factsheet

Pork Information Gateway

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Estimating Genetic Merit

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Introduction

In estimating the genetic merit of an animal, breeders are trying to determine the animal's value as a parent, its breeding value. The phenotype of an animal (the traits we see and measure) is a combination of genetic and environmental effects. Genetic effects are the result of the genes inherited from parents. Environmental effects are the result of conditions the animal experienced, such as level of nutrition, stocking density, temperature, or health status.

The challenge to the breeder is to determine how much of an animal's superiority (or inferiority) for a trait is due to additive genetic effects, since this is what will be passed on to its progeny through its own genes. Defining what constitutes genetic merit is an important first step in this process.

Favorable performance for a characteristic is an obvious way to rank animals; however, it should be done relative to other animals that are of similar age and housed and raised under similar conditions. It is best to compare an animal's performance record to the average of the group of animals that they were raised with. This can be done by calculating performance deviations from the group average or the ratio of animal's performance with the group average. For example, a gilt has an average daily gain of 1.9lb/day for the grow-finish period while the other gilts of similar age and raised in the same building averaged 1.8lb/day for average daily gain. The gilt in question would have a performance deviation of 0.1lb/day, which is favorable and a ratio of 105.6 (1.9/1.8). This is the first step in evaluating an animal's genetic merit for performance characteristics. For further examples see Table 1.

Two terms are often used in discussing genetic merit. The first term, Estimated Breeding Value (EBV) is the estimated genetic merit of animal, expressed as a deviation. The second term, Expected Progeny Difference (EPD) is one-half an animal's Estimated Breeding Value and can be used to determine the expected performance change of progeny if the animal in question is used as a parent. Methods to estimate genetic merit in swine have evolved considerably this century. As breeders have been able to incorporate increasing amounts of information to assess an animal's breeding value, methods have grown from simple visual appraisal to complex statistical techniques. The purpose of this fact sheet is to discuss these alternative methods.

Selection Based on Visual Appraisal

This method has been used for centuries to assess genetic merit, in which selection candidates are only visually evaluated to assess their potential to produce progeny to perform in the herd. Characteristics that would

be evaluated in a visual appraisal could include feet and leg structure, soundness, underlines, and external genitalia, since these could affect a candidate's ability to produce progeny. In any swine breeding program, visual appraisal is an important component, and there are scoring systems that have been developed for assessing feet and leg soundness. However, relying solely on visual appraisal to assess genetic merit in a swine breeding program is strongly discouraged as it can be highly subjective (relative to the appraiser), and methods that also use performance information are key in a genetic improvement program.

Gilt Ear Notch	Average Daily Gain Record	Group Average	Performance Deviation	Performance Ratio
14-2	1.9	1.8	0.1 (1.9-1.8=0.1)	105.6 ((1.8/1.9)*100=105.6)
6-8	1.85	1.8	0.05 (1.85-1.8=0.05)	102.8 ((1.85/1.9)*100-102.8)
17-11	1.7	1.8	-0.1 (1.7-1.8=-0.1)	94.4 ((1.7/1.8)*100=94.4)

Table 1. Relative comparisons of gilts within a Contemporary Group for Average Daily Gain.

Gilt Ear Notch	Heritability for Average Daily Gain	Performance Deviation	Estimated Breeding Value
14-2	0.3	0.1	0.03 (0.3*0.1=0.03)
6-8	0.3	0.05	0.015 (0.3*0.1=0.015)
17-11	0.3	-0.1	-0.03 (0.3*-0.1=-0.03)

Table 2. Breeding Value Estimation for Average Daily Gain.

Selection Based on Phenotype

In situations where breeders have defined improvement of a single trait as their breeding goal, and information is limited to the contemporary test group, estimating genetic merit is straightforward. An estimated breeding value from a single trait assessment, EBVST, can be calculated with the following equation:

$$EBV_{ST} = h^2 (P - GA); \qquad EPD_{ST} = EBV_{ST}/2$$

Where EBV_{ST} is the estimated breeding value using single trait and contemporary group information, h2 is the heritability of the trait, P is the animal's record, GA is the group average of the contemporaries of the animal, and EPD_{ST} is the expected progeny difference.

This method strives to account for environmental effects by taking the animal's deviation from the test group average and multiplying that deviation by the heritability of the trait. An example of this method can be found in Table 2.

The advantage of this method is that it is relatively easy to calculate for animals completing a performance test, but does have disadvantages relative to other methods. First, as noted in NSIF-FS9, more than one trait is usually of economic importance to swine breeders and commercial producers. Second, when obtaining EBVs in this way, it is difficult to compare animals from different test groups because their records have been deviated from different group averages. And third, this method does not use information from relatives or other traits that may have been recorded for other test groups from the breeding herd. This information can be used in other methods to increase the accuracy of estimating genetic merit.

Relative Information

Members in families have some of their genetic background in common. Animals that are closely related (full or half sibs) have more in common than animals that are not closely related (cousins, etc). Since family members have some of their genetic background in common, tendencies among their performance records also have genetic similarity. This information can be used to better calculate an individual's EBV or EPD. An example of this is calculating and EBV based on an individual's own performance as well as performance from full and half sibs tested in the same contemporary group as follows:

$$EBV_{SIB} = b_1(P-GA) + b_2(FS-FSGA) + b_3(HS-HSGA)$$

Where, EBV_{SIB} is the estimated breeding value of the animal using sib information, b_1, b_2, and b_3 are the weighting factors associated with records on the animal, its full-sibs and half-sibs, respectively, P, FS and HS

are the records or average records for the animal, its full-sibs and half-sibs, respectively, and GA, FSGA and HSGA are the group averages for contemporaries of the animal, its full-sibs and half-sibs, respectively.

