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## Selection Guidelines for the Seedstock Producer

(Key Words: Breeding, Genetics, Genetic Improvement)

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### Introduction

The primary function of seedstock producers is to direct genetic progress for economically important traits and provide those improved genetics to the commercial industry through healthy boars and gilts. To effectively cause genetic progress, a well-planned breeding program must be implemented in seedstock herds. The breeding program must include economically important traits that can be measured objectively, and it must emphasize those traits in a way that reflects the needs of the commercial customer.

This factsheet will address principles that should be incorporated into the breeding program of seedstock producers. Consult the references at the end of this publication for additional information about performance testing and genetic improvement strategies.

### Basics of Genetic Improvement

Since the late 1700s, livestock improvement has emerged as a mixture of art and science. Until the post World War II era livestock improvement came about mostly by visual appraisal and did cause improvement in type, conformation and breed character. With the consolidation of the commercial pork industry and the increased pressure placed on the meat industry by consumers, the science of livestock improvement has become the cornerstone of herd improvement programs. These scientific programs can cause predictable genetic change in seedstock herds. Using these programs, seedstock producers will be more able to provide boars and gilts to the commercial pork industry to improve their competitiveness along with the product provided to the consumer.

Before a performance testing program can be put into place, a selection objective for a particular herd or line must be established. This selection objective is a commitment to what the herd or line will be known for and how it will be used in commercial crossbreeding systems. Lines that are for terminal boar production will be selected primarily for postweaning growth traits and body composition, while maternal lines will be selected for a balance of reproductive, growth and body composition traits.

**Accuracy of trait measurement.** Gathering data for a performance testing program must be a routine part of the day to day management of a seedstock herd. Data collected for use in a performance program must be gathered in a way so that the measurements are repeatable. For example, a scale is needed to weigh pigs and calculate days to 230 lb. The scale needs to be accurate so that if a pig was weighed several times each weight measurement would be within a pound or two of the others and estimate the actual weight of the pig.

**Adjustment factors.** Once data are collected they should be adjusted to correct for nongenetic factors so that pigs are fairly evaluated for the traits of interest. This includes simple things like age and weight at market for postweaning traits or parity of the sow for reproductive traits.

**Heritability.** Biological traits have an interesting characteristic. Pigs of similar ancestry that are managed uniformly will still have some variability in performance. Only a portion of this variability of like animals is under genetic control. The portion of the variability that can be influenced in a genetic improvement program is called heritability. The symbol often used to represent heritability is  $h^2$ . In general, reproductive traits are considered to have low heritability, postweaning growth and effi-

ciency traits are of moderate heritability while carcass traits are highly heritable (Table 1).

Item	Heritability (h <sup>2</sup> )
<b>Reproductive Traits</b>	
Age at Puberty	.32
Pigs Born	.10
Pigs Born Alive	.07
Litter Birth Weight	.29
Prewaning Survival	.05
Pigs Weaned	.06
Litter 21 Day Weight	.15
Rebreeding Interval	.23
<b>Postweaning Traits</b>	
Days of Age at 230 lbs	.25
Average Daily Gain	.30
<b>Postweaning to Market Wt.</b>	
Feed/Gain	.30
Average Daily Feed Intake	.24
<b>Body Composition Traits</b>	
Average Backfat Thickness	.41
Tenth Rib Backfat Thickness	.52
Loin Muscle Area	.47
Lean Percent	.48

Traits that are lowly heritable will tend to respond to selection at a slower rate than traits that are highly heritable. Before traits are chosen for a selection program the ability to make progress (i.e., heritability) and the economic value should be considered. If traits are lowly heritable but are of economic significance to the selection objective of the herd, they should be included in the selection program. While the rate of change in the trait may slow, the value could be high.

**Selection intensity.** Genetic improvement over time is measured as improvement in average performance. For a given trait, if the goal is to desirably change average performance then replacement animals must be better than average. The difference between the average performance of the selected replacement animals and the average of the contemporary group is called the selection differential. The magnitude of the selection differential is referred to as selection intensity. If the performance records of the animals selected are not much different from group average the selection intensity is very small and genetic progress will occur very slowly if at all. If

performance of animals selected ranks in the top 10% then the selection intensity is much greater and genetic progress occurs at a greater rate.

Figure 1 is a representation of potential genetic change per generation for days to 230 lb. In this example, selection intensities for gilts ranged from 50% (top one-half) to 25% (top one-fourth) while selection intensities for boars ranged from 50% to 1%. Dramatic differences in potential genetic improvement occur as boars and gilts are selected more intensely.

**Generation interval.** Once an animal is conceived, its genetic makeup and therefore its ability to contribute to genetic progress is fixed. In an ongoing genetic improvement program, the average genetic merit of the new generation should be better than the genetic merit of the parents that produced them. Therefore, genetic progress is enhanced when an older animal is replaced with a younger animal that is genetically superior.

