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# **Identification of genetic factors affecting tail biting in pigs**

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## **Research Organisation**

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## Executive Summary

Tail biting is a behaviour in pigs that leads to considerable 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. 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 partly due to the fact that data about incidence of tail biting is limited. Previous research has focussed on tail biters and only recently has first information about genetic factors affecting the incidence of victims of tail biting become available. These first results indicate that selection of pig genotypes that have a lower risk of being victims of tail biting offers an opportunity to change the predisposition of pigs to become victims of tail biting.

This project aimed to identify genetic and non-genetic factors that affect the risk of being a victim of tail biting on farms. Currently, most pig farmers do not routinely monitor the incidence of tail biting on farms. However, tail biting recorded as a need for medication or a cause of removal was available from three populations. These data were used for genetic analyses to identify genetic and non-genetic factors affecting incidence of tail biting in pigs.

Medication records were available from 2011 to 2017 for Large White pigs (population A). Removal data were available from 2011 to 2017 for population B and from 2008 to 2014 from population C. Both of these two populations included purebred pigs from multiple lines as well as crossbred pigs. These medication or removal data were combined with corresponding pedigree and performance records of purebred pigs available from each farm. In all three populations, records about tail biting victims that could be used for genetic analyses were reduced considerably due to incomplete information for tail biting records. In population A, information about 459 tail-biting victims were combined with 12,051 growth and backfat records for estimation of genetic parameters. There were 349 purebred pigs available from population B and the incidence was too low for genetic analyses. In population C, 441 purebred victims of tail biting were included in genetic analyses to estimate line differences for the incidence of tail-biting victims. The incidence of removal of pigs due to tail biting victims was also too low in population C to estimate heritabilities or genetic correlations.

Medication or removal of tail-biting victims was defined as a binary (0/1) trait. Pigs that were medicated or removed due to tail biting were defined as 1 while non-treated pigs that were recorded for growth and backfat received a 0. Analyses were based on general linear mixed models which assume that errors have normal distribution. This assumption is not correct for binary traits like tail biting and logistic models that fitted a logit link function to connect expected value of the outcome variable with a linear function of the explanatory variable in the model were also used. Heritability estimates were based on sire models fitting both linear and logistic models. Sire models rather than animal models were used because sire models are more robust than animal models for genetic analyses of binary traits. The implications of poor cross-classification of tail-biting victims with definitions of contemporary groups were explored.

The incidence of tail-biting victims was heritable based on medication records. The heritability of tail biting was 0.09 ( $\pm$  0.02) based on a linear sire model fitting month of birth as a contemporary effect. This heritability increased to 0.12 ( $\pm$  0.03) when contemporary group was defined for a time period of three months. Heritability estimates based on logistic sire models were 0.25 ( $\pm$  0.09, for month as contemporary group) and 0.32 ( $\pm$  0.10 for three-month time period as contemporary group). Higher heritability estimates for logistic models in comparison to linear models are usually observed in animal-

breeding applications and estimates found in this study follow expectations. Further, line differences between incidences of removal due to tail-biting was found in population C. Together, these results demonstrate genetic effects affecting the incidence of tail-biting victims on farms. The genetic differences between sires can be used for selection of pigs that are less likely to be victims of tail biting. Information about victims of tail biting was based on medication records. Incidence of medication due to other health issues was not heritable. Therefore, the low heritability for overall medication records was due to incidence of tail-biting victims rather than a disease challenge.

Incidence of tail-biting victims had no genetic association with growth rate or backfat of growing pigs. These results indicate that current selection strategies for higher lean meat growth do not affect the incidence of tail-biting victims. This result is favourable in the sense that current selection strategies do not lead to higher incidence of tail biting. However, it also implies that selection emphasis has to be placed on tail biting in order to achieve genetic gain in incidence of tail-biting victims.

The gender of pigs affected incidence of tail-biting victims in each herd. However, the direction of this effect was not consistent between farms. Further, the effects of calendar month on incidence of tail biting varied between populations indicating that other temporary and unknown factors exist that lead to an outbreak of tail biting at a specific time and in a specific group of pigs within each farm. It is therefore important to monitor incidence of tail biting on farms closely and to record when and where outbreaks occur within the piggery in order to identify farm-specific factors leading to an outbreak of tail biting in specific sections of the piggery.

Incidence of tail-biting victims was higher in autumn and winter in two farms of this study. Further, a higher incidence of tail biting was observed for pens that are expected to have higher levels of draughts due to the vicinity of fans for these pens. Indoor climate factors including higher levels of draughts, lower temperatures and higher chill factors have been shown to influence the incidence of tail biting in other studies. Farmers should evaluate micro-climate of individual pens within sheds in order to reduce incidence of tail biting for specific pens.

A simple binary medication score that identified victims of tail biting (score of 1) from pigs that did not need medication due to being a victim of tail biting (score of 0) was heritable. No heritability estimate was found in the literature about medication score of tail-biting victims and this first heritability estimate provides opportunities for pig breeding programs to select pigs that are less likely to become victims of tail biting. Information about medication of pigs is collected on farms for veterinary reasons. These data should be incorporated into electronic databases to facilitate selection of pig genotypes with reduced incidence of becoming a victim of tail biting.

In recent study conducted in France, the incidence of injury due to tail biting had a similar heritability than the heritability of medication due to tail biting found in this study. Injury due to tail biting can be easily noted when pigs are recorded for weight and backfat. This simple score should be implemented by breeding companies in order to facilitate selection of pigs that are better able to ward off tail biters.

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## **I. Background to Research**

Tail biting is a behaviour in pigs that leads to considerable pain, injury and in severe cases mortality in victims of tail biting. Further, biters start tail biting because their own welfare is compromised. The current management practice of tail docking is a painful procedure which is becoming less acceptable in pig industries worldwide. Therefore, new strategies are required to reduce the incidence of tail biting and the need for tail docking in growing pigs. This project was developed in response to the call by APL for projects that will lead to continued improvement in the welfare of pigs on farms. The importance of tail biting in the industry is reflected in the high response rate from industry expressing interest to participate in the project.

The causes of tail biting are multi-factorial. A number of genetic and non-genetic factors have been identified that lead to higher incidence of tail biting on farms. Comprehensive data are required for complex statistical models that can disentangle multiple effects and take into account the non-normal distribution of the incidence of tail biting.

This project aims to identify genetic and non-genetic factors that increase the risk of being a victim of tail biting on farms. Currently, pig breeders have no systematic approach to monitor the incidence of tail biting on farms. However, tail biting recorded as a cause of removal or need for medication is available from three populations. These data allow first genetic analyses to identify genetic and non-genetic factors leading to a higher incidence of tail biting in pigs.

Genetic analyses of existing data about victims of tail biting quantify the heritable component of being a victim of tail biting. This information is useful for breeding companies to identify selection avenues to reduce the incidence of tail biting. Further, estimation of genetic association between incidence of tail biting and growth or backfat shows whether current selection strategies for efficient lean meat growth affect the incidence of behavioural problems like tail biting. The consequences of selection for productivity and efficiency on behaviour and welfare of pigs is a question which is of concern to society overall. So far, information about these genetic associations could not be found in the literature.

This project will provide genetic parameters for traits describing incidence of tail biting which are required by pig breeding programs to consider tail biting in selection decisions. Genetic associations between tail biting and growth or backfat will illustrate whether current selection for lean meat growth affects incidence of being a victim of tail biting. Further, models used in genetic analyses include non-genetic factors which provide information about non-genetic avenues to reduce the incidence of tail biting.



## **2. Objectives of the Research Project**

This project has two objectives. These are:

1. Identification of genetic factors affecting tail biting on farm
2. Estimation of genetic association between incidence of tail biting and performance of pigs.

