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Genetic analysis of pig survival up to commercial weight in a crossbred population

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ABSTRACT

Records from 99,384 crossbred pigs from Duroc sires and Large White × Landrace dams were used to estimate genetic parameters for survival traits at different stages of the fattening period, and their relations with final weight. Traits analyzed were preweaning mortality (PWM), culling between weaning and harvesting (C_{all}), culling during the farrowing period (C_{far}), in the nursery site (C_{nur}), during the finishing phase (C_{fin}), and hot carcass weight (HCW). Because of the binary nature of PWM and culling traits, threshold-linear models were used: Model 1, including PWM, C_{all}, and HCW; Model 2, including PWM, C_{far}, C_{nur}, C_{fin}, and HCW. Both models included sex and parity number as fixed effects for all traits. Contemporary groups were considered as fixed effect for HCW and as random effects for the binary traits. Random effects were sire additive genetic, common litter, and residual effects for all traits and models. Heritability estimates were 0.03 for PWM, and 0.15 for HCW with both models, 0.06 for C_{all} with Model 1, and 0.06 for C_{far}, 0.14 for C_{nur}, and 0.10 for C_{fin} with Model 2. Litter variance explained a large part of the total variance and its influence declined slightly with age. For Model 1, genetic correlations were −0.36 between PWM and C_{all}, −0.02 between PWM and HCW, and −0.25 between C_{all} and HCW; correlations for litter effect were −0.15 between PWM and C_{all}, −0.19 between PWM and HCW, and −0.21 between C_{all} and HCW. For Model 2, genetic correlations were all positive between PWM and culling traits, except between PWM and C_{nur} (−0.61). Genetic correlations between HCW and the other traits were moderate and negative to null. Correlations for common litter effect were all negative between traits, except between C_{far} and C_{fin}, and between C_{nur} and C_{fin}. Heritability of PWM and culling traits increased with age period. Therefore, selection for survival after weaning may be more efficient. The low genetic correlations between PWM and culling traits suggest that different genes influence pre and postweaning mortality. The HCW was not correlated with the other traits. However, relationships are not strongly unfavorable, therefore selection for survival and high final weight is possible.

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1. Introduction

Parameters used to measure performance in grow-finish pigs include mortality rate, growth and feed conversion. Increased mortality rates within the finishing period can result in a significant loss of investment and

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is an indication of poor animal health and/or animal welfare practices. Many studies have focused on farrowing and preweaning piglet mortality (e.g., Arango et al., 2005, 2006;Ibáñez-Escriche et al., 2009) or sow mortality (e.g., Chagnon et al., 1991; Sasaki and Koketsu, 2008). However, losses at higher age are even more economically important because of increasing rearing costs with age (Fuerst-Waltl and Sørensen, 2010) and to our knowledge, no genetic studies have investigated pig mortality between weaning and final market weight. Growing pig mortality includes pigs that die naturally as well as pigs that are euthanized. Pigs are usually euthanized to relieve the animal from pain or poor living conditions due to low body condition, poor health and hernia ruptures. These pigs are not only considered economically unprofitable but are also considered to be at risk of spreading disease to the rest of the herd and are discarded before the next phase of growth.

Environmental factors (i.e., management, housing, and hygienic status) also play a major role in growth and survival but may not be consistent over time. In contrast, genetic progress is permanent and cumulative across generations. However, additive genetic variation for survival must exist for improvement to occur (Henderson et al., 2011). Genetic analyses of survival until production age has been done in dairy cows and sheep (e.g., Fuerst-Waltl and Sørensen, 2010; Hatcher et al., 2010; Henderson et al., 2011). Those studies revealed that estimated direct heritabilities of survival traits during different periods are low. However, a sufficient genetic variability could still allow developing selection strategies for overall better survival (Henderson et al., 2011).

The objective of this study was to estimate genetic parameters for survival traits at different stages of the fattening period, from weaning to harvesting, and their genetic relations with the final market weight in a commercial crossbred population of pigs.

2. Materials and methods

Animal Care and Use Committee approval was not obtained for this study because data were obtained from an existing database.

2.1. Data

Data were provided by Smithfield Premium Genetics (Rose Hill, NC). The final dataset consisted of 99,384 records after discarding animals with incomplete or inconsistent information; the pedigree file included information for 103,980 animals. Data were recorded in a crossbred population of pigs between 2008 and 2010 on 1 commercial farm. Crossbred pigs were produced from the mating of purebred Duroc boars with crossbred Large White × Landrace sows. Pedigree data were not available for crossbred dams. Sows had records for ≤ 10 parities, but records for parities 7–10 were grouped together; percentages of records available by parity number are shown in Table 1.

Five survival traits were analyzed: preweaning mortality (PWM), which was the mortality of liveborn piglets before weaning at <21 d of age; culled during the farrowing phase (C_{far}), which were piglets that survived until weaning but could not be moved to the nursery site at <30 d of age because of low weaning weight (<2.7 kg), poor body condition, or poor health; culled during the nursery phase (C_{nur}), which were pigs that survived past 60 d of age but could not be moved to the finishing site because of poor body condition or poor health; culled during the finishing phase (C_{fin}), which were pigs that survived past 150 d of age but had poor body condition or poor health that required removal from the herd by euthanasia or had some other defect that resulted in the animal being sold to a discount market from the finishing site rather than being sent to the packing plant; and hot carcass weight (HCW). All culling traits were also grouped together and considered as 1 trait (C_{all}). Mortality and culling (PWM, C_{far}, C_{nur}, C_{fin}, and C_{all}) were considered to be binary traits (0 if the pig was still alive or not culled and 1 if the pig died or was censored at weaning or moving time); HCW was a continuous trait.

Table 1
Percentages of records by parity number.

Parity number	Percentage of records
1	17.0
2	18.5
3	17.5
4	15.0
5	12.0
6	10.0
7–10	10.0

A description of the data is shown in Table 2. The PWM status (dead or alive) was available for 99,384 animals. Of those pigs, 58,989 had C_{far} records, 58,856 had C_{nur} records, and 58,691 had C_{fin} records. The HCW was available for 51,933 of the pigs still in the system after the finishing phase. Mean age at slaughter was 194 ± 13 d. A total of 302 different purebred Duroc sires had progeny with PWM status recorded, and 229 of those sires had progeny with the other traits recorded. Mean parity number was 3.5 ± 1.9. Among the 1671 dams, 1413 had pigs recorded in parity >1. Contemporary groups were defined on the basis of piglets born during the same year and month because all animals at the commercial farm were managed similarly.

2.2. Statistical analysis

Single- and multiple-trait analyses with a sire model were used to estimate variance components. Only results from multiple-trait analyses are presented. The equation for the general multiple-trait model was

$$\boldsymbol{y} = X\beta + \boldsymbol{Zs} + \boldsymbol{Wl} + \boldsymbol{Qc} + \boldsymbol{e}$$

where $\boldsymbol{y}$ is a vector of observations (PWM, culling status, or HCW), β is a vector of fixed effects, $\boldsymbol{s}$ is a vector of additive genetic effects of the sire; $\boldsymbol{l}$ is a vector of common litter effects assigned by litter of the dam, $\boldsymbol{c}$ is a vector of random contemporary group effects; $\boldsymbol{X}$, $\boldsymbol{Z}$, $\boldsymbol{W}$, and $\boldsymbol{Q}$ are incidence matrices that relate observations to effects, and $\boldsymbol{e}$ is a vector of residual effects. Sire genetic effect was defined as

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