

# SWINE GENETICS



## Fact Sheet Number 7

### Performance Records on Relatives

Estimating the genetic merit of all individuals in a herd is required before a comprehensive selection and genetic improvement program can be successful. Performance records need to be collected on as many animals as possible, ideally on every animal in the herd. Since animals have relatives and progeny in the herd, the records on these relatives or groups of relatives can be used to improve the estimation of the genetic merit of an individual animal. Animals are related when they receive some identical genes from a common ancestor. When they have genes in common, the performance of one individual for a given trait can be used to help estimate genetic merit for other related individuals.

Genetic evaluations conducted by the majority of breed organizations and breeding stock companies use the animal model and best linear unbiased prediction (BLUP) procedures. This technology is used to determine expected progeny differences (EPDs) for the animals evaluated. An EPD is the predicted average performance difference of the offspring from a breeding animal compared to the average performance of the offspring from other animals in the same population. The animal model not only uses the individual's performance record, but also utilizes information from all related animals (full-sibs, half sibs, sire, dam, grand sire, grand dams, etc.) when estimating an individual's EPD. Because information is available on relatives, this system of genetic evaluation adjusts the EPD of a superior-

performing individual from a poor-performing family downward in comparison to the performance of the individual itself. Likewise, the EPD of a relatively poor performing animal from a superior performing family adjusts upward, but is still below the family average. That is, compared to their phenotypic values, breeding values tend to regress toward the population mean. Fact Sheet No. 5, "Estimating Genetic Merit," of the National Swine

Improvement Federation Swine Genetics Handbook provides a more detailed explanation of breeding value estimation.

#### Connectedness

Information on relatives is important to provide links between contemporary groups on a within herd basis and links to other herds so that across-herd analyses can be conducted. These links provide genetic ties or connections for

**Figure 1.** Example of disconnected herds and sires.<sup>1</sup>

Herds	Sires			
	A	B	C	D
1	X	X	—	—
2	X	X	—	—
3	—	—	X	X

<sup>1</sup>— indicates that there were no offspring performance records from a sire in a given herd, while X indicates that a sire has produced at least one (hopefully more) offspring with a performance record in a given herd.

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different contemporary groups within a herd and to other herds within the same population to provide the basis for unbiased prediction of an animal's genetic worth. A complete explanation of contemporary groups can be found in Fact Sheet No. 5, "Performance Records for Selection Programs," in the National Swine Improvement Federation Swine Genetics Handbook. Without genetic ties or connectedness to other herds, EPDs from different herds within a breed can not be accurately compared. Exchanges of genetic material through live breeding animals and more so with

**Figure 2.** Example of connected herds and sires.<sup>1</sup>

Herds	Sires			
	A	B	C	D
1	X	X	—	—
2	—	X	X	—
3	—	—	X	X

<sup>1</sup>—indicates that there were no offspring performance records from a sire in a given herd, while X indicates that a sire has produced at least one (hopefully more) offspring with a performance record in a given herd.

artificial insemination, improves the genetic ties across herds and allows for more accurate comparisons of EPDs across herds. Data that is well connected more accurately identifies superior performing breeding animals and results in faster genetic progress. Examples of disconnected and connected herds and sires are shown in Figures 1 and 2, respectively.

In the example in Figure 1, herds 1 and 2 are connected because they have used sires A and B. Likewise, sires C and D are connected through their use in the same herd (3). Sires A and B are completely disconnected from sires C and D because they were not used in the same herds. Herds 1 and 3 are not connected because they have not used a common sire. The same can be said for Herds 2 and 3. Thus, comparison of EPDs for animals across Herds 1 and 3 or 2 and 3 are not valid, because the herds do not have related progeny. Across-herd comparisons are valid between Herds 1 and 2 because related offspring exist through the use of common sires. Disconnected data have to be analyzed on a within-set basis.

In the example from Figure 2, all herds and sires are connected. Herd 1 is connected to Herd 3 through Herd 2's use of sires B (also used in Herd 1) and C (also used in Herd 3). The use of common sires among the three herds results in offspring that are related. Similarly, sire D is connected to sire A because Herd 2 used sire B and C and Herd 1 used sire A and B, while Herd 3 used sires C and D. Connectedness between herds and between contemporary groups within herds provides the basis for unbiased predictions of an animal's genetic worth.

