

Genetic Evaluation of Longevity Traits

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Introduction

Sow longevity or what is called length of productive life (LPL) in some livestock species is an important trait to consider from a productivity, profitability and animal welfare perspective in modern pork production systems. First of all, net present value increases in a commercial breeding herd when sow longevity or the parity at removal are improved whether we are talking about a breed-to-wean (Stalder et al., 2003) or a farrow-to-finish operation (Stalder et al., 2000). From previous literature, heritability estimates have ranged between 0.02 and 0.34, being somewhat population and trait definition dependent (Serenius and Stalder, 2004). Moreover, some evidence exists which indicates that sow longevity, prolificacy and / or conformation traits are genetically associated. Additionally, the U.S. pork industry is experiencing additional animal welfare pressure due to a variety of factors including the type of housing that our sow's experience during the gestation period. When housing issues are combined with poor sow longevity, welfare concerns may arise because a large portion of sows in commercial breeding herds do not remain productive for more than one or two parities. Thus, there is interest among swine breeders and commercial pork producers to select for improved LPL (or sow longevity as it has been more commonly referred to) in breeding programs, and this interest has increased in recent years. The objective of this paper is to outline the alternative for defining different sow longevity traits and to examine different methods of conducting genetic evaluations for sow longevity traits in order to make improvements through selection.

Selection of the appropriate longevity trait to evaluate

Before sow longevity can be improved or the reasons that sows vary in their longevity can be examined, the trait itself needs to be defined. The appropriate sow longevity trait definition might even be different depending on type of study being conducted. Studies involving economic analyses might be concerned with lifetime productivity in order to derive some economic function where sales dollars are needed, either net or gross. Genetic, nutritional or other studies might be concerned with length of life, herd life, productive life, parity removed, or some similar measure where the trait being examined defines lifetime length and / or some removal activity. D'Allaire et al. (1992) suggested that there are several ways to evaluate longevity in swine operations including removal rate, culling rate, replacement rate, percent gilts in herd, mean parity of females in inventory, and mean parity at removal. In the past, U.S. pork producers have tended to focus on culling and replacement rates as a measure of how herds are doing with the retention of females within their operations (Deen et al., 2002). However, when making comparisons across herds or to other studies, culling and replacement rate values can differ based on methods used to calculate values (D'Allaire et al., 1987). In

many cases, some of these values may be difficult to measure or obtain. For example, it may be difficult to obtain actual birth dates if producers are purchasing replacement gilts. There is no way to accurately calculate an actual length of life measure and in this case what must be done is calculate herd life or time from herd entry to removal.

Measures examined in retrospective studies of field data can be deceiving. From strictly a management and productivity standpoint, Deen (2003) has made the argument that parity, age at removal, and removal rate are not appropriate measures of longevity because old, less productive sows can be retained just to improve parity or age structure of the herd. From a management perspective, the target longevity value should be the proportion of the herd removed in early parities or conversely the percentage of females remaining after parities one, two or three. To accomplish this, Deen and Matzat (2003) suggest that the appropriate longevity measure may be average parity at removal. The trait “pigs weaned per day of life” was used as a measure of longevity in a study reported by Culbertson and Mabry (1995). From a strict economic perspective, it is this value, pigs produced per day of life (herd or actual life) that may be most valuable. This trait provides the advantages that as sows become more productive (i.e. more pigs born alive, more pigs weaned, or some defined output criteria) the number gets larger. Furthermore, a sow that is productive but not consistent in rebreeding (i.e. non-productive days is increased), the animal becomes penalized in this situation as the output produced is divided by a greater number of days. It is clear that appropriate measures of longevity are dependent upon the objectives of the study.

Careful examination is required of all potential traits before one is actually selected for use. If possible, it is desirable to have the ability to calculate the longevity trait from data that is already collected as a routine practice at the farm level. Asking producers to capture additional data can be challenging especially at the beginning of any new program. Furthermore, an understanding of the trait that is chosen is critical. For example, are we going to use a categorical type trait like parity at removal or survival to some specific parity? Alternatively, a linear trait could be recorded; for example, lifetime herd life, lifetime pigs born alive or weaned are all examples of continuous traits that are related to sow longevity where selection could improve the trait. The type of trait, discrete or continuous, can impact the heritability estimates and variance components, both of which are critical if we expect to make genetic progress to improve sow longevity. In order to make genetic improvement the trait must be heritable and sufficient variation in the trait must exist within the population undergoing selection in order to expect quantitative selection for longevity to be successful. Literature heritability and variance component estimates suggest that there are at least some differences in the estimates depending on which longevity trait is evaluated (Stalder et al., 2004). Additionally, as we will see later, the type of trait impacts how the data will ultimately be analyzed having both desirable attributes and limitations.

