# INTRODUCTION TO COLOR COAT INHERITANCE IN THE CANE CORSO

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The NHGRI (National Human Genome Research Institute) a division of the government agency – National Institute of Health, describe the canine genome as others have described the human genome. A dog's body, like the human body is comprised of trillions of cells each with a nucleus and organelles that contain the genes that make up what and who the dog is and what diseases the dog has a greater propensity to develop and what coat color the dog will present. In each nucleus, there are 38 autosome pairs (non sex chromosomes) and 1 pair of sex chromosomes. So, each nucleus has 78 autosomal chromosomes and 2 sex chromosomes. Each of the genes found on the 78 autosomal chromosomes can present one of 2 forms each called alleles, dominant or recessive. However, the 2 sex chromosomes are either X or Y, but the alleles on each are also in either allelic form. Chromosomes are made up of DNA (Deoxyribonucleic Acid), the genetic code for sustaining life. During fertilization, the embryo receives half it's chromosomes the sire and half from the dam. So, the offsprings are a product of a recombination of genes from the parents.

DNA is made up of small chemical building blocks called "nucleotides" or "bases," which come in four types: adenine (A), guanine (G), cytosine (C) and thymine (T). All living organisms, including humans, use this four-letter code. The bases are paired in fixed units of adenine-thymine (A-T) and guanine-cytosine (G-C). Dogs have approximately three billion base pairs in each cell. Genes are defined by a unique sequence of nucleotides which can be as few as a hundred bases or as many as a million. The sequence of each gene is called its "code." For example, the code from one gene may lead to proteins that add color to a hair shaft, the code from another gene produces enzymes to digest food, and a third gene will direct the formation of antibodies that fight diseases. For a given gene the code is a very precise; a single mistake in the DNA sequence could have disastrous consequences for the health of your dog.

Each of the 78 chromosomes contains the codes for hundreds of genes. Genes encode the necessary machinery for manufacturing proteins, which in turn make up the body's physical structure. Proteins are needed for all of the key systems in the body such as the nervous system or the digestive system. Each gene has a specific code that is passed from parent to offspring. The term "canine genome" refers to the entire sequence of the dog genome including all the genes and the spaces in between. Genes can determine how your dog will develop from the color of his fur to his personality traits and, in some cases, the diseases your dog will be susceptible.