### Accuracy of Estimates

A very important concept in estimation of breeding value is the accuracy of the estimate. Accuracy is defined as the relationship or correlation between the estimate of breeding value and the animal's true breeding value. The true breeding value of an animal is not known because we cannot look directly at the thousands of genes or identify each gene that an animal possesses. Therefore, we must estimate the true breeding value using the animal's and its relatives' performance. The accuracy of the estimate of the breeding value is generally dependent upon the heritability of the trait and the number of records from the individual and/or its relatives used in the evaluation procedure.

Accuracy can range from 0, when there is no information on the breeding value, to 1.00, when the breeding value is known exactly. Records on close relatives affect the accuracy more than on those on distant relatives because close relatives have more genes in common with the animal being evaluated. For example: On average, twice as many genes are alike between a parent and its progeny than between an animal and its grandparent.

Accuracy is a measure of precision associated with estimated breeding values or expected progeny differences. Higher accuracy values for a given trait can be used to gauge the level of confidence that predicted values are near the true genetic value. Low accuracy values indicated that predicted values may vary as more information (performance records on relatives) becomes available. Breeding values or expected progeny differences having relatively high

accuracy values do not vary as greatly compared to breeding values with a lower accuracy when more information becomes made available.

Accuracy is very important in selection programs because the accuracy of the estimated genetic merit affects the response to the selection program. The heritability of a specific trait is considered fairly constant, but the heritability values of different traits can vary considerably. Most heritability estimates for economically important traits can vary considerably and range from .1 to .7 on a possible scale of 0 to 1.00. As noted before, heritability affects the accuracy since the proportion of the performance owing to genetic merit is larger with larger heritability values. In general, it then follows that traits with high-heritability values can be predicted more accurately than traits with low-heritability values.

### Individual Performance Record(s)

If only the animal's own record is used to estimate genetic merit, the accuracy of the estimate is given by the square root of the heritability of the trait. Therefore, the accuracy is the same for all animals with only one record for the same trait. But the accuracy is different for different traits with one record on the individual. The following are examples of accuracy values for different heritability values assuming one record per individual:

Heritability	Accuracy
.10	.32
.25	.50
.50	.71
.75	.87
1.00	1.00

Most heritability values range from .1 to .70 for traits of economic interest, thus the accuracy values range from .32 to .84, assuming one record on the individual being evaluated.

Increasing the number of records on an individual increases the accuracy. However, for each additional record added, the increase in accuracy is marginally less. So moving from one to three records increases accuracy more than increasing from 10 to 12 records.

Remember though, 10 or 12 records will provide more accuracy than three records.

The concept of repeatability enters into accuracy calculations when more than one record is available on an individual. Repeatability measures the degree of association between records on the same animal for traits expressed more than once in an individual's life. Traits that may be measured more than once include number born, litter weight, and number weaned. By definition, repeatability must be greater than or equal to heritability for a given trait. Repeatability includes all the genetic effects plus the permanent environmental effects, such as damaged teats or any effects of nutrition on mammary development that would affect all subsequent lactations. Permanent environmental effects do not affect the genetic merit of an individual but do influence the performance and, therefore, all records on an individual. For repeatable traits, observing the performance of an individual several times increases the accuracy of the estimated breeding value compared to an estimate based on a single observation. Table 1 contains examples of accuracy values for different levels of heritability, repeatability, and number of records.

If more than one record is collected, the accuracy is influenced by the number of records, heritability and repeatability. The increase in accuracy depends upon the ratio of repeatability to heritability, but the increase in relative accuracy is greater for lowly heritable traits than for highly heritable traits.

The reason that accuracy increases less when repeatability is higher is that the higher repeatability means that the similarity between observations is due to nontransmittable effects, permanent environment, and nonadditive genetic factors.