Efficiently turning over the breeding herd can have a large impact on genetic improvement, since it relates directly to generation interval. The generation interval is the average age of parents when they produce an offspring. Generation interval is often expressed in months or years. If the number of months or years it takes to complete a generation is high, due to the slow replacement of older animals with younger animals, genetic progress per year will be very slow. If the number of months or years it takes to complete a generation is low then genetically superior young animals are replacing genetically inferior older animals at a faster rate and genetic progress per year is greater. A reasonable range for generation interval within seedstock herds can be 14 to 20 months. There is additional discussion of generation interval later in this publication.

## Performance Testing

Performance testing is the evaluation of objectively measurable traits so that desirable individuals will be

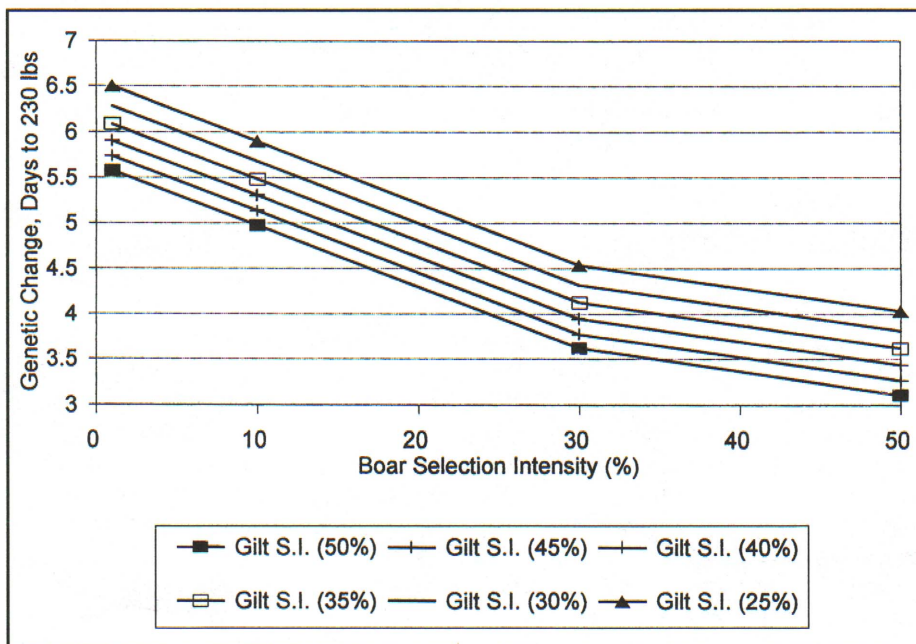


Figure 1. Selection intensity (S.I.) effect on genetic change.

chosen as parents for the next generation. Procedures must be implemented so that the data collected reflect differences between animals that are largely genetic.

**Contemporary groups.** To conduct a performance testing program the initial comparison that is made is within a contemporary group. Pigs are compared to the contemporary group average for the performance trait. How that contemporary group average is selected becomes critical to the evaluation outcome for the pigs within that group. Contemporary groups must be defined so that animals within that group are of the same breed and gender, are of similar age, have had similar care, eaten similar feeds and been housed within the same facility during a defined time period.

The definition of contemporary groups will vary depending on the traits measured. For grow-finish traits, litters that were farrowed in distinguished groups and then managed in an all-in/all-out system would be a contemporary group. For herds that farrow continuously, or do not farrow litters of the same breed or breed cross during a distinctive period, the seedstock producer will have to use wise judgment in defining contemporary groups. The seedstock producer must balance keeping the age range among pigs to a practical minimum and yet have enough pigs within the contemporary group to make the comparisons meaningful.

Sometimes within a contemporary group, pigs will be managed or housed somewhat differently. If this occurs, pigs managed or housed differently cannot be directly compared to each other. If this occurs pigs will need to be divided into subcontemporary groups. For instance, if half the gilts are kept in one building while the other half are put into another facility, these females will need to be categorized into different subcontemporary groups. Initial comparisons or performance deviations should then be made within subcontemporary groups.

Animals within contemporary groups can be measured for growth traits at different times, but pigs in the same pen should remain together until all animals within a pen have been evaluated. It is best if animals that are to be measured for traits that are adjusted to a common weight be evaluated near the target weight (e.g., days to 230 lb, backfat adjusted to 230 lb). As animals are weighed and returned to their pens, only those animals that met the weight criterion would be considered off-test. If animals are removed from the pen after reaching the off-test weight criterion, changes in pen stocking density will alter the performance of those pigs yet to be evaluated. If this occurs then animals should be designated into subcontemporary groups.

