In breeding beef cattle, choosing traits for which to select is only part of the battle. Once the choice or choices have been made, a breeder must have some way to accurately establish each animal's breeding value for those desired traits. Here, authors Wilkes and Dr. Turner discuss methods that can help take the guesswork out of that process.

Third in a series designed as a guide to basic genetics.

Genetic Improvement Aids to Selection

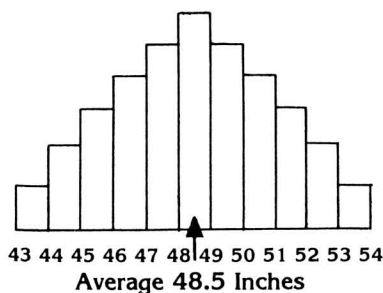by Darrell L. Wilkes
and Thomas B. Turner, Ph.D.

In the last article we briefly discussed several selection methods for improving more than one trait in beef cattle. Regardless of the method used, we are assuming that each trait can be accurately measured. To be more specific, we are assuming that the animals we choose to keep are better than those we discard. Since this is the backbone of genetic improvement, discussing methods which help improve our accuracy of selection—namely, progeny tests, pedigree information and records on collateral relatives—is worthwhile. For reasons that follow, these aids to selection are more useful in some instances than in others.

For the time being, let us assume that we are interested in improving a single trait. If heritability for this trait is high, we know the record on the individual is our single most valuable piece of information. Traits such as yearling weight and frame score (as well as many others) fall into this category. For the most part, if we are selecting for frame score, for example, we will select replacements based only on their own individual records for that trait. In doing so, we probably will not make many mistakes. That is, the animals we select are probably those with the highest breeding values for frame score. However, as business persons, we want to know the degree of emphasis placed on the word "probably."

Concept of Probability

Most of us are familiar with the mathematical concept of probability. By making a statement containing the word "probably," we are making reference to this concept. Those of us who occasionally take in the leisure of a poker game have applied our knowledge of probability either successfully or otherwise. Now let us apply this concept to cattle breeding.

In order to appreciate this application, we need to be able to visualize what a population (herd) of cattle looks like on paper. We know we have a few individuals that are extremely tall and a few that are extremely short. Most of them, however, are pretty close to the average. If we set up a bar graph where each bar represents a 1-inch spread in hip height at one year, we might have a distribution as follows:

43 44 45 46 47 48 49 50 51 52 53 54
Average 48.5 Inches

The height of each bar represents the proportion or percentage of calves that fall into a particular category. For example, we can see that the bar representing calves between 48 and 49 inches is higher than the one representing calves between 53 and 54 inches. As we move closer to the average (48½ inches), we notice that the bars get taller. That is, we expect most of the calves to be close to the average. Of course, the average will be different in each herd, but the basic distribution will be similar to that shown in the graph.

The Bell-Shaped Curve

Now if we break this same calf crop down into ½-inch rather than 1-inch intervals, we would have twice as many bars and the graph would begin to smooth out. If we continue, we would eventually have a smooth curve as shown:

Short   Tall
**Average
48.5 Inches**
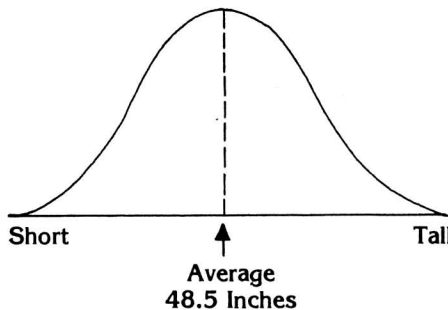
This is the familiar bell-shaped curve referred to by statisticians as the *normal curve*. You can think of it as a calf crop.

Far out in the right-hand tail you will find those very tall show heifer prospects. Of course, there are not many of those, so the curve is not very high there. Far out in the left-hand tail you will find the "belt buckle" heifers you will cull if selecting for frame score. From either extreme, as you move toward the middle, you will start finding more animals closer to the average. The area under the curve represents your entire calf crop (separate curves for bulls and heifers). The height of the curve represents the proportion of your calves that take on some particular value.

Since we can view this normal curve as a calf crop, we can begin to assign probabilities to our selections. Also, we can see how our aids to selection come into play. If you decide to keep 50% of your heifers from a calf crop and are selecting on frame score, you could just count down the top half and select them, culling all others. If we knew that the phenotype of an animal was perfectly associated with its genotype, we would make *no* mistakes in our selections. However, since the heritability of frame score is not 100%, we do not have this luxury.