FIG. 1

**Adapted from NHGRI Intramural Publication Support Office DNA image, dog images courtesy of © AKC/Mary Bloom**

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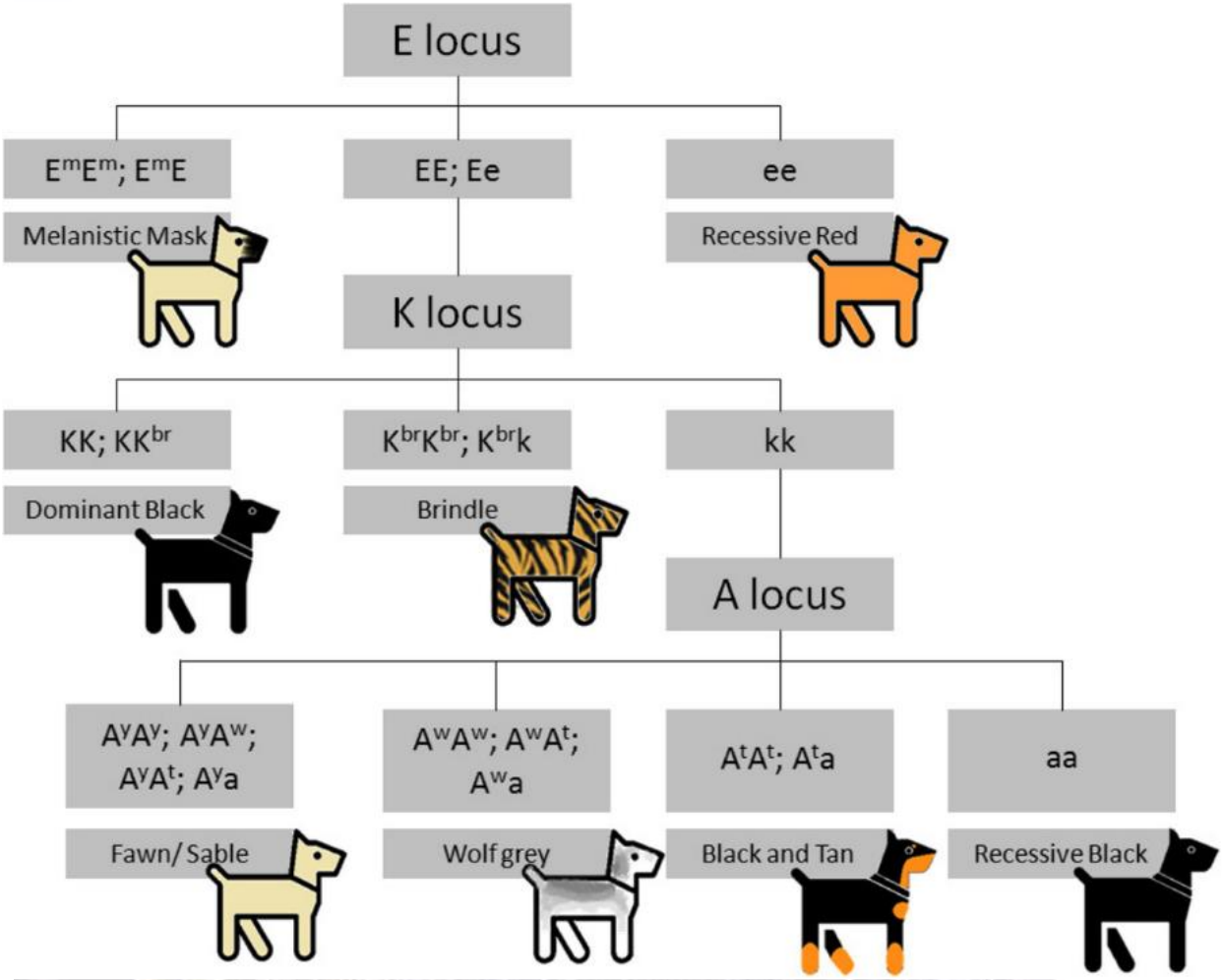
There are many ways in which traits are passed from one generation to the next. From the simplest to understand – simple dominance- to a very complex multi-factoral transmission. In the simplest form, the presence of one dominant allele will dictate the presence of a phenotype, i.e. B_ will present black and bb will be the recessive phenotype. Unfortunately, in the real world, this form of genetic transmission is rare. To make genetics more complex, we have recognized that many genes are linked suggesting a more complex or inconclusive segregation ratio calculation due to undeclared gene linkages. A segregation ratio in Mendelian genetics is defined as the proportion of offspring that can be expected to be of a particular genotype or phenotype. So when one gene is phenotypically presented, the distribution of offspring phenotype classes, whereas genetic transition probabilities refer to the distribution of offspring genotype classes. linked genes are also presented which may not be detected immediately. For example, in horses the dominant allele W (white) is considered a lethal gene. The W allele is linked to the gene that causes the Lethal White Foal Syndrome which is the trigger for ileocolonic agangliosis, which basically means the middle to lower intestine does not function and the foal will not survive. So, what about Cane Corsos…

In an article published in March 2019, by Korec, E., et.al., ***Inheritance of coat colour in the cane Corso Italiano dog,*** analyzed data from 23,271 dogs and bitches using the Cane Corso Italiano Pedigree Database. For the first time the coat colour segregation ratios in Cane Corso Italiano offspring arising from crosses between parents of all possible coat colour combinations is documented. Breeders are continually bombarded with requests for certain colors of puppies. For as long as purebred dogs, cats, or horses have been available, people have their favorite colors. How does a certain color of Corso present? Over the years, many genes that play a role in coat color genetics have been described. However, a generalized, widely accepted nomenclature for gene names and symbols in domestic dogs does not exist; some genes were named historically by the scientists who first described them, and some genes were named according to their role in humans or a model organism. This continues to be confusing for breeders as well as for scientists. A review summarized the issue of dog coat colour genetics, introduced a modified version of the historical nomenclature and identified 12 coat colour loci in dogs. However, biological mechanisms are still unknown for some coat colour phenotypes.

Newton, et.al., was the first to discover the Melanocortin 1 receptor (MC1R) by a molecular genetic analysis in dogs. This gene can be identified with allelic locus E, and mutations in this gene commonly result in a distribution of eumelanin and pheomelanin. An important breakthrough was the discovery that pigment type-switching (black eumelanin and yellow pheomelanin) is controlled by three genes in dogs: Melanocortin 1 receptor (MC1R), Agouti signalling protein (ASIP) and β–Defensin 103 (CBD103) by Candille, et.al and Oguro-Okano M, et al. These genes are associated with characteristic allelic influence (locus E, locus K and locus A) for a dog's coat colour. Allelic dominance and the hierarchy of individual loci are summarized in Fig. 2 according to several reviews of literature. Melanin is the pigment in skin cells that give color. In humans, the melanin pigment acts as an umbrella over the nucleus to protect from UV radiation. There are three basic types of melanin, EUMELANIN that is expressed as black or brown colors, PHAEOMELANIN is expressed as yellow to red colors, and NEUROMELANIN which is a dark pigment only found in the central nervous system and is not directly linked to coat color expression. The table below shows the summary of the Korec article. **E-Locus** (Recessive Yellow, Melanistic Mask Allele) Description: MC1R, also known as the extension gene, controls production of pigment in melanocytes. The dominant form of the gene, the "**E**" allele, allows the dog to produce eumelanin, which is a black pigment. **K-Locus** (Dominant Black). Description: Coat coloration is controlled by several different genes

in dogs. One of these gene is referred to as "Dominant Black. **A-Locus** (Fawn/Sable, Tricolor/Tan Points, Solid Black).

