Genetic associations of sow longevity with age at first farrowing, number of piglets weaned, and wean to insemination interval in the Finnish Landrace swine population

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ABSTRACT: The objective of the study was to estimate genetic parameters for length of productive life (LPL), and determine its genetic correlation with age at first farrowing (AFF), number of piglets weaned at first farrowing (NW), and first wean-to-insemination interval (W2I) in the Finnish Landrace swine population. Data from the Finnish national litter recording scheme were utilized to estimate the genetics of LPL, and genetic associations between LPL, AFF, NW, and W2I. Data from the Finnish Landrace sow records were utilized from farms that farrowed more than 20 gilts annually from 2000 through 2005. The data set included information from 11,222 sows, all of which had AFF and NW information available. The sows producing the records evaluated were daughters of 1,267 sires, and there were 3,684 animals in the pedigree when all of the sires were traced back to founder animals. All data were obtained from FABA Breeding (Vantaa, Finland). Multivariate Bayesian analysis of Gaussian, right-censored Gaussian, and categorical traits was utilized to estimate (co)variance parameters of LPL, AFF, NW, and W2I of the sow. From these traits, AFF and NW were treated as Gaussian, LPL as right-censored Gaussian, and W2I as categorical traits. Estimated posterior means of heritabilities were 0.22, 0.16, 0.09, and 0.08 for LPL, AFF, NW, and W2I, respectively. A relatively large proportion of variance due to farm-year interaction was observed (posterior means of \( f^2 \) ranged between 0.03 and 0.26). The LPL was moderately genetically correlated with NW and AFF (posterior means were –0.20 and 0.36, respectively), whereas no clear association was found between W2I and LPL. Favorable genetic correlations between AFF and W2I and between NW and W2I were also observed. Additionally, an unfavorable genetic correlation between AFF and NW was observed in the present data set. Because LPL is genetically associated with other economically important prolificacy traits, it should be included in a multiple trait swine breeding value estimation system.

Key words: Bayesian analysis, correlation, genetics, length of productive life, multiple trait

INTRODUCTION

Length of productive life (LPL) is an important trait to consider from a productivity, profitability, and animal welfare perspective in modern pork production systems. Net-present value increases with the LPL of the sow (Stalder et al., 2003). Animal welfare concerns may arise when sows cannot remain productive for more than 1 or 2 parities. Thus, the interest to select for LPL in breeding programs has increased in recent years.

Alternative breeding value estimation methods have been presented for LPL and similar traits. Survival analysis is a well-accepted method for estimating breeding values for LPL, similar traits, or both. However, it has not been possible to conduct a multiple trait analysis that estimates breeding values for survival traits and other types (such as Gaussian and categorical) of traits simultaneously (Ducrocq and Stößner, 2001). Recently, Damgaard and Korsgaard (2006) introduced bivariate survival and Gaussian trait analysis, where both environmental and genetic correlations are modeled. Alternatively, LPL can be analyzed as a Gaussian trait when censoring is accounted for (Korsgaard et al., 2003). Successful, right-censored Gaussian trait analy-
Table 1. Number of observations (N), phenotypic means and SD for length of productive life (LPL), age at first farrowing (AFF), wean to successful insemination interval (W2I), and number of piglets at first weaning (NW) from the Finnish Landrace swine population.

<table>
<thead>
<tr>
<th>Item</th>
<th>n</th>
<th>Mean</th>
<th>SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>LPL</td>
<td>11,222</td>
<td>493.2</td>
<td>376.8</td>
</tr>
<tr>
<td>AFF</td>
<td>11,222</td>
<td>353.7</td>
<td>36.4</td>
</tr>
<tr>
<td>NW</td>
<td>11,222</td>
<td>8.9</td>
<td>2.0</td>
</tr>
</tbody>
</table>

*LPL was defined as interval from first farrowing to culling or censoring of sow, and W2I was defined as interval from first weaning to successful insemination or culling of sow.

sis of LPL has been reported in pigs by Arango et al. (2005) and Guo et al. (2001) and in fish by Kettunen et al. (2007).

Previous literature heritability estimates for LPL have ranged from 0.02 to 0.34, being population and trait definition dependent (Serenius and Stalder, 2004). Previous research results have not provided a consensus regarding the genetic associations between measures of sow longevity and other efficiency related traits. Reliable estimates of these correlations are needed to develop breeding value estimation routines for sow longevity. Thus, the objective of the current study was to estimate genetic parameters for LPL, and determine its genetic correlation with age at first farrowing (AFF), number of piglets weaned at first parity (NW), and first wean to insemination interval (W2I) after the first litter in the Finnish Landrace swine population.

