

Genetic Principles

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To fully understand breeding management, it is important to know some basic genetic principles. Knowing the role genetics plays in each economically important trait of beef cattle can assist in making wise selection decisions. It is necessary to know which traits can be altered through breeding management (selection and/or crossbreeding) and which traits should be altered by other management techniques.

Trait is the term used to describe a characteristic in cattle. This can refer to either the appearance or performance of an animal and can also be referred to as the *phenotype*; for example, black coat color, horned, 550 pound weaning weight, etc. For most performance traits (e.g., weaning weight), the phenotype of an animal is controlled by two factors: the environment in which the animal lives and the animal's genetic makeup or *genotype*. The environment consists of not only the weather but also how the cattle are managed. Creep feed, forage quality and quantity, and health programs are examples of environmental effects. Environmental effects on economically important traits are controlled through management techniques such as nutrition and health programs.

For the purposes of this manual, the focus will be on the genetic component of the phenotype. The genetic component of all living things is expressed through the production of proteins at the cellular level. Cells can turn on or turn off the production of proteins through signals from other cells, environmental changes, age, or other factors. The code for this protein production is found in DNA (deoxyribonucleic acid), which comes in long strands that form *chromosomes*. Cattle have 30 pairs of chromosomes; humans have 23. Each

animal inherits one of each pair from its sire and the other from its dam.

The term *gene* refers to the basic unit of inheritance, and it is a specific segment of the chromosome that codes for a precise protein. There are also parts of the chromosome that are thought to play no role in inheritance. The location of the gene on the chromosome is called the *locus* (Figure 1). The term *allele* refers to one of the chemical or functional possibilities that can be present at a locus (i.e., coat color extension locus has two possible alleles: red and black).

In terms of genetics, traits are usually referred to as either *simply inherited* or *polygenic*. Simply inherited traits are usually affected by only one gene. The classic example of a simply inherited trait in beef cattle is red/black coat color. Some genetic disorders are also simply inherited. Simply inherited traits are typically observed as either/or: either the animal is black, or they are red. Additionally, simply inherited traits are affected little by the environment. If an animal has the genotype for black coat color, environmental conditions are not likely to make it red.

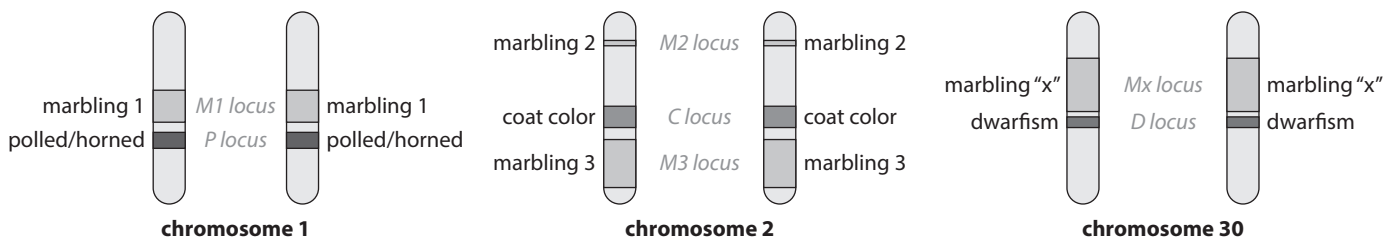
As implied in the name, polygenic traits are controlled by many genes, and most of the economically relevant traits are in this category. The number of genes involved depends on the trait, and there is currently little information on how many genes are involved for each trait. Examples of some common polygenic traits in cattle are calving ease, weaning weight, milking ability, marbling, tenderness, etc. Besides being controlled by many genes, polygenic traits are also influenced by the environment. We will illustrate the basic concepts of genetics using simply inherited traits and will then come back to polygenic traits.