The b_1, b_2, and b_3 values are calculated using information on the number of records, inheritabilities, relationships between an animal and its sibs and genetic correlations. The main advantage of using this method to estimate genetic merit over visual appraisal or single trait assessment is that the breeder can incorporate information from relatives in the calculation of estimated breeding value. This improves the accuracy of that estimate over those from the previously mentioned methods. Also it is easier to calculate estimated breeding values using this method than some other alternatives. The main disadvantage of this method is that records are deviated from contemporary group averages and comparisons of breeding value across test groups or herds are not valid.

Best Linear Unbiased Prediction (BLUP)

Best Linear Unbiased Prediction (BLUP) is a statistical procedure that allows breeders to make better use of information than previously discussed methods of estimating genetic merit. EBVs and/or EPDs (Expected Progeny Differences – ½ of the estimated breeding values) of animals are calculated from a system of simultaneous equations. This system incorporates information from all known/recorded relatives of the animal in calculating its breeding value. It does this by utilizing a relationship matrix that accounts for all relationships among relatives within a herd or breed. Some animals may not have a record for the trait of interest but solely provide a genetic tie among animals that do have records. Unrelated animals would have a 0 as their relationship, a sire and its progeny would have ½ as their relationship, since the sire contributes ½ of the genes of the progeny, a grandsire would have ¼ as its relationship to its grandprogeny, etc. Additionally, animals are connected that were raised in the same environment or contemporary group (the same herd, building, week of off-test, for example). Finally, information on other traits recorded on the animal can be used to estimate the breeding value of an animal for a specific trait if those other traits are genetically correlated to that trait. For example, backfat measures tend to be correlated to growth rate so this additional information can be used to estimate a more accurate breeding value.

With an animal model, the BLUP procedure defines base animals (oldest animals in the data set, e.g., born in 1995) and an equation for each trait in the analysis for every animal. For example, in an analysis of days and backfat for animal A, two equations would be defined. In the equation for backfat for A, information used would include A's own backfat measurement, backfat measures on contemporaries and relatives and growth data from A, its contemporaries and relatives, weighted by appropriate correlations. When equations have been defined for all traits and animals in the analysis, the system of equations is solved and estimated breeding values produced. EBVs are given as deviations from the base animals. An animal with a backfat EBV of –0.20″ (a backfat EPD of –0.10″) would be expected to have 0.2 in. less backfat than base animals, and this would be a genetic difference. It is important, especially with across-herd evaluations, that records used in the analysis are connected. Connectedness takes two forms. The first form of connectedness entails genetic ties across herds. These ties can be AI sires with progeny in several herds or animals sold as breeding stock and producing progeny in other herds. These ties across herds need to exist and be maintained for optimal BLUP evaluations to be performed. The second form of connectedness entails the contemporary group. Because the BLUP system of equations is simultaneously solved for genetic and environmental effects, it is important to have good connectedness within contemporary groups. Unrelated animals are "connected" by being in that group. Contemporary groups need to be as large as resources and facilities will allow and should represent progeny from a minimum of 2-3 sires. Advantages of BLUP evaluation include: 1) Estimated breeding values of animals in different herds or contemporary groups can be compared; 2) Estimated breeding values can be obtained for traits not expressed by an animal (litter size EBVs/EPDs for boars, for example); 3) Recorded information is more optimally used, thereby producing a more accurate estimate of breeding value than previously discussed methods of estimating genetic merit; and 4) Genetic trends can be calculated, which allows breeders to monitor genetic progress for traits in the breeding goal. Disadvantages of BLUP evaluation include: sophisticated computer programs are required to solve the system of equations and EBVs/EPDs are generated for individual traits rather than a single value to rank animals for selection.

Accuracy of EBVs or EPDs

EBVs/EPDs are estimates of the true genetic merit. Theses estimates of genetic merit can change once more information on relatives (e.g. younger sibs, progeny, etc.) become available. Accuracy values, which provide the user some sense of how much EBVs/EPDs could change, can be calculated. Accuracies are means to

determine how "close" the estimate of genetic merit is to the true genetic merit an animal. Accuracies are often reported in one of two ways. The first is as probability that the estimate will change when more information is included in the calculation of EBVs or EPDs. For example a boar off-test will have an EPD calculated for growth rate. When further relative information becomes available (e.g. sibs, progeny, etc.) new EBVs will be calculated including this information that was unavailable at the initial EBV calculation. These probability values range from 0.0 to 1.0. Low values (0.0 to 0.4) suggest that as more information becomes available EBV estimates have a greater chance to change, either in a favorable or non-favorable direction compared to high accuracy values (0.7 to 1.0).

Another method of reporting accuracy is to report an estimate of "possible change." This value would indicate how large a range of possible values the true breeding value would lie within and indicate how much the EBV or EPD may change once more information is included in the estimate. For example, a young boar with an EPD for days to 250 lb of –3.0 could have a possible change value of + 1.0. This would suggest that as more information from relatives is included in estimate of the EPD, the value could improve to –4.0 or increase to –2.0. An older boar with progeny data would have a smaller possible change value.

Summary

Estimating genetic merit is a critical component of any performance testing and genetic improvement program. Simple measures such as deviations, ratios, and EBVs including only the animal's performance record are more accurate than visual appraisal or raw performance records. However, genetic merit estimated using an individual's record and performance information on relatives leads to more accurate estimates of genetic merit and can improve rates of genetic change.