Breeding Value Versus Actual Value

Let us recall our objective: We want to select those heifers with the highest *breeding values* for frame score regardless of their *actual value* for this trait. Since frame score is fairly highly heritable (70%), we know that, on the average, the tallest heifers will have the highest real breeding values. However, we should not ignore that, if heritability is 70%, nonheritability is 30%. That is, 30% of the difference in frame score between any two heifers is due to non-genetic causes. When comparing two heifers then, we must realize that the tallest one does not automatically have the highest breeding value for frame score.

Now that we have established a basic understanding, let us start selecting heifers. We want to achieve the highest possible likelihood that the heifers we select will be above average. If we look at the tallest heifer, we see that she has a hip height of 54 inches—well above the average. Now what is the probability that she is above average in *breeding value* for frame score? Since we know that heritability for frame score is high, we feel fairly certain that this heifer is at least above average. If the truth were known, she may not have the highest breeding value for frame score, but she is at least above average—isn't she? If we let the phenotypic standard deviation be 2.5 and heritability be .70, we calculate the probability as .969. This is very close to being absolutely certain. We interpret this value as follows: If we had 1,000 calf crops like the one we have described and each one contains a 54-inch heifer, .969 of these 54-inch heifers would have above average breeding values in their respective herds. We cannot do much better than this.

Battle of the Bulge

As we continue to move down the list of heifers, our certainty that each one is genetically above average starts to decrease. As we get near the average heifers—of which there are many—it becomes almost a guessing game. This is where we need some information from relatives to help make the right decisions. This is what the authors refer to as the "battle of the bulge." Winning this battle is a key step in winning the overall war against innocent mistakes in selection.

If we recall our normal curve and represent the "battlefield" by the shaded region, we have the following:

**Average
48.5 Inches**
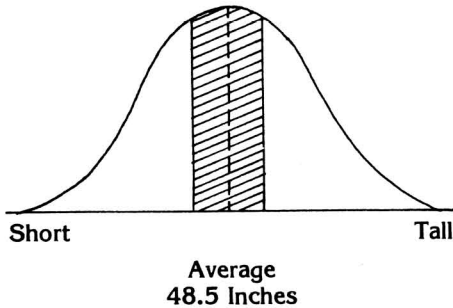
By using additional information (records on relatives), we can get a more accurate ranking of the animals that happen to be in the battlefield area. The width of the battlefield depends upon the heritability of the trait. Recall that if heritability is equal to 100%, there would be no battlefield at all. In contrast, if heritability is low, the battlefield would be much larger and, in fact, could cover the entire area under the curve. This is why records on relatives are so much more helpful when ranking animals for a trait low in heritability.

Now that we have seen when our aids to selection are useful, let us discuss some of them.

Progeny Testing

Even without possessing detailed knowledge of genetics or statistics, the concept of a progeny test is one with which most of us are familiar. In fact, before Gregor Mendel actually had discovered the true nature of inheritance in the mid-19th Century, livestock breeders were advocating that sires of proved excellence be used to their fullest capacity.

We have come a long way since the rediscovery of Mendel's work in the early 1900s and today have a better handle on the principles of progeny testing—both from a genetic and statistical standpoint. For example, we know that a progeny test is more useful for some traits than for others. Indeed, there are several traits that cannot be measured in a bull at all without a progeny test. For example, although we may be able to get a little information from the pedigree of a bull for estimating his breeding value for maternal traits, we know that the most informative data come from his daughters. This requires a progeny test.

In other cases, if the record is available on the individual, the progeny test may or may not add much information. The amount of additional information that can be obtained from a progeny test is largely dependent on the heritability of the trait being evaluated. Table 1 shows the accuracy of the estimated breeding value that is due to the individual's record versus records on progeny.

TABLE OF ACCURACY VALUES

	Heritability						
	.10	**.20**	**.30**	**.40**	**.50**	**.60**	**.70**
Self	.316	.447	.548	.632	.707	.775	.837
10 Progeny	.452	.587	.669	.725	.767	.799	.825
20 Progeny	.582	.715	.787	.830	.860	.883	.900
Self Plus 10 Progeny	.492	.615	.688	.742	.787	.828	.868

Immediately, one can see that information on progeny is useful in improving accuracy. However, it also should be clear that information on progeny is accompanied by the law of diminishing returns for traits that are highly heritable. For example, inspection of the accuracy figures in the column for .70 heritability reveals that the individual's own record is more informative than the records on 10 progeny. However, for traits that are lowly heritable, progeny information can help improve accuracy quite dramatically. The obvious suggestion from geneticists is that each individual be measured for each trait of importance in your herd. If this is done and progeny information eventually becomes available, both sources of information can be used to predict the breeding value of an animal.