Alleles at a locus can influence the trait by themselves but can also affect the phenotype through interactions with other alleles. Alleles can interact in two ways, referred to as *dominance* and *epistasis*. There are varying degrees of dominance, and this refers to how the two alleles that an animal has at a locus interact. The classic form of dominance is complete dominance. With complete dominance, one allele can completely mask the expression of the other allele. This results in heterozygote animals having the exact phenotype as homozygote dominant animals. This is the type of dominance we see in red/black coat color, where black is dominant to red. Cattle that have two black alleles are black (homozygous dominant), cattle that have one black and one red allele are also black (heterozygous), and red animals are the result of having two red alleles (homozygous recessive). When dealing with traits with complete dominance, heterozygous animals are often called carriers because they are carrying the recessive allele and can pass it to their offspring even though they do not express the trait themselves. It is possible to breed two black cattle and get a red calf because each parent was a red allele carrier.

Coat color is a good trait to demonstrate how alleles interact in a trait with complete dominance. For this example, we will mate an Angus bull to Hereford cows. The Angus bull is homozygous dominant, which means he has two black alleles (BB). The Hereford cows are homozygous recessive, which means they have two red alleles (bb). When mated, all offspring will be heterozygotes (Bb). The Punnett square in Figure 2 illustrates this mating.

If we were to breed these heterozygous heifers back to a Hereford bull, we would

Figure 1. Chromosomes with hypothetical location of genes that control some common traits in cattle.



get 50% heterozygous black (Bb) calves and 50% homozygous red (bb) calves (Figure 3). If we were to mate the Hereford x Angus heifers to Hereford x Angus bulls, then we would get all three possibilities: homozygous black (BB), heterozygous black (Bb), and homozygous red (bb) (Figure 4). The expected ratio would be 25%:50%:25%, respectively. The expected phenotypic ratio would be 75%:25% black to red.

Traits controlled by one gene, with complete dominance, are easy to understand but can cause problems because of the possibility of carriers. For some traits, the only way to detect carriers is through progeny testing, which is costly and time consuming. However, with advancements in molecular technologies, carriers can be identified for some traits by conducting a DNA test on a tissue sample (typically hair, blood or semen), which will be discussed in the chapter titled *DNA-Based Technologies*.

Besides complete dominance, there are other types of interactions between the two alleles at a locus, including: partial dominance, no dominance, and overdominance. As implied by their names, partial dominance means that the heterozygote favors the dominant characteristic but does not express to the full extent as the homozygous dominant. No dominance means that the heterozygote is the average of the homozygote dominant and recessive and is also referred to as additive because the phenotype of the heterozygote is the sum of the effects of the two alleles individually. Overdominance is when the heterozygote's phenotype is more extreme than either homozygote.

Dominance is a way to describe how alleles interact with each other at a locus. The term epistasis is used to describe how genes interact with genes at other loci. A classic example in cattle is the diluter genes in Charolais. When Charolais are crossed with red or black cattle, the offspring are off-white. This is the result of the diluter genes at different loci overriding the red/black genes.

Another type of inheritance interaction that can happen is sex-related inheritance. Sex-related inheritance can be categorized in three ways: sex-linked, sex-influenced, and sex-limited. Sex-linked traits are determined by genes located on the X chromosome. Sex-influenced trait expression occurs when phenotypes are different between males and females with the same genotype. An example is scurs, which occur at a higher rate in males than females.

Figure 2. Punnett square for coat color when mating a homozygous black bull to a homozygous red cow. The joining of the gametes shows the potential offspring and their color.

		Bull Gametes	
		B	B
Cow Gametes	b	Bb black	Bb black
	b	Bb black	Bb black

Figure 3. Punnett square for coat color when mating a homozygous red bull to a heterozygous black cow. The joining of the gametes shows the potential offspring and their color.

		Bull Gametes	
		b	b
Cow Gametes	B	Bb black	Bb black
	b	bb red	bb red

Figure 4. Punnett square for coat color when mating a heterozygous black bull to a heterozygous black cow. The joining of the gametes shows the potential offspring and their color.