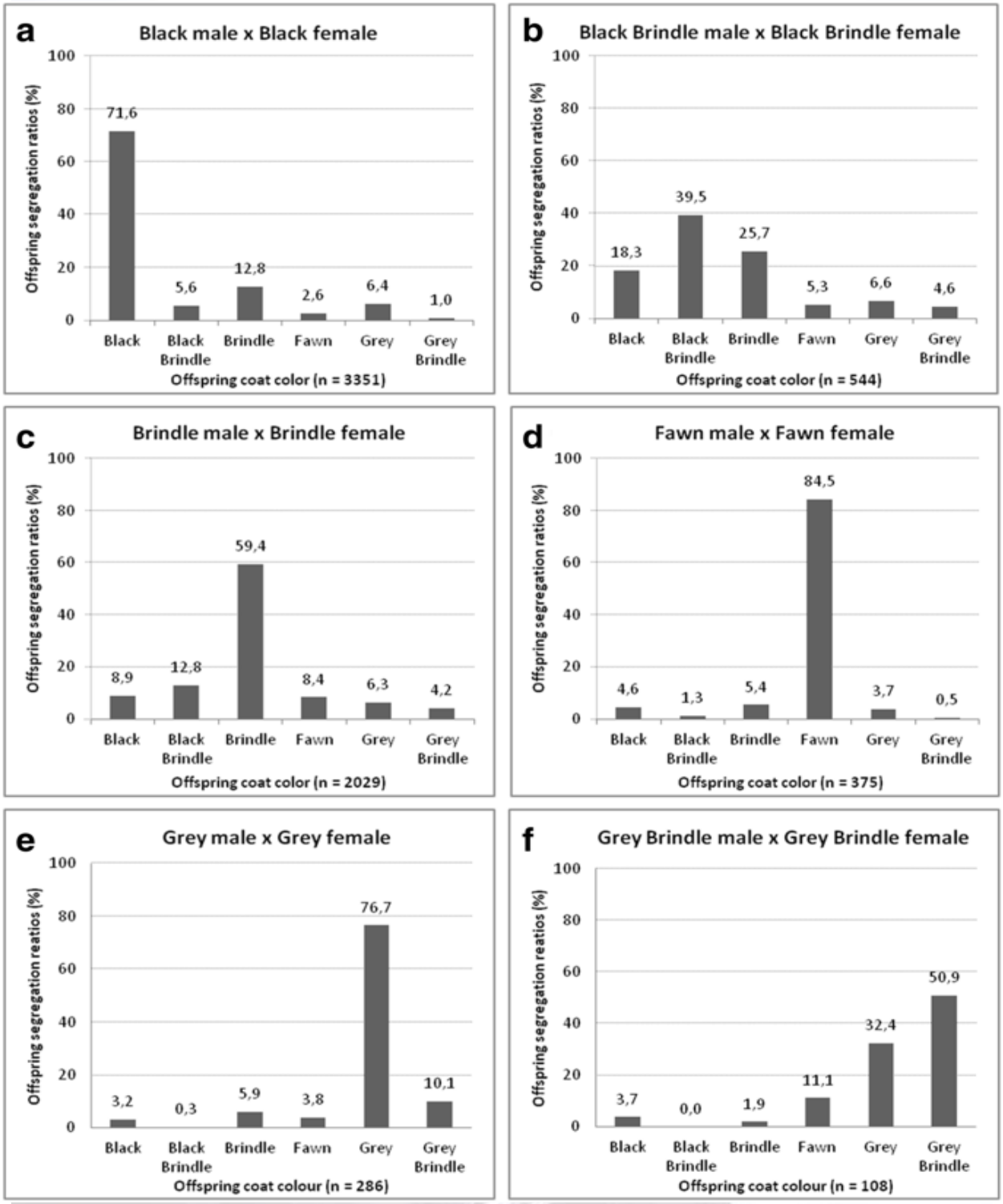
FIG.2




Inheritance of the basic coat colour loci. Locus E affects the distribution of eumelanin and pheomelanin. In dogs, there are three alleles with specific dominance ($E^m > E > e$). $E^m$ is responsible for melanistic mask and e is responsible for recessive red. The K locus is hypostatic for the E locus, and there are also three alleles with a specific hierarchy ($K > K^{br} > k$). The K allele is responsible for dominant black and $K^{br}$ is responsible for brindle colour. Locus A has four alleles, and the dominance of these alleles is $A^y > A^w > A^t > a$. Allele $A^y$ is responsible for fawn or sable colour. Allele $A^w$ represents wild colouration, which is ancestral. Allele $A^t$ represents black and tan or saddle and tan colouration, and allele a is responsible for recessive black. Alleles E and k are wild-type, and coat colour is under the control of hypostatic loci.

Korec, et.al., summary suggests the following: The main aim of this study was to identify the principles of inheritance of coat colours in Cane Corso Italiano breed. First, they attempted to verify whether the principles of Mendelian inheritance of the coat colour could be applied. The first crosses analyzed were between males and females of the same colour are summarized in Fig. 3.

**Fig. 3**




Male and female crossing of the same colour in the Cane Corso breed. **a** crossing two black parents. **b** crossing two black brindle parents. **c** crossing two brindle parents. **d** crossing two fawn parents. **e** crossing two grey parents. **f** crossing two grey brindle parents

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Korec's summary of data collected suggested that black is the most frequent coat colour in the Cane Corso breed. The segregation ratio of the offspring produced by crossing two black parents is summarized in Fig. 3a. Of the offspring, 71.6% were black, and 28.4% were other colours.

Crossing two black brindle parents resulted in segregation of the offspring, where only 39.5% of the offspring were black brindles, 25.7% were brindles and 34.8% had other colours (Fig. 3b). Crossing two brindle parents resulted in 59.4% brindle offspring and 40.6% other-colour offspring (Fig. 3c). Crossing two fawn parents resulted in 84.5% fawn offspring and 15.5% other-colour offspring (Fig. 3d). Crossing two grey parents resulted in 76.7% grey offspring and 23.3% other-colour offspring (Fig. 3e), and grey brindle parents produced 50.9% grey brindle offspring and 49.1% other colour offspring (Fig. 3f).