### 3. Introductory Technical Information

Severe cases of tail biting lead to injury of animals and pose an important welfare concern. Cutting the tip of the tail in young piglets, called tail docking, is currently practiced in pig industries worldwide to reduce the incidence of tail biting. For example, this management practice reduced incidence of tail lesions from 23% or 89% in non-tail-docked pigs to zero percent or 48% in tail-docked pigs in the studies by Lahrmann et al. (2017) or Li et al. (2017). However, this management practice in itself is now also regarded as a growing welfare concern (ter Beek, 2013; Pig Progress). Therefore, other strategies are required to reduce the reliance on tail docking as a management practice for the prevention of tail biting.

The incidence of tail biting is often poorly recorded. Monitoring of tail damage on carcasses at abattoirs is the most common method to estimate the incidence of tail biting in Europe according to a review by the European Food and Safety Authority (EFSA, 2007). Although this method is simple and allows rapid monitoring of animals from many farms, this approach underestimates the real prevalence of tail biting on farms because pigs most severely affected will have died on farm or were euthanized prior to slaughter. Further, the review (EFSA, 2007) highlighted considerably lower incidence of tail biting in routine monitoring schemes in comparison to specific scientific investigations. Overall, the incidence of pigs with tail lesions at abattoirs was about 3% in tail-docked pigs and 6-10% in pigs whose tail had not been docked although extremely high incidence of 30% damaged tails has been reported in individual scientific studies. These levels of lesions observed in abattoirs were lower than percentages of pigs with lesions observed on farms in the more recent studies by Lahrmann et al. (2017) and Li et al. (2017). Overall, this wide range of incidence indicates that recording of lesions may need to be more specific and precise for a true estimate of tail biting incidence observed on farms or in abattoirs.

The causes of tail biting are multifactorial and the prevalence of tail biting may depend on interactions between some factors of the environment and the animal. Risk factors include the gender of pigs, herd size, stocking density, age and weight of pigs, floor material, feeding regime, health status, environmental enrichment, air quality and genetics (e.g. Schroder-Petersen and Simonsen, 2001; Sonoda et al., 2013). This long and comprehensive list of factors suggests that a holistic approach will be required to reduce the incidence of tail biting in pigs.

Sodona et al. (2013) summarized breed differences in aggressive, foraging and exploratory behaviour which are thought to be related to tail biting. Within breeds, Breuer et al. (2005) identified genetic variation in tail biting in Landrace pigs but found no genetic differences in the incidence of tail biting among Large White pigs. Further results by Breuer et al. (2005) indicate that selection for increased leanness and growth rate may increase the incidence of tail biting in pigs. However, Sodona et al. (2013) point out that information about genetic influences on tail biting is sparse and inconsistent.

## 4. Research Methodology

### 4.1. Genetic analyses of medication records to identify tail-biting victims – Population A

#### 4.1.1. Overview of data

Medication records were available from January 2011 until September 2017. These pigs were born from September 2010 to June 2017. Medication records were based on hand-written documents of medication records available from this herd. Scripts were developed to identify missing information in the data. Incomplete records were eliminated when it was not possible to get complete information even with additional manual data edits of individual records.

The data included 1256 pigs with medication records available on farm. Pedigree information was available for 927 medicated pigs. Tail biting was the main reason that pigs required medication. There were 781 pigs from multiple breeds that had been treated for tail biting and most of these pigs (615 pigs) had pedigree information available. Genetic analyses were based on Large White pigs only (N = 553). A proportion of these pigs had information about sex missing leaving 459 Large White victims of tail biting with complete information for genetic analyses.

These data were combined with other performance data available for 12,051 pigs recorded on farm during the same time period as medication records were available. Data included only Large White pigs which were recorded for growth and backfat at an age of 126 days and a body weight of 85.7 kg.

#### 4.1.2. Definition of incidence scores

Three different incidence scores were defined to quantify the incidence of medication, incidence of tail biting, incidence of a disease other than tail biting. Pigs that were medicated for any disease were defined as 1 for the medication incidence while non-treated pigs received a 0. This incidence score quantifies the incidence of any disease. Pigs that were medicated specifically for tail biting were defined as 1 for the tail-biting incidence versus a 0 for pigs not treated for tail biting. Similarly, pigs that were medicated for any disease other than tail biting were defined as 1 for the medication incidence versus those pigs that were not treated for any other disease. Finally, the 0 score was based on pigs born from September 2010 until June 2017 that had performance records available. This number of pigs was lower than the number of pigs raised on farm. Overall, there were 12,051 pigs that had information about pedigree, medication and growth or backfat records available.

Whether the incidence observed on farm is higher or lower than the incidence reported here is not known because the number of pigs reported as medicated for tail biting or any other disease is incomplete due to missing pedigree information. Further, the number of pigs assumed to be healthy was based on the number of pigs recorded for growth and backfat which was lower than the number of pigs raised on farm. Therefore, the incidence reported for these scores should only be regarded as an indication of the true incidence for tail biting.

#### 4.1.3. Genetic analyses of tail biting scores

Heritability estimates. Genetic analyses were firstly based on general linear mixed models that included month of birth and sex as fixed effects. Random effects of the model were sire and common litter effect which were fitted for tail biting score with the procedure MIXED (SAS, 2014). These models were also used to estimate least squares means for sex and month of the year for tail biting incidence.

In these models, it is assumed that errors have normal distributions. This assumption is not correct for tail biting or medication scores because these traits have a binomial distribution. Tail biting score was modelled more appropriately by fitting a logit link function to connect expected value of the

outcome variable with a linear function of explanatory variables fitted in the model. The procedure GLIMMIX (SAS, 2014) was used to fit logistic sire models for tail biting and other medication scores. In animal breeding, logistic sire models are mostly used instead of logistic animal models because convergence is often not achieved for logistic animal models (e.g. Jamrozik et al., 2012; Baeza-Rodriguez et al., 2017) due to the frequency of extreme subclasses in which all observations are either zero or one (Misztal et al., 1989).

Convergence was not achieved for tail biting using the logistic sire model in this study when the standard model with birth month as the contemporary group was fitted. This lack of convergence may have been due to confounding of sire progeny with birth of month resulting from the low incidence of tail biting. This aspect was further investigated by sequentially removing individual months of birth that had at least two, three, four or five observations of tail biting. These limitations on data aimed to achieve better cross-classification of sire effect with birth month. Both the logistic and linear sire model were applied to these reduced data sets with improved data structure. However, this approach is not ideal because high proportions of the data were eliminated from analyses. Therefore, alternative models with different definitions of contemporary group effects were also explored.

Further, information about sex of animals was missing for 94 victims of tail biting representing 17% of tail-biting victims. These animals were not included in models that fitted the significant sex effect. Subsequently, alternative models with different contemporary group effects were implemented without fitting the sex effect in order to have more tail-biting victims included in the analyses.

The additive genetic variance is four times the sire variance. Heritability estimates were then derived as additive genetic variance divided by phenotypic variance. The common litter effect estimate was also expressed relative to the phenotypic variance by dividing variance due to common litter effect by the phenotypic variance.

Phenotypic variance was the sum of variances due to each random effect fitted in each model and the residual variance. Variance components are not directly comparable between linear and logistic models because linear models express variances on the observed scale while logistic models express variances on the logistic scale. The linear sire model was run with outcome variable (tail biting) being binomially distributed and no adjustment to the residual variance was made as outlined above. In comparison, the logistic link function converted the outcome variable to a standard logistic distribution with a mean of 0 and a residual variance of 3.29.

Heritabilities from linear versus logistic models should be put on the same scale for a comparison of estimates (Dempster and Lerner 1950). Heritability on the observed scale (heritability based on linear model) was converted to heritability on the underlying scale (heritability based on logistic model) using a formula outlined by Van Vleck (1972). For this conversion, the heritability on the observed scale was multiplied by the proportion of pigs with tail bite ( $p$ ) and the proportion of pigs that were not victims of tail biting ( $1 - p$ ). This product is then divided by the square of the standard normal curve ordinate at the threshold point where it cuts an area that is equal to the proportion of pigs with tail bite ( $z$ ). The proportion of pigs that were victims of tail biting was 0.045 which corresponds to a  $z$  value of -1.7 or 2.89 for the square value of  $z$ . The low proportion of pigs that were victims of tail biting implies that the heritability on the underlying scale was lower than the heritability on the observed scale for heritability estimates based on the linear sire model.