For sow productivity traits, contemporary farrowing groups must be designated. In general, herds that have distinct farrowing groups will be able to uniquely identify contemporary farrowing groups. For herds that farrow continuously, or do not, farrow sows of the same breed or breed cross within a distinctive group, the seedstock producer will again have to use wise judgment in designating farrowing groups. For instance, some producers designate all sows of the same breed that farrow within a particular month as a contemporary farrowing group. However, sows of the same breed that farrow at a similar time but differ in the genotype of their litter should be in different sub-contemporary groups. It

would be unfair to compare sows of the same breed for litter 21 day weight if a portion of them had purebred litters while others had crossbred litters.

**Whole-herd testing.** A key point of comparing individuals and using data in genetic evaluation programs is the notion of whole-herd testing. Whole-herd testing is nothing more than testing all animals that are healthy and can contribute a record. For sow productivity traits all females that farrow a litter should be measured. Furthermore, litter size should be standardized soon after farrowing. Thus if litter size between sows is relatively the same, differences in the number and weight of pigs at weaning will more closely reflect genetic differences among the sows.

For postweaning traits, all healthy barrows, gilts and boars that grow normally should be included. Records of pigs that grow extremely slow compared to pigs of similar age or those that have been ill, acutely or chronically, such that their ability to reach market weight has been hampered should not be included in the evaluation. A potential guideline could be as follows: pigs whose adjusted record for days to 230 lb, which is more than 32-39 days higher than their contemporary group average could be excluded, especially if the individual had been noted as ill or injured during its growth phase.

Partial herd testing or selective testing of animals is a detriment to long-term genetic improvement in the herd. If, for example, only the very good pigs from an average sire are tested along with a greater number of pigs from an above average sire, the average sire may be evaluated to be better than he truly is. In this scenario the few good performing progeny from an average sire may have a higher mean performance than the larger number of progeny tested from an above average sire. This could lead to more progeny selected from the average sire than desirable and therefore diminish the amount of genetic change possible.

Including only some of the records from a contemporary group can also bias a genetic evaluation by changing the average to which an individual's record is compared. For example, the genetic value of a boar or gilt may be underestimated if only records from the best performing pigs of a contemporary group are included in the group average.

## Expected Progeny Deviations (EPDs)

Expected Progeny Deviations (EPDs) are estimates of genetic merit that can be more powerful in driving genetic progress than selection based on individual performance records alone. These EPDs are defined as the difference from average in performance of subsequent progeny if an individual is mated to average mates.

In some literature or industry programs estimates of genetic merit are presented as Estimated Breeding Values or EBVs. The EBV is an estimate of the genetic merit of an individual. The EPD of an animal is nothing more than one-half of its EBV. Calculation and use of these two estimates of genetic merit are virtually the same.

In the calculation of EPDs, the individual's performance record is used along with the performance record

of other relatives, such as full- or half-sibs, sire, grandsires, dam, granddams and progeny. All performance records are deviated from their contemporary group average and weighted by the heritability of the trait. In the case of records of relatives, the records are also weighted by the relationship between the relative and the individual of interest. This weighting of relative records also takes into account the number of records per relationship class. For instance an animal may have more half-sib records to include in the calculation than full-sibs.

An EPD may have a positive or negative sign. These signs are important in their interpretation and use. EPDs with positive signs signify more or greater while EPDs with a minus sign indicate less or fewer. For example, a gilt may have an EPD of -.2 for number born alive. If mated to average mates resulting daughters would be expected to farrow .2 pigs fewer per litter. However, if the EPD was +.2, the opposite would be true.

Some genetic evaluation systems do deviate from the above mentioned convention concerning the sign of the EPD or EBV. For instance, the Nebraska SPF EBV program uses a different convention for signs of the estimates. A minus sign implies detrimental genetic merit estimates, while EBVs with positive signs are desirable estimates. When using EPDs or EBVs from different systems, care should be taken to understand the convention used in regard to the sign of the estimates.

**Accuracy of EPDs.** As performance records regarding an individual and its relatives occur, an EPD estimate can be calculated. The EPD estimate should be a reliable appraisal of a pig's true genetic value. As more performance records from relatives are collected and included in the calculation, the EPD estimate improves in reliability. The measure of the reliability of the EPD is called accuracy. The accuracy of an EPD can be thought of as the closeness of the estimate of an animal's genetic merit to its true genetic merit.

**Across-herd EPDs.** With the use of modern statistical methods and the decrease in cost of high-speed computers along with the genetic ties between herds created through the expansion of artificial insemination, EPDs that can account for non-genetic differences between herds can now be estimated. This provides the user with an accurate method of directly comparing animals that were tested in different herds. Across-herd evaluations are now available for most major pure breeds. A more in-depth discussion of across-herd estimation of EPDs can be found in the National Swine Improvement Federation's Factsheet No. 13, *Across-Herd Genetic Evaluation*.

## Managing the Purebred Herd for Genetic Improvement

Much of the discussion to this point has been directed toward a

better understanding of how to uncover genetic differences and exploit them in a selection program. However, there are other factors that must be managed to sustain long-term genetic improvement.