MATERIALS AND METHODS

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

Data

Data from the Finnish litter recording scheme were utilized to estimate the genetics of LPL, and genetic associations between LPL, AFF, NW, and W2I. Data from Finnish Landrace sow records were utilized from farms that farrowed more than 20 gilts annually from 2000 through 2005. Moreover, observations were removed from the data if they were not within a logical or normal range of values (AFF: 240 to 500 d; NW: 1 to 20; W2I: 2 to 150 d). The data set included information from 11,222 sows, all of which had AFF and NW information available (Table 1). The sows producing the records evaluated were daughters of 1,267 sires, and there were 3,684 animals in the pedigree when all of the sires were traced back to founder animals. All data were obtained from FABA Breeding (Vantaa, Finland).

The LPL was defined as the natural logarithm of time (d) from first farrowing to culling or censoring (sow is still alive); AFF was defined as the interval from the birth of the sow to her first farrowing; and W2I was defined as the interval from first weaning to successful insemination or culling date. Because of the skewed distribution and the nature of W2I records, W2I records were categorized into 3 classes (1 = under 16 d; 2 = 16 to 40 d; 3 = over 40 d). This categorization was based on the distribution of W2I records in the current data set. The basis for these categories is as follows: First, a normal W2I would likely be between 1 and 16 d postweaning, albeit anything above 8 d would typically be considered a long W2I interval. The second category is represented from the end of the first category plus an additional estrous cycle (i.e., 16 d plus 21 to 24 d). Finally, the third W2I category is anything above the previously defined category. Based on our subjective evaluation of the W2I data and the biology of the estrous cycle in swine, these categories were developed. In the current data, there was very little crossfostering, and thus, no adjustment for the number of piglets allowed to nurse was made in the evaluation of NW records.

Statistical Analyses

Multivariate Bayesian analysis of Gaussian, right censored (animals considered still in production or status unknown at the time of the evaluation) Gaussian, and categorical traits was utilized to estimate (co)variance parameters. Gibbs sampling and data augmentation were implemented as described by Korsgaard et al. (2003). To keep the computation time reasonable, 6 separate 2-trait analyses were carried out. In matrix notation, the 2-trait statistical model utilized can be written as

\[ y = X b + W f + Z s + e, \]

where \( y \) is the vector of observations, \( b \) is the vector of fixed effects, \( f \) is the vector of random farm-year interaction effects, \( s \) is the vector of additive genetic sire effects, \( e \) is the vector of random residual effects, and \( X, W, \) and \( Z \) are known incidence matrices. The intercept was the only factor included in \( b \) of LPL. For all other traits, first farrowing year-month interaction was included in \( b \). In addition, the linear covariate of AFF was included in the statistical models of NW and W2I, if it was not one of the correlated characters. For NW, the fixed effects of breed of the litter (purebred vs. crossbred), weaning age, and mating type (AI vs. natural mating) were included in the \( b \) vector.

A priori, additive genetic sire effects were assumed normally distributed \( N(0, \mathbf{A} \otimes \mathbf{G}) \), where \( \mathbf{A} \) is additive genetic relationship matrix between sires (standard additive genetic relationship matrix) in \( s \), and \( \mathbf{G} \) is additive genetic sire (co)variance matrix. A priori, random residual effects were assumed to follow an inverted Wishart distribution. For a more detailed description...
of multiple trait analyses of Gaussian, right censored Gaussian, and categorical traits, see Korsgaard et al. (2003).

A blocked Gibbs sampler (Garcia-Cortes and Sorensen, 1996) was developed using C++ programs from a workshop given by Fernando and Kachman (2005). The Gibbs samplers were run as single chains of 101,000 cycles, where the first 1,000 were treated as a conservative burn-in. After burn-in, all of the samples were stored (i.e., 100,000 samples were retained to describe posterior distributions). Because 6 different, 2-trait chains were generated, posterior distributions of heritability estimates and proportion of variance due to the farm-year interaction effect were described with 300,000 (3 × 100,000) samples in total.