An alternative approach is to derive pseudo identifications for pigs without performance records from weaning records. The information about the litters weaned each week can be used to derive pedigree for pigs that were expected to be weaned from each litter each week. This approach was evaluated

by Guy et al. (2018) who found similar heritabilities for medication score when non-treated pigs were based on performance records or weaning records.

Genetic associations between tail biting and other traits were explored by fitting a sire model in ASReml (Gilmour et al., 2009) which considered genetic relationships between sires that were ignored in genetic analyses outlined above. Both linear and binary models outlined above were fitted in ASReml using a sire model. In addition, a linear animal model was also explored for comparison of estimates of heritabilities and genetic correlations.

Genetic models for average daily gain and backfat included month of birth as contemporary group and sex of the animal which were both fitted as fixed effects. The weight of the animal at recording was fitted as a linear covariable for backfat. Genetic associations were estimated using both a sire and an animal model for trait combinations.

#### **4.2. Genetic analyses of mortality records to identify tail-biting victims – Population B**

Data about removal of pigs recorded from 2011 to 2017 were extracted from the on-farm herd recording system. Victims of tail biting were identified based on removal records available on farm. The data included 488 records about purebred and crossbred pigs that had been removed from farm due to tail biting. This number of observations was reduced to 349 purebred pigs which had been removed from the herd due to tail biting over these seven years.

This low number of observation represents a removal due to tail biting of below 0.2% which is too low for statistical analyses because the cross-classification of tail biting incidence with other factors was insufficient.

The number of observed removals due to tail biting was derived based on data from 2011 to 2016 for illustration of seasonal effects.

#### **4.3. Genetic analyses of mortality records to identify tail-biting victims – Population C**

Data about victims of tail biting based on removal records were extracted from the on-farm herd recording system. The data extract contained pre-weaning and post-weaning removal of purebred and crossbred pigs collected from 2008 until 2015. Recording of removal reasons varied over years and information about removals of pigs due to tail biting was insufficient for subsequent years. These data included 1,722 pigs that were removed due to tail biting.

Data were edited to ensure good cross-classification of effects which is paramount for analysis of a binary trait; e.g. both scores (0 and 1) should be well represented across all other factors included in models.

Removal data for 2015 were not sufficiently cross-classified with other effects and were excluded from analyses. Data were limited to post-weaning removals that occurred between 25 to 199 days of age. Analyses was based on male and female pigs only. After implementing these data limits, a total of 1,265 tail-biting victims remained in the overall data set. The majority of these pigs were crossbred pigs leaving 441 purebred pigs that were victims of tail biting used in genetic analyses.

Information was available about 13 pigs that were removed from the population because they were identified as a tail-biting pig. Similarly, the incidence of removal due to other aggressive behaviour was

also low (0.11 % of all mortalities). The incidence of tail biters and aggressive behaviours in general was too low to warrant any further investigation of these mortality categories.

Information about tail biting was combined with performance data which was available for 90,501 pigs from seven different lines that were recorded from 2008 until 2014. These pigs were recorded for growth rate and backfat at an age of 154 ( $\pm 9.96$ ) days and a body weight of 96.7 ( $\pm 12.3$ ).

Incidence score for removal due to tail biting was defined as 1 for pigs that had been removed due to tail biting and 0 for pigs with performance records. Further incidence scores were defined to identify purebred pigs that were removed due to unspecified injuries or trauma (trauma, N=650) or due to unspecified leg issue (legs, N=4117) which may have been related to biting behaviour of pigs within a group.

Analyses were based on general linear mixed models using the GLM procedure (SAS, 2014). These models included line (7 levels), sex (2 levels) as well as month (12 levels) and year (7 levels) of recording as fixed effects which were significant factors affecting incidence of tail biting, trauma and legs.

Random effects were explored with the procedure MIXED (SAS 2014) fitting sire as a random effect. Log likelihood for tail biting incidence was too flat (infinite) and it was not possible to estimate variance components for this trait. Analyses converged for incidence of trauma and legs. However, no sire variance was detected for the incidence of trauma. Further, heritability for removal of pigs due to leg problems was below 0.001 which was too low for inclusion of this traits in pig breeding strategies. Overall, these analyses demonstrated that it was not possible to detect genetic differences between sires within lines based on these trait definitions. The low incidence of removal due to tail biting or trauma (< 1% for each trait) may have contributed to the difficulty in detecting genetic differences between sires within lines.

## 5. Results

### 5.1. Results based on analyses of medication records – Population A

#### 5.1.1. Incidence of tail biting observed on farm

First investigations were based on all medication records in order to characterise the incidence of tail biting for different groups of pigs (e.g. weaner, porker or grower pigs) and different pens within the grower, the porker and the weaner sheds. The information presented in this report summarises the occurrence of tail biting for different pens within each shed. Pigs are allocated evenly to individual pens within each shed over time. Therefore, observed incidence of tail biting for individual pens gives first indications about actual differences in the incidence of tail biting for specific pens within a shed.

Information about location of pigs was only available for a proportion of medicated pigs and it was therefore not possible to apply statistical models to these medication data to quantify significance levels of pen effects.

The number of pigs medicated in the weaner, porker and grower shed is shown in Table A1 including the number of pigs that had information available about pen number within each shed. A proportion of pigs (47% of all medicated pigs) were moved to the sickbay for treatment and the pen number within each shed where pigs got sick before being moved to the sickbay was not known. This overview further illustrates that most pigs (676 pigs or 60%) were medicated in the grower shed followed by the weaner shed (24%). Tail biting was the main cause that pigs needed medication accounting for 47%, 71%, 66% of medications in the weaner, porker and grower shed, respectively.

Table A1. Number of pigs treated overall (Medication) and specifically for tail biting (tail biting) that had information about pen location (Pen) available within in each shed.

		Pen	Sickbay	Total
Weaner shed	Medication	141	124	265
	Tail biting	85	39	124
Porker shed	Medication	72	112	184
	Tail biting	62	68	130
Grower shed	Medication	385	291	676
	Tail biting	258	192	450

As pigs were moved from the weaner to the porker and then to the grower shed, they were housed in different pens within each shed. The pen information relates to the pen of the pig at the time the pig was medicated. Non-medicated pigs had no pen information available and it was therefore not possible to fit pen as a specific effect in a statistical model. However, it is expected that all pens within each shed were allocated the same number of pigs over time. Therefore, a higher incidence of tail biting for individual pens indicates that the risk of tail biting was higher in some pens.

The number of tail bites observed for each pen within the grower, porker and weaner shed differed between pens in each shed. A higher incidence of tail biting was observed for pens 11 to 15 and 21 to 25 in the grower shed (Figure 1). The location of fans and the direction of each fan within the grower shed is also illustrated in Figure 1 illustrating that more tail biting was observed for pens that were close to these two fans in the grower shed. A similar observation was made for the porker shed where pen 4, 5 and 6 had a higher incidence of tail biting observed (Figure A2). Fans moved wind to pens 4

and 6 while pen 5 is located under a window in the corridor of the porker shed. The location of fans in the weaner shed also corresponded to higher observation of tail biting (Figure 5).

Jointly, these observations indicate that wind turbulences created by fans installed in these sheds may have contributed to a higher incidence of tail biting in specific pens of these sheds.

