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Comparison of survival analysis and a linear mixed model for predicting genetic parameters of tail-biting incidence in pigs

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Introduction

Tail biting in pigs is a social behaviour that affects welfare and health of pigs, and the profitability of pork-producing companies worldwide. Despite ongoing efforts to reduce tail biting through methods such as tail docking and providing enrichment, such as straw, tail biting still occurs. Therefore, alternatives such as genetic selection, which are cheap, permanent and welfare-friendly, are required (D'Eath *et al*., 2014). To select for tail biting, large-scale identification of tail biters is needed. Identifying tail biters is difficult, but tail lesions on victims can serve as a proxy for tail biting in genetic improvement programs.

Genetic parameters of tail-biting incidence are often estimated using linear mixed animal models. However, these models typically do not handle the non-linearity of binary traits or censored records (animals that have not experienced a tail bite at the end of the observation period). Consequently, heritability estimates for tail biting tend to be low, impeding the rate of genetic progress (Hegedűs *et al*., 2025; Reda *et al*., 2025). Survival analysis can effectively address both issues of censoring and non-linearity in longitudinal data. Survival analysis is used to analyse either the duration of time an animal 'survives' an event or the time until the event happens. The Cox proportional hazards survival model measures the conditional probability of an event prevailing given that the animal has not experienced the event up to a specific time of observation (Kachman, 1999).

Survival analysis has been applied to estimate the genetic parameters of cannibalism in chickens (Ellen *et al*., 2008), resulting in higher accuracy of genetic merits compared to linear models. However, survival models have not been applied in genetic studies of tail biting in pigs, except in epidemiological studies evaluating the efficacy of interventions during outbreaks (Chou *et al*., 2019). This paper aims to estimate genetic parameters for the risk of receiving a tail bite using linear and survival models.

Materials & Methods

Animals and data collection. Longitudinal data was collected on 33,758 tail-docked grower-finisher pigs between August 2022 and December 2023 at a commercial pig breeding farm. These data covered three pig lines (14,920 Large White, 14,278 Landrace, and 4,560 Duroc) with pedigree including 224 sires, 2,834 dams, and 3,783 litters. Phenotypes were collected weekly from weaning until 19 weeks of age, when other performance parameters were also measured. Pigs were scored four times a week for tail biting based on observed tail lesions using a three-point scoring system, where 1 was no tail lesion, 2 was mild tail lesions, and 3 was severe or infected tail lesions.

Trait definition. Two traits were analysed, survival time (days) and bite status. Survival time was the number of days from weaning to the first tail-biting episode. If a pig did not have a tail bite, it was allocated the number of days from weaning to date of performance weight, with a

maximum age of 175 days. Note that the term "survival" should not be confused with mortality, but it was defined to refer to a period without a bite. Bite status was coded as if tail biting was absent (0 = score 1) or present (1 = score 2 or 3) for the first tail-biting event, as repeated events were also available. Tail-biting rate was defined as the percentage of pigs bitten (incidence rate) at the end of the observation period. All pigs that had a tail-biting incidence before the end of the observation period were considered failures or uncensored (event = 1). In contrast, pigs that did not exhibit tail biting during the observation period were considered censored (event = 0). Pigs that were removed from the pen, sick, or died for reasons other than tail biting (n = 8,926) were also censored, and these records were filtered from the analysis to avoid bias in parameter estimates.

Analysis. Survival curve of tail biting incidence for the three pig lines was plotted with R version 4.3.1 (R Core Team, 2023) using the R package "survminer" (Kassambara *et al*., 2025). Three methods were compared to estimate variance components and heritabilities for survival days and bite status, both within-line and across lines. First, a bivariate threshold linear animal model was fitted to obtain precise estimates of heritability for survival days (BTLMT) and bite status (BTLMS), assuming a normal distribution for both traits (Damgaard and Korsgaard, 2006). These estimates were identical to those from traditional linear models. Second, the survival time model (STM) was implemented by fitting a linear animal model to the observed survival days (Ellen *et al*., 2008). Finally, a generalised linear mixed model using a complementary log-log (cloglog) link was fitted for the bite status (0/1) on the log of survival days, which is equivalent to the Weibull proportional hazards model (Southey *et al*., 2003). All genetic analyses were performed with ASReml v.4.2 (Gilmour *et al*., 2021). The model included fixed effects of year-season (3-month periods) at birth (7 levels), sex (2 levels), line (3 levels), and the interaction between line and sex (6 levels). The model included random effects of additive (animal) genetics and the common litter effect. The same fixed and random effects were used across all models. In the model with a cloglog transformation, the residual variance on the liability scale was $\pi^2/6$ (Ducrocq and Casella, 1996).

Results

The probability of surviving a tail-biting incident differed significantly between piglet lines (Figure 1). Duroc had the highest likelihood of remaining unbitten and the longest survival time. In contrast, Large White had the lowest likelihood of staying unbitten and the shortest survival time.

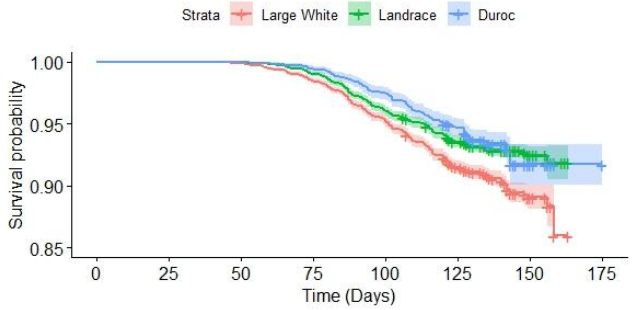

Figure 1. Kaplan-Meier survival curves of tail-biting incidence among three pig lines.