RESULTS

Posterior means, standard deviations, and first and third quartiles of posterior distributions of heritability ($h^2$) and proportion of variance due to farm-year interaction ($f^2$) are presented in Table 2. The heritability estimates for LPL and AFF are moderate, posterior means ($\pm$standard deviation) being 0.22 ± 0.04 and 0.16 ± 0.03, respectively. Similarly, estimated posterior means were 0.09 ± 0.02 and 0.08 ± 0.05 for NW and W2I, respectively.

In general, a moderate proportion of variation for the traits evaluated can be explained by including the farm-year interaction effect in the statistical model (Table 2). The greatest $f^2$ was estimated for AFF and LPL (posterior means were 0.26 and 0.23, respectively). Thus, a relatively large farm and farm-year variation in culling policy, management, farm conditions, or a combination of these, affecting AFF and LPL was observed in the present analyses. A large farm or management effect was expected by definition of lowly heritable traits such as reproductive traits in swine. Additionally, the estimated $f^2$ for W2I (0.10) was greater than the corresponding heritability estimate (0.08). Estimated posterior mean for $f^2$ of NW was less than (0.03) the estimates for the other traits evaluated in the present study.

Sow longevity (LPL) was moderately genetically associated with AFF and NW (posterior means were −0.20 and 0.36, respectively), whereas W2I was not correlated with LPL (posterior mean of $r_p = −0.05$; Figure 1). Both of the moderate genetic correlations observed were favorable (i.e., selection for large litters and short AFF would simultaneously improve LPL as well). Favorable genetic correlations between AFF and W2I and between NW and W2I were also obtained (Figure 1). However, the genetic correlation between AFF and NW was unfavorable (i.e., selection for large NW would increase AFF if both traits are not properly accounted for in a total merit index).

In general, estimated phenotypic correlations were very low (absolute values of posterior means being less than 0.10), but they had the same sign as the corresponding genetic correlation estimates (Table 3). However, there was one exception, a moderately negative genetic correlation between NW and W2I (−0.34), whereas the phenotypic correlation was positive (0.04). All of the standard deviations of posterior distributions for the genetic correlations were very low (≤0.02).
Heritability estimates appear to indicate that sufficient additive genetic variation exists such that it should be possible to improve the population for LPL, NW, AFF, and W2I through an effective genetic selection program implemented in an efficient swine-breeding program.

The farm and year interaction effect explained a relatively large proportion of phenotypic variation, posterior means for \( f^2 \) estimates ranging from 0.03 to 0.26. The greatest \( f^2 \) were estimated for LPL and AFF (0.23 and 0.26, respectively). These estimates indicate that relatively large variation differences exist for between farm-year variation, which is influenced by culling policies and breeding practice differences implemented for replacement gilts from year to year within a given farm and across farm of replacement gilts. An alternative explanation for the relatively large between farm-year variation in LPL and AFF of the sow could be that relatively large variation exists for individual pork producer’s management skills, facility conditions, or both.

### Table 3. Posterior means and (SD) for phenotypic correlations between length of productive life (LPL) of the sow, age at first farrowing (AFF), number of piglets weaned at first farrowing (NW), and wean-to-last insemination interval (W2I) from the Finnish Landrace swine population

<table>
<thead>
<tr>
<th>Item</th>
<th>AFF</th>
<th>NW</th>
<th>W2I</th>
</tr>
</thead>
<tbody>
<tr>
<td>LPL</td>
<td>−0.03 (0.02)</td>
<td>0.07 (0.02)</td>
<td>−0.04 (0.02)</td>
</tr>
<tr>
<td>AFF</td>
<td>0.08 (0.01)</td>
<td>0.02 (0.02)</td>
<td></td>
</tr>
<tr>
<td>NW</td>
<td></td>
<td>0.04 (0.01)</td>
<td></td>
</tr>
</tbody>
</table>

\( ^1 \)LPL was defined as interval from first farrowing to culling (data transformed using the natural logarithm) or censoring of sow; W2I was defined as interval from first weaning to successful insemination or culling of sow.

**Figure 1.** Estimated posterior distributions, and their means and SD of genetic correlations between length of productive life (LPL), age at first farrowing (AFF), number of piglets weaned at first farrowing (NW), and wean-to-last insemination interval (W2I) in Finnish Landrace population. The LPL was defined as the natural logarithm of time (days) from first farrowing to culling or censoring (meaning the sow is still producing in the breeding herd).
in the present study. For example, if estrous detection or breeding practices are not well managed in a given herd, AFF will automatically be greater (or variance is greater) due to large number (or large variation) of estrous cycles. Similarly, LPL will automatically be poor if a large number of gilts/sows are culled due to reproductive failure, which relies heavily on management skill when humans become involved with estrous detection and when AI is utilized.