Levels of carbon dioxide and ammonia describe aspects of air quality within a shed. A previous study conducted in this herd showed that measures of the environment were variable over time (Hermesch et al., 2015; Final Report 2B-103, Pork CRC). In this previous study, air quality measures were recorded on six days from May 2013 to July 2013 in the porker and finisher shed. The average carbon dioxide and ammonia levels for each pen recorded in the previous study are shown in Figure 2 and Figure 4 for the grower and porker shed. Although carbon dioxide and ammonia levels varied between pens in the grower shed, an association between air quality measures and incidence of tail biting was less obvious. This lack of association is partly due to the fact that air quality measures were only available for a proportion of the time period that had tail-biting observations recorded. Despite this reduced overlap of environmental measures with tail-biting observations, a weak association between a higher incidence of tail biting in pens 24 to 28 of the grower shed and higher levels of ammonia and carbon dioxide may be noted. The variation in air quality over time and to some extent the variation in air quality between pens within a shed warrants the recommendation to measure air quality for individual pens within a shed over time and to investigate the effect of air quality on the incidence of tail biting for individual pens. In particular, air quality of all individual pens within a shed should be recorded when a tail biting outbreak has occurred in some pens.



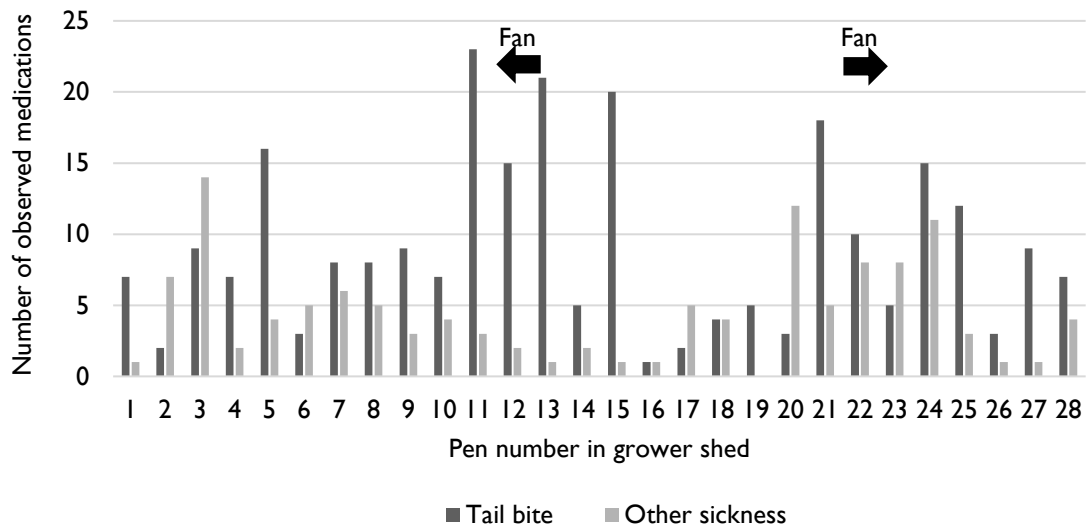


Figure 1 Number of observed pigs medicated for tail biting or any other sickness in each pen of the grower shed.

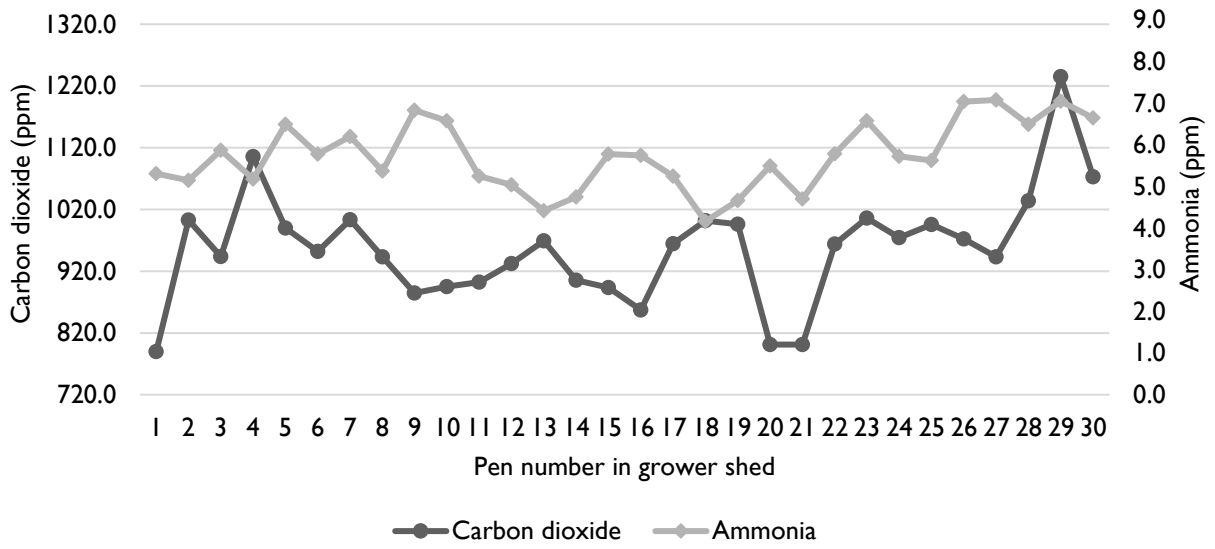


Figure 2 Observed carbon dioxide and ammonia levels for pens in the grower shed (observations based on data outlined in Hermes et al., 2015)

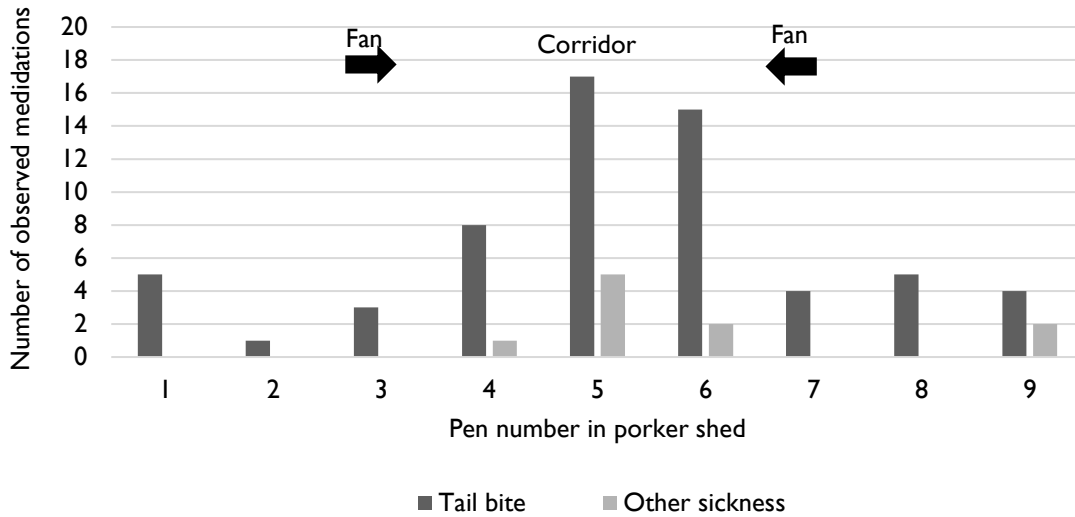


Figure 3 Number of observed pigs medicated for tail biting or any other sickness in each pen of the porker shed.

