# Breeding Winners to Winners

and the Unhappy Results

# Part I

By Dr. Carmen L. Battaglia

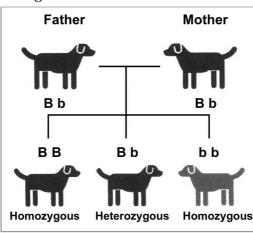
This is a report about an unpublished study and the interviews with breeders who had bred quality bitches to high quality males. Some of the litters were graded as average and not up to the quality of their sire or dam, others produced pups that fell short of the traits expected, and a few produced a litter with one good pup but its littermates were average or below average in quality. The wide range of unimpressive results prompted a study about breedings that involved the "Best to the Best". The lingering question about these results was why were there so many disappointing litters. A closer look at the methods and information used to select sires and dams led to a preliminary conclusion that while some breeders experienced success, most did not because they relied on the idea that breeding the "best to the best" would produce better than average results. Further analysis shed light on the fact that most of the decisions about the breeding partners involved emphasis on just one or two traits and only a few breeders reported having any knowledge of genetics or how the genes would behave in a breeding. Most did not have a plan that included pedigree analysis and only a few knew the strengths and weaknesses of their sire and dam's pedigree. As the interviews continued, I was reminded of a lesson learned early in my career as a breeder while studying genetics. It was a phrase often repeated in class ... "how much you know will determine how far you will go". That reminded me about the decision making process of these breeders and the frustration they endured.

#### Mendel

History shows that advances in genetics and breeding began with an Austrian monk named Gregor Johann Mendel, who, in 1843, entered the Augustinian Monastery in Old Brno where he lived. In 1851, he became an ordained priest and a member of the Natural Science Society which provided him the opportunity to lecture about his experiments. His ideas were new and not well understood-in part because of his heavy emphasis on mathematics, which at the time were not part of scientific reporting. His famous lecture in 1865 was not published until 1866 and his discovery would not become public until the early 1900s. They would lead a new scientific community to a different way of thinking about inheritance. Mendel focused on how traits were passed down from one generation to the next. What he called the "factors" or "particles" of inheritance were actually the genes. To better understand his ideas, others began to use letters of the alphabet to represent the alleles he wrote about. Lower case letters (b, w,) represented recessive alleles and upper case letters (BW) represented dominant alleles. Mendel's "First Law" of genetics proved that genes do not blend together, instead they retain their individual character, even when a recessive gene is present and masked by a dominant gene. It took from 1790 to 1866 before the solution to this genetic puzzle was beginning to be understood. Figure 1 represents Mendel's First Law which involves dominant and reces-

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sive traits. Imagine if, as a breeder, you bred two black dogs. Both are black because they both carry one dominant gene for black (B) and one recessive gene (b) for the recessive color liver, which sometimes is called chocolate. Most breeders would expect black puppies. The problem for most breeders is not knowing if their dogs are carriers of the recessive gene. Figure 1 illustrates how two black parents produced a litter of three pups, two black pups (Bb, BB), and a third pup (bb) a chocolate. These results illustrate Mendel's discovery of what can be expected when information about the parents is known. In this case, when just one

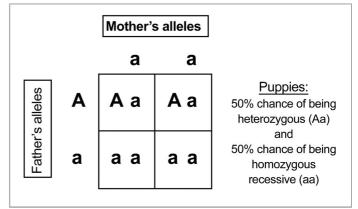


a litter of pups could have coats that are long or short, strait or curly, rich in color or pale in color. If the parents have the same two coat traits, such as a short and a color-rich, it does not guarantee their pups will have those same traits, but it raises the expectation. As already mentioned, there could be pups in some litters that might have long, straight and pale coat colors unlike those of their parents. To avoid the unexpected, pedigree analysis can be used to code the ancestors on paper in order to identify any recessives that might be hiding among the different phenotypes.

Mendel proved that DNA is the build-

ing structure for the traits that can be passed on to the offspring. It is the mechanism that allows the parents to each have two alleles for every gene: one allele is inherited from their mother and the other one is inherited from their father. The combination of the two





alleles is what is called a genotype. When a puppy receives the exact same allele from its father and its mother it is said to be homozygous for that allele and it will have a homozygous genotype for that gene. Alternatively, when a puppy receives different alleles from its mother and father, it is said to be heterozygous and that

### pup occurs with the recessive trait, it confirms that both parents were carriers of the recessive gene.

Figure 2, is another illustration regarding what can be expected in a breeding. The percentages are the mathematical frequencies (50%) that could occur if the breeding was repeated several times. Breeders can learn more about their pedigrees and their potential for producing certain traits by collecting information about the ancestors and what they produced in prior litters. Key information is often missed because it is in the third and fourth generation (see Figure 3).

