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Complex Traits

Using Dogs as a Model for Modern Genetics
Nancy P. Moreno, Ph.D.



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- Page 32: Mosher, D., Quignon, P, Bustamante, C., Sutter, N., Mellers, C., Parker, H., et al. (2007) A Mutation in the Myostatin Gene Increases Muscle Mass and Enhances Racing Performance in Heterozygote Dogs. *PLoS Genet* 3(5): e79. doi:10.1371/journal.pgen.0030079. Public domain. <http://journals.plos.org/plosgenetics/article?id=info:doi/10.1371/journal.pgen.0030079>
- Page 33: Clark, L., Wahl, J., Rees, C., and Murphy, K. Retrotransposon insertion in SILV is responsible for merle patterning of the domestic dog. *Proceedings of the National Academy of Sciences*. 1376–1381, doi: 10.1073/pnas.0506940103. Open access. Used with permission. Fig. 1. <http://www.pnas.org/content/103/5/1376.full>

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Materials

1. Dogs — A Model for Modern Genetics (p. 1)

- Complex Traits slide set (slides 2–10), available at: <http://www.bioedonline.org/slides/classroom-slides1/genetics-and-inheritance/complex-traits/>
- Computer and projector, or interactive whiteboard
- Copies of “The Domestic Dog and Related Species” (one per student or group)
- *Optional:* Copies of “Examples of the Dog and Related Species”

2. Genotyping a Mixed Breed Dog (p. 7)

- Complex Traits slide set (slides 11–15), available at: <http://www.bioedonline.org/slides/classroom-slides1/genetics-and-inheritance/complex-traits/>
- Computer and projector, or interactive whiteboard
- Copies of student page, “Dog Breeds Diagram” (one per student or one per group)

3. Mapping a Mutation (p. 11)

- Complex Traits slide set (slides 16–23), available at: <http://www.bioedonline.org/slides/classroom-slides1/genetics-and-inheritance/complex-traits/>
- Computer and projector, or interactive whiteboard
- Copies of the student page (one per student)

4. Genotypes and Phenotypes (p. 17)

- Complex Traits slide set (slides 24–26), available at: <http://www.bioedonline.org/slides/classroom-slides1/genetics-and-inheritance/complex-traits/>
- Computer and projector, or interactive whiteboard
- Copies of the student sheets (one set per student)

5. Categorizing Hair Types in Dogs (p. 21)

- Complex Traits slide set (slides 27–41), available at: <http://www.bioedonline.org/slides/classroom-slides1/genetics-and-inheritance/complex-traits/>
- Computer and projector, or interactive whiteboard
- Set of eight Dog Breed Cards copied onto cardstock (see p. 25–26; one set per group)
- Copy of “Genetics of Dog Coats” (p. 27, one per student)
- Copy of “Confirmed Hair Phenotypes,” to be distributed after students have completed Part 2, item 6 (see p. 24 for details, one per student)

6. Genetic Testing and Designer Dogs (p. 29)

- Complex Traits slide set (slides 42–45), available at: <http://www.bioedonline.org/slides/classroom-slides1/genetics-and-inheritance/complex-traits/>
- Computer and projector, or interactive whiteboard
- Copies of the student sheet (one per student)
- Access to the Internet

OVERVIEW

Students explore variation among dog breeds, and compare variation within domesticated dogs to variation within wolves. Students also determine relationships among the dog and its closest relatives using a phylogenetic tree.



Dogs — A Model for Modern Genetics

From the tiny, long-haired Pekingese to the tall, short-haired Great Dane, domestic dogs show immense variety in their sizes, shapes, coat colors and textures, and behaviors. Selective breeding by humans for desirable genetic changes or mutations generated this variability. Today, more than 400 distinct breeds of dogs are recognized.

Because of its wide range of characteristics, the domestic dog (*Canis familiaris*) has become an important model for modern genetic studies. However, most of this diversity is found only between dog breeds. The characteristics of individuals within a particular dog breed are very uniform—genetically and



PEKINGESE

GREAT DANE



MACKENZIE GRAY WOLF

in appearance. In other words, dogs are homogeneous in their appearance (phenotype) and genetic makeup (genotype) within breeds, and are phenotypically and genetically heterogeneous among or between breeds. This pattern of variability, in which particular traits are accentuated within breeds, results from inbreeding (breeding of close relatives).

Dogs are members of the Canidae family of mammals. This group also includes coyotes, foxes, jackals, and wolves. The gray wolf is the closest relative of the dog. However, the gray wolf (*Canis lupus*) does not show the wide range of phenotypic variability found in the dog.

Even though dog breeds appear quite distinct, they still freely interbreed without physical or other barriers. In other words, all domestic dogs are members of the same species. Even with their wide range of appearances, dogs are more similar to one another genetically than they are to grey wolves, their closest relatives.

Dogs and wolves, which are separate species, also occasionally do interbreed. Normally, the two species maintain separate identities, have different physical characteristics and have different evolutionary histories. In addition, dogs and wolves usually are isolated reproductively (in natural circumstances, dogs and wolves rarely interact or have opportunities to breed).

Experts believe that the domestication and divergence of dogs from wolf populations began about 15,000 years ago. Most modern dog breeds originated within the past few hundred years. Domestication led to selection for and retention of certain favorable traits, such as herding or tracking behaviors, in addition to preferred physical characteristics.

FAST FACTS

A dog's ears are usually large relative to head size; its tail may curl upward, especially when running; the chest is broad so legs are separated; feet typically are not splayed; and its eyes may be blue.

A wolf's ears are small relative to its head size; its tail does not curve upward, even when running; the chest is very narrow so legs are close together; feet may splay outward; and its eyes are never blue. (Source: California Department of Fish and Wildlife.)



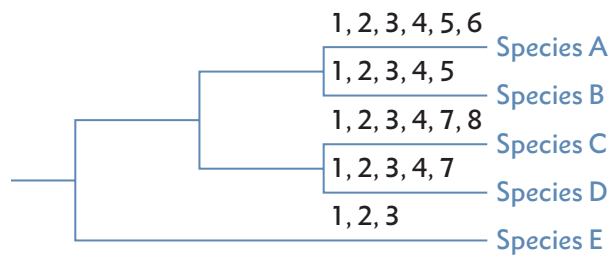
DID YOU KNOW?

Wolves tend to walk more directly when traveling, and circle widely rather than varying off of a path. Its hind foot tracks are placed within or directly in front of its forefoot tracks. (See track pattern, upper left.)

Dogs tend to walk all over—they have no need for stealth. As a result, a dog’s hind foot tracks seldom register within its forefoot tracks