Proc. Assoc. Advmt. Anim. Breed. Genet. 26: 66-69

GENETIC PARAMETERS OF BEING A TAIL-BITING RECIPIENT IN PIGS

A.A. Reda[1, 2], M.N. Aldridge[1], P.M. Gurman[1] and S. Hermesch[1]

[1] Animal Genetics Breeding Unit*, University of New England, Armidale, NSW, 2351, Australia
[2] School of Veterinary Medicine, Wollo University, Dessie, 1145, Ethiopia

SUMMARY

This study aimed to estimate the heritability of being a tail-biting recipient and to evaluate the genetic associations with performance traits in pigs. Tail bite lesions were recorded weekly from weaning until finisher test (TBPW) and as a single observation at finisher test, with an average age of 147 days (TBFT) on 13,458 pigs from 6 genetic lines between August 2022 and December 2023. Genetic analysis was carried out using linear and binomial animal models. Three models were investigated: fitting the direct genetic effects (M1), fitting common litter (M2), and the line group effects (M3) as additional random effects. The heritability for TBPW was 0.13 ± 0.02 for M1 with a linear model. The heritability estimates dropped to 0.05 ± 0.01 when the litter effect (M2) and line group effects (M3) were fitted. Estimates for the proportion of variance explained by the common litter effects were 0.05 and 0.06, and the line group effects were 0.03 for TBPW. The heritability for TBFT was 0.06 ± 0.01 for M1 with a linear model. Similarly, the heritability for TBFT decreased to 0.03 ± 0.01 for M2 and M3. Heritability estimates for TBPW and TBFT for M1, based on a logit liability scale within a binomial model, were 0.18 ± 0.03 and 0.17 ± 0.04, respectively. Both tail-biting traits had no significant genetic correlations with performance traits, including average daily gain, back fat thickness, and eye muscle depth. Overall, TBPW had a higher estimate of heritability than TBFT. Thus, TBPW should be used in selection strategies of pigs to reduce tail-biting and improve pig welfare.

INTRODUCTION

Socially driven behavioural traits, primarily vulva, ear, and tail-biting, are common in modern pig farming and negatively affect animal welfare, health, and production (Canario *et al.* 2020). Pig breeding companies globally are interested in using genetic selection techniques to lessen the prevalence and effects of harmful behavioural traits, primarily tail-biting. Heritability estimates have been presented for tail-biting recipients recorded at performance testing in finisher pigs in a Tai Zumu line (Canario and Flatres-Grall 2018) and using medication records as a proxy for tail-biting in Large White Australian pigs (Hermesch and Guy 2018). However, the genetic components of tail-biting recipients and their relationship to key breeding goal traits have not been studied in post-weaned pigs. This study aimed to estimate the genetic parameters of alternative traits for recording tail-biting recipients and evaluate their genetic associations with performance traits using data collected post-weaning (TBPW) and at the finisher test (TBFT) at an Australian commercial pig farm.

MATERIALS AND METHODS

Data. Tail-biting and production measurements of post-weaned and finisher pigs were obtained from one piggery in Australia. Tail-biting was recorded between August 2022 and December 2023 on 13,458 tail-docked pigs from six maternal and sire lines of three breeds (Landrace, Large White, and Duroc). Pigs with tail-biting records descended from 1,762 litters, 1,353 dams, and 155 sires.

---

[*] A joint venture of the NSW Department of Primary Industries and Regional Development and the University of New England

Pigs were housed in commercial conditions, with males and females housed in separate pens. Tail-biting phenotypes were obtained in growing pigs post weaning. Post-weaning tail-biting (TBPW) was based on weekly observations of pigs from weaning until the end of the performance test at an average age of 147 days. Only the first observation of tail-biting was used for this study. In addition, finisher-test tail-biting (TBFT) was recorded when other performance traits were recorded. Tail-biting was scored based on observed tail lesions as an ordinal categorical variable (0 = no tail lesions, 2 = mild tail lesions, 3 = severe tail lesions, infected tails, and/or tail losses). The categorical scores were converted into a binary trait as tail lesions present (1) or not (0) for the genetic analysis. Performance traits, including average daily gain (ADG) from birth to test, backfat thickness at the P2 site (BFT), and eye muscle depth (EMD), were collected at the end of the test period when pigs reached market weight of 95.2 kg on average.