### Performance Records of Sibs and Other Relatives

Performance records on full-sibs and half-sibs (full-and half-brothers and sisters) are very useful to evaluate traits that cannot be measured on potential breeding animals. The most common examples include the carcass traits, such

**Table 1.** Accuracy Values for different heritabilities, repeatabilities and number of records on an individual.\*

Heritability	Repeatability	Number of records			
		1	3	5	10
.10	.25	.32	.45	.50	.55
	.50	.32	.39	.41	.43
	.75	.32	.35	.35	.36
.25	.25	.50	.71	.79	.88
	.50	.50	.61	.65	.67
	.75	.50	.55	.56	.57
.50	.50	.71	.87	.91	.95
	.75	.71	.78	.79	.80

\*Accuracy values calculated using the following formula:

$$nh^2 \div [1+(n-1)r]$$

where: n = number of records, h<sup>2</sup> = heritability, and r = repeatability

**Table 2.** Accuracy Value with either half-sib or full-sib records at different heritability values, assuming no environmental correlation.

Number of sibs	Heritability							
	.10		.30		.50		.70	
	half	full	half	full	half	full	half	full
1	.08	.16	.14	.27	.18	.35	.21	.42
3	.13	.26	.22	.42	.27	.50	.31	.56
5	.17	.32	.27	.48	.32	.56	.36	.60
10	.23	.42	.34	.57	.38	.62	.41	.65

as loin eye area, carcass length, and muscling score as well as on and maternal traits for males, such as litter size. Testing of sibs is used at some central test stations where two or three full- or half-sib barrows may enter the test at the same time as the boar. The barrows are grown to slaughter weight and then carcass information is collected on them and used to estimate breeding values for carcass traits on the remaining related animals in the population.

The additive genetic relationship or the percent of genes in common between full-sibs is one-half or 50% and for half-sibs is one-quarter or 25%. The accuracy of estimates from sib data depends upon the heritability of the trait, the number of sibs, the additive genetic relationship between the sibs, and the animal being evaluated and an environmental correlation effect. Table 2 contains accuracy values with varying

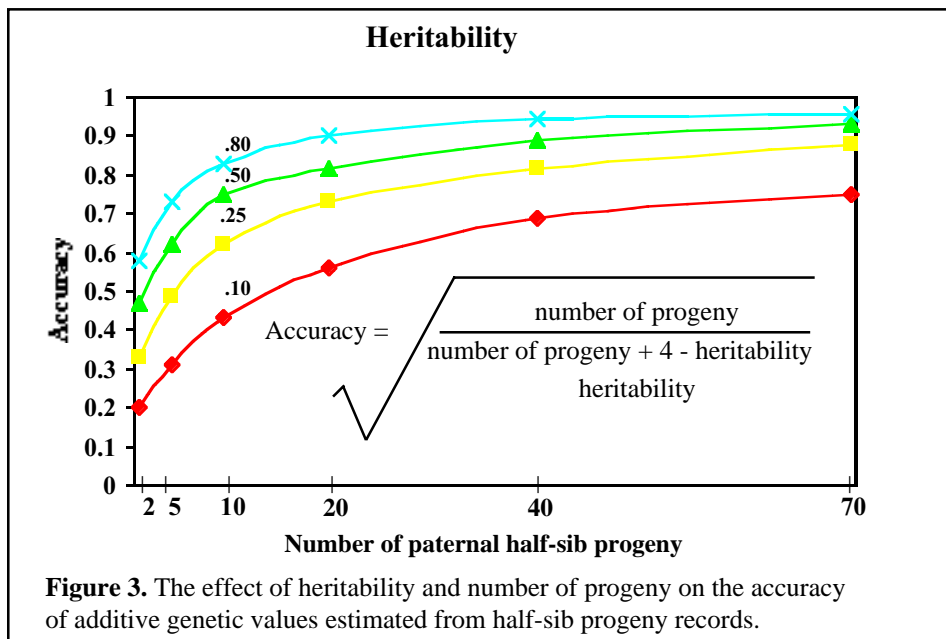
numbers of records on half-sibs or full-sibs and different heritabilities but with no environmental correlation.

The general trend is for accuracy to increase as the number of sibs increases and as the heritability of the trait increases. Full-sib records produce larger accuracies than half-sib records within heritability values because full-sibs are more closely related to the animal being evaluated.

