

HOW SNP WORKS

A mammalian genome consists of DNA packed in the nucleus of a cell. The DNA is bundled into chromosomes that vary in number depending on the species.

DNA is essentially made of only 4 base chemicals: adenine (A), guanine (G), cytosine (C), and thymine (T). These bases are held together in a long strand of sugar-phosphate- containing polymers. The A binds to a T and the G binds to a C to create a double stranded complimentary DNA molecule of these bases, positioned together in pairs called base-pairs. The dog genome is composed of around 2.5 billion bases compared to 3.2 billion in the human.

Within the long DNA strands of an animal, there are many millions of similarities between two individuals of the same species (e.g. humans, dogs, cats, horses, etc.) that dictate how they physically appear. Each individual differs from the next by about 1 base pair in every 1,000. Some of these differences dictate whether they carry genetic diseases. >From these small genetic differences, variations are expressed as in hair color, eyesight, nose shape, foot size, some allergies and to some extent, behavior. These single-base pair differences are called single nucleotide polymorphisms or SNPs (pronounced “snips”). Some SNPs are linked to particular populations and, the case of humans, can be used to trace human migration that occurred thousands of years ago.

For the most part, SNPs are neither good nor bad; they are just different. Some SNPs have functional significance and some do not. SNPs that have no consequence can be used as a “fingerprint” to give a unique profile to an individual. Other SNPs can be used to determine the genetic basis of animal coat color. Other SNPs, if they are located in a particular gene, can be unfortunate if they result in the loss or change of a peptide that leads to the development of a genetic disease.

The pure-bred dog population consists of greater than 300 partially inbred genetic isolates called breeds. Each year over 1 million purebred dogs are registered in the United States, alone. Breeders keep meticulous records and genealogies of their animals. The manipulation of canine genetics by centuries of human intervention has led to a variety of relatively young modern dog breeds, the majority of which having been developed within the last 300 years. Highly inbred animals may be more prone to breed-specific genetic diseases because the disease gene is kept within a relatively small gene pool. A SNP profile will be very informative for dog breeders to choose appropriate sires and dams to reduce the risk of genetic diseases.

In SNP detection, there are three possibilities for the paternal and maternal chromosomes.

Paternal Chromosome	Maternal Chromosome
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In (I), a Cytosine (C) is present at the site of both the paternal and maternal chromosomes; in (II), a C is present on the paternal chromosome and a thymine (T) on the maternal chromosome (or vice versa); and in (III) a T is present on both. A series of these sites with different bases, or SNPs serve to characterize a stretch of DNA.

SNPs are detected in the Pawsitive ID system by use of two different fluorescently tagged stretches of complementary DNA that flank either side of each SNP (polymorphism) to be identified. Through a process known as the polymerase chain reaction, many millions of copies of the fluorescent tags are produced and thus serve as markers for the SNPs. The process is automated and robust.