One of these is sampling enough progeny from particular sires to determine their genetic ranking. The number of litters a boar sires within and across contemporary groups will affect the accuracy of his EPD. The number of sires represented within a contemporary group, as well as the number of contemporary groups a sire has progeny tested in, are important. Equations have been developed to better understand this concept.

Figure 2 shows the effect on accuracy when from 1 to 12 sires have progeny in each contemporary group and a given sire has progeny in 3, 6 or 12 groups. A moderately heritable trait ( $h^2=.3$ ) was assumed for this example. The largest improvement in accuracy of sire evaluations occurred when the number of sires used per contemporary group increased from 1 to 2. Also, it is evident that the improvement in accuracy begins to diminish beyond the addition of 4 to 5 sires per contemporary group. Further investigation, not shown here, demonstrated that having more than 4 to 5 sires per contemporary group could not be justified economically, solely for the purpose of increasing accuracy.

Along with managing the number of sires represented within a contemporary group, is the need to adequately represent a sire across contemporary groups. Figure 3 is an evaluation of 3, 4, 5 and 12 sires with progeny in 1 to 12 contemporary groups. The largest increase in accuracy occurs when sires had progeny evaluated in 2 to 6 contemporary groups. Thus seedstock producers should have a boar's progeny tested in more than 2 contemporary groups.

Some seedstock herds do not introduce new animals into the herd after selection has begun. These herds are considered closed to outside genetic influence. A concern of closed herds is the potential detrimental change in performance due to inbreeding. Inbreeding can cause a decrease in genetic variability as well as cause a

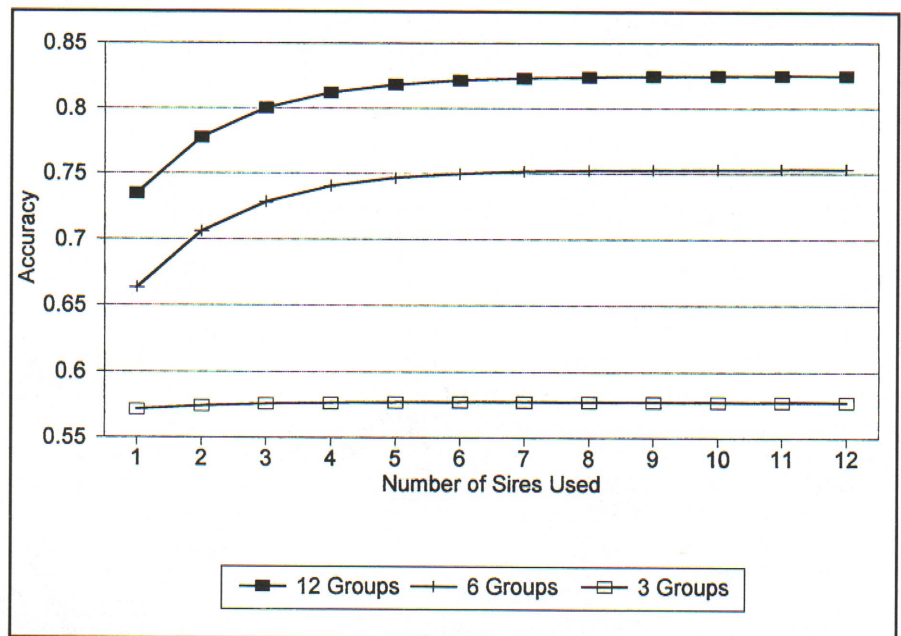


Figure 2. Impact of differing sire usage on accuracy of sire EPDs.

fixation of undesirable genes. Not only can the frequency of undesirable qualitative traits increase (e.g., cleft palate), but also undesirable chronic effects on performance traits can occur. Increases in inbreeding can cause a steady, chronic performance decrease in lowly heritable traits over time. As noted in Figure 4, a 10% increase in the inbreeding coefficient of the litter will cause a reduction of .28 pigs weaned.

Within closed populations, mating strategies can be developed to delay the increase in the average inbreeding coefficient. This can be easily done by maintaining a reasonable number of herd sires per generation in comparison to the number of sows within the herd.

An example of this is found in Figure 5. This is an evaluation of how the change in the average inbreeding coefficient for the first generation of selection is affected by the number of sows and boars used. The number of sows within a herd is not as important in minimizing the change in the average inbreeding coefficient as the number of boars used per generation. By using 12 herd sires per generation, the change in the average inbreeding coefficient is about 1% per generation, regardless of sow herd size.

Reducing the average change in the inbreeding coefficient will cause genetic variability to decrease at a slower rate. This is important in terms of the impact on heritability. When the genetic variability of a trait declines the heritability will also decline, since heritability is the proportion of the total variability of a trait due to genetic influence. Figure 6 depicts the percentage decline of heritability due to a decrease in genetic variability from inbreeding. In this example, the heritability used is .3 (e.g., days to 230 lb). One generation of selection when using only one herd sire caused heritability to decline 16%. On the other hand using 12 herd sires caused heritability to decrease less than 1%. Maintaining a reasonable number of herd sires will diminish inbreeding buildup and cause heritability to decline at a slower rate.

