Directions: Read the following article and answer the questions

Meet Tasha, a boxer dog (Figure 1). In 2005, scientists obtained the first complete dog genome sequence using Tasha’s DNA. Like all dogs, Tasha’s genome consists of a sequence of 2,400,000,000 pairs of nucleotides (A, C, T, and G) located on 39 pairs of chromosomes. What do scientists do with this information? This article will introduce you to an approach for using genome sequence data to identify genes associated with an organism’s characteristics, or phenotypes, called genome wide association studies (GWAS). GWAS involve scanning DNA sequences across the genomes of a large number of individuals—in this case, many different dogs—to find differences, or variations, associated with particular phenotypes, to then guide the identification of the responsible genes.

SNPs Are Common Variations in DNA Sequences

GWAS use DNA “markers” across the genome called single nucleotide polymorphisms, or SNPs (pronounced “snips”). A SNP is a variation in a single nucleotide at a particular position in the genome (Figure 2). Not all single nucleotide changes are SNPs. To be classified as a SNP, the change must occur in more than 1% of the population.

SNPs Are Identified by Comparing Many Genomes

After sequencing Tasha’s genome, scientists sequenced the genomes of many dogs from a variety of breeds, comparing them to one another. They identified millions of common variations among these genomes and their locations on chromosomes. Specific locations are denoted by the chromosome number followed by the nucleotide number along the chromosome. For example, at a particular location some dogs have an A, while other dogs have a C (Figure 2). Dogs can have two copies of the C allele in this location, two copies of the A allele, or one of each allele.

SNPs Are Used to Find the Locations of Genes Associated with Particular Traits

Once we know where the SNPs are located in an organism’s genome, they can be used to home in on the genes of interest. In a GWAS, scientists typically compare SNPs in two groups of individuals: one with one version of a trait (for example, dogs with long fur) and one with another version of the trait (for example, dogs with short fur). They then identify SNPs that are found to occur significantly more frequently in dogs with one version of the trait than the other (for example, short versus long fur). Those SNPs serve as “markers” for the region of the dog genome where a gene responsible for determining coat length resides.

Why are certain SNPs correlated, or associated, with certain traits? SNPs that occur within a gene or in a regulatory area near a gene may directly affect that gene’s function and the resulting trait. For example, the change from an A to C in the Figure 2 example may itself be responsible for a dog having long rather than short
hair. However, a SNP does not have to be responsible for causing a trait in order to be correlated with that trait. If a SNP is close enough to a trait-causing allele, they may be inherited together (Figure 3).

**Variants in Three Genes Account for Most Dog Coat Differences**

Variants in just three genes acting in different combinations account for the wide range of coat textures seen in dogs -- from the poodle’s tight curls to the beagle’s sick-straight fur. A team led by researchers from the National Human Genome Research Institute (NHGRI), part of the National Institutes of Health, reported these findings October 2015.

“This study is an elegant example of using genomic techniques to unravel the genetic basis of biological diversity,” said NHGRI Scientific Director Eric, Green, M.D., Ph.D. “Genomics continue to gain new insights from the amazing morphological differences seen across the canine species, including many that give clues about human biology and disease.”

Until now, relatively little was known about the genes influencing the length, growth pattern and texture of the coats of dogs. The researches performed a genome-wide scan of specific signposts DNA variation, called single-nucleotide polymorphisms, in 1,000 individual dogs representing 80 breeds. These data were compared with descriptions of various coat types.

“What’s important for human health is the way we found the genes involved in dog coats and figured out how they work together, rather than the genes themselves,” said Elaine A. Ostrander, Ph.D., chief of the Cancer Genetics Branch in NHGRI’s Division of Intramural Research. “We think this approach will help pinpoint multiple genes involved in complex human conditions, such as cancer, heart disease, diabetes, and obesity.”

Artificial selection, at the heart of breeding for desirable traits in domesticated animals, has yielded rapid change in a short span of canine history. While researchers estimate that modern dog breeds diverged from wolves some 15,000 years ago, the genetic changes in the dog genome that create multiple coat types are more likely to have been pursued by breeders in just the past 200 years. In fact, short-haired breeds, such as the beagle, display the original, more wolf-like versions of the three genes identified in the study.
Modern dog breeds are a part of a unique population structure, having been selectively bred for many years. Based on this structure, the researchers were able to break down a complex phenotype --coat-- into possible genetic variations. “When we put these genetic variants back together in different combinations, we found that we could create most of the coat varieties seen in what is among the most diverse species in the world --the dog,” Dr. Ostrander said. “If we can decipher the genetic basis for a complex trait such as the dog’s coat, we believe that we can do it as well with complex diseases.”

(Excerpt from NIH publication, 27 August 2009)

**Questions**

1. How many pairs of chromosomes do dogs have? How many more is this than what humans possess?

2. How many genes account for the wide variety of coat textures in dogs? ______________

3. In two or three sentences, describe how scientists went about identifying these genes.

4. In this reading, why are SNPs referred to as “genetic markers” or “signposts”?

5. Why do you think it is important to analyze the DNA of many dogs when doing this research?

6. Do humans have SNPs?

7. How might the dog genome benefit humans?