Feasibility of reducing mortality of pigs from birth to slaughter by genetic selection

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Abstract

Pig mortality is a big welfare and economic challenge. This study investigated the feasibility of reducing mortality of pigs from day 5 to slaughter and from birth to slaughter by breeding. Data of 163,782 female pigs were from DanBred Yorkshire breeding herds. Variances and breeding values were estimated using a linear, a logit and a probit model based on mortality record (0, 1) at individual level. Estimates of direct heritabilities ranged from 0.013 to 0.017 and maternal heritabilities from 0.005 to 0.017. Estimated breeding values (EBVs) from the three models were highly consistent. Although low heritabilities, validation accuracies of EBVs ranged from 0.415 to 0.420 for direct EBVs, from 0.192 to 0.392 for maternal EBVs, and from 0.357 to 396 for total EBVs. The results indicate that reducing pig mortality by breeding is feasible, and linear model is efficient for genetic evaluation of pig mortality.

Introduction

Pig mortality in modern pig production has become a major welfare and economic concern. It has been reported that pre-weaning mortality rates vary between 12% and 25% (Alonso-Spilsbury et al., 2007). In addition to pre-weaning mortality, previous studies have shown that mortality rates ranged between 1.9% and 4.2% in nursery phase, and between 1.6% and 4.6% in finisher phase (USDA, 2015; Christiansen, 2018). In Denmark, selection for number of piglets alive at day 5 has been implemented since 2004, which is expected to improve both litter size and piglet survival before day 5 (Su et al., 2007). However, the mortality from day 5 to slaughter has not directly been taken into account yet. So far, the knowledge in efficiency of breeding for reducing pig mortality is very rare, especially for mortality after weaning.

Pig mortality is usually recorded at litter level and considered as a trait of sow. However, mortality is a complex trait that is also affected by the pig's own genotype. It may therefore be more appropriate to perform genetic evaluation of mortality at pig individual level using a model including direct and maternal additive genetic effects. Furthermore, since pig mortality at individual level is a binary trait, a standard linear Gaussian model may be not appropriate for analysing such data, and more sophisticated models should be considered.

The objective of this study is to evaluate feasibility of reducing mortality of pigs before slaughter by estimating variance components and heritability of pig mortality and validating accuracy of genetic evaluation of mortality using a linear, a logit and a probit model, based on data from Danish Yorkshire breeding herds.

Materials & Methods

Population and data. The data used in this study included 163,782 female pigs, collected from DanBred Yorkshire breeding herds from October 2018 to November 2021. Male pigs were not used in this study since relevant information was missing, e.g. castration. The traits in the analysis were mortality from day 5 to slaughter (Mort5S), and mortality from birth to slaughter (MortBS). Since all females were born in nucleus herds, slaughter age was set to 150 days for

all pigs. A pig was scored 1 if the pig died before slaughter, otherwise 0. Based on the data, Mortality rate was 16.6% for Mort5S and 23.8% for MortBS in this population.

Statistical models. Variance components and breeding values of mortality were estimated using the following single-trait models.

Linear mixed model: $\mathbf{y} = \mathbf{Xb} + \mathbf{Z_c c} + \mathbf{Z_l l} + \mathbf{Z_d a_d} + \mathbf{Z_m a_m} + \mathbf{e}$

Logit model: $\boldsymbol{\eta} = \mathbf{Xb} + \mathbf{Z_c c} + \mathbf{Z_l l} + \mathbf{Z_d a_d} + \mathbf{Z_m a_m}$

Probit model: $\boldsymbol{\rho} = \mathbf{Xb} + \mathbf{Z_c c} + \mathbf{Z_l l} + \mathbf{Z_d a_d} + \mathbf{Z_m a_m}$