If we ask commercial producers in a field setting to record additional data not currently collected, challenges may occur in getting accurate field data especially early on in the process. Another very important point is revealed here as well. If much field data is to be used in the evaluation of sow longevity from commercial herds should be the case, it is imperative that data is recorded and calculated in the same manner across data management software packages. Additionally, our work has demonstrated that a significant portion of data may have errors associated with it (Knauer et al., 2007). As is

the case with any attempt at the analysis of a data set, the frequency of errors and their type can significantly impact the results obtained and likewise influence the decisions made based on the result.

Analysis methods to evaluate longevity

In recent years genetic evaluations for longevity have been conducted especially in other species. The beef cattle industry has for many years had a trait they call stayability. This is a binary trait representing whether an animal has reached some fixed parity. In the beef cattle case, it represents the probability that a cow is in the herd at six years of age, the age determined to be when most cows would reach a positive net present value, given the cow was in the herd as a two year old (Cowley, 1998). Stayability provides the beef cattle producer with an estimate of how long a sire's daughters will stay in the herd. In essence it gives beef cattle producers a chance to evaluate females from a business or accountant perspective to determine the asset's, in this case the cow's, depreciable life. Some of the breed organizations in the beef cattle industry effectively use the stayability values to arrive at a length of productive life for the cows in their populations.

Survival analysis is another common method to evaluate genetic differences for longevity in livestock species. In survival analysis, longevity is defined as the probability of a sow removal at any given time (failure rate at time t) given she is alive or in the herd at time -1 . In this case, some underlying hazard function is assumed to impact the animal's lifespan. Other items can be modeled such as a treatment, breed etc. which has an effect on the hazard function and in some cases are said to have a constant or proportion affect across the hazard function and hence are termed proportional hazards models.

In this type of analysis, data censoring is quite common. Data censoring is most commonly used for animals that have not yet finished producing their record, base animals with no known record for the trait, and females that may have been sold to another herd. However, genetic parameter estimates can be biased by the degree of censoring in the data being evaluated. Limitations to this type of analysis include the assumption that the risk of an effect that is being modeled over time is always proportional. While there may be some methods to handle the proportionality differences, these methods need further refinement to ensure that the correct adjustments are being made. Time dependent variables can be added. A time dependent variable allows some variable to differ over time, for example culling differs across years because of some health problem in the herd or many herds.

The most commonly used software to conduct survival analysis is called the Survival Kit (Solkner and Ducrocq, 1999). The survival kit allows for change in culling policy and for environmental factors to be accounted for in the survival analysis by treating them as time-dependent effects as previously mentioned. Some of the limitations of this software are that only a single trait can be evaluated, in this case a defined longevity trait. While longevity breeding values are obtained, their association with other linear traits and improvement in the estimates due to information from correlated traits is not possible. Additionally, the typical model used is a sire, maternal grand-sire model. This type of evaluation is commonly done for the dairy breeds in France.

Another method to evaluate longevity traits is using repeated binary records. In this case, an animal is either still alive or remains in the breeding herd or is not (0 or 1) each time period as defined by the users (day, week, month, year, etc.). In this case it has been shown that repeatability or random regression models can be used to estimate breeding values (Meuwissen et al., 2002; Veerkamp et al., 1999). Multiple trait analyses are possible. Time dependent variables can be modeled similarly to the survival analysis, and it appears to be relatively straight forward to implement. The draw back to this process is that the records are binary in nature and the procedure treats them as linear traits. This may not be an optimal way to evaluate longevity. What impact this has on the accuracy of the variance component and breeding value estimates is not as well understood, but is needed in order to implement the procedure into routine breeding value estimation.