Comparing Different Herds

The foregoing principles and suggestions apply directly to a closed herd where no outside sires are used. Since many breeders opt to use bulls from other herds via A.I., the progeny test becomes more useful to them. Why? Because it is difficult to compare *actual* weights and measures from different herds. The use of ratios does not solve this problem either, since the reference point of a ratio—100—is not the same in any two herds. If we were able to obtain two bulls of identical genotype and grow them out in two different herds, there is little doubt they would have different yearling weights. In all likelihood, they would have different ratios as well. Nevertheless, if they were progeny tested together in the same herd(s), their progeny would be equal in merit, assuming dam contributions were held constant.

Considering this, the value of the Angus Sire Summary is obvious to breeders who choose to use some bulls A.I. In addition, it allows every breeder the opportunity to compare his/her herd sire not only to the bulls he/she actually uses, but to other bulls included in the summary which were not used in his/her own herd.

Pedigree (Information on Ancestors)

If one already has obtained a highly reliable estimate of an individual's breeding value by a progeny test or some other means, there is really no need to look back through the pedigree. Regardless of whether its parents had them or not, an animal cannot transmit genes it does not have. Likewise, an animal cannot transmit genes its parents did not have.

While those statements may seem obvious, it is no secret that many good individuals are shunned because they have some "undesirable" ancestor. On the other side of the coin, many poor individuals are kept because they have a "good" pedigree. We have used quotation marks around the words *undesirable* and *good* because no two breeders seem to agree when and where they apply. There is no telling the amount of progress that has been sacrificed over the years because of this kind of thinking. Needless to say, it has been substantial.

Objectively appraising an animal's pedigree is not an art—it is a science. For the breeder who has decided which traits to select for, pedigree and the information contained therein can be a great aid in selection. However, for the breeder without specific goals and without a clear understanding of the science involved, the pedigree serves only as a nemesis to real progress.

Too Much Emphasis on Pedigree

It has been our general observation that too much emphasis is placed on the pedigree, especially on the more distant ancestors. If we can be honest with ourselves for a moment, we realize that very little valuable information is contained in a typical pedigree. Names and registration numbers are basically worthless unless the breeder has some additional information on these animals on which to base his decisions. Even then, such information is rarely used to its fullest potential. Instead, inappropriate bits and pieces of information are extracted and used far beyond their bounds. Structured performance pedigrees, while they are potentially very useful, do not preclude this abuse either.

The practical limitations on usefulness of pedigree selection are imposed primarily by two factors—Mendelian chance at segregation and previous selection.

Mendelian Chance at Segregation

It is well understood that any animal gets half of its genes from each parent. Now a parent never gives the same set of genes to any two progeny (the probability of this happening is basically zero). This implies that, even if we know exactly the genotype of each parent, we could not predict exactly what the genotype(s) of their progeny would be. The best we can do, if we know the genotypes of the parents, is a multiple cor-

relation of .71 between the genotypes of the parents and the breeding value of an offspring. So what? Well, if heritability is .50, we can do just as well by measuring the trait on the individual and predicting its breeding value from that!

Previous Selection

The fact that all of the animals in a pedigree have been selected implies that calves which would have had poor pedigrees are never born. The final result of this is that there is generally a small spread in the overall merit of any particular set of

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pedigrees. One possible exception would be where selection for a new trait is just beginning. If this were the case, however, accurate records on ancestors likely would not be available anyway.

We do not want to give the impression that ancestors should be ignored. Certainly the authors realize that the pedigree of a purebred animal has a very substantial influence on the marketability of that animal, and this is not at all bad. Our objective is to point out that pedigree information—or the lack of it—traditionally has been subject to gross misuse. However, we should point out with equal vigor that pedigree information has its usefulness if taken in the proper perspective.

Obvious Value

If we think of the amount of information a pedigree can contain if the breeder has diligently kept records on all animals, the real value of the pedigree becomes obvious. Each ancestor essentially has been through a progeny test. This implies that even for traits of low heritability, the ac-

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curacy with which we can estimate breeding value of ancestors is potentially high. In fact, quite commonly breeding value of the sire can be estimated with accuracy in excess of .90. When this can be accomplished, this information should be used.

We suggest that breeders who would like to use pedigree information more objectively set the stage by measuring all traits they feel are important whether they are selecting for them now or not. By so doing, that information will be available when

needed; and more important, by personally measuring traits, a breeder will have confidence that the records are reliable.