In the models, **y** is the vector of binary observations $y_i = \{0,1\}$, **η** is the vector of logits with $\eta_i = \log(\pi_i/(1-\pi_i))$ where π_i is probability of death of animal i, and **ρ** is the vector of expected liabilities of death with $\rho_i = \Phi^{-1}(\pi_i)$ where Φ is cumulative normal distribution function, **b** is the vector of fixed effects including parity, herd, and year-month, **c** is the vector of random herd-year-month effects, ***l*** is the vector of random litter effects, $\mathbf{a_d}$ is the vector of direct additive genetic effects, $\mathbf{a_m}$ is the vector of maternal additive genetic effects. The scales of **b**, ***l***, **c**, $\mathbf{a_d}$ and $\mathbf{a_m}$ in the three models are different. It is assumed that $\mathbf{c} \sim N(\mathbf{0}, \mathbf{I}\sigma_c^2)$, $\boldsymbol{l} \sim N(\mathbf{0}, \mathbf{I}\sigma_l^2)$, $\begin{bmatrix}\mathbf{a_d}\\ \mathbf{a_m}\end{bmatrix} \sim N\left(\mathbf{0}, \begin{bmatrix}\sigma_{ad}^2 & \sigma_{adam}\\ \sigma_{adam} & \sigma_{am}^2\end{bmatrix} \otimes \mathbf{A}\right)$. The residuals are assumed to $\mathbf{e} \sim N(\mathbf{0}, \mathbf{I}\sigma_e^2)$ in the linear model, set to $\mathbf{e} \sim N(\mathbf{0}, \mathbf{I})$ in the probit model, and logistic distribution with variance ≈ 3.29 in the logit model. Phenotypic variance was defined as $\sigma_p^2 = \sigma_l^2 + \sigma_{ad}^2 + \sigma_{am}^2 + \sigma_{adam} + \sigma_e^2$ (Willham, 1972). The models were implemented using DMU package (Madsen et al, 2010).

Validation of genetic prediction. For validation of genetic prediction using the above models, the full data were divided into reference data and validation data by dam's birth date with 2019-10-01 as a cut-off date. Accuracy of EBV was measured as the correlation between EBV and corrected phenotype ($\mathbf{y_c}$) divided by accuracy of y_c. EBV from all three models were compared with the y_c from the linear model. The y_c was defined as $y_c = \hat{a}_d + \hat{a}_{m(dam)} + \hat{l} + \hat{e}$. By the definition, the accuracy of y_c was $r_{yc} = \sqrt{\frac{\sigma_{ad}^2 + \sigma_{am}^2 + \sigma_{adam}}{\sigma_l^2 + \sigma_{ad}^2 + \sigma_{am}^2 + \sigma_{adam} + \sigma_e^2}}$. Dispersion bias for each model was measured by the regression of EBV from full data on EBV from reference data.

Results

For all traits and models, the estimates of direct and maternal heritabilities were very low, ranging from 0.005 to 0.017 (Table 1). For MortBS, direct heritabilities in underlying scale from the logit and the probit model were not higher than those in observed scale from the linear model, which was unexpected, indicating a challenge of analysing binary traits. Maternal heritabilities for MortBS was higher than those for Mort5S. The correlations between direct and maternal additive genetic effects was low and not significantly different from zero.

Table 1. Phenotypic variance, proportion of litter variance, direct (a_d) and maternal (a_m) heritability, correlation between a_d and a_m, as well as their standard error (±).

Trait	Model	σ_p^2	lit^2	h_{ad}^2	h_{am}^2	r_{adam}
Mort5S	Linear	0.134	$0.051_{\pm 0.0021}$	$0.015_{\pm 0.0026}$	$0.005_{\pm 0.0017}$	$-0.119_{\pm 0.1747}$
	Logit	3.648	$0.071_{\pm 0.0038}$	$0.017_{\pm 0.0033}$	$0.010_{\pm 0.0031}$	$0.006_{\pm 0.1884}$
	Probit	1.107	$0.069_{\pm 0.0039}$	$0.016_{\pm 0.0030}$	$0.010_{\pm 0.0031}$	$0.032_{\pm 0.1879}$
MortBS	Linear	0.177	$0.061_{\pm 0.0021}$	$0.015_{\pm 0.0026}$	$0.010_{\pm 0.0022}$	$-0.182_{\pm 0.1451}$
	Logit	3.665	$0.076_{\pm 0.0031}$	$0.013_{\pm 0.0024}$	$0.014_{\pm 0.0031}$	$-0.069_{\pm 0.1613}$
	Probit	1.128	$0.084_{\pm 0.0035}$	$0.014_{\pm 0.0025}$	$0.017_{\pm 0.0034}$	$-0.050_{\pm 0.1608}$

Although variance components and heritabilities were somewhat different among the three models, the EBVs from the three models are highly consistent (Table 2). For the validation animals, correlations between EBVs from logit and probit model were higher than 0.998. Correlations between EBVs from the linear model and the other two models were about 0.990 for direct EBVs and total EBVs, and ranged from 0.928 to 973 for maternal EBVs.

Table 2. Correlations (upper diagonal for Mort5S and lower diagonals for MortBS) between EBVs from different models.