		Bull Gametes	
		B	b
Cow Gametes	B	BB black	Bb black
	b	Bb black	bb red

Sex-limited traits are those traits that can only be expressed in one sex or the other. Examples in cattle would be milking ability, which can only be expressed in females, and scrotal circumference, which can only be expressed in males.

The terms used to describe how traits are expressed are *categorical* or *continuous*. Most simply inherited traits in cattle are categorical traits, which mean they fit a certain discrete category. For the phenotype of horned/polled, there are only the two choices, horned or polled, which make this trait a categorical trait. Categorical traits that are polygenic are referred to as *threshold* traits. Dystocia is typically expressed as either assisted or unassisted or is measured numerically: no difficulty = 1; easy pull = 2; hard pull = 3; caesarean section = 4; and abnormal presentation = 5. Nevertheless, it is obvious that many factors can affect dystocia, including birth weight and pelvic area, which are both polygenic traits that are expressed on a continuous scale. Continuous refers to the fact that, in theory, there are infinite possibilities for the trait phenotype. Most measurement traits fall into this category.

As discussed in the beginning of this chapter, all traits are controlled by two effects: genetics and environment. In actuality, the impact of genetics can be divided into two types of action: *additive* and *non-additive*. Additive genetic action refers to the effect of genes that is independent of other genes and the environment. In other words, there is no influence of dominance or epistasis. These

genetic effects are additive in nature, which means for a polygenic trait, you can take one additive gene and add it to the effect of another additive gene, and so on, for all additive genes that influence that trait. The sum of all genes influencing a trait for an animal is called its *breeding value* for that trait. A simple case for weaning weight is illustrated in Figure 5.

The proportion of differences we see between animals for a trait that is controlled by additive genetics is called *heritability*. For example, yearling weight has an estimated heritability of around 0.40 in many beef cattle populations, which means that about 40% of the differences we see in yearling weights between cattle in a herd are caused by additive genetic effects. If a trait has a low heritability, this indicates that non-additive genetic effects and/or the environment have a much larger influence on that trait. High heritability indicates that additive genetics play a

Figure 5. Simplified illustration of combining the additive genetics for weaning weight to determine the animal's weaning weight breeding value.

Allele	Effect
A	+ 25 lb
a	+ 5 lb
B	+ 15 lb
b	- 5 lb
C	- 10 lb
c	- 15 lb
D	+ 0 lb
d	- 5 lb

Genotype of Bull A:
AABbCcDd

$$\text{Breeding Value} = 25 + 25 + 15 + (-5) + (-10) + (-15) + 0 + (-5) = 30 \text{ lb}$$

Genotype of Bull B:
AaBbCCdd

$$\text{Breeding Value} = 25 + 5 + 15 + (-5) + (-10) + (-10) + (-5) + (-5) = 10 \text{ lb}$$

relatively large role in the trait. The level of heritability in a trait will have an impact on selection decisions. Progress tends to be much slower in lowly heritable traits when attempting change through selection. With higher heritability, we usually can achieve more rapid progress through selection due to greater accuracy in selection decisions.

Both the sire and the dam pass on half of their genetics to their offspring. For definition purposes, sperm and egg cells are called *gametes*. Each gamete that a parent produces gets a random sampling of that parent's genes. For a single gene, a heterozygous *Zz* animal produces 50% *Z* gametes and 50% *z* gametes. That means that there is variation in the genetic makeup of the gametes produced, which is termed *Mendelian sampling*. Mendelian sampling can be clearly observed when you compare full-sibs, and humans are perfect examples. The fact that male and female children can be born to the same parents is one example of Mendelian sampling. Now compare brother to brother and sister to sister within a family; there are often similarities because full sibs have half of their genes in common on average, but there are also differences, which can be dramatic. An example in cattle would be to compare flush-mates in an embryo transfer program; there is often variation in these full-sibs, even when raised in similar environments.