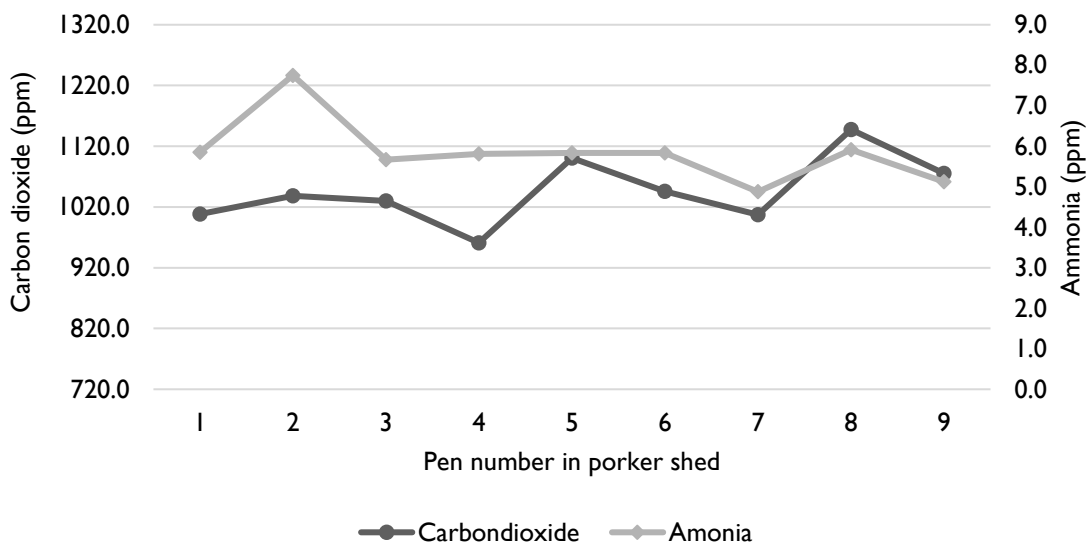


Figure 4 Observed carbon dioxide and ammonia levels for pens in the porker shed (observations based on data outlined in Hermes et al., 2015)

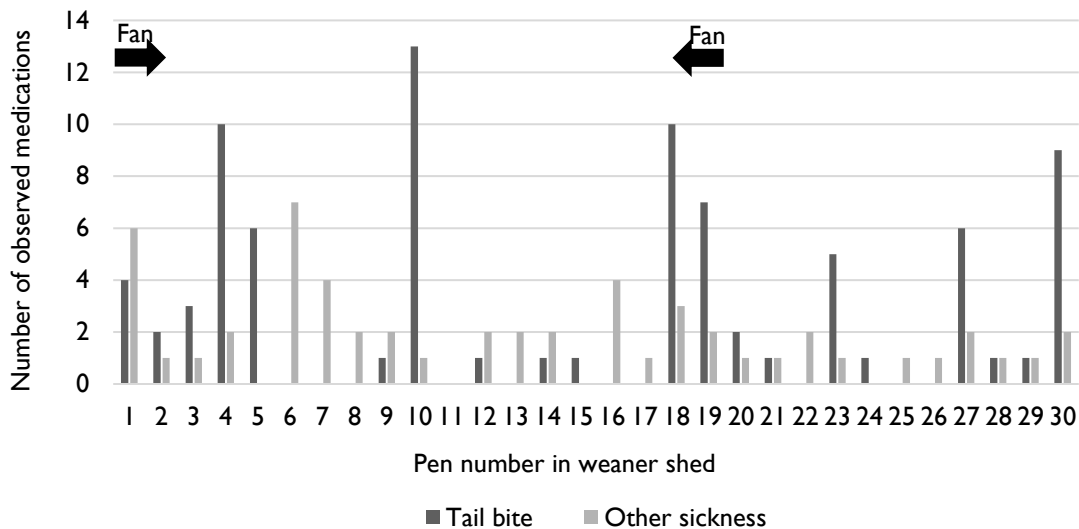


Figure 5 Number of observed pigs medicated for tail biting or any other sickness in each pen of the weaner shed.

### 5.1.2. Factors affecting incidence of tail biting

Males were more likely to be a victim of tail biting than gilts. The predicted incidence of tail biting in males was 9.85% ( $\pm$  0.63%) versus 7.13% ( $\pm$  0.57%) in gilts. A higher incidence of tail biting in males has been reported previously in the literature (review by Schroder-Petersen and Simonsen, 2001 and Diaz et al., 2017).

Incidence of tail biting was higher for pigs born in January to April of each year (Figure 6). The incidence of tail biting occurred mostly three months after the month of birth which implies that incidence of tail biting was higher in the autumn and winter months. The specific reason for the higher incidence of tail biting are not known, however, multiple indoor-climate factors which may be more prevalent in autumn and winter have been shown to be associated with higher tail biting incidence (Schroder-Petersen and Simonsen, 2001). These indoor-climate factors include lower temperatures, poor ventilation, draught and extreme chill factors. Therefore, particular attention should be given to these indoor-climate factors and their effects on tail biting.

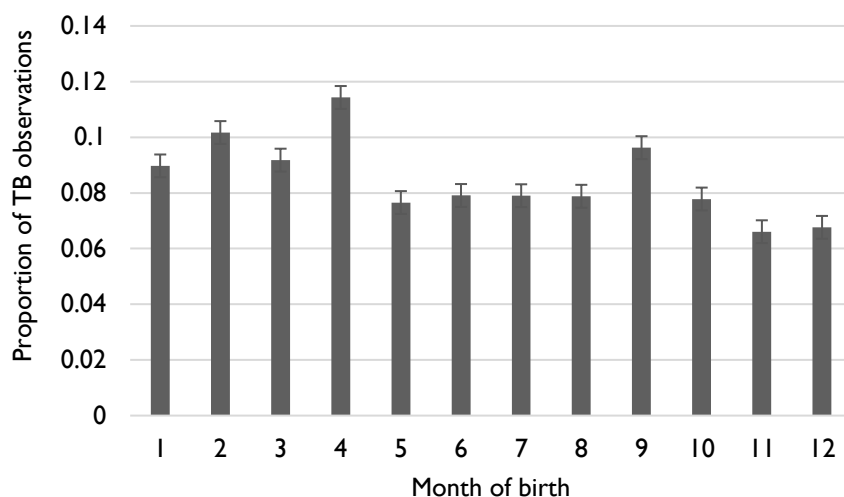


Figure 6 Proportion of tail biting (TB) observations for each month of birth (Note: Incidence of medication was mostly observed 3 months after month of birth)

### 5.1.3. Heritability estimates for tail biting incidence

#### Effect of data structure on heritability estimates

Using the full data set and a linear sire model, heritability for tail biting score (TB) was 0.11 when sire was the only random effect fitted in the model (Table A2). This heritability was reduced slightly to 0.09 when common litter effect was added to the model. The estimate of common litter effect was 0.11 which did not change significantly when the data set was modified by removing months that had at least 2, 3, 4, 5 or 6 TB victims per month. In contrast, heritability for TB increased continuously to 0.18 when more TB victims were present in each month. This increase in heritability indicates that the contemporary group effect (month of birth in this example) accounts for a proportion of the sire variance when the incidence of TB is low for each month. Therefore, higher incidence of TB is required for each contemporary group in order to disentangle genetic from environmental factors reliably.

Phenotypic variance increased when months with less tail biting victims were removed because the remaining data had a higher proportion of tail biting victims. This increase in phenotypic variance is expected for a binomial trait like tail biting score, because the variance of a variable that assumes the value of 1 with a probability of  $p$  is  $p*(1-p)$ . Given this formula, variance is smaller for a lower proportion of pigs that were victims of tail biting.

The logistic sire model did not converge when all data were used and birth month was fitted as a contemporary group effect. This model only converged when data were restricted to ensure that at least six observations of TB was present for every month of birth. Heritability estimate was 0.41 for the logistic sire model which fitted only sire as a random effect. This heritability is expected to be lower when common litter effect is fitted as a second random effect.

Table A2 Sire ( $V_{sire}$ ), common litter effect ( $V_{pe}$ ), residual ( $V_{res}$ ) and phenotypic ( $V_p$ ) variances along with estimates of heritability ( $h^2$ ) and common litter effect ( $c^2$ ) for tail biting (TB) fitting linear sire models and applying restrictions to the data set.