Statistical analysis. Variance components for tail-biting traits defined as binary traits were estimated using a single-trait animal model with REML assuming a Gaussian distribution. Additionally, the heritabilities of tail-biting traits were calculated based on a binomial distribution employing a logit link function with the residual error variance fixed at $\pi^2/3$ (Gilmour *et al.* 2021). Three models were tested, M1: direct additive genetics effects, M2: common litter effects, and M3: line group effects as additional random effects were compared. Fixed effects of sex (2 levels) and month of birth (16 levels) were fitted for all models, while line (6 levels) was fitted as a fixed effect for M1 and M2. Furthermore, a linear covariate for test weight was fitted for BFT and EMD. All the analyses were conducted using ASReml version 4.2 (Gilmour *et al.* 2021), and the models can be summarised in matrix notation as:

$$\boldsymbol{y} = \boldsymbol{X}\boldsymbol{b} + \boldsymbol{Z}_1\boldsymbol{a} + \boldsymbol{Z}_2\boldsymbol{c} + \boldsymbol{Z}_3\boldsymbol{g} + \boldsymbol{e},$$

where $\boldsymbol{y}$ is the vector of phenotypes; $\boldsymbol{b}$ is the vector of systematic effects; $\mathbf{a}$, $\mathbf{c}$, and $\mathbf{g}$ is the vector of the random additive genetic effects; random common litter effects and random line group effects, respectively, while $\mathbf{e}$ is the vector of residuals. Individual observations were linked to their respective levels of systematic, random additive genetics, common litter, and random line group effects through incidence matrices $\mathbf{X}$, $\mathbf{Z_1}$, $\mathbf{Z_2}$, and $\mathbf{Z_3}$, respectively. Genetic correlations between all traits were estimated using a series of bivariate animal models assuming a Gaussian distribution.

RESULTS AND DISCUSSION

The overall prevalence of tail-biting recipients was 4.42% and 2.72% in TBPW and TBFT, respectively. The weekly observations of TBPW resulted in a higher detection rate of tail-biting compared to the single observation at the end of the growing phase when pigs were performance tested.

Heritability estimates. The heritability of TBPW was 0.13 ± 0.02 for M1 with a linear model (Table 1). When including the litter effect and line genetic effects, heritability estimates decreased to 0.05 ± 0.01. This was expected because the common litter effect accounted for 5 to 6% of the phenotypic variation in TBPW (M2). The line group effect explained 3% of the phenotypic variation in TBPW (M3). The heritability of TBFT was 0.06 ± 0.01 for M1 with a linear model. When the common litter effect and the line group effects were included in models (M2 and M3), heritability estimates for TBFT decreased to 0.03 ± 0.01. This reduction was due to the common litter effect, which accounted for 4% of the phenotypic variation for TBFT, and the line group effect, accounting for 2% of the phenotypic variation in TBFT. Based on binomial models, heritabilities ranged from 0.06 (M2, M3) to 0.18 (M1), and common litter effects varied from 0.11 to 0.13 for both tail-biting traits. Fitting lines either as a fixed or random effect did not significantly affect estimates of additive genetic effects or common litter effects, and genetic lines may be fitted as a fixed or random effect in genetic models. These findings show that the expressions of tail-biting recipient traits were influenced by the pig's additive genetic effect, the common litter effect, and genetic differences between lines.

Line-wise heritabilities were estimated for TBFT using M1 with a linear model. Estimates were highest in the Duroc terminal sire line (0.13 ± 0.05), followed by the Duroc maternal line (0.05 ± 0.02), Landrace maternal line (0.04 ± 0.02), Large White terminal sire line (0.02 ± 0.02), Landrace sire line (0.01 ± 0.02), and the Large White maternal line (0.00 ± 0.00). These estimates indicate the need for line-specific estimates of genetic parameters for tail-biting traits.

The current heritability estimates for TBFT were within the range of heritability estimates found in previous studies using linear models, which ranged from 0.06 to 0.08 (Canario and Flatres-Grall 2018). Moreover, heritabilities for both tail-biting traits from the binomial models were higher than the linear models, which agrees with the findings of Hermesch and Guy (2018). The heritability estimate of TBPW was higher than TBFT, indicating the potential for a response to selection. However, recording TBPW is more time-consuming and costly.

Table 1. Heritability and standard errors (h^2 ± SE), common litter effects (c^2 ± SE), line group effects (g^2 ± SE), and phenotypic variance (σ_p^2) for post-weaning tail biting (TBPW) and finisher-test tail biting (TBFT) traits, backfat thickness (BFT, mm), eye muscle depth (EMD, mm), and average daily gain (ADG, g/day) in recipient pigs