Note, it would take large numbers of half-sibs to get an accuracy value close to one. Records on parents or progeny of an animal increases accuracies by a value similar to full-sibs since the degree of relationship is the same. Records on more distant relatives (cousins, grandparents, etc.) do not improve the accuracy greatly. As with full-versus half-sibs, the further the relative is removed (smaller genetic relationship) from the individual being evaluated, the

**Table 3.** Accuracy values with full-sib records given different heritability levels and an environmental correlation ( $c^2$ )\*.

Number of full-sibs	Heritability							
	.10 $c^2$		.30 $c^2$		.50 $c^2$		.70 $c^2$	
	0	.10	0	.10	0	.10	0	.10
1	.16	.16	.27	.27	.35	.35	.42	.42
3	.26	.24	.42	.39	.50	.47	.56	.53
5	.32	.28	.48	.43	.56	.51	.60	.56
10	.39	.33	.57	.48	.62	.55	.65	.59



less their records improve the accuracy of estimation.

The environmental correlation ( $c^2$ ) represents a nongenetic likeness between sibs caused by the sibs sharing a common environment. For example: All littermates have a common mother whose milking ability and mothering ability contributes to all of her progeny in that litter. If the sow is above average for milk production, probably all the pigs will have above average 21-day weights owing in part to the common effect of the good milking sow. This is clearly not an additive genetic effect, but does influence performance of the pigs in the litter. The environmental correlation is probably different for full-sibs than for half-sibs and may even be different for different groups of half-sibs raised under different environments.

The effect of the environmental likeness is to reduce the accuracy of the estimate of breeding value.

The effect of an environmental correlation (Table 3) is demonstrated using records from full-sibs and an environmental correlation ( $c^2$ ) of .10, which is common in swine data. The common environmental effects cause a reduction in the accuracy regardless of the number of full-sibs or the heritability of the trait, because some of the similarity between records is due to nongenetic factors.

### Progeny Performance Records

Traits that are not necessarily expressed in both sexes (sex-limited) or for which data cannot be collected on breeding animals are good candidates for genetic evaluation using progeny

records. Examples of such traits are number born, litter weight and milking ability on males and carcass traits on breeding animals. Progeny tests are commonly used to estimate breeding values of male animals because males leave more progeny in a shorter period of time than females. Generally, full-sib and paternal half-sib progeny are used to estimate breeding values. Paternal half-sib progeny are progeny from the same sire but different dams. Accuracy is dependent on the heritability and the number of full- and half-sib progeny. The relationship among the number of half-sib progeny, heritability, and the accuracy level is illustrated in Figure 3. Within a given heritability, an increase in the number of progeny increases the accuracy of the estimate. However, the amount of increase in accuracy depends upon how many progeny are already available. For instance, moving from one to five progeny will increase accuracy much more than going from 60 to 64 progeny. As in other cases, the higher the heritability the more accurate the estimate of breeding value.

### Combinations of Individual, Sib, and Progeny Records

Different combinations of information can be used to improve the accuracy of the estimated breeding values while keeping the response to selection at an acceptable level. Swine performance records are generally collected on the individual, its full- and half-sibs, and if it is kept as a breeding animal then information is available on its full- and half-sib progeny. Table 4 contains accuracy values using combinations of performance records from different sources with varying heritability values.

Records on the individual produce a relatively high accuracy of prediction for traits with large heritability. Adding progeny or parent records to an individual's record on traits with high heritability increases the accuracy only slightly unless there are large numbers of progeny available. Adding sib and/or progeny records to traits of low heritability can result in marked improvement in accuracy. Compare the accuracy values in Table 4 for individual, individual plus 10 half-sibs, and individual plus 10 half-sib progeny at

**Table 4.** Accuracy values given different sources of records and heritability levels.\*

Source of records	Heritability		
	.10	.30	.50
Two parents only	.23	.39	.50
Individual	.32	.55	.71
Individual + 2 parents	.38	.67	.76
Individual + 5 full-sibs	.41	.64	.76
Individual + 10 full-sibs	.48	.68	.78
Individual + 10 half-sibs	.34	.57	.72
Individual + 50 half sibs	.46	.64	.75
Individual + 5 half-sib progeny	.44	.67	.79
Individual + 10 half-sib progeny	.52	.71	.84
Individual + 40 half-sib progeny	.73	.82	.93

\*Environmental correlation assumed to be zero.