Since the mathematical operations involved in properly weighting the various sources of pedigree information are sometimes very complex, it may be worthwhile to use the performance pedigrees available from the Angus association if you are selecting for traits they include. If not, your state university is staffed with people who are paid by you to do such things, and they are usually very eager to help.

Information on Collateral Relatives

Relatives such as half sibs are referred to as collateral relatives. Generally, collateral

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relatives make their records in the same herd—and often in the same year—as the individual being considered for selection. Exceptions occur when an animal has collateral relatives in several other herds—usually via A.I.

Basically, records on collateral relatives furnish a progeny test of one of the parents of the individual being considered. If taken in this perspective, the primary advantage is to improve the accuracy with which we can estimate breeding value of the common parent(s) and, ultimately, accuracy of the predicted breeding value of the individual.

In summary, the foregoing aids to selection help the breeder win the "battle of the bulge." Regardless of the fact that some animals appear to be obvious keepers, if additional information shows them to be less than expected, they should be dealt with accordingly. Finally, once the breeder has obtained the most accurate possible estimate of the breeding value of each animal for each trait, it is then time to use these estimates in the selection and mating system the breeder has chosen.

Regardless of the fact that some animals appear to be obvious keepers, if additional information shows them to be less than expected, they should be dealt with accordingly.

The next article will deal with systems of mating. It will show that some mating systems can render much data useless unless the breeder is aware of potential biases they can introduce.   Ⓐ

Medfly Not the Only Insect Invader in U.S.

The European corn borer rode into this country on broom corn imported from Hungary or Italy about 1908.

The gypsy moth, a major defoliator of hardwood forests, was brought to Massachusetts in 1869 by a physician who was going to cross it with the silkworm to produce a better variety of silk. A few moths escaped.

And, of course, the Mediterranean fruit fly wasn't named after California.

"A number of our major insect pests and many minor ones can be traced back as invaders from other countries," University of Illinois entomologist Robert Metcalf says.

We've introduced our share of pests to other countries, most notably the Colorado potato beetle into Europe on a shipment of potatoes to Germany in relief efforts after World War II.

All Will Be Here Soon

He predicts that within a few years most of the insect pests throughout the world that can exist in our climate will be here. That's what all the recent furor in California has been about. Metcalf notes that the Medfly has come to the southern U.S. a number of times; first to Florida in 1929, then again

in 1956 and a couple of times subsequently, causing the destruction of millions of pounds of fruit.

The flies were eradicated with an enormous spraying effort in urban and suburban areas with a Malathion bait insecticide. The pest apparently went to California from Hawaii, where it has been endemic for at least 30-40 years, Metcalf says.

"That's why inspectors at various ports of entry in the U.S. are so diligent about looking at baggage," he adds. "But they can't control the person who brings something to eat or some plant material in his pocket, goes through inspection and discards it somewhere else.

Easier Life for Insects

"We've done everything to make life easier for insects. We've provided the best kind of luxurious air transportation. It used to be that many insects couldn't survive a 2-month sea voyage, but most can live through an 8-hour flight," he continues.

Instead of the scattered patches of diverse crops Indians had, we grow thousands of acres of contiguous corn and soybeans.

"We can see for miles in every direction—nothing but corn and soybeans. This makes it a lot easier for those invaders to become very damaging. And then we've stored enormous amounts of grains and shipped them all over the world," Metcalf says.

In their native habitats where insect pests have evolved through millions of years, they exist in a fair amount of harmony with their environment. There are a great number of suppressive factors—such as insect diseases, parasites and predators—that keep the population regulated in some kind of respectable numbers.

Population Explosion

"When the pest is brought from abroad, those factors are left behind and typically there's an explosion as the pest enters a new set of ecological niches," he notes. "It takes many years to restore any kind of equilibrium. And with some pests like the corn borer and the gypsy moth, we never really have."

Agricultural scientists are encouraging the spread of this whole complex of natural enemies as part of integrated pest management programs. They also are trying to find crop varieties that are relatively resistant to insect attacks. Sometimes the best place to look for those is the homeland of the pest where plants have developed resistant characteristics and where beneficial insects and enemies are most numerous.

According to Metcalf, some disease-causing organisms are important regulating factors, and some of the microbiological products they produce actually are being marketed as insecticides. Ⓐ

How Many Billions In a Trillion?

The Tax Foundation has estimated that federal, state and local governments will spend $1.07 trillion in fiscal 1981, or $4,678 for each American. Ⓐ