Traits	M	AIC	σ_p^2	h^2 ± SE	c^2 ± SE	g^2 ± SE
TBPW - linear	M1	-30396	0.040	0.13 ± 0.02		
	M2	-30463	0.040	0.05 ± 0.01	0.06 ± 0.01	
	M3	-30488	0.041	0.05 ± 0.01	0.05 ± 0.01	0.03 ± 0.02
TBPW - binomial	M1	61366	4.013	0.18 ± 0.03		
	M2	61077	4.091	0.07 ± 0.04	0.13 ± 0.03	
	M3	60912	4.589	0.06 ± 0.03	0.12 ± 0.03	0.11 ± 0.07
TBFT - linear	M1	-35673	0.026	0.06 ± 0.01		
	M2	-35709	0.026	0.03 ± 0.01	0.04 ± 0.01	
	M3	-35738	0.026	0.03 ± 0.01	0.04 ± 0.01	0.02 ± 0.01
TBFT - binomial	M1	66665	3.979	0.17 ± 0.04		
	M2	66176	4.076	0.06 ± 0.04	0.13 ± 0.04	
	M3	65897	4.569	0.06 ± 0.04	0.11 ± 0.04	0.11 ± 0.07
BFT	M1	27154	3.523	0.54 ± 0.02		
	M2	27059	3.389	0.37 ± 0.03	0.08 ± 0.01	
	M3	27062	3.690	0.34 ± 0.04	0.07 ± 0.01	0.08 ± 0.05
EMD	M1	59249	36.579	0.34 ± 0.02		
	M2	59220	35.800	0.24 ± 0.03	0.05 ± 0.01	
	M3	59241	47.085	0.18 ± 0.03	0.03 ± 0.01	0.24 ± 0.12
ADG	M1	125773	5816.300	0.59 ± 0.03		
	M2	125623	5357.500	0.28 ± 0.04	0.12 ± 0.01	
	M3	125662	5752.000	0.26 ± 0.04	0.11 ± 0.01	0.07 ± 0.04

M: model, M1: σ_a^2, M2: $\sigma_a^2 + \sigma_c^2$, and M3: $\sigma_a^2 + \sigma_c^2 + \sigma_g^2$, AIC: Akaike Information Criterion.

Genetic correlations. There was a very high genetic correlation between TBPW and TBFT ($r_g = 0.95 \pm 0.02$), indicating that the two tail-biting traits are genetically identical. Hence, selection against tail-biting at the end of the finisher test will improve tail-biting at weaning. No genetic correlations were found in the literature between alternative traits describing tail-biting. At the phenotypic level, Hakansson and Hans (2020) found that pigs that received tail-biting earlier or during the post-weaning phases are most likely to get tail bitten in later stages (i.e., finishing phases). Moreover, the genetic correlations between tail-biting traits and performance traits were not significantly different from zero (Table 2). In line with our results, previous studies have reported no significant genetic associations between tail biting and production traits in pigs (Hermesch and

Guy 2018). Together, these results indicate that the current selection for improved productivity does not impact the prevalence of tail-biting recipients. These tail lesion scores could be incorporated into breeding programs using a multiple-trait selection index to mitigate tail biting, thereby improving pig welfare and productivity.

Table 2. Genetic and phenotypic correlations with their standard errors (SE) between both tail-biting traits, post-weaning tail biting (TBPW) and finisher-test tail biting (TBFT) in recipient pigs, and back fat thickness (BFT), eye muscle depth (EMD), and average daily gain (ADG)

Traits	**Genetic correlations ± SE**		**Phenotypic correlations ± SE**	
	TBPW	TBFT	TBPW	TBFT
TBFT	0.95 ± 0.02		0.62 ± 0.01	
BFT	0.02 ± 0.07	0.08 ± 0.08	-0.01 ± 0.01	-0.01 ± 0.01
EMD	0.01 ± 0.06	-0.20 ± 0.09	0.00 ± 0.01	-0.03 ± 0.01
ADG	-0.07 ± 0.06	-0.09 ± 0.08	-0.03 ± 0.01	-0.03 ± 0.01

CONCLUSIONS

Heritability estimates for TBPW and TBFT were low to moderate based on linear and binomial models. Selection lines differed genetically in their susceptibility to receive tail bites, which was also reflected in differences in heritabilities for tail-biting recipients between lines. None of the tail-biting traits showed any antagonistic genetic associations with performance traits that would impede selective breeding against this behaviour. Despite labour and logistical challenges, TBPW had a higher estimate of heritability than TBFT. Therefore, TBPW offers more opportunities for selection to reduce the incidence of tail-biting recipients in pigs.

ACKNOWLEDGEMENTS

This project was partially funded by the Australian Government (DISR) CRC-P program. The leading author is a recipient of the UNE IPRA, DAP, and APRIL top-up scholarships. The authors acknowledge SunPork and its staff for organising a farm visit and providing data for this study.

REFERENCES

Canario L. and Flatres-Grall L. (2018) *Proc. World Cong.Genet. Appl. Livest. Prod.* **11**: 572.

Canario L., Bijma P., David I., Camerlink I., Martin A., Rauw W.M., Flatres-Grall L., Zande Lvd., Turner S.P., Larzul C. and Rydhmer L. (2020) *Front. Genet.* **11**: 611073.

Gilmour A.R., Gogel B.J., Cullis B.R., Welham S.J. and Thompson R. (2021) ASReml User Guide Release 4.2. VSN International Ltd, Hemel Hempstead, HP2 4TP, UK.

Hermesch S. and Guy S.Z.Y. (2018) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **23**: 334.

Hakansson F. and Houe H. (2020) *Prev. Vet. Med.* **184**: 105160.