

Basic Horse Genetics

ANR-1420

Understanding the basic principles of genetics and gene-selection methods is essential for people in the horse-breeding business and is also beneficial to any horse owner when it comes to making decisions about a horse purchase, suitability, and utilization. Before getting into the basics of horse-breeding decisions, however, it is important that breeders understand the following terms.

Chromosome - a rod-like body found in the cell nucleus that contains the genes. Chromosomes occur in pairs in all cells, with the exception of the sex cells (sperm and egg). Horses have 32 pairs of chromosomes, and donkeys have 31 pairs.

Gene - a small segment of chromosome (DNA) that contains the genetic code. Genes occur in pairs, one on each chromosome of a pair.

Alleles - the alternative states of a particular gene. The gene located at a fixed position on a chromosome will contain a particular gene or one of its alleles. Multiple alleles are possible.

Genotype - the genetic makeup of an individual. With alleles A and a, three possible genotypes are AA, Aa, and aa. Not all of these pairs of alleles will result in the same phenotype because pairs may have different modes of action.

Phenotype - characteristics of an animal that can be seen or measured—for example, color, birth weight, speed.

Qualitative traits - traits that are controlled by a single pair or a few pairs of genes. Qualitative traits are easily sorted into distinct categories and are not highly affected by environmental influences; therefore, it is usually simple to determine an animal's genotype for a particular qualitative trait. An example of a qualitative trait in horses is chestnut versus black coat color.



Quantitative traits - traits that show a continuous range of phenotypic variation. Quantitative traits usually are controlled by more than one gene pair and are heavily influenced by environmental factors, such as track condition, trainer expertise, and nutrition. Because of these conditions, quantitative traits cannot be classified into distinct categories. Often, the important economic traits of livestock are quantitative—for example, cannon circumference and racing speed.

Heritability - the portion of the total phenotypic difference (variation) among animals that is caused by the part of its genetic makeup that can be passed from generation to generation.

Homozygous - an individual whose genes for a particular trait are the same. For example, a black horse may be homozygous dominant for the black gene (EE), while a chestnut horse is homozygous recessive for that gene (ee).

Heterozygous - an individual whose genes for a particular trait are different. For example, a phenotypically black horse may be heterozygous (Ee) for the black gene.



Selecting Qualitative Traits: Basic Color Genetics

Selecting qualitative traits is a good place to review some basic genetic principles because most horse colors are controlled by relatively few genes and are easily identified phenotypically. The key to basic genetics is to remember that the horse contributes only one gene for any allele that he or she has to the offspring. For example, the base coat color of any horse may be either black with a genotype of EE or Ee or chestnut (sorrel) with a genotype of ee. The homozygous black horse (EE) can contribute only an E gene to the offspring. The homozygous chestnut horse (ee) can contribute only the e gene to the offspring. However, the heterozygous black horse (Ee) can contribute either an E or e to the offspring. This is an example of simple dominant gene action. An easy way to determine the chances of getting a black or chestnut horse is to simply write down the possible genes contributed from both parents (in bold letters below) in a Punnett square as shown:

Dominant gene - an allele that is expressed when carried by only one of a pair of chromosomes. For example, the E allele for the black versus chestnut coat color is dominant, while e is recessive. Horses that have one copy of the dominant E allele (EE or Ee) will be black unless that color is modified by other genes.

Recessive gene - an allele that is expressed only when the dominant allele is absent—for example, the e allele for the black versus chestnut coat color. Horses that have the e allele on both chromosomes of a pair (ee) will be chestnut unless that color is modified by other genes.

Additive - a gene effect that occurs when the heterozygous phenotype is intermediate between the two homozygous phenotypes—for example, aa = no product; Aa = product; AA = two times the product. Many economically important traits in livestock are influenced by many pairs of additive genes.

Locus - the place on a chromosome where a gene is located. The plural of locus is loci.