Along with maintaining a reasonable number of herd sires, matings of pigs that are closely related should be avoided. This will cause the average increase in inbreeding coefficient to be further reduced. Therefore, a general rule is that matings among animals that have a relationship of half-sibs or closer should be avoided. This should reduce the increase in inbreeding by approximately 50%.

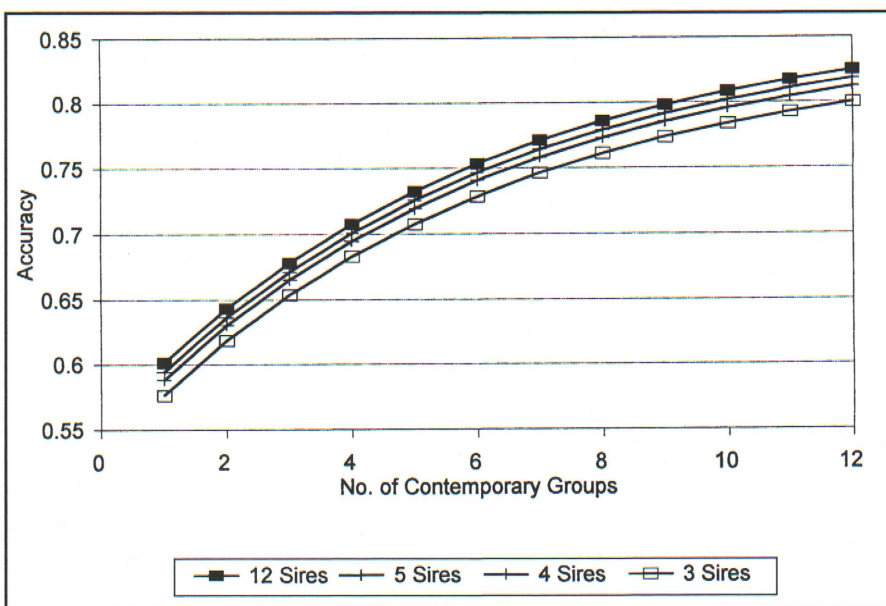


Figure 3. Impact of contemporary group number on sire EPD accuracies.

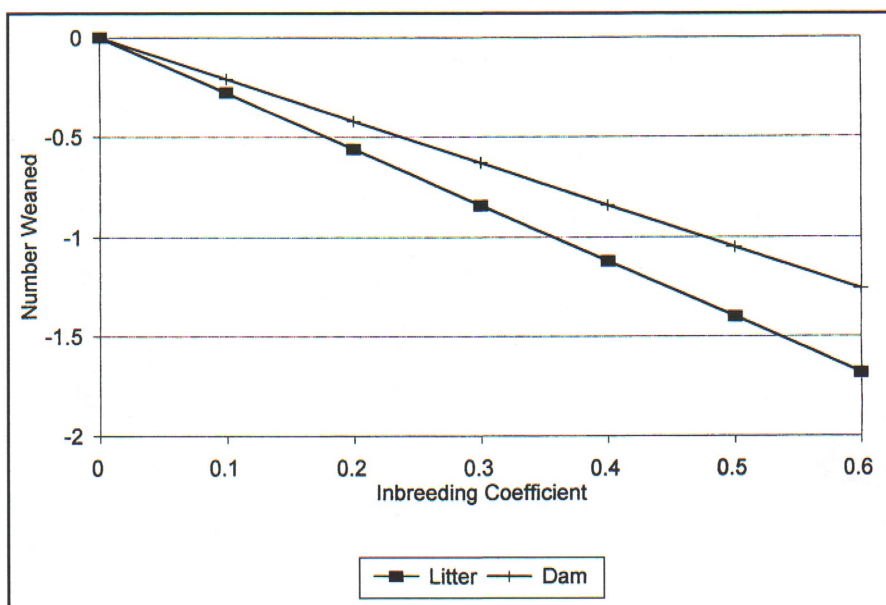


Figure 4. Inbreeding effects on number weaned.

Improvement in genetic merit is often expressed as the change that has occurred within a generation. However, a generation can be a variable length of time. In the business of raising pigs, profit and loss is measured on a yearly basis. Therefore, the shorter the generation interval the more impact genetic improvement will have on yearly profit.

Figure 7 is an evaluation of response per year for a moderately heritable trait ( $h^2=.3$ ), when the average generation interval of sows and boars differ. The generation interval is defined as the average age of parents when they have offspring. In this example it was assumed that replacement gilts would rank in the top one-third and replacement boars would rank in the top 10%.

