GENETIC ANALYSIS OF TAIL-BITING VICTIMS IN PIGS

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SUMMARY

Tail biting is a welfare concern in pigs for both victims of tail biting and tail biters. This study aimed to estimate genetic parameters for tail-biting victims using medication records routinely collected on farm. Medication records for 771 pigs were available from 2011 until 2017 and most pigs (n = 459) needed medication due to tail-biting injury. There were 10,335 pigs with growth and backfat records that had not been medicated during this time period. Three different health traits were analysed as binary traits, defined as medication due to tail-biting injury, overall medication and medication for any health issue other than tail biting. Linear and logistic sire models were used to estimate genetic parameters. Heritability estimates for tail-biting victims were 0.09 (± 0.02) and 0.25 (± 0.09) based on a linear and logistic sire model, respectively. Medication due to other sicknesses was not heritable indicating that heritabilities for overall medication reflected additive genetic effects for tail-biting victims. There were no genetic associations between being tail bitten and growth rate or backfat indicating that current selection emphasis for these performance traits does not affect tail-biting victims. These first genetic parameter estimates of being a tail-biting victim indicates opportunities to select pigs less prone to becoming a victim of tail biting.

INTRODUCTION

Tail biting is a behaviour in pigs that causes pain, injury and in severe cases mortality in victims of tail biting. Further, biters start tail biting because their own welfare is compromised. The causes of tail biting are multi-factorial and the prevalence of tail biting may depend on interactions between some factors of the environment and the animal (Sonoda *et al*. 2013). This makes it difficult to find solutions to reduce the incidence of tail biting. So far, information about genetic factors affecting tail biting is limited. Previous research has focussed on tail biters (Breuer *et al*. 2005). Only recently has the first information about genetic variation for the incidence of victims of tail biting been reported (Canario and Flatres-Grall 2018), where tail-biting injury was recorded as a binary trait observed when pigs were approximately 100 kg. Alternatively, medication records available on farms for veterinary purposes may be used to identify victims of tail biting.

This study aimed to estimate heritability for tail-biting victims in pigs using medication records and to estimate their genetic correlations with growth rate and backfat.

MATERIALS AND METHODS

Medication records were available from January 2011 until September 2017 for 771 Large White pigs. Most pigs required medication due to tail biting (n = 459 pigs). These medication data were combined with other performance data recorded on farm during the same time period. Three different health traits were defined according to the reason for medication: due to having a tail-bite injury, overall medication and due to sickness other than tail biting (Other sickness). For these health traits, any pigs that were medicated were defined as 1 (case) while non-treated pigs received a 0 (control) for these health traits. There were 10,335 pigs with performance data that had not been medicated. These non-medicated pigs were recorded for growth rate and backfat at an average age of 126 days and an average body weight of 85.7 kg. There were 326 medicated pigs and 179 tail-bite victims that

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were also recorded for growth and backfat. The prevalence of tail-biting victims was estimated as the proportion of pigs recorded for growth and backfat which were also medicated for tail bite. Overall, pigs were the progeny of 180 sires and 1,082 dams.

The three health traits were analysed as binomial variables using generalized linear mixed models which were fitted on a sire level with a logistic link. Therefore, a logistic distribution was assumed for the underlying liability scale. In addition, variance components were estimated for health traits applying a linear sire model which was also used to estimate genetic correlations between health traits and growth or backfat. Genetic models for health traits as well as average daily gain and backfat included month of birth as contemporary group and sex of the animal fitted as fixed effects. The weight of the animal at recording was fitted as a linear covariate for backfat. Random common litter effect was fitted as an additional random effect for all traits. For sire models, additive genetic variance was calculated as four times the estimated sire variance. Further, the residual variance was specified as $\pi^2/3 \approx 3.29$ for logistic sire models. Genetic parameters were estimated using ASReml (Gilmour *et al*. 2009).

RESULTS AND DISCUSSION

Prevalence of tail biting. The prevalence of tail-biting victims based on medication records was 4.2% in this study. However, the prevalence observed in this study should only be regarded as an indication of the true prevalence of tail biting because both the number of tail-biting victims needing medication and the number of pigs not being a victim of tail biting were estimated from incomplete data. The prevalence of tail-biting victims was 6.6% and 10.8% in two different herds based on a binary trait to identify pigs with tail damage (Canario and Flatres-Grall 2018). These two prevalence scores are not directly comparable because only a proportion of pigs with tail damage require medication and a higher prevalence of tail damage score is expected.

Heritability estimates. Tail biting had a heritability of 0.09 (± 0.02) based on a linear sire model (Table 1). In comparison, the heritability estimate of tail-biting victims was higher (0.25 ± 0.09) based on a logistic sire model (Table 2). A higher heritability based on a logistic sire model in comparison to a linear sire model has been observed in other studies (Baeza-Rodriguez *et al*. 2017). In comparison, Canario and Flatres-Grall (2018) found a heritability of 0.06 (± 0.01) based on an animal model that also included social genetic effects. Jointly, these results indicate that the incidence of tail-biting victims has a genetic component that can be used for selective breeding.