When DNA tests are available, they can be used to identify which dogs are affected, carriers or clear. See Table 1 for a better understanding of what can be expected.

Figure 3, illustrates what would be known if a breeder collected information about all of the ancestors in a pedigree. This kind of record keeping takes more time, but it uncovers the strengths and weaknesses needed by breeders. This example also makes clear that when DNA tests are available, each ancestor can be coded as a carrier, clear or affected. Test results can also tell breeders the risks they are making with each breeding.

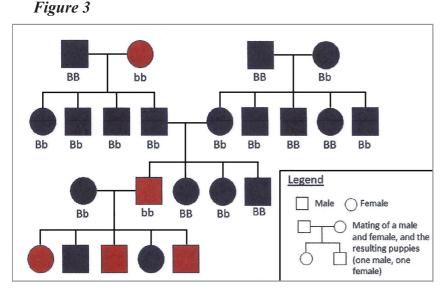
Today we know that the genes are arranged in DNA sequences which provide the framework that produces each and every trait. The coat color example above illustrates this point and provides a good understanding of how the genes work. In the illustration (Figure 1), only one trait (coat color) is discussed because it is a characteristic found in all dogs regardless of their breed. In this regard,

Table 1: The chances of producing affected, carrier and clear puppies based on the genetic test status of both parents for Mendelian traits

	Clear father	Carrier father	Affected father
Clear mother	All puppies are clear	50% chance puppy is clear 50% chance puppy is a carrier	All puppies are carriers
Carrier mother	50% chance puppy is clear 50% chance puppy is a carrier	25% chance puppy is clear 50% chance puppy is a carrier	50% chance puppy is a carrier 50% chance puppy is affected
Affected mother	All puppies are carriers	50% chance puppy is a carrier 50% chance puppy is affected	All puppies are affected

#### Figure 1

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puppy will have a heterozygous genotype for that gene. What complicates this is that some genes only exist in two forms. For example, in canines there are genes for white spotting and agouti which

can have more than two alleles, each resulting in a different phenotype, but there are other factors that determine which traits will be expressed. For example, the abundance of different alleles within a breed population, referred to as "allele frequency" also influences the outcomes. Therefore, the more abundant an allele is in a breed, the higher the frequency and the more likely that phenotype will be observed in the breed. A good example is the allele governing short coats. If it has a very high frequency within a breed population, then the breed will be characterized by its short coat. This can be seen in the Doberman, German Shepherd Dog, Cane Corso, and many other breeds including many hunting breeds. Another example of

the high frequency of an allele is the allele for wither height which is a characteristic found in the German Shepherd Dog. Breeds with a high frequency of alleles for one or more traits are typically expected to produce that trait in most of the individuals in that breed. Another factor influencing a trait and the likelihood of something happening is called the process of "recombination". It takes place during the gamete formation and it occurs when some chromosomes swap segments of DNA with each other and become recombined. This is not bad because recombination creates genetic diversity by shuffling the alleles between chromosome pairs. There are other concepts that influence the outcomes such as when two genes are close to each other on the same chromosome. In these instances, there is a lower chance that recombination will happen between them when their alleles begin to shuffle. This is why the alleles of genes that are physically close to one another on a chromosome tend to be inherited together. When this happen the genes are said to be "linked".

Knowing all of this makes us better educated as breeders, but it does not help us make better breeding decisions or increase our chances of producing more quality litters. To do this, a different method has been suggested. It begins with the terminology we use

because words matter-especially when information is passed from one of us to another. In this regard, there are three terms that are often used: phenotype, genotype and type breeding. Phenotype refers to the characteristics that can be seen, meaning their external appearance. Hence, a dog that is observed to be black (phenotype) may not produce only black puppies. It could have a genetic make-up (genotype) that includes the genes for other colors. Since the genotype cannot be seen directly, indirect methods must be used to learn about them. Indirect methods are not estimates or guessing games. Instead, they require detailed information about each ancestor and their littermates, usually for three generations. Those who do not collect information usually rely on "type" breeding which means the selection of sires and dams be based on appearance rather than on the traits observed in their pedigrees. Many times "type" breeding is used to breed the winners to the winners,

or the "best to the best". In practice, these breeding's fail to take advantage of what the science of genetics has taught us about inheritance and pedigree analysis. To avoid this trap, a pedigree better