Epistasis - one locus masks, or controls, the expression of another locus. A locus, or loci, controlling the early steps in a pathway can be epistatic to genes occurring later in the pathway. For example, in horses, if an early step in a pathway that produces pigment (color) precursors is masked by the dominant white gene, it does not matter what base color the animal was supposed to be—it will have a white coat.

black (EE) × black (EE) =
all offspring homozygous
black (EE)

	E	E
E	EE	EE
E	EE	EE

black (Ee) × chestnut (ee) = ½
heterozygous black (Ee) and ½
chestnut (ee)

	e	e
E	Ee	Ee
e	ee	ee

black (Ee) × black (Ee) =
¼ homozygous black (EE),
½ heterozygous black (Ee)
¼ chestnut (ee)

	E	e
E	EE	Ee
e	Ee	ee

black (EE) × black (Ee) = all
offspring black; ½ homozy-
gous (EE), ½ heterozygous (Ee)

	E	e
E	EE	Ee
E	EE	Ee

black (EE) × chestnut (ee) = all
offspring heterozygous black
(Ee)

	e	e
E	Ee	Ee
E	Ee	Ee

chestnut (ee) × chestnut (ee) =
all offspring chestnut (ee)

	e	e
e	ee	ee
e	ee	ee

The problem lies with identifying whether the parent with the black base coat is homozygous or heterozygous for that trait. Since we know that chestnut horses can only be homozygous recessive (ee), performing test matings of a black horse to chestnut horses will give the breeder a clue to the black horse's genotype. The more matings that are performed in which no chestnut offspring are produced, the more assurance there is that the black horse is homozygous (EE). If even one chestnut horse is produced, we know that the black horse has to be heterozygous (Ee). Recent mapping of the horse's genome has reduced this tedious process to a simple DNA diagnostic test performed on samples of the horse's hair roots. Most breeds include both black and chestnut horses; however, some breeds have been selected for only the dominant allele, such as Friesians and Cleveland Bays, and others have been selected for only the recessive, such as Suffolks and Haflingers.

The next obvious question is, if the base coat color of a horse is either black or chestnut, why are there so few true black horses? It is because there are other diluting genes that restrict or dilute the base coat color. For example, the bay (agouti) gene (A), which has several alleles (A, a+ and a), restricts the black color to the "points" (the legs, ear rims, mane, and tail). Depending on the "dose" of the bay gene received by the horse from its parents, a black horse can remain a true black (EEaa or Eeaa) or may become bay (strong dilution with at least one parent contributing an A) or seal brown (less dilution than bay with at least one parent contributing an a+). It is not clear how, or even if, this bay dilution gene interacts with the chestnut base coat.

Another example of a diluting gene is the dun (D) gene, which commonly is found in stock-type horses, ponies, and the Norwegian Fjord. The homozygous dominant (DD) or heterozygous (Dd) combination of this gene dilutes the base coat to grullo if the horse is black, to dun if the horse is bay, and to red dun if the horse is chestnut. The D gene also contributes a darker dorsal stripe and often darker shoulder and leg bars. The cream gene (c^{cr}) also dilutes the coat color and has an additive, or dosage, effect. A single dose (Cc^{cr}) with a chestnut coat color results in a palomino and with a bay color results in a buckskin. A single dose of the cream gene on a black or seal brown coat results in a horse that is phenotypically similar to black or seal brown but is termed a smokey black by some organi-

zations. A c^{cr} contributed from each parent (a double dose, c^{cr} c^{cr}) dilutes the chestnut color to cremello (ivory coat, pink skin, blue eyes) and the bay color to perlino (ivory coat, pink skin, blue eyes, and a darker mane and tail). The silver dapple gene (Z) is also a diluting gene that results in a dark chocolate color with a black coat, a silver-maned bay on a bay coat, and no effect on a chestnut coat. Horses with the silver dapple gene do not have to be dappled, and the gene is most commonly found in Rocky Mountain horses and Shetland and Icelandic ponies and is rarely seen in Quarter Horses, Morgans, and Peruvian Pasos.