Table 1. Phenotypic (Vp) variances, heritability (h^2) and common litter effect (c^2) estimates (standard errors, se) for tail biting, health and performance traits fitting linear models

Trait	Vp	h^2	se	c^2	se
Tail biting[1]	0.0377	0.09	0.02	0.11	0.01
Overall medication[1]	0.0602	0.07	0.02	0.08	0.01
Other sickness[1]	0.0276	0.00	0.01	0.04	0.01
Growth rate[2]	2668	0.22	0.03	0.12	0.01
Backfat[2]	1.74	0.23	0.02	0.07	0.01

[1] a linear sire model was fitted; [2] a linear animal model was fitted

No genetic variation was evident in the health traits defined by sickness other than tail biting indicating that heritability found for overall medication was predominantly due to tail biting incidence. Medication records were explored in detail by Guy *et al*. (2019) who used a subset of the data presented in this study. Alternative approaches to derive pseudo identifications for pigs without performance

records from weaning records were explored. Information about litters weaned each week was used to derive pseudo pedigree for pigs that were expected to be weaned from each litter each week. Heritabilities for medication incidence from a logistic sire model were similar for both approaches which defined controls based on performance-tested pigs (reduced-control: 0.06 ± 0.04) or based on pigs weaned per litter (full-control: 0.04 ± 0.03).

Estimates of common litter effects were 0.11 (± 0.01) and 0.14 (± 0.03) for tail-biting victims based on the linear and logistic sire model, respectively. Litter mates are likely to be housed in the same pen post weaning which may have contributed to these significant common litter effects for tail-biting victims.

Table 2. Phenotypic (Vp) variances, heritability (h^2) and common litter effect (c^2) estimates (standard errors, se) for tail biting and health traits fitting logistic sire models

Trait	Vp	h^2	se	c^2	se
Tail biting	4.14	0.25	0.09	0.14	0.03
Medication	3.84	0.13	0.06	0.11	0.03
Other sickness	3.61	0.02	0.06	0.08	0.05

Genetic correlations. Estimates of genetic correlations between tail biting and growth rate or backfat were not significantly different from zero (Table 3). Other correlations between tail biting and growth rate were lowly negative demonstrating that higher prevalence of tail biting was associated with lower growth rate at the residual, common litter and phenotypic level. These negative non-genetic associations between tail biting and growth rate were not found for backfat. Further, estimates of genetic and non-genetic associations between overall medication and growth rate or backfat were like associations between tail biting and growth rate or backfat. Genetic correlations were also not significantly different from zero indicating that selection for higher growth rate and lower backfat will not adversely affect tail-biting victims or overall medication.

Table 3. Genetic (r_g), common litter (r_c), residual (r_r) and phenotypic (r_p) correlations (with standard errors) between tail biting or overall medication and growth rate or backfat fitting linear sire models

Trait	r_g (se)	r_c (se)	r_r (se)	r_p (se)
		Tail biting		
Growth rate	0.03 (0.18)	-0.14 (0.06)	-0.06 (0.01)	-0.07 (0.01)
Backfat	-0.09 (0.19)	-0.09 (0.07)	-0.01 (0.01)	-0.02 (0.01)
		Overall medication		
Growth rate	0.03 (0.19)	-0.11 (0.07)	-0.10 (0.01)	-0.09 (0.01)
Backfat	-0.01 (0.19)	-0.09 (0.08)	-0.01 (0.01)	-0.02 (0.01)

Medication due to other sickness was not heritable and genetic correlations with other traits could therefore not be estimated. No information was found in the literature regarding genetic associations between being a victim of tail biting and growth rate or backfat. Estimates of genetic correlations between tail biters and growth or backfat presented by Breuer *et al.* (2005) are not comparable because the behaviour of tail biting is different to the behaviour of a tail-biting victim.

Selection strategies. Medication records were used in this study to identify victims of tail biting in pigs. This measurement of tail-biting prevalence does not capture all victims of tail biting because only a proportion of tail-biting victims require medication. Therefore, a binary score identifying

tail damage as was used by Canario and Flatres-Grall (2018) may be a better measure of tail-biting victims because the prevalence of such a score is expected to be higher than the prevalence based on medication records. A higher prevalence of a score identifying tail-biting victims results in a higher variance for the binary trait. Overall, it is recommended that tail damage of pigs is recorded when pigs are performance tested for weight or fat depth in order to verify these initial heritability estimates available for tail-biting victims.

Tail biting leads to economic losses because tail-bitten pigs are at higher risk of infections, carcase condemnation, reduced weight gain and increased medication and labour costs (review by Valros and Heinonen 2015). Often these cost components are difficult to quantify and information about medication records provides information about additional medication and labour costs.

The prevalence of tail biting is high when an outbreak of tail biting occurs. Generally, tail biting is not observed continuously and the overall prevalence of tail-biting victims is low. This is desirable of course, however, a low prevalence implies that variance for tail-biting victims is low which in turn limits opportunities for genetic improvement. Therefore, selection criteria that can be recorded easily on all pigs to reduce biting behaviour and prevalence of tail biting are desirable. First indications that social genetic effects for growth are associated with multiple biting behaviours including tail biting were presented by Camerlink *et al*. (2015) and should be investigated further. Social genetic effects for prevalence of tail-biting victims were found by Canario and Flatres-Grall (2018). However, estimating these social genetic effects for tail-biting victims directly is difficult due to the low prevalence and binary nature of this trait. Therefore, investigating social genetic effects for growth as an indirect selection criterion for tail biting in pigs may be a more feasible alternative. This approach also requires information of tail-biting victims and recording a simple (binary) score to identify tail-biting victims should be priority.

CONCLUSIONS

Being a tail-biting victim, identified by medication records, was heritable. No genetic associations were found between tail-biting victims and growth rate or backfat. Simple (binary) scores to identify victims of tail biting based on medication records or observations of tail damage of pigs on farms should be considered as new welfare traits in pig breeding programs.

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