In the first year there was a difference in genetic improvement of .26 genetic units between generation intervals of 12 and 30 months. After 5 years; however, there was a difference of 1.21 genetic units between selected programs that had generation intervals of 12

and 30 months. In reference to a trait like days to 230 lb this would equal a difference of 3.4 days after 1 generation and 17 days after 5 generations. Managing the generation interval to speed genetic improvement will allow continued improvement of commercial replacement stock.

## Managing EPD Usage in a Selection Program

Use of EPDs in selection programs offers the user much more potential genetic gain than basing selection on individual performance records alone or traditional selection indexes. Research in this area has shown that using EPDs will improve selection response of lowly heritable traits (e.g., reproductive traits) by 21% to 70%, moderately heritable traits (e.g., growth traits) by 10% to 30% and highly heritable traits (e.g., body composition traits) by 3.5% to 12% compared to selection on the individual performance record alone.

EPDs cause greater improvement in genetic gain because of inclusion of information from relatives and better correction for environmental factors. The result is improved accuracy in the prediction of true genetic merit of an individual. Thus, a greater percentage of chosen replacement animals have a more desirable genetic merit.

The use of EPDs can be thought of as a more effective way to identify desirable families within a breed or line, as well as desirable animals within a family. This greater reliance on family information causes a culling of less desirable families from a population or line at a faster rate than selection based on individual performance alone. This may cause the relationship among individuals within a breed or line to increase at a faster rate.

The escalated increase in relationship among individuals will cause the average inbreeding coefficient to increase at a faster rate. Subsequently, heritability can decrease. This has been substantiated in simulation studies that compared selection results of selection conducted with either EPDs or individual records only. In small herds (less than 100 sows), heritability decreased at a faster rate than when selecting on the performance records alone. In larger closed herds (more than 200 sows) the decline in heritability was not as severe. This

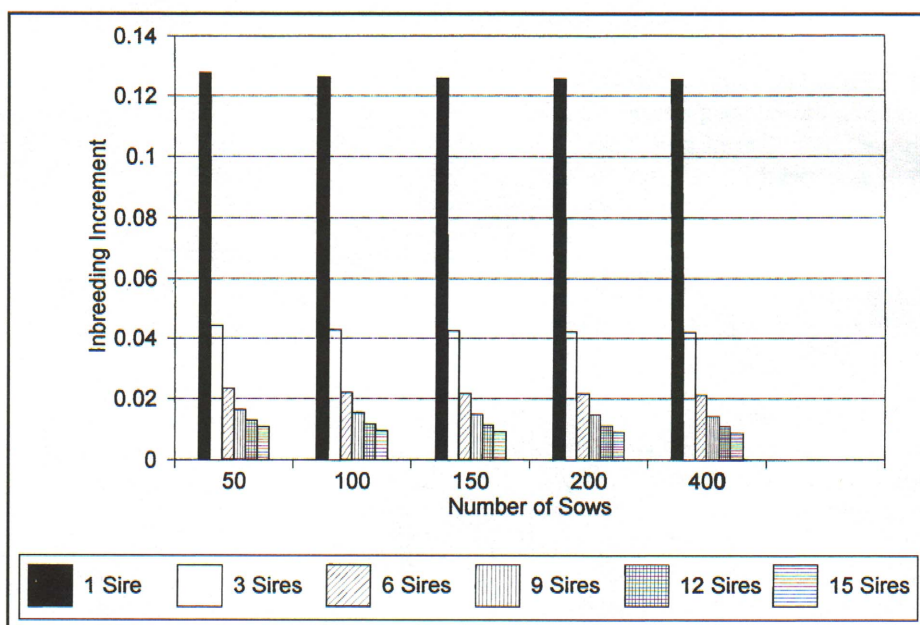


Figure 5. Effects of sow and boar numbers on increase in inbreeding.