Since only half of each parent's total genetic material is in each gamete, the average of all gametes produced by an animal is half of its breeding value. This is termed the parent's *transmitting ability*. Expected Progeny Differences (EPD) are estimates of an animal's transmitting ability and will be discussed in detail later. Selection decisions are made to change the additive genetics in the herd because additive genetics are passed on from one generation to the next; animals with favorable EPD tend to have higher proportion of alleles with favorable additive effects on that trait.

Most traits are controlled to some degree by both additive and non-additive genetic action. In beef cattle breeding, we can take advantage of additive genetics through our selection decisions, but we can also take advantage of non-additive genetics. Non-additive genetic actions involve interactions between alleles at the same loci (dominance), interaction between genes at different locus (epistasis), and the interaction between genes and the environment.

Epistasis and genetic-environmental interactions are difficult to account for, but dominance can be taken advantage of through a crossbreeding program. Pure breeds or lines of cattle have been developed over time through selection and inbreeding. Both practices increase the level of homozygosity in that breed; i.e., animals tend to have the same alleles at a locus. But this homozygosity will be different in other breeds or lines; i.e., animals in other lines tend to have a greater proportion of other alleles. Therefore, when these breeds or lines are crossed, there is a great increase in number of loci for which the offspring will be heterozygous. For both simply-inherited and polygenic traits, the dominant alleles are often the advantageous alleles. With complete dominance, there are no differences in performance between the homozygous dominant and heterozygous individuals. The result is that instead of the offspring performing average to the parental lines, as would be the case with additive genetics, they perform at a higher level than the average of the parental lines. The term for this increase in productivity is called heterosis. Heterosis tends to be highest for lowly heritable traits (such as reproduction) because these traits tend to have larger non-additive effects, and lowest for highly heritable traits (such as carcass traits). Crossbreeding might result in relatively small amounts of heterosis for a given trait, but these effects tend to accumulate to produce large increases in overall productivity. In some instances, a portion of this advantage is passed on to future generations, but to optimize the benefits, a crossbreeding program should be implemented (discussed in detail in the chapter on crossbreeding).

Another genetic effect that is important when making selection decisions is genetic correlations. A genetic correlation is reflected when you select for one trait and another trait is affected. There are two ways that traits can be genetically correlated: *linkage* and *pleiotropy*. Linkage is when genes that affect two traits are located close together on the chromosome. In that case, they do not segregate randomly but tend to segregate similarly (the closer together, the less random the segregation). Pleiotropy is when a gene influences more than one trait. It is easy to understand that some of the genes that impact weaning weight are also going to impact yearling weight and birth weight; this is an example of pleiotropy.

The effect of one trait on the other can be either complementary or disadvantageous. For example, as selections are made for increased weaning weight, yearling weight is also increased because of the positive genetic correlation between those traits. An example of a disadvantageous correlation would be that as selections are made for increased weaning weight, calving ease tends to decrease. Conversely, as selections are made to improve calving ease, weaning and yearling weights tend to decrease unless attention is paid to simultaneously select against this. The implications of genetic correlations for many traits for which EPD are calculated are presented in Table 1.

The breeding management program of most seedstock producers is handled primarily through their selection practices. A sound breeding management program for most commercial cattle producers should include both selection and crossbreeding. The following chapters will go into detail about practices that are available for both selection and crossbreeding.

Table 1. Effect of genetic correlations when selecting for other traits.

	Weight			Milking Ability	Calving Ease	Mature Size
	Birth	Weaning	Yearling			
CED EPD	-	-	-	0	+	-
WW EPD	+	+	+	-	-	+
YW EPD	+	+	+	-	-	+
Milk EPD	0	-*	-*	+	0	0

+ = as EPD goes up, this trait also tends to increase.

- = as EPD goes up, this trait tends to decrease.

0 = no relationship.

* Increased milk EPD tend to decrease growth rate for the first generation due to a negative genetic correlation between milk and growth. However, grand progeny would have increased WW and YW due to added milk production in the daughters.