Other genes that dilute the base coat color are the Champagne (Ch) gene and the Pearl (PrI) gene. Champagne is a dominant gene that can dilute any coat color or modification of the base colors. Champagne dilutes a black base coat to brown and a chestnut coat to gold. Champagne horses have amber eyes and lavender-colored skin that becomes speckled with darker pigmented spots as the horse ages. The Champagne dilution is common in Tennessee Walking Horses, Missouri Fox Trotters, Miniatures, and Spanish Mustangs. The Pearl gene is a rare dilution that is recessive. That is, it takes two doses of the gene to change a base chestnut coat to a light apricot color. A single dose of the gene does not affect the horse's base coat color unless it is combined with the cream gene; then, the resulting coat color is phenotypically similar to the double cream dilution (perlino, cremello), but in effect, the horse is a pseudo-cremello or pseudo-perlino. That is, the color looks like cremello or perlino, but it is caused by a different genetic action. The Pearl gene is found in Andalusians, Lusitanos, Quarter Horses, and Paints. In Quarter Horses and Paints, it historically has been referred to as the "Barlink Factor."

Another form of coat color modification is the grey gene (G). The homozygous dominant (GG) and heterozygous dominant (Gg) both result in a horse that progressively develops more white hairs in its coat with age. Grey horses are born with a normal, or almost normal, coat color and eventually turn white with advancing age. The skin and eyes of grey horses remain dark. Because the grey gene has a dominant gene action, at least one parent of a grey horse must be grey. Grey occurs in many breeds of horses, and it is the predominant color in several breeds such as Lippizans and Andalusians. Melanomas (skin tumors) are more common in gray horses. While the condition may be disfiguring, most of the tumors are benign.

Basic colors and results from common modifications or dilutions

Base Color	Modified/diluted with	Result	Further modified/diluted with	Result
black	aa	black	dd	black
black	AA, Aa ⁺ , Aa	bay	dd	bay
black	a ⁺ a ⁺ , a ⁺ a	seal brown	dd	seal brown
black	AA, Aa ⁺ , Aa	bay	DD or Dd	dun
black	a ⁺ a ⁺ , a ⁺ a	seal brown	DD or Dd	dun or brown grullo
black	aa	black	DD or Dd	grullo
chestnut			dd	chestnut
chestnut			DD or Dd	red dun
black	aa	black	CC	black
black	aa	black	Cc ^{cr}	smokey black
black	AA, Aa ⁺ , Aa	bay	Cc ^{cr}	buckskin
black	AA, Aa ⁺ , Aa	bay	c ^{cr} c ^{cr}	perlino
black	a ⁺ a ⁺ , a ⁺ a	seal brown	Cc ^{cr}	diluted seal brown smokey black
chestnut			CC	chestnut
chestnut			Cc ^{cr}	palomino
chestnut			c ^{cr} c ^{cr}	cremello
black	aa	black	zz	black
black	aa	black	ZZ or Zz	chocolate with silver mane and tail
black	AA, Aa ⁺ , Aa	bay	ZZ or Zz	bay with lightened points and silver mane and tail
chestnut			zz	chestnut
chestnut			ZZ or Zz	chestnut

Champagne (Ch) dilution possibilities with basic colors. In this scheme, the recessive Ch gene is identified by N. All offspring of homozygous dominant horses (ChCh) should show the Champagne dilution phenotypically. (from Cook et al., 2008)

Base color	Modified with	Result	Further modified with	Result
any			NN	homozygous recessive for Ch. No change in the horse's coat color from Ch gene.
black	aa		NCh or ChCh	dark tan with brown points
black	AA, Aa ⁺ , Aa	bay	NCh or ChCh	tan with brown points
chestnut			NCh or ChCh	gold

Pearl (PrI) dilution possibilities with basic coat colors. In this scheme, the dominant PrI gene is identified by N, and the recessive is identified by PrI. (from Veterinary Genetics Laboratory, 2011)

