Genetic parameters of novel behaviour traits derived from social network analysis in pigs

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Abstract

Social network analysis (SNA) has provided novel traits that describe the role of individual pigs in aggression. The objectives were to estimate the genetic parameters for these SNA traits and quantify their genetic association with skin lesions. Pigs were video recorded for 24h post-mixing. The observed fight and bullying behaviour of each animal was used as input for the SNA. Skin lesions were counted on different body parts at 24h (SL24h) and 3wk (SL3wk) post-mixing. A Bayesian approach estimated the genetic parameters of SNA traits and their association with skin lesions. SNA traits were heritable (h^2=0.18 to 0.26) and strongly genetically correlated (rg>0.88). Positive genetic correlations were observed between 3 of the 4 studied SNA centrality traits with anterior SL24h, although they showed negative genetic correlations with anterior SL3wk. This study provides a first step towards potential integration of SNA traits into a multi-trait selection index for improving pigs' welfare.

Introduction

Grouping of unacquainted pigs is a common procedure in commercial farms, but can lead to elevated aggression and injuries (Boumans *et al*. 2018). Genetic selection could help in providing a long-term solution for controlling aggression in pigs (Turner 2011). Skin lesions have been considered as a practical indicator traits for aggression (Wurtz *et al*. 2017). However, they are inadequate for identifying individuals that contribute most to the aggression in a pen. On the other hand, Social Network Analysis (SNA) provides quantitative 'centrality traits' that describe the position of each animal in the social structure (Agha *et al*. 2020). Previous studies have shown strong phenotypic association between SNA centrality traits and skin lesions at the pen level (Foister *et al*. 2018). However, the existence of a genetic component contributing to SNA traits is still unknown. Our objectives were to (1) estimate the genetic parameters for SNA centrality traits, and (2) quantify the genetic association between SNA and skin lesion traits.

Material and Methods

The dataset consisted of 1146 commercial pigs, 698 of them were purebred Yorkshire and 448 were Yorkshire × Landrace. The animals were the progeny of 82 sires and 217 dams. The total number of animals in the two-generation pedigree was 2427. Animals were distributed into 78 pens, i.e. social groups, each containing 15 animals with the same sex and breed which were formed using 3 animals from each of 5 litters. Fresh skin lesions were counted for each body region 24h (SL24h) and 3 weeks (SL3wk) post-mixing. The body regions were identified as anterior (head, neck, forelegs, and shoulders), central (flanks and back) and posterior (hind legs and rump). The skin lesion records were log transformed ($y= \log_e (x + 1)$) to approach the normal distribution (Full details in Desire *et al*. 2016).

Animals were video recorded for 24h post-mixing. Each animal that initiated or received an aggressive interaction was registered. Aggressive interactions consisted either of fighting or bullying behaviour. Fighting was defined as aggression that lasted at least one second where both pigs engaged in biting, pushing or head knocking the opponent, whereas bullying was defined as when one pig

received or delivered aggression with no observable retaliation occurring (Turner *et al*. 2009). All of these aggression interactions were entered in the SNA as undirected, allowing for bidirectional initiation of interactions, and unweighted, i.e. the frequency or duration of interactions between a given dyad were not considered. SNA was applied to transform the numerical data of aggressive interactions between animals into graphs, where the animals are displayed in terms of nodes (Farine and Whitehead 2015). The SNA traits for each animal describe its position in the network, i.e., the pen (Table 1). The SNA traits considered in this study were derived from Foister *et al*. (2018) using the "igraph" package in R (Csárdi *et al*. 2016). All the listed centrality traits showed considerably skewed distributions; therefore, a square root transformation was applied to reduce skewness.

Table 1. The definition of the social network analysis traits considered in this study.

Measures	Interpretation
Degree centrality	The number of animals that a particular animal directly engaged with.
Eigenvector centrality	Takes into consideration both the number of aggressive interactions of the focal individual and the number of aggressive interactions that its social partners have.
Betweenness centrality	Measures the relative importance of the animal in connecting different subgroups directly engaging in aggression.
Clustering coefficient	Quantifies what proportion of an individual's social partners are also connected, and divides this by the possible number of theoretical connections that could have occurred between the social partners.

A series of univariate and bivariate analyses were used to estimate the genetic variance components of all transformed SNA and skin lesion traits using the following linear animal model

$$\mathbf{y=Xb + Za + Wc + e}$$

where **y** is the vector of records for the traits, and **X, Z** and **W** the incidence matrices of systematic effects, genetic effects and environmental (pen) effects, respectively. Vectors **b, a, c** and **e** represent systematic effects (genetic line, sex, batch), additive direct genetic effects, common environmental pen effects and residual error, respectively, whereas body weight at time of mixing was fitted as a covariate. Bayesian analyses were performed using BLUPF90 software (Misztal *et al*. 2018). Heritability and genetic correlations between traits were calculated.

Results

The posterior means of heritability for SNA traits ranged from 0.18 to 0.26. SNA traits were strongly genetically correlated (Table 2).

Table 2. Posterior means of heritability (diagonal) and genetic correlations (off-diagonal) and the 95% highest posterior density intervals (HPD95%) of the SNA traits.

Trait	Degree centrality	Eigenvector centrality	Betweenness centrality	Clustering coefficient
Degree centrality	0.26 (0.11, 0.41)	0.98 (0.96, 1)	0.99 (0.95, 1)	-0.88(-0.99, -0.72)
Eigenvector centrality		0.22 (0.10, 0.36)	0.94 (0.84, 0.99)	-0.95 (-0.99, -0.85)
Betweenness centrality			0.26 (0.11, 0.40)	-0.95 (-0.99, -0.90)
Clustering coefficient				0.18 (0.06, 0.29)

Positive genetic correlations were observed between all SNA traits and anterior SL24h, except for clustering coefficient, which was weakly negatively correlated with anterior SL24h with HPD95% covering zero (Table 3).