Model	EBV_{ad}			EBV_{am}			EBV_{ad+am}		
	Linear	Logit	Probit	Linear	Logit	Probit	Linear	Logit	probit
Linear	1	0.992	0.989	1	0.948	0.928	1	0.993	0.989
Logit	0.993	1	0.999	0.973	1	0.998	0.994	1	0.999
Probit	0.991	0.999	1	0.965	0.999	1	0.993	0.999	1

Regression coefficients of the EBVs obtained from full data on the EBVs from reference data for validation animals ranged from 0.932 to 1.194 (Table 3), indicating that dispersion bias was small for all models and traits. Regression coefficients for the logit and probit models were slightly less far from 1 than the counterparts from the linear model, indicating slightly less bias.

Table 3. Regression coefficients of EBVs from full data on EBVs from reference data.

Trait	Model	EBV_{ad}	EBV_{am}	EBV_{ad+am}
Mort5S	Linear	0.948	1.194	0.932
n=22,364	Logit	0.986	1.139	0.942
	Probit	1.002	1.103	0.946
MortBS	Linear	0.978	1.081	0.956
n=24,628	Logit	1.028	1.047	0.975
	Probit	1.038	1.038	0.978

Despite low heritability, accuracy of EBV were not low (Table 4). Validation accuracies ranged from 0.415 to 0.420 for direct EBVs, from 0.192 to 0.392 for maternal EBVs, from 0.357 to 0.396 for total EBVs. The validation accuracies were very similar between the three models, except that accuracy of maternal EBV from the linear model was lower than those from the other two models. According to the results from the linear model, the total genetic variance for observed phenotypic values ($\sigma^2_{ad} + \sigma^2_{am} + \sigma_{adam}$) was 0.00248 for Mort5S and 0.00398 for MortBS. Selection on the sum of EBV_{ad} and EBV_{am} would reduce mortality by 1.95% for Mort5S, or 2.25% for MortBS, given selection intensity of 1.

Table 4. Validation accuracy of EBVs from different models

Trait	Model	EBV_{ad}	$EBV_{am(dam)}$	$EBV_{ad+am(dam)}$
Mort5S	Linear	0.420	0.236	0.392
n=22,364	Logit	0.418	0.378	0.396
	Probit	0.419	0.392	0.395
MortBS	Linear	0.415	0.192	0.357
n=24,628	Logit	0.418	0.255	0.358
	Probit	0.419	0.259	0.357

Discussion

This study assessed feasibility of reducing pig mortality before slaughter by investigating genetic parameters and selection accuracy using three models. With the binary output of mortality at individual level, it was expected that the logit model and the probit model would perform better than the linear model in which the normality assumption is violated. However, the results showed that the EBVs from the linear model were highly consistent with the EBVs from the logit and probit models. The validation accuracies of the three models were also similar to each other. The negligible difference in prediction accuracy between linear model and probit or logit model have been found in simulation studies (e.g., Meijering and Gianola, 1985) and in the studies on mastitis in cattle (e.g., Koeck et al., 2010). These results indicates that linear model is robust to violation of normality hypothesis, and thus it could be a good choice for genetic evaluation of pig mortality because it is simple to implement.

Heritabilities for the two mortality traits were lower than 0.02. However, accuracies of EBVs were moderate for direct EBV and total EBV, though relatively low for maternal EBV. This could be due to large information from relatives contributing to the estimation of breeding values. In the current study, an individual had, on average, about seven full-sibs and about 200 half-sibs in the data. According to the genetic parameters and accuracy of EBV obtained in this study, selection on total EBV would reduce mortality by i×1.95% for Mort5S, and i×2.25% for MortBS, where i is selection intensity. The realized reduction of mortality by including mortality in selection index will depend on the weight on mortality and the relationship of mortality with the other traits in the selection index.

Accuracies of EBV and expected genetic gains presented above are based on conventional selection. Genomic selection has been widely used in pig breeding. It has reported that selection accuracy and genetic gain increased up to 50% when changing conventional selection to genomic selection (e.g., Knol et al., 2016). In most pig breeding companies, pure pigs in test are genotyped. When genomic information is used for prediction of pig mortality, the accuracies of EBV and the genetic progress in reducing mortality is expected to increase largely.

We conclude: even though heritability for mortality traits is low, accuracy of EBV is acceptable for selective breeding; linear mixed model is efficient for predicting breeding value of mortality traits; and selection to reduce pig mortality before slaughter is feasible.

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