would be desirable to arrive at more accurate conclusions.

Table 1. Variance component estimation under additive genetic model (GM), social binary model (SBM), and social continuous intensity model (SCIM).

Model	σ^2_{pen}	σ^2_d	σ^2_s	σ_{ds}	σ^2_{Phe}	h^2_d	$\sigma^2_{spen}/\sigma^2_{Phe}$
GM	0.15±0.02	0.04±0.01	-	-	0.31±0.05	0.15±0.04	-
SBM	0.07±0.02	0.07±0.02	0.004±0.001	0.01±0.01	0.36±0.04	0.19±0.05	0.13±0.04
SCIM	0.12±0.02	0.04±0.01	0.002±0.000	0.00±0.00	0.32±0.02	0.15±0.05	0.06±0.02

Abbreviations: σ^2_{pen}= pen variance, $\sigma^2_{d=}$ direct genetic additive variance, σ^2_s=social genetic additive variance, σ_{ds}= direct-social genetic covariance, h^2_d= direct heritability, $\sigma^2_{spen}/\sigma^2_{Phe=}$ proportion of the phenotypic variance explained by the genetic social pen variance calculated as $(n-1)\sigma^2_s$.

Table 2 shows percentages of overlap between the best 20% animals selected under different criteria (EBVs from GM model versus TBV from the three social models). These results show important differences between selection based solely on EBVs and selection based on TBVs. In contrast, rankings derived from TBVs across both social models show much higher agreement with each other, with a value of 62.5%.

Table 2. The percentage of coincidence between the best 20% animals selected under different criteria.

Criteria[1]	TBV SBM	TBV SCIM
EBV GM	41.56	29.84
TBV SBM	-	62.5

[1] GM: classical animal model; SBM: social binary model; SCIM: social continuous intensity model.

Overall, these values of overlapping are lower than those reported by Ragab *et al.* (2019), who found coincidences between 0.69 and 0.89 for ADG. Our preliminary results indicate that selecting candidates based on EBV or TBV can lead to markedly different outcome. It should be noted, however, that the estimation of social effects is generally less accurate than that of direct additive values. Hence, because TBV is defined as EBV + (n-1)SBV, the social values contribute multiple times to the TBV, and particularly to the σ^2_{TBV}, underscoring the need for accurate estimation of social effects before implementing TBV-based selection. In this context, more data is expected to be added to re-estimate EBV, SBV, TBV and their respective correlations with more accurate results.

Conclusions

Social intensities are an interesting approach to solve a classical problem of collinearity between additive direct effects, social effects and pen effects in pigs reared in groups. A reliable measure of intensity can be obtained from automatic feeders, which may be applied at a large scale without additional work or cost. Model with intensity showed lower correlation between additive direct and social genetic effects, which may indicate better identifiability. Rankings based on EBV and TBV showed low coincidence between criteria. In this regard, careful consideration of TBV is recommended, as the precision in social estimates may importantly affect TBV estimation. These results will be expanded with new phenotypes and simulation studies to achieve more accurate results.

Acknowledgements

Pedro Nuñez specially acknowledges the PRE2021-097003 scholarship, financed by the Spanish Ministry of Science and Innovation. This study was funded by the Spanish Ministry of Science and Innovation in Project PID2024-157480OB-I00 and European Union's Horizon Europe research and innovation programme under the grant 01059609 (Re-Livestock Project).

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