Table 3. Posterior means of the genetic correlations and the 95% highest posterior density intervals (HPD95%) of SNA and skin lesions recorded 24h post-mixing.

Trait	Anterior skin lesions 24h (HPD95%)	Central skin lesions 24h (HPD95%)	Posterior skin lesions 24h (HPD95%)
Degree centrality	0.62 (0.34, 0.88)	0.01 (-0.46, 0.44)	-0.02 (-0.60, 0.56)
Eigenvector centrality	0.54 (0.15, 1.00)	-0.19 (-1.00, 0.39)	-0.13 (-1.00, 0.59)
Betweenness centrality	0.46 (-0.01, 0.87)	-0.10 (-0.71, 0.40)	-0.27 (-1.00, 0.41)
Clustering coefficient	-0.14 (-0.56, 0.34)	0.63 (0.08, 1.00)	0.73 (0.24, 1.00)

Conversely, estimated genetic correlations between the majority of SNA traits and anterior SL3wk were found to be negative with the HPD95% not including zero, except for clustering coefficient, which was found to be moderately to strongly positively correlated with both anterior and central SL3wk post-mixing (Table 4).

Table 4. Posterior means of the genetic correlations and the 95% highest posterior density intervals (HPD95%) of SNA skin lesions recorded 3 weeks post-mixing.

Trait	Anterior skin lesions 3wks (HPD95%)	Central skin lesions 3wks (HPD95%)	Posterior skin lesions 3wks (HPD95%)
Degree centrality	-0.37 (-0.66, -0.06)	-0.18 (-0.56, 0.20)	0.06(-0.53, 0.80)
Eigenvector centrality	-0.47 (-0.84, -0.10)	-0.23 (-0.67, 0.19)	-0.17(-0.76, 0.40)
Betweenness centrality	-0.57 (-0.99, -0.24)	-0.49 (-0.87, -0.09)	-0.78 (-1.00, 0.18)
Clustering coefficient	0.68 (0.28, 1.00)	0.62 (0.26, 0.97)	0.40 (-0.22, 0.98)

Discussion

To the best of our knowledge, the genetic parameters for SNA traits for aggressive behaviour in pigs and genetic associations to skin lesions have not been previously estimated. The magnitude of the heritability of SNA traits indicates that these traits are partially under genetic regulation and could be utilized for selective breeding. Remarkably, heritability estimates for SNA traits, which partly capture social interactions between group members other than the individual in question, were at similar magnitude as those of dyadic behavioural traits previously estimated from the same dataset (Desire *et al*. 2016) and fall within the range of heritability estimates for skin lesions at 24h post-mixing (Turner *et al*. 2009; Wurtz *et al*. 2017).

Positive genetic correlations between 3 of the 4 SNA centrality traits with anterior SL24h, and their negative genetic correlations with anterior SL3wk suggests that individuals with genetic predisposition for high centrality immediately after mixing would tend to suffer high injuries on the anterior part of the body at this stage but would tend to have lower injuries in the stable group. Except for anterior lesions 24h post-mixing, clustering coefficient was the only trait that was found to be positively genetically correlated with skin lesions at both time points suggesting that using this trait at mixing as selection criterion may not inflict a trade-off for reducing lesions at different time points or different body parts. However, this study only provides a first step towards potential integration of

SNA traits into a multi-trait selection index for improving animal welfare by reducing both aggressive interactions as well as resulting injuries. The recent advances in automated capture of animal behaviour would facilitate the application of SNA to derive novel behavioural phenotypes that describe an animal's relative contribution to pen level aggression in commercial pig farms.

In conclusion, SNA provides promising new phenotypes to reduce aggression and resulting injuries in pigs through selective breeding. Future studies are needed to determine the response to selection for these traits on pen level aggression and other economically important traits in order to simultaneously improve the performance and welfare of pigs.

References

Agha S., Fàbrega E., Quintanilla R., and Sánchez J.P. (2020). Animals 10. doi:10.3390/ani10112123.

Boumans I. J. M., Imke J., de Boer M., Hofstede G. J., and Bokkers E. A. M. (2018). Physiology and Behavior 194: 23–40. doi:10.1016/j.physbeh.2018.04.032.

Csárdi G., Nepusz T., and Airoldi E.M. (2016). InterJournal, Complex Systems, 1695. Available at: https://igraph.org.

Desire S., Turner S. P., D´Eath R. B. , Lewis C. R. G., and Roehe R. (2016). Animal 10: 1243–1253. doi:10.1017/S1751731116000112.

Farine D. R. and Whitehead H. (2015). Journal of Animal Ecology 84 (5):1144–63. doi:10.1111/1365-2656.12418.

Foister S., Doeschl-Wilson A., Roehe R., Arnott G., Boyle L., and Turner S. P. (2018). PLoS ONE 13(10). doi:10.1371/journal.pone.0205122.

Misztal I., Tsuruta S., Lourenco D. A. L, Masuda Y., Aguilar I., Legarra A., *et al.* (2018). BLUPF90 software. Available at: http://nce.ads.uga.edu/wiki/doku.php?id=documentation.

Turner S. P., Roehe R., D'Eath R. B., Ison S. H., Farish M., *et al.* (2009). Journal of Animal Science 87(10):3076–82. doi:10.1007/s10519-007-9171-2.

Turner S. P. (2011). Applied Animal Behaviour Science 134(1):1–9. doi:10.1016/j.applanim.2011.06.001.

Wurtz K. E., Siegford J. M., Bates R. O., Ernst C. W., and Steibel J. P. (2017). Journal of Animal Science 95(10):4310–4317. doi:10.2527/jas2017.1757.