Data set	$V_{sire}$	$V_{pe}$	$V_{res}$	$V_p$	$h^2$	$c^2$
Full – month only sire	0.00106		0.0364	0.0374	0.11	
Full – month	0.00087	0.00400	0.0329	0.0378	0.09	0.11
2 TB victims/month	0.00100	0.00394	0.0338	0.0387	0.11	0.10
3 TB victims/month	0.00132	0.00422	0.0367	0.0423	0.12	0.10
4 TB victims/month	0.00156	0.00423	0.0381	0.0439	0.14	0.10
5 TB victims/month	0.00193	0.00489	0.0396	0.0464	0.17	0.11
6 TB victims/month	0.00224	0.00539	0.0414	0.0490	0.18	0.11

Effect of fixed effect model on heritability estimates

Linear sire models that only included year and sex as well as month or season resulted in similar heritability estimates for tail-biting victims of 0.17 or 0.18 (Table A3a). This heritability estimate is similar to the heritability estimate obtained with the reduced data set that had at least 5 or 6 tail-biting victims per birth month outlined previously (Table A2). When a year-by-season interaction was fitted, heritability estimate was 0.13 (Table A3a) in comparison to a heritability of 0.09 for a model that included birth month as a contemporary group effect (Table A2). Season was defined in three-month periods and contemporary group sizes for year-season were larger than contemporary group sizes based on birth month. These results further support the observation that fitting smaller contemporary group sizes reduced estimates of heritabilities for tail biting due to a confounding of the incidence of tail biting of progeny from specific sires and contemporary groups.

Table A3a Sire ( $V_{sire}$ ), common litter effect ( $V_{pe}$ ), residual ( $V_{res}$ ) and phenotypic ( $V_p$ ) variances along with estimates of heritability ( $h^2$ ) and common litter effect ( $c^2$ ) for tail biting (TB) fitting linear sire models and applying different models.

Fixed effects in model	$V_{sire}$	$V_{pe}$	$V_{res}$	$V_p$	$h^2$	$c^2$
Year + sex	0.00183	0.00648	0.0328	0.0411	0.18	0.16
Year + month + sex	0.00178	0.00647	0.0328	0.0410	0.17	0.16
Year + season + sex	0.00181	0.00645	0.0328	0.0411	0.18	0.16
Year + season + year*season + sex	0.00128	0.00524	0.0331	0.0396	0.13	0.13

It was possible to include more tail-biting victims in analyses when the significant effect of sex was omitted from the model. Heritabilities from these analyses were slightly higher for the less complex models (Table A3b) in comparison to the previous models indicating that genetic differences between sires may be detected more easily for higher incidence of tail biting.

Table A3b Sire ( $V_{sire}$ ), common litter effect ( $V_{pe}$ ), residual ( $V_{res}$ ) and phenotypic ( $V_p$ ) variances along with estimates of heritability ( $h^2$ ) and common litter effect ( $c^2$ ) for tail biting (TB) fitting linear sire models and applying different models.

Fixed effects in model <sup>1</sup>	$V_{sire}$	$V_{pe}$	$V_{res}$	$V_p$	$h^2$	$c^2$
Year	0.00276	0.00597	0.0377	0.0464	0.24	0.13
Year + month	0.00256	0.00593	0.0377	0.0462	0.22	0.13
Year + season	0.00267	0.00597	0.0377	0.0463	0.23	0.13
Year + season + year*season	0.00122	0.00518	0.0379	0.0443	0.11	0.123

<sup>1</sup> sex was omitted from model in order to include more tail-biting victims in analyses

### Heritability estimates for all traits

Following these explorations of models and data structure, final estimates of heritabilities and common litter effects are shown in Table A5 for all traits. These estimates were based on linear sire models that consider genetic relationships between sires. As expected, heritability and common litter effect estimates for tail biting (Table A4) were equivalent to estimates presented in previous Tables which ignored relationships between sires.

Overall medication score had lower heritability than tail biting incidence because it included both medication due to tail biting and medication due to other health issues. Medication due to other health issues had not significant heritability and heritability of overall medication score was therefore lower than heritability for medication due to tail biting.

Animal models are usually used in animal breeding applications which consider all genetic relationships between animals. Heritability estimates were lower for tail biting or medication scores using an animal model (Table A5) in comparison to using a sire model indicating that an animal model is less able to detect genetic differences between animals. Moderate heritabilities of 0.22 and 0.24 for growth and backfat corresponded to heritability estimates usually found for these traits.

Tail biting score had a moderate heritability based on a logistic sire model that also included the litter effect (Table A6). A higher heritability based on a logistic sire model in comparison to linear sire models has been observed in other studies (e.g. Doyle et al, 2000; Baeza-Rodriguez et al., 2017).

Table A4 Additive genetic ( $V_a$ ) and phenotypic ( $V_p$ ) variances along with estimates of heritability ( $h^2$ ) and common litter effect ( $c^2$ ) and their standard errors ( $se$ ) for tail biting and health traits fitting linear sire models with different contemporary group (CG) effects.

Trait	CG effect	$V_a$	$V_p$	$h^2$	$se$	$c^2$	$se$
Tail biting	Birth month	0.0032	0.0377	0.09	0.02	0.11	0.01
	Birth season	0.0049	0.0396	0.12	0.03	0.13	0.01
Medication	Birth month	0.0040	0.0602	0.07	0.02	0.08	0.01
	Birth season	0.0053	0.0620	0.09	0.03	0.10	0.01
Other sickness	Birth month	0.0001	0.0276	0.004	0.007	0.04	0.01
	Birth season	0.0002	0.0280	0.008	0.009	0.04	0.01

Table A5 Additive genetic ( $V_a$ ) and phenotypic ( $V_p$ ) variances along with estimates of heritability ( $h^2$ ) and common litter effect ( $c^2$ ) and their standard errors (se) for tail biting, health and performance traits fitting linear animal models with different contemporary group (CG) effects.

Trait	CG effect	$V_a$	$V_p$	$h^2$	se	$c^2$	se
Tail biting	Birth month	0.0014	0.0375	0.04	0.01	0.11	0.01
	Birth season	0.0017	0.0392	0.04	0.01	0.14	0.01
Medication	Birth month	0.0017	0.0600	0.03	0.01	0.08	0.01
	Birth season	0.0016	0.0616	0.03	0.01	0.10	0.01
Other sickness	Birth month	0.0007	0.0276	0.003	0.005	0.03	0.01
	Birth season	0.0003	0.0280	0.001	0.005	0.04	0.01
Growth rate	Birth month	876	2668	0.22	0.03	0.12	0.01
	Birth season	941	2632	0.23	0.03	0.13	0.01
Backfat	Birth month	0.42	1.73	0.24	0.03	0.06	0.01
	Birth season	0.39	1.74	0.23	0.02	0.07	0.01

Table A6 Additive genetic ( $V_a$ ) and phenotypic ( $V_p$ ) variances along with estimates of heritability ( $h^2$ ) and common litter effect ( $c^2$ ) and their standard errors (se) for tail biting, health and performance traits fitting logistic sire models with different contemporary group (CG) effects.

Trait	CG effect	$V_a$	$V_p$	$h^2$	se	$c^2$	se
Tail biting	Birth month	1.0305	4.1367	0.25	0.09	0.14	0.03
	Birth season	1.357	4.248	0.32	0.10	0.15	0.03
Medication	Birth month	0.515	3.837	0.13	0.06	0.11	0.03
	Birth season	0.669	3.895	0.17	0.06	0.11	0.03
Other sickness	Birth month	0.0001	0.0276	0.004	0.007	0.04	0.01
	Birth season	0.0002	0.0280	0.008	0.009	0.04	0.01

### 5.1.3. Genetic associations

Genetic associations between tail biting and growth or backfat are shown in Table A7. Estimates of genetic correlations were not significantly different from zero varying from -0.09 to 0.13 for different trait and model combinations. Other correlations between tail biting and growth rate were negative and significantly different to zero demonstrating that higher incidence of tail biting were 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.

Estimates of genetic and non-genetic associations between medication score and growth rate or backfat were similar to associations between tail biting and growth rate or backfat (Table A8). In particular, genetic correlations were also not significantly different to zero indicating that selection for higher growth rate and lower backfat will not affect medication score adversely.