#### Figure 4 Factors used in predicting traits

- 1. Has the sire or dam produced the trait?
- 2. How many ancestors have produced the desired trait?
- 3. Are there good-producing ancestors on both sides of the pedigree?
- 4. Were the desired traits observed in the littermates of the sire or dam?
- 5. What is the heritability of the trait(s)?
- 6. Will in-breeding or line-breeding be used?

than the Traditional Pedigrees is needed because traditionally pedigrees only collect information about each dog's name and title–neither of which are heritable.

Over the years, many have tried a wide array of breeding methods but it was Mr. Lloyd Brackett (1950s), a breeder who became a legend in his is own time, who addressed this problem in another way. Brackett was well-educated and well-read with a passion for writing about what he found and believed. He became known by his many successes and his ability to speak out on topics of interest to breeders. He often was quoted as saying that breeders need to learn "how to breed by direction rather than by chance". His method for success focused on pedigree analysis. Brackett knew that in a three generation pedigree there were 14 ancestors. Each could be evaluated based on seven traits of conformation (head, ears, neck, front, back, rear and tail). Simple math convinced him that 14 ancestors with seven traits meant he had to know about 98 traits in order to understand the strengths and weaknesses of a three generation pedigree. Given the discussion about the genes and how they can behave, it was clear that he needed a pedigree that would capture information and display it in a way that made understanding easy. In addition, he needed a reminder about the factors that

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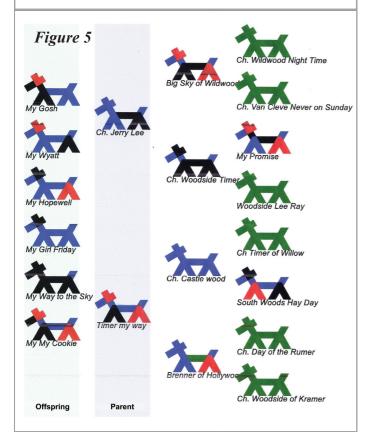
could be used to predict traits in a litter.

The pedigree most suited for capturing and displaying this kind of information is the Stick Dog pedigree. It allows breeders to evaluate each ancestor and seven traits of conformation based on a breed standard. The logic underlying this pedigree is that each ancestor will be drawn as a stick figure that can be coded with more than just names and titles which are heritable. The four mutually exclusive colors used to code the seven structural parts are shown in Table 2.

Using the codes in Table 2, we can begin with the color blue, which means the trait is correct based on the breed standard. In Figure 5, the ears of "Jerry Lee" are coded blue and the ears on his son "My Gosh" are coded "red". This means that "Jerry Lee" has correct ears based on the breed standard but his son "My Gosh" has faulty ears. When the seven traits of each ancestor are coded in this manner, the strengths and weaknesses of a pedigree are known. A software program written for Microsoft computers supports this pedigree and it automatically codes ancestors whose traits are unknown with the color green. Again using Figure 5, the

## Table 2Color Coding of Traits

CODE	RANK TRAITS FOR QUALITY
Blue	Correct based on breed standard
Black	Could be improved
Red	Is a fault
Grey	A serious fault or disqualification
Circle/Green	Missing information



strengths and weaknesses of only 8 of 14 ancestors are known, the remaining 6 are coded green meaning their traits are not known. Knowing the amount of missing information is significant when it comes to decision making. It points to what can be expected in a litter and the risks a breeder is willing to take. Therefore, it is not surprising in the breeding of "Jerry Lee" to "Timer My Way", that four pups occurred with a major fault.

The stick dog pedigree has proven to be of one the most useful tools for planning and predicting a breeding. Information about this software is available at www.breedingbetterdogs.com. Part II of this study about breeders will focus on another problem faced by these breeders. It is called knowing when to use "inbreeding" and when it is useful.

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#### About The Author

Carmen L. Battaglia holds a Ph.D. and Master's Degree from Florida State University. An AKC judge, researcher and writer, he is a leader in promoting ways to breed better dogs. He is the author of many articles, several books and is a popular TV and radio talk show guest having appeared on Animal Planet several times. His seminars on breeding dogs, selecting sires and choosing puppies have been well received by breed clubs all over the country. Those interested in learning more about his articles and seminars should visit the website http://www.breedingbetterdogs.com