.10 heritability. The accuracy increases from .32 to .34 to .52, respectively; a substantial improvement.

However, waiting for large numbers of progeny to be born and tested increases the testing costs and time, lengthen the generation interval, and possibly lowers the selection intensity. All of these factors have to be balanced against the need for the extra improvement in accuracy received by adding more progeny. In general, getting as much progeny information as possible, plus records on the individual being evaluated, is a good practice for lowly

heritable traits (less than .20). Traits with high heritability don't require as many progeny or relative records, if records on the individual are available, to attain an acceptable level of accuracy.

Remember that all genetic improvement programs begin with a good record-keeping program. Collect performance records on as many animals in the herd as possible because this allows you to use many combinations of records to evaluate animals without reducing the progress from your selection program. Of course, even the best record system doesn't result in herd

improvement until the records are used to make selection decisions.

Improving accuracy is not strictly dependent on increasing the number of records used to estimate an animal's breeding value. Whether or not the individual has a performance record for a given trait is a large determinant of the accuracy associated with the EPD, particularly for highly heritable traits. Improving accuracy is also dependent on a number of other factors including: 1) relatives in different herds, 2) contemporary groups and their size (groups of fewer than 20 animals are of little value), 3) sires used in each contemporary group (single sire contemporary groups contribute little or no information, a minimum of two sires should be used and the use of five are better), etc. Thus, it is common for an EPD for an animal having fewer relatives with records that are spread out over a number of herds and contemporary groups to have a higher accuracy associated with its EPD compared to an animal having more records from relatives but those records are from fewer herds and contemporary groups.

### EPDs, Accuracy, and Risk Management

The difference between the predicted breeding value and true breeding value is known as the error of prediction.

The error of prediction has an equal chance of being above or below the current predicted breeding value.

The possible changes associated with different accuracy levels for a given trait are shown in Table 5.

Accuracy can be used to manage risk. When making mating decisions, a breeder should select animals having EPDs that improve the trait of interest most. If a breeder selects an individual animal having a high EPD and an associated high accuracy, he/she should be confident that the average performance of its offspring is extremely close to the predicted value. If a breeder selects an individual with a high EPD with a low associated accuracy, the performance from the progeny is likely to be more variable and may exceed or

**Table 5.** Possible positive or negative changes associated with accuracy for maternal and terminal swine traits<sup>1</sup>.

Accuracy	Maternal Traits		Terminal Traits	
	Number Born Alive	21-day litter Weight, lbs	Days to Market	Backfat, in.
.10	.52	5.54	3.38	.034
.20	.51	5.46	3.33	.033
.30	.50	5.31	3.24	.032
.40	.48	5.10	3.12	.031
.50	.45	4.82	2.94	.029
.60	.42	4.45	2.72	.027
.70	.37	3.98	2.43	.024
.80	.31	3.34	2.04	.020
.90	.23	2.43	1.48	.015

<sup>1</sup>Adapted from A guide to interpreting STAGES reports for breeders and their clients, Purdue University, West Lafayette, IN 47907-1151.

fail to meet predicted performance.

However, as more information becomes available, the EPD moves closer to the true value and accuracy improves.

Because it is just as likely for the EPD to be under predicted as over predicted, using individuals having an EPD with low accuracy can result in offspring with outstanding performance. Producers should remember that this same individual (high EPD, low accuracy) may produce offspring that are poor performing.

Breeders in a position to take risk might consider using several individuals that have high EPDs, but low accuracy values. On average he/she will have the same number of individuals exceeding performance expectations as those which perform poorly. The “outstanding” sire will be identified from among the young sires. Breeders that do not wish to take risk should rely heavily on individuals that have desirable EPDs for a given trait and high accuracy associated with them. If your breeding herd is large enough, a breeder may consider using a combination of high EPD, high accuracy and high EPD, low accuracy breeding animals in order to balance risk.