It was not possible to estimate genetic correlations between medication due to other health issues and growth rate or backfat because this medication score was not heritable.

Table A7 Genetic (rg), common litter (rc), residual (rr) and phenotypic (rp) correlations (with standard errors) between tail biting and growth rate or backfat fitting linear animal or sire models.

Trait	Model	rg	rc	rr	rp
Growth rate	Animal model	0.13 (0.15)	-0.21 (0.07)	-0.08 (0.02)	-0.07 (0.01)
	Sire model	0.03 (0.18)	-0.14 (0.06)	-0.06 (0.01)	-0.07 (0.01)
Backfat	Animal model	-0.08 (0.15)	-0.13 (0.10)	-0.01 (0.02)	-0.02 (0.01)
	Sire model	-0.09 (0.19)	-0.09 (0.07)	-0.01 (0.01)	-0.02 (0.01)

Table A8 Genetic (rg), common litter (rc), residual (rr) and phenotypic (rp) correlations (with standard errors) between overall medication score and growth rate or backfat fitting linear animal or sire models.

Trait	Model	rg	rc	rr	rp
Growth rate	Animal model	0.10 (0.16)	-0.17 (0.08)	-0.11 (0.02)	-0.10 (0.01)
	Sire model	0.03 (0.19)	-0.11 (0.07)	-0.10 (0.01)	-0.09 (0.01)
Backfat	Animal model	-0.14 (0.16)	-0.11 (0.11)	0.00 (0.02)	-0.02 (0.01)
	Sire model	-0.01 (0.19)	-0.09 (0.08)	-0.01 (0.01)	-0.02 (0.01)

## 5.2. Results based on analyses of removal records – Population B

Pigs were removed from the herd due to tail biting at an average age of 126.3 days (standard deviation of 30.2). More pigs were removed due to being a victim of tail biting in autumn and winter (Figure 7) corresponding to results from Herd A. This repeated observation indicates that indoor climate conditions affect outbreaks of tail biting as was outlined by Schroder-Petersen and Simonsen (2001) in their review.

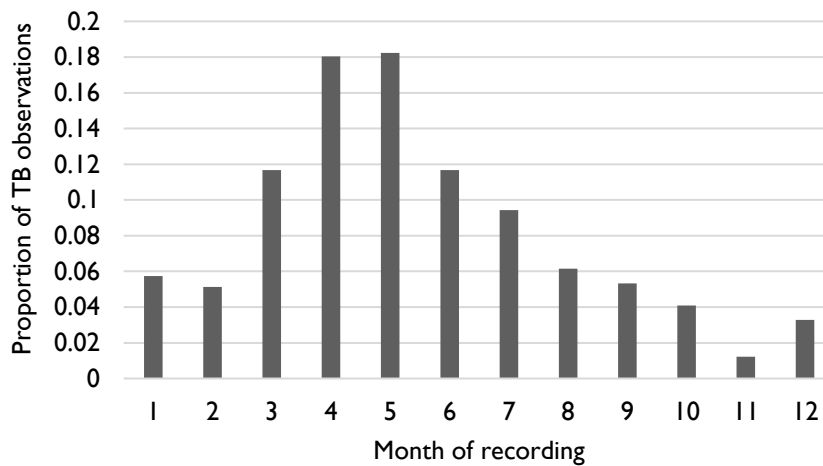


Figure 7 Proportion of removals due to tail biting for each month of recording

## 5.3. Results based on analyses of removal records – Population C

Pigs were affected by tail biting at an average age of 123.7 days (standard deviation of 35.3 days) which was considerably higher than the average mortality age of pigs that died post weaning (90.4 days with



standard deviation of 49.3 days). This higher age of pigs affected by tail biting implies higher costs attributed to tail biting in comparison to mortality of pigs due to other causes.

### 5.1.2. Factors affecting incidence of tail biting

In this population, males were less likely to be a victim of tail biting than gilts. The predicted incidence of removal due to tail biting in males was 0.21% ( $\pm 0.035$ ) versus 0.67% ( $\pm 0.038$ ) in gilts. This finding contradicts results from Population A in this study and results presented in the literature (review by Schroder-Petersen and Simonsen, 2001 and Diaz et al., 2017).

Incidence of tail biting was higher in June to December each year based on the month of recording (Figure 8). The specific reasons for the higher incidence of tail biting in the second half of the year are not known.

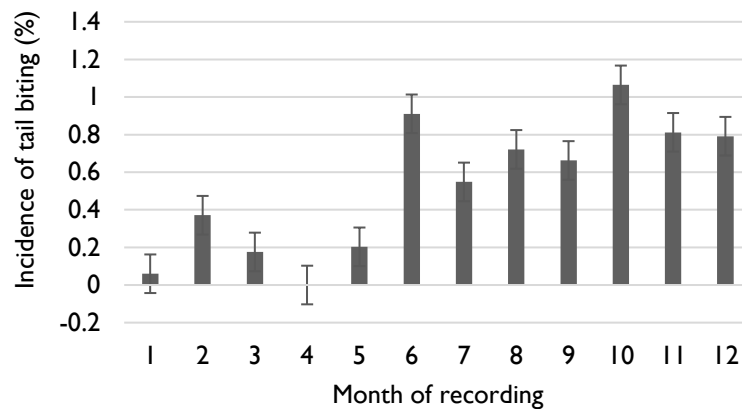


Figure 8 Incidence of removal due to tail biting for each month of recording

Incidence of removal due to tail biting different between lines (Figure 9). Breed differences for tail biters have been reported previously (Schroder-Petersen and Simonsen, 2001).

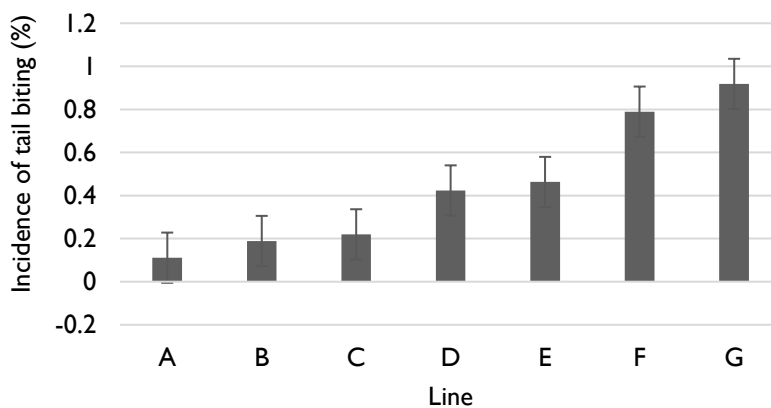


Figure 9 Incidence of removal due to tail biting for different lines

## **6. Discussion**

### **6.1. Heritability estimates**

Tail biting had low to moderate heritability estimates depending on the model used. These heritability estimates for medication due to tail biting were higher than heritability estimates for medication due to other health issues. Tail biting represents a behaviour rather than a health issue and behaviour traits have been shown to be heritable as demonstrated in the extensive review by Canario et al. (2013). Further, Canario et al. (2018) found a heritability of 0.06 for a binary score (0/1) identifying victims of tail biting at a body weight of around 100 kg based on observed injury to the tail. No further studies were found in regard to genetic analyses of tail biting victims.

Tail biting was defined as a binary (0/1) trait which does not have a normal distribution. Different models were explored to account for the non-normal distribution of tail biting scores. The heritability on the observed scale from the linear model was higher than the corresponding heritability on the underlying scale given the low incidence of tail biting. Therefore, heritability estimates were considerably lower for linear sire models than for logistic sire models which has also been observed in other studies (e.g. Baeza-Rodriguez et al., 2017; Doyle et al., 2000). Similarly, Breuer et al. (2005) found heritability of 0.05 in Landrace pigs for clinical tail biters and a corresponding heritability of 0.25 as a continuous trait on the underlying scale. However, Breuer et al. (2005) did not find a heritability for tail biters in Large White pigs.