The heritability of survival days across all lines using the STM was 0.15 ± 0.02 (Table 1). Heritability was highest in Duroc (0.19 ± 0.04), which also had the highest survival probability and the longest survival days, compared with Landrace (0.15 ± 0.02) and Large White (0.15 ± 0.02). Combining all lines and using BTLMT and BTLMS, respectively, the heritability estimates for survival days and bite status were 0.14 ± 0.02 and 0.06 ± 0.01, respectively. As

the across-line estimates were used for comparison, the within-line estimates from BTLMS were not shown. Similar heritability estimates (0.15 ± 0.03) were obtained for bite status using a cloglog model. However, the common litter effect was high in cloglog and BTLMT. Variance components were not estimable for the Large White on the cloglog due to convergence issues. Overall, heritability estimates for survival days were identical in both STM and BTLMT (Table 1).

Table 1. Number of pigs with phenotype (n), tail biting rate (%), mean survival days, heritability (h^2), common litter effect (c^2), and phenotypic variance (Vp) and their standard errors (± SE) of being a tail-biting victim across and within three lines in pigs using a survival-time model (STM), bivariate threshold-linear model for survival time (BTLMT) and bite status (BTLMS), and a complementary log-log (cloglog) for bite status using animal models.

Line	n	Tail biting (%)[1]	Survival days[2]	Model	h^2	c^2	Vp
Large White	10,832	9.2 ± 0.3	167 ± 0.5	BTLMT	0.14 ± 0.02	0.07 ± 0.01	158.8 ± 2.4
				STM	0.15 ± 0.02	0.06 ± 0.01	159.7 ± 2.5
				Cloglog	-	-	-
Landrace	10,445	6.8 ± 0.2	169 ± 0.2	BTLMT	0.14 ± 0.02	0.10 ± 0.01	122.0 ± 2.0
				STM	0.15 ± 0.02	0.08 ± 0.01	122.2 ± 2.0
				cloglog	0.14 ± 0.05	0.23 ± 0.04	2.6 ± 0.1
Duroc	3,555	6.3 ± 0.4	170 ± 0.4	BTLMT	0.23 ± 0.05	0.08 ± 0.02	87.8 ± 2.5
				STM	0.19 ± 0.04	0.12 ± 0.01	89.3 ± 2.5
				cloglog	0.22 ± 0.10	0.12 ± 0.08	2.5 ± 0.2
All lines	24,832	7.8 ± 0.2	168 ± 0.2	BTLMS	0.06 ± 0.01	0.08 ± 0.01	0.1 ± 0.0
				BTLMT	0.14 ± 0.02	0.08 ± 0.01	132.9 ± 1.4
				STM	0.15 ± 0.02	0.08 ± 0.01	133.6 ± 1.4
				cloglog	0.15 ± 0.03	0.21 ± 0.02	2.6 ± 0.1

[1] Tail biting rate, percentage of pigs bitten (incidence rate) at the end of the follow-up period.
[2] Restricted mean survival day, average number of days from weaning until the onset of the first tail biting or date of performance recording, with an upper limit of 175 days.

Discussion

This study presented genetic parameters for the risk of tail biting in pigs using alternative survival models. Heritability estimates for survival days and bite status were similar across the models, although the cloglog model had high standard errors. Because the incidence rate was low, the cloglog link function is asymmetric and approaches zero at extreme values, additive and litter effects seemed to overlap. Comparable studies applying these models to tail biting in pigs were not found. In pig breeding, the trait of survival days could be more useful than the binary trait because survival days reflect when a pig was bitten, whether early or late in the growing phase. Also, survival days provide continuous data on how long an individual animal stays normal before being bitten or removed from the cohort. The heritability estimates for survival days (0.14 to 0.23) using STM and BTLMT, and for bite status (0.14 to 0.22) using cloglog, found in this study, are within the upper range of previous literature, between 0.03 and 0.16 (Gorssen *et al*., 2024; Hegedűs *et al*., 2025; Reda *et al*., 2025). This suggests greater potential for genetic improvement by selecting pigs for longer survival days without being bitten. Heritability estimates for survival days obtained using the STM in this study are higher than those reported for cannibalism in chickens, ranging from 0.02 to 0.10 (Ellen *et al*., 2008). A BTLMT can serve as a method for validating heritability estimates from the STM and linear models, as in genetic analyses of continuous and survival traits (Damgaard and Korsgaard,

2006). Furthermore, a cloglog model for binary status, regressed on log survival days, can yield estimates similar to those from STM and bivariate models. This method is analogous to the proportional hazards model used in a discrete-time analysis of lamb mortality (Southey *et al*., 2003). Overall, survival models tend to yield higher estimates of genetic parameters than linear models. Higher heritability estimates were also obtained using Cox proportional hazards animal or sire models (results not shown) compared with the alternative models tested here. However, standard Cox models are computationally demanding for large-scale genetic studies and difficult to combine with other breeding goal traits in genetic evaluation programs.
As the survival models also captured the genetic variance on censored records by accounting for non-linearity , which can increase the rate of genetic gain for tail biting. This approach has broader implications for other time-to-event traits that typically have low heritabilities, such as disease and welfare traits. Thus, we recommend further investigation for its application in pig breeding programs using robust model comparison methods. However, tail biting status varies over time, meaning that an individual pig may experience multiple victimisation statuses at any point during the rearing phase. This temporal variation can be accounted for using discrete-time survival and disease transmission dynamics models, which will be explored in future studies.

Conclusions

Using alternative survival models captured a greater proportion of the additive genetic variance than typical linear models, yielding higher heritability and the potential to increase genetic gain. This enables breeders to select pigs less likely to become victims of tail biting.

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