Another approach that has been used in recent years was discussed by Damgaard and Korsgaard (2006) who introduced bivariate survival and Gaussian trait analysis, where both environmental and genetic correlations are modeled. However, they indicated that more research is needed in order to estimate breeding values in a reasonable amount of time when large datasets like those available from the swine industry are evaluated. Alternatively, LPL can be analyzed as a Gaussian trait when censoring is accounted for (Korsgaard et al., 2003). In practice, successful right censored Gaussian trait analysis 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). In the study by Guo and co-workers (2001) they reported heritability estimates using these procedures for length of productive life and lifetime prolificacy of 0.22 to 0.25. These values are moderately heritable and appear to hold promise for simultaneously evaluating these types of traits. This procedure is relatively easy to implement, and multiple trait analyses are possible with various trait types (Gaussian, right censored Gaussian, categorical, binary). In order to develop a breeding value estimation routine for LPL, knowledge about genetic variation of LPL, and its genetic association with other traits is needed.

In a recent study in our group (Serenius et al., 2009) we estimated genetic parameters for LPL, and determine its genetic correlation with age at first farrowing, number of piglets weaned at first farrowing and first wean-to-insemination interval in the Finnish Landrace swine population using procedures similar to those outlined by Korsgaard et al. (2003). 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). In order to reduce computation time, six separate 2-trait analyses were carried out. In this evaluation, heritability estimates for length of productive life (0.22 ± 0.04) and age at first farrowing (0.16 ± 0.03) were in the moderate range. Similarly, the heritability estimates for number weaned (0.09 ± 0.02) and weaned to estrus interval (0.08 ± 0.05) generally in the low range of values.

Use of related traits

Studies have consistently demonstrated a relationship between leg soundness traits and measures of sow longevity. Overall leg action has been shown to be favorably associated with length of productive life as has individual leg traits like weak front

pasterns. Conversely, bucked kneed front legs and weak rear legs have a negative relationship with sow productive lifetime (Lopez-Serrano et al., 2000; Serenius et al., 2001; Serenius et al., 2006; and Serenius and Stalder, 2004). Sow longevity has also been favorably associated with reproductive traits including age at first farrowing, farrowing interval, and wean to estrus interval (Tholen et al., 1996; Serenius and Stalder, 2004; Serenius et al., 2006; Serenius et al., 2009). The relationship between longevity and production traits and carcass composition are generally slightly unfavorable and the strength and sign of the relationship can vary depending on the population being evaluated (Tholen et al., 1996; Lopez-Serrano et al., 2000; Serenius and Stalder, 2004).

Molecular tools to improve longevity

Molecular markers may be available to identify traits important for a variety of traits impacting sow productive lifetime. Recent studies completed by ISU researchers have identified several potential useful genes that may improve sow longevity. Association analyses of several genes found that CALCR, HDBP, CALCA, MTHFR, OXTR, IHH, ANKH, LRCH1 and OPN genes were significantly associated with leg and body conformation traits such as leg action, pasterns (weak or upright), body length (short or long) and depth (deep or shallow bodied) (Onteru et al., 2008). Further investigations by the ISU researchers (Fan et al., 2008) identified 6 body conformation traits which could be combined into two principal factors, each explaining greater than 20% of the total variation, and which accounted for body volume and side-view, respectively. Additionally, another 11 feet and leg traits were summarized into three principal factors, which generally described leg movement, leg defects and uneven toes, respectively. The association analyses between the SNPs and the principal factors were evaluated and the genes COL9A1, hDBP, APOE, DK, PPARGP and PAPPB were associated with body volume ($P < 0.05$). Furthermore, the SNPs in COL1A2, CALCR, FBN1 and OXTR were associated with side-view. Leg movement was significantly associated with SNPs in COL1A2, CALCR, BMP8, OPG, PTHR and OXTR. Leg defects were significantly associated with SNPs in ALOX15, ALOX5, COL9A2 and WNT16. These results appear to indicate that genes involving cartilage development and fatness seem to function in skeletal structure, and genes relevant to cartilage and bone formation are likely to play important role for feet and leg soundness in pigs. These results demonstrate that molecular markers may become useful for feet and leg soundness and other traits related to sow longevity.

Summary

Sufficient variation exists such that genetic improvement for sow longevity should be possible. Use of molecular markers to improve sow longevity and associated traits like leg soundness hold promise to speed genetic improvement progress towards a more robust sow herd. There are a variety of tools available currently to conduct an accurate genetic evaluation for sow longevity. However, when attempting to conduct an evaluation of both longevity traits and normally recorded reproduction and production traits may take additional research to identify the most optimal methods for analysis.

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