Base color	Modified with	Result	Further modified with	Result
any			NN or NPrI	no change
black	AA, Aa ⁺ , Aa	bay	NPrI and c ^{cr}	pseudo-perlino
chestnut			NPrI and c ^{cr}	pseudo-cremello
chestnut			PrIPrI	apricot body, mane, and tail

Grey(G), Roan (RN) and White (W) coat color modifications

Base color	Modified with	Result
any	GG, Gg	grey
any	gg	no change
any	RNRN (probably lethal), RNrn	roan
any	rn	no change
any	Ww	white
any	ww	no change

Roan (RN) is another gene that lightens the base coat color in horses by mixing white hairs and colored hairs on the body. The amount of white hairs may vary between the summer and winter coats, but overall, the horse remains the same color throughout its life. The head and leg colors of roan horses are darker than the body. The roan color is a dominant trait, but there is some controversy as to the possibility that the homozygous dominant condition is lethal in the early embryonic state. There are other genes that contribute to an uneven roaning pattern, typically around the flank, barrel, and top of the tail in horses.

The white gene (W) modifies the normal coat so that the horse is white from birth. Typically, this gene results in pink skin and dark eyes. This is also a dominant trait, but research indicates that the homozygous dominant (WW) is a lethal condition in early embryonic development. There is evidence that two normal parents can produce a white foal, which indicates that some white foals are produced from a gene mutation. The W gene is rare in all breeds but can be found in the Tennessee Walking Horse, Miniatures, and American Albino breeds and has occurred in Thoroughbreds, Arabians, and Standardbreds.

Tobiano (TO) and Overo (O) spotting patterns

Base color	Modified with	Result
any	TOTO, TOto	tobiano
any	toto	no change
any	Oo	overo
any	oo	no change

The tobiano spotting color pattern (TO) in which white crosses the horse's back between the withers and tail is found in horse breeds throughout the world. It is a dominant trait that can occur on any coat color. The overo spotting color pattern (Oo) in which white originates from the horse's belly and usually does not cross the back between its withers and tail also is found in horse breeds throughout the world. Because an overo offspring can result infrequently from the mating of two solid-colored horses, it had been assumed that the overo color pattern is caused by the homozygous recessive (oo). However, transmission of the overo spotting pattern does not follow a recessive pattern and is now known to be inherited as a dominant trait in which the homozygous dominant is a lethal condition in the early embryonic stage. This is not to be confused with the lethal white foal syndrome, which also is associated with the overo color pattern. Foals with the lethal white foal syndrome are almost always the result of two overo parents and are typically either blue-eyed white foals or may have only a few colored spots around the muzzle, ears, or tail. The lethal white foal syndrome causes intestinal blockage due to missing portions of the digestive tract or lack of nerve cells that control movement of the intestinal tract. The sabino color pattern is another spotting pattern in which the horse has irregular spotting on the legs, belly, and face and often has roaning in the colored portions of its coat. Sabino patterns in different breeds may be controlled by different genes.

Leopard complex (LP) appaloosa color pattern

Base color	Modified with	Result
any	LPLP, LPlp	appaloosa
any	lp lp	no change

The appaloosa color pattern is a combination of spotting and/or diffuse roaning, which usually is fairly symmetrical on the horse's body. Appaloosa color patterns are found worldwide in various breeds of horses and ponies. Until recently, the inheritance of the pattern was unknown, but gene mapping of the horse genome has greatly increased the understanding of this color pattern. The gene responsible for the appaloosa pattern is termed the leopard complex (LP). The "complex" portion of the term is to include all types of appaloosa patterns that are not leopard. It is believed that LP functions as a dominant gene to cause the appaloosa coat pattern, along with other appaloosa characteristics such as mottled skin, white sclera, and vertically striped hooves. To have the color pattern, the horse must have an LP gene. However, modifying genes may influence the expression of the LP gene; therefore, a horse that has minimal white modifying genes may not exhibit the LP gene. To further confuse the issue, many researchers have hypothesized that the LP gene may act as an incomplete dominant gene. That is, a horse that inherits an LP from both parents (LPLP) will exhibit more white than the heterozygous horse (LPlp), which only receives the dominant form of the gene from one parent. Horses that are homozygous dominant are few-spot leopards, while heterozygous horses are leopard, blanket, varnish roan, snowflake, and frosted patterns.