These results suggest that the inheritance of coat colour is much more complicated and that additional genes are involved. The segregation ratios of offspring produced by the parental crossing of all possible colour variations suggest that at least one gene responsible for coat colour is located on a sex chromosome. To verify this hypothesis, the sex ratio was analysed in offspring of all colour groups using statistically significant data. A ratio of 50% males and 50% females should be found if all genes responsible for coat colour are located only on autosomes. A ratio of 1:1 was found in most colour groups and was confirmed by the chi-square test. For brindle offspring, when brindle males were crossed with grey brindle females, 90 males and 55 females were produced. This result did not confirm a ratio of 1:1 using the chi-square test ($p = 0.0037$). For black offspring, when black males were crossed with brindle females, 524 males and 615 females were produced. This result did not confirm a ratio of 1:1 using the chi-square test ($p = 0.007$). A ratio of 1:1 was not confirmed in an additional 6 offspring colour groups using statistically significant data. So, what does all this mean?

Korec and fellow researchers found that crossing black-, fawn- and grey-colour individuals (male and female of the same colour) resulted in a greater than 70% probability that offspring would present the same colour as their parents. On the other hand, the coat colour of offspring arising from crossing individuals of black brindle, grey brindle and brindle was much more dependent on the genetic background. Crossing parents of the same colours can produce a litter with multiple colour variations. This is an important finding because there is a demand for specific colours within the community of breeders.

The results of sex segregation ratios confirmed their hypothesis that at least one gene responsible for coat colour is located on a sex chromosome. It is possible that one of the control mechanisms or biochemical pathways controlling the expression of coat colour could be regulated by sex chromosomes. Our hypothesis is supported by the fact that a gene located on a sex chromosome determines orange colouring in cats. This gene is still unknown, but its effect on coat colouring has been known for decades.

In dog coat colour genetics, there are many unknown mechanisms that lead to the expression of some colour phenotypes other than the basic colours (for example, ticking, progressive greying and tweed phenotypes). Hypothetically, the intensity of fawn, red, brindle or grey colours could be affected by gene or genes that are still unknown.

There are so many other factors that must be addressed with looking at the intricacies of genetics. However, at this time, we hope you will chew on this bit of information and think about the WHOLE dog, not just the color of its coat…

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Korec, E., Hančl, M., Bydžovská, M. *et al.* Inheritance of coat colour in the cane Corso Italiano dog. *BMC Genet* **20,** 24 (2019). https://doi.org/10.1186/s12863-019-0731-2

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