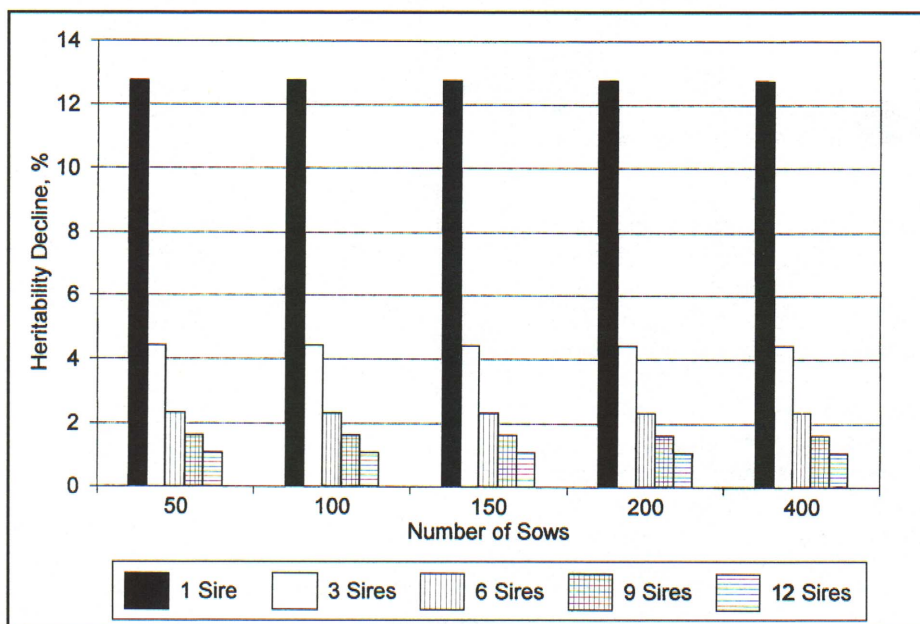


Figure 6. Effects of sow and boar numbers on decline of heritability.

suggests that using EPDs within small, closed herds can lead to a decrease in the heritability of trait. Therefore, closed herds should be relatively large in size when plans are to use EPDs in the selection program.

This research modeled selection programs in closed herds. These closed herds did not introduce outside, non-related animals into the herd after the initial generation of selection. This scenario may not hold true for smaller herds that participate in national or regional genetic evaluation programs. Herds that participate in such programs can routinely sample high ranking non-related boars, through artificial insemination or the purchase of high ranking sons. This provides herds two important herd management tools. The first is not closing the herd, allowing the inbreeding level to remain low and maintaining greater heritability. The second is less genetic risk in sampling unrelated boars.

## Managing Qualitative Traits

Qualitative traits are traits that are controlled by one or just a few gene pairs. They often express themselves as all or none phenotypes. For instance, baby pigs with cleft palate will have parents that do not exhibit the trait. However, each parent is a carrier of the trait and it then manifests in the offspring. The term for carrier animals, those that carry one normal and one defective gene, is heterozygous. If animals carry either two normal or two defective genes they are homozygous.

Some qualitative traits have an economic impact on commercial pig production. Many of these such traits are classified as genetic defects. Often the genetic control is that of a recessive gene. This means that if a parent carries one normal and one recessive gene, the detrimental phenotype is not expressed. However, the parent will pass the recessive gene on to one-half of its progeny. If that parent is mated to an animal that also carries a recessive gene for the trait in question, on average 25% of the offspring will express the trait.

Screening a genetic defect from a population is a matter of how detrimental it is to the population and how prevalent the phenotype is. If the occurrence of a genetic defect is uncommon and a pig exhibits the defect, culling the parents of that individual and its full sibs would further reduce the number of animals in the herd that would be carriers and therefore decrease the probability of the occurrence of the genetic defect. However, if animals that have progeny with genetic defects are not screened from the herd and therefore contribute progeny, the genetic defect will become more prevalent. At some future point the defect would occur at a large enough incidence that more drastic elimination measures may be needed. These could include culling affected families or lines.

Direct tests are becoming available to determine the genotype (homozygous or heterozygous) for some qualitative traits. A tissue or blood sample is subjected to laboratory tests. From the laboratory results, it can be determined if an animal carries, zero, one or two copies of a favorable or detrimental gene. Currently, a

test for the PSS (Porcine Stress Syndrome) gene is available to the industry.

**Porcine Stress Syndrome.** An example of a trait caused by a recessive gene is Porcine Stress Syndrome. It is considered a genetic defect but may have some beneficial effects. Animals that are homozygous for the PSS gene can suffer sudden death near market weight due to stress. If they reach slaughter, upon sanguigation they will exhibit on average, pale, soft and exudative (PSE) pork. These animals, on average, will have a higher lean yield of some primal cuts. Animals that are carriers of the PSS gene do not exhibit PSS characteristics and will have a greater yield of some primal cuts compared to normal pigs, but have a greater incidence of PSE than normal pigs. See PIH - 26, "Porcine Stress Syndrome" for an in-depth discussion of this condition.

Until recently, PSS could only be accurately tested with the use of halothane gas. This method could only determine animals that are homozygous for the PSS gene. Scientists have developed a blood test that can detect both the homozygous and heterozygous PSS animals. This test can then be used to determine the frequency of the gene within a herd or line.

Once the frequency is known, strategies concerning the gene can be planned. Primarily, it should be decided if the PSS gene will be maintained within a herd or line or eliminated. If it is to be eliminated then the rate of elimination should be determined. The rate of elimination may very well be tied to the frequency of the gene. For lines that have the gene at a moderate or high frequency, elimination of the gene may be done in a systematic fashion so as not to decrease the number of families and thus potentially reduce herd size.

## Use of Artificial Insemination in Seedstock Herds

Artificial insemination is just reaching its potential within the United States pork industry. For seedstock producers it provides a simple tool for sampling genetic lines within a breed without taking physical ownership of the boar. Semen from a particular boar can be used to produce a representative number of pigs for testing and comparison to other sires used within the herd. If the progeny of the boar do not perform as well as progeny from other sires then all that is lost is the cost of the semen and testing costs.