In general, farm-year (+season) interaction is modeled in breeding value estimation. If breeding value estimation is routinely conducted, solutions for farm-year interaction classes would be available for producers to utilize. These estimates have potential use for improved sow management, as described previously (Rydhmer, 2000). For example, seasonal trends of farm-year solutions may be indicative of problems relating to weather changes. Based on management solutions, a producer or management consultant may focus on heating or cooling systems, or other practices that could be modified as the seasons change throughout the year and that affect each pork operation in a slightly different manner. Similarly, when new practices are implemented, management solutions (obtained when estimating breeding values) are indicative of the positive or negative impact on the traits of interest that different management practices may have.

A great deal of data collection is required before farm-year-season solutions can be routinely utilized in this type of management consulting. Moreover, data should be collected from commercial operations to obtain solutions for these operations, as well as nucleus and multiplier operations. However, if nucleus and commercial operations are very different, performance records and pedigree information from commercial operations should be used to augment traditional breeding value estimation (Bijma and van Arendonk, 1998). In other words, if genetic correlation between same traits measured in nucleus and commercial operations is low, information from commercial operations should be utilized in breeding value estimation of the purebred or great-grandparent and grandparent portions of the population to genetically improve the commercial pigs—because that is the ultimate objective of commercial swine breeding programs. Thus, we suggest animal breeders develop tools to present farm-year-season solutions for management consulting purposes. As a positive side effect, the amount of data available for breeding value estimation may increase remarkably.

**Genetic and Phenotypic Correlations**

According to current results, sow longevity (LPL) is moderately associated with NW and AFF in a favorable manner. These findings are in agreement with our earlier study (Serenius and Stalder, 2004). However, other studies (Tholen et al., 1996) have reported an unfavorable correlation between stayability and number of piglets born alive at first farrowing. They also reported that W2I was favorably associated with stayability. Similarly, farrowing interval was genetically favorably correlated with LPL of the sow in our earlier study (Serenius and Stalder, 2004). In the current study, no clear associations were observed between LPL and W2I of the sow. However, it should be remembered that W2I and farrowing interval are not the same traits and the definition of sow longevity between the present findings and previously reported studies differed as well.

A moderately favorable genetic correlation was observed between AFF and W2I, and between NW and W2I. Moreover, AFF and NW were only slightly genetically unfavorably associated (i.e., selection for high NW will result in indirect selection pressure for greater AFF). Farrowing interval has been genetically favorably associated with AFF and NW in our previously reported studies (Serenius et al., 2004; Serenius and Stalder, 2004). Thus, the current findings are in agreement with our earlier studies.

Because of the relatively large genetic correlations between LPL of the sow and other reproduction traits, breeding value estimation for these traits should be based on multiple trait analyses. Hence, current types of analyses, where LPL is modeled as a right-censored, Gaussian variable (Korsgaard et al., 2003) should be utilized in breeding value estimation of LPL. Alternatively, survival analysis (Ducrocq and Casella, 1996; Damgaard and Korsgaard, 2006) or a random regression model fitted for binary observations (Veerkamp et al., 2001) can be utilized in breeding value estimation for sow longevity. Meuwissen et al. (2002) indicated that a random regression model, which utilizes binary information, is almost as accurate as survival analysis when single trait breeding values for longevity are estimated. Similarly, Kettunen et al. (2007) reported that single trait breeding values from Gaussian, right-censored Gaussian, and survival analysis were highly correlated when evaluating a fish health data set. Thus, the different models seem to work similarly in the single trait analysis situation. However, it is not clear if the utilization of information that is provided through genetic correlations from other traits would change the results or interpretations from the Gaussian, right-censored Gaussian, random regression, and survival analysis comparisons. More research is needed to compare different breeding value estimation methods in the analysis of sow longevity data.

One of the advantages of survival analyses is the capability to model time-dependent effects (Ducrocq and Casella, 1996). For example, the culling policy of different facilities may change over time due to economic situations, farm owner changes, disease outbreaks, or other similar types of reasons. However, it may be possible to model similar types of effects in a linear model setting. One such approach may be to include farm-year-season as a nested effect by the number of months an individual sow has been in the corresponding farm-year-season class. More research is needed to develop the idea of accounting for time-dependent effects when
Gaussian types of analyses are employed for longevity traits.

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