In this publication, the genes that control color are discussed individually, and prominent breeds exhibiting a particular color pattern are given. However, it is important to realize that all horses have a pair of genes for every color gene discussed and many that are not discussed. For example, a chestnut horse would have the color genotype of ee dd CC gg ww zz toto oo lp lp rnrn. Genetic tests for some color genes exist. For example, a test can be done to determine whether an animal is homozygous or heterozygous for the black gene.

The Quandary with Quantitative Traits

Quantitative traits often result from additive gene action. That is, many genes affect the trait, and the

effect of each gene is small. At the same time, the environmental effects are high for quantitative traits. This combination tends to blur the distinction between phenotypic classes. One horse may look better than its genetic makeup would indicate because it has been in a good environment, while another may look worse than its genetic makeup would indicate because it has been in a bad environment. As a result, when selecting breeding animals, we may choose a horse with a good phenotype due to a superior environment which, in reality, may or may not have the genotype we desire. Similarly, we may pass up a horse because its phenotype is undesirable due to a poor environment, while its genotype actually may be highly desirable for a specific breeding goal. In other words, the best performers may not always have the most desirable genes, and environmental factors can enhance or mask genetic effects.

Unfortunately, many of our economically important traits for horses are quantitative traits. Performance traits, such as racing speed, jumping ability, and cutting ability, are all quantitative traits, and evaluation of performance usually has a combination of objective (such as speed and jump height) and subjective (such as conformation and disposition) measurements. Animal breeders have a variety of formulas for predicting genetic change through breeding. These formulas take into account a variety of factors that influence genetic change. A simple formula is as follows:

$$\text{yearly genetic change} = \frac{\text{heritability} \times \text{selection differential}}{\text{generation interval}}$$

Some horse traits have been investigated to the extent that scientists have estimated the heritability of that trait. A highly heritable trait generally means that horse breeders can make more accurate selection decisions about that trait and can more rapidly influence the amount of genetic change with their decisions. Heritability estimates for various horse performance traits range from 0.04 (cow sense) to 0.63 (withers height). Different populations of horses may show different heritability estimates for the same trait because their genetic and environmental backgrounds are different. For example, if the population studied is an elite group of horses performing at the top level of competition, these horses probably would be more similar in environment and genetics than a group of horses performing at the local or regional level of the same sport. To use an example from color genetics, if all horses in a population are chestnut, there is little chance of producing a black. Whenever possible, addi-

tional information from relatives, weighted properly according to each relative's relationship to the animal being selected, will increase the selection accuracy regardless of the heritability for that trait.

The selection differential is the difference between the selected individual and the population average. Breeders who cannot predict (many economically important traits may not be measurable until the animal matures) or recognize superior animals probably will not make a lot of genetic change or may end up with the wrong type of change for their goals. Also, breeders who have only a limited number of horses to utilize in their breeding program are at a disadvantage for this factor. More intense selection, through retaining only the highest quality animals, allows breeders to increase the mean genetic level of their herd. Breeders with a limited number of breeding animals often do not want to intensely cull animals because it may reduce their herd size to a number that is not economically viable. However, producing animals of limited usefulness to the horse industry probably is not economically viable either.

The long generation interval of horses also reduces the rate of genetic change in horse breeding. The generation interval is the average time from the birth of one generation to the birth of the next, and in horses the generally accepted generation interval is about 10 years. Genetic change can occur more rapidly with shorter generation intervals. The long generation interval also means that the average horse breeder has very few opportunities to influence genetic change in horses in his or her lifetime. Poor selection decisions or constantly changing breeding goals will negatively influence the amount of genetic change a breeder can realize. Also, when the long generation interval is combined with poor reproductive efficiency (only about 50 percent of mares bred produce a foal), this factor can greatly retard genetic change. Increasing the reproductive efficiency can decrease the generation interval and increase selection intensity in a herd, resulting in more rapid genetic change.