Logistic sire models, rather than logistic animal models are often used in animal breeding for binary traits because logistic sire models are more robust than logistic animal models due to better cross-classification of effects in the model. In this study, multiple logistic sire models were also used and heritability estimates from these logistic sire models for tail biting corresponded well with estimates by Breuer et al. (2005) for tail biters in Landrace.

Predictive ability and goodness of fit of linear models versus logistic models have been compared in animal breeding applications. Multiple studies suggested to use linear models for binary traits (e.g. Baeza-Rodriguez et al., 2017; Abdollahi-Arpanahi et al., 2013) because the best fit and prediction was found for linear models.

In conclusion, linear sire models were more robust than logistic sire models and it is recommended to use linear sire models for genetic evaluation of tail biting. For genetic evaluation of tail-biting observations, the incidence of tail biting has to be evaluated and contemporary groups have to be sufficiently large to ensure good cross-classification of effects in the model. Therefore, contemporary groups may be based on three-monthly time periods rather than monthly definitions of contemporary groups.

### **6.2. Genetic associations**

Both tail biting and medication scores had no significant genetic associations with either growth rate or backfat. Therefore, current selection strategies for improved growth rate and lower backfat level are not expected to lead to higher incidence of tail biting or medication score. However, a lack of genetic association between tail biting and performance traits also implies that breeding programs have to include tail biting in selection decisions and put selection emphasis on this trait in order to achieve genetic gain in tail biting (reduced incidence of tail biting).

No information was found in the literature about genetic associations between being a victim of tail biting and growth rate or backfat. Only two studies were found that may be compared indirectly.

Breuer et al. (2005) investigated clinical tail-biters, rather than victims of tail biting. Being a tail biter (0/1 trait) was identified as a heritable trait in Landrace pigs. In this population, tail-biting was unfavourably genetically correlated with lean tissue growth rate ( $rg$  of 0.27), and back fat (BF) thickness at 90 kg ( $rg$  of -0.28). These results indicate that current selection strategies may increase the incidence of tail biters at least in this Landrace population. A higher frequency of tail biters has been reported for some Landrace populations (Schroder-Petersen and Simonsen, 2001).

Camerlink et al. (2015) evaluated biting behaviour of pigs divergently selected for indirect genetic effects for growth. Indirect genetic effects are heritable effects of an individual on the performance of other animals in the group which may result from social interactions. Pigs selected for high indirect genetic effects for growth were found to have less aggressive biting, less ear biting and less biting on enrichment material. These pigs also had a lower tail damage score and were therefore less likely to be a victim of tail biting.

Results from these studies are not directly comparable because different aspects of tail biting (tail biter versus victim of tail biting) and selection (direct genetic effects versus indirect genetic effects for growth) were presented. This overview illustrates that specific aspects of each study need to be taken into account when comparing results. However, results from these studies jointly demonstrate that tail biting behaviours are influenced by genetic effects that can be used for development of selection strategies to reduce incidence of tail biting in pigs.

### **6.3. Use of removal information for analyses of tail biting**

The incidence of removal due to tail biting was low for both Population B and Population C. As a result, it was not possible to estimate heritabilities for removal due to tail biting in these data sets.

Line differences were detected indicating genetic effects. However, estimates of genetic effects are not always clear (ESFA, 2007). Given the low incidence of removal due to tail biting, confounding of line or month of recording with other unknown factors may have occurred and may have affected estimates of these factors.

### **6.4. Estimates of non-genetic effects on incidence of tail biting**

Gender of pigs affected incidence of tail biting in multiple populations in this study. However, the effect of sex was not consistent between populations.

A higher incidence of tail biting was observed for pens that are expected to have higher levels of draughts due to the vicinity of fans for these pens. Indoor climate factors including higher levels of draughts have been shown to influence the incidence of tail biting (Schroder-Petersen and Simonsen, 2001).

Calendar month was a significant effect on incidence of tail biting in all populations. More tail biting was observed during autumn and winter months in two populations indicating that unfavourable indoor climate variables such as cold temperatures and chill factors may lead to higher incidence of tail biting which has been observed previously (e.g. Schroder-Petersen and Simonsen, 2001).

However, the effects of calendar month on incidence of tail biting varied between populations indicating that other temporary and unknown factors exist that lead to an outbreak of tail biting at a specific time and in a specific group of pigs within each farm. It is therefore important to monitor incidence of tail biting on farms closely and to record when and where outbreaks occur within the piggery in order to identify farm-specific factors leading to an outbreak of tail biting.

## 7. Implications & Recommendations

A simple binary medication score that identified victims of tail biting (score of 1) from pigs that did not need medication due to being a victim of tail biting (score of 0) was heritable. No heritability estimate was found in the literature about medication score of tail-biting victims and this first heritability estimate provides opportunities for pig breeding programs to select pigs that are less likely to become victims of tail biting. Information about medication of pigs is collected on farms for veterinary reasons. These data should be incorporated into electronic databases to facilitate selection of pig genotypes with reduced incidence of becoming a victim of tail biting.

Further, in a recent study conducted in France, the incidence of injury due to tail biting had a similar heritability than the heritability of medication due to tail biting found in this study. Injury due to tail biting can be easily noted when pigs are recorded for weight and backfat. This simple score should be implemented by breeding companies in order to facilitate selection of pigs that are better able to ward off tail biters.

Genetic correlations between medication score for tail biting and growth or backfat were not significantly different from zero. This result implies that current selection emphasis for higher lean meat growth does not affect incidence of tail biting. This result is favourable in the sense that current selection strategies do not lead to higher incidence of tail biting. However, it also implies that selection emphasis has to be placed on tail biting in order to achieve genetic gain in incidence of tail-biting victims.

Heritability estimates were affected by the choice of model. It is recommended to use sire models rather than animal models which are more robust in detecting genetic differences for a trait like tail biting that has a low incidence. Further, linear models had better convergence than logistic models and may be preferable in practical breeding applications. Heritabilities were higher for logistic sire models in comparison to linear sire models which is usually observed when applying these kind of models to binary traits.

The incidence of removal of pigs due to tail biting victims was too low for genetic analyses and these data are not useful for selection strategies to reduce incidence of tail biting in pig populations. Line differences were observed in one population providing further evidence for genetic influences on victims of tail biting.

Incidence of tail biting victims was higher in autumn and winter in two populations of this study. Indoor climate factors such as cold temperatures and chill factors have been shown to affect tail biting outbreaks which may have contributed to the higher incidence of tail biting in autumn and winter in two populations.

More tail-biting victims were observed for specific pens within grower, porker and weaner sheds. These pens were in the vicinity of fans and wind draught is expected to be higher in these pens. Farmers should evaluate micro-climate of individual pens within sheds in order to reduce incidence of tail biting for specific pens.

## 8. Technical Summary

Snapshot title: Genetics affects victims of tail biting

Purpose:

- To identify genetic and non-genetic factors affecting victims of tail biting

Take home messages – max 6 dot points (key outcomes for producers):

- A simple medication score to identify victims of tail biting was heritable offering new selection avenues to reduce incidence of tail biting on farms.
- Current selection strategies for higher lean meat growth are not expected to affect incidence of tail biting victims because no genetic associations between lean meat growth and tail biting were found in this study.
- Incidence of tail biting was higher in autumn and winter in two populations investigated in this study. Farmers should monitor indoor climate such as cold temperatures and chill factors in order to reduce the incidence of tail biting in autumn and winter.
- More tail-biting victims were observed for specific pens that were in the vicinity of fans. These pens had higher wind speed due to the position of fans within the shed. Farmers should evaluate micro-environments of individual pens within sheds in order to reduce incidence of tail biting for specific pens.

## 9. Literature cited

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## **10. Publications Arising**

No publications have been prepared from this Project so far.