However, when herds participate in across herd genetic evaluation summaries, sires from other herds that rank higher can be used to further genetic progress. For example, using sires that rank within the top 10% of the breed should improve genetic change within a herd (Figure 1). However, further improved progress will be achieved when using boars that rank within the top 1% (Figure 8).

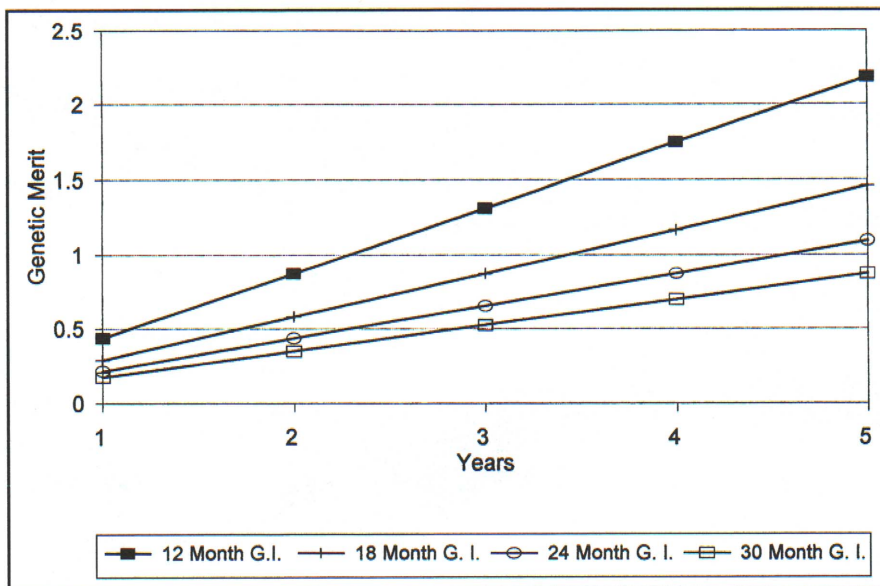


Figure 7. Generation interval (G.I.) effect on genetic change over time.

For herds that conduct their own within-herd genetic evaluation program, there is a catch in using semen from boars outside the herd. Since ancestral information is used in EPD calculations, boars with no ancestral data within a herd database will be at a disadvantage in these genetic comparisons. Therefore it is important to properly sample a sire with no previous ancestral information. Within a EPD selection program, an outside sire with no ancestral data is considered average when introduced into a breeding herd. If that sire is mated to only poor ranking or high ranking females then the evaluation of that sire will be biased and will not provide an accurate assessment of his genetic value to the herd. It is important that an outside sire be mated to an equal number of low, medium and top ranking sows so that the resulting evaluation will accurately reflect the sire's potential genetic contribution to the herd. Since the boar's assumed genetic merit is average and if he is mated to sows whose combined genetic merit is herd average then if the resulting genetic evaluation is average or better, his superior offspring may be kept for replacements.

## Conclusion

Implementation of principles discussed in this Factsheet will lead to predictable genetic progress. Seedstock producers that desire to maintain a viable genetic improvement program must incorporate these principles into their management programs.

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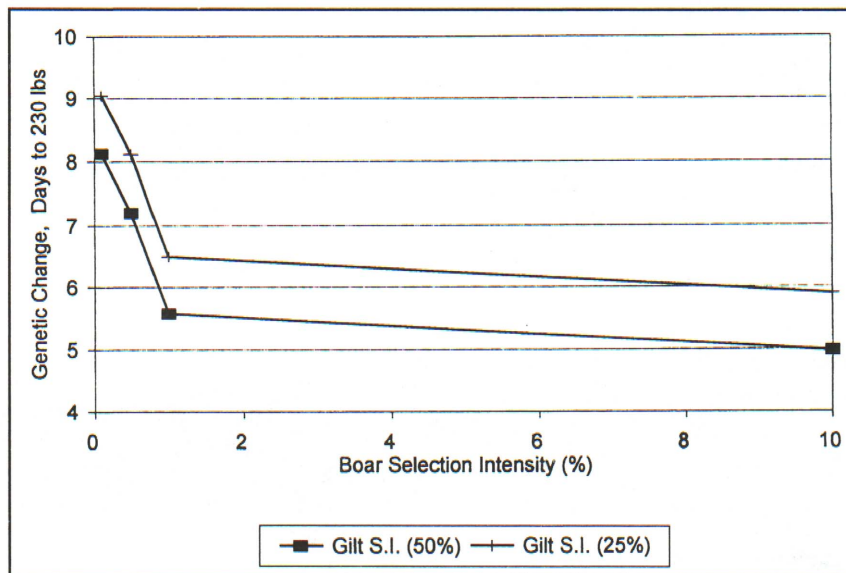


Figure 8. Selection intensity (S.I.) effect on genetic change.

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