Finally, the very nature of the horse industry can influence the amount of genetic change made by individual breeders. Historically, many desirable stallions were accessible to only a few breeders due to factors such as high cost and geographical location. This did not retard the genetic change of the breed, but it did slow the genetic change realized by the average breeder. With the increased use of shipped semen in the horse

industry, this problem is beginning to be alleviated in most breeds. Through the use of artificial insemination, selection intensity from the male side can be greatly improved.

Evaluating Individuals

Breeding stock selection is usually based on a variety of individual preferences of the breeder. Some breeders put more weight on pedigree, some on performance of the horse or its relatives, and some on appearance of the horse. Are some of these considerations more important than others? It depends on the trait in question. Highly heritable traits (0.4 or higher heritability) respond well to selection procedures based on individual performance, assuming that environmental effects are minimized. Individual performance is also a useful selection criterion for economically important traits and when genetic turnover is fast. Traits with low heritabilities (less than 0.2) respond well to selection based on family background (pedigree, performance of relatives) because the individual's own performance is not an accurate assessment of the animal's genetic merit. Pedigree also can be a useful selection tool for a young horse that has not had a chance to prove itself or for a horse that was injured prior to proving itself. Pedigree also may be a useful tool when dealing with genetic abnormalities, traits expressed later in life, or traits expressed by only one sex. However, breeders should realize that the pedigree decreases in value in the selection process as the individual animal gains performance and progeny records. In addition, breeders should remember that the individual horse will not have any genes that its parents did not have. So, when utilizing the pedigree as a selection tool, breeders should emphasize the individual's parents and grandparents. The genetic contribution of more distant relatives such as great grandparents is very minor.

Performance tests, in which horses are put into a common environment for a period of time before traits are measured and compared, and progeny tests, in which a stallion is bred to number of mares to evaluate his offspring relative to those of other stallions for certain traits, have been used as selection tools. Other livestock species commonly evaluate potential breeding animals using this scheme. The performance test commonly is used as a selection tool for young stallions of warmblood breeds.

Basic Breeding Schemes

Breeding schemes of outcrossing and inbreeding do have genetic consequences that may be either good or bad, depending on the goals of the breeder. Outcrossing is mating unrelated families within a breed. It tends to increase heterozygosity, strengthen traits related to fitness (such as fertility), and cover up recessive genes. Crossbreeding is a more extreme form of outcrossing in which horses from different breeds are mated. Crossbreeding has the same genetic effects as outbreeding, plus it decreases genetic purity. Crossbreeding is common with some types and uses of horses. Many of our modern light horse breeds were formed by crossbreeding, and it is still used today to introduce desirable genetics into horse populations. For example, Thoroughbred and Arabian genes were introduced into native horse populations to refine the appearance and increase the athletic ability of warmblood breeds. Outcrossing is sometimes used for corrective mating—for example, breeding a splay-footed mare to a pigeon-toed stallion. These two conditions potentially are caused by two separate genetic mechanisms, and it is difficult to predict what type of leg structure would result from the breeding. A far better strategy would be to breed the mare to a stallion with the most correct structure that fits into the breeder's economic restraints and other selection criteria.

Inbreeding is breeding closely related individuals (father-daughter, brother-sister). The genetic consequences of inbreeding are to increase homozygosity of both dominant and recessive genes. Inbreeding does not create undesirable genes, but it does increase the possibility that recessive genes will be paired and expressed phenotypically. Inbreeding also decreases traits related to fitness, such as fertility, disease resistance, and longevity. Linebreeding is a mild form of inbreeding that breeds horses related to a common ancestor, and it has the same genetic consequences of inbreeding. Inbreeding and linebreeding are used to set phenotypic type in qualitative (morphological) traits, to concentrate the influence of an outstanding ancestor, and to form lines for future outcrossing purposes. Neither outcrossing nor inbreeding is “good” or “bad.” The use of these breeding schemes depends on what is appropriate to reach the breeding goals set by the breeder.

Selection Methods

After setting goals and examining performance records, pedigrees, relationships between animals, and test results as appropriate, horse breeders can use a variety of methods of multiple trait selection. Before getting started, breeders need to realize that as the number of traits selected for increases, the possible amount of change in a single trait decreases. One method is to select for one trait exclusively until the goal for that trait is reached, then start selecting for the next trait. This is termed tandem selection and is probably the least effective method of selection because traits often are correlated genetically. That is, one gene may affect more than one trait. So, selecting for each individual trait separately may alter, either positively or negatively, the genetic change made for the previous trait(s).

A second selection procedure is to set minimum standards for several traits, and if a horse does not measure up to one of those standards, it is culled. This method is called an independent culling level and is used to some degree by most breeders and breed associations. The problem with this method is that a horse that is outstanding in one trait may be culled if it does not meet the standards for another trait. This type of selection is most useful if the breeder is dealing with only a small number of traits and a small percentage of the offspring are needed to replace the parents. Neither of these requirements is common to the horse population.

A selection index is a more effective method of trait selection than tandem selection or setting independent culling levels, but it is more difficult to set up. Selection indices are mathematical formulas that utilize information from traits of importance and weight those traits according to importance. Information is obtained from the animal itself and from its relatives to calculate a single score for an animal, and selection is based on the score. If multitrait evaluations are used, the selection index method simply weighs the traits by their relative economic values and sums them. Drawbacks to the selection index are that it is difficult to formulate, and it often is difficult to obtain the information needed. Also, what may be important for one horse breeder and be weighted heavily in his or her index would not necessarily be a highly important trait to another breeder. However, formulating a selection index may be a useful exercise because assigning a relative economic value to each trait allows the breeder to realize which traits are of true economic importance to his or her breeding goals.

Another method of selection that is commonly used in other livestock species and is beginning to be available for horses in Europe is the expected progeny difference (EPD). In this method, all available information about a trait from the individual and its pedigree, properly weighed according to the relationships to the animal being evaluated, is used to calculate the expected difference in the offspring's performance for that trait. That is, an EPD is the expected difference in performance from future offspring of a sire compared to the performance of the base population. The EPD combines into one figure a measurement of the genetic potential for a particular trait based on the individual's performance and performance of related animals. In other species, EPDs are reported as positive or negative values for each trait of importance. For example, a beef bull may have an EPD of -0.4 for birth weight (slightly below the average of his peers), a weaning weight EPD of +38 (38 points above the average of his peers), and a yearling weight EPD of +82. So, if a particular breeder were looking for a bull that sires calves of average birth weight that will grow rapidly after birth, this might be a bull to consider. Also, the procedure can be used to rank the bull on traits that cannot be measured directly from him, such as maternal ability traits and carcass traits. The EPD scores come with an accuracy score attached. The more offspring the sire has, the more accurate the EPD score and the more the breeder can rely on it to remain relatively unchanged with additional data.

In horse breeding, the EPD would be a good selection tool. Most breeders have too few mares to cull them intensely. Instead, they correctly put more emphasis on selection of the stallion. With the use of transported semen, stallions are able to have more offspring in many different herds. Properly recording the performance of these offspring would allow for EPD estimation so that the stallions could be compared more objectively by the breeder.

Whether the breeding goal is to produce a palomino foal or to produce the next Olympic winner, the same basic genetic principles should guide the selection process.

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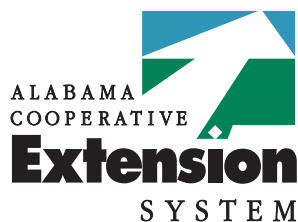
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ANR-1420

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Web Only, **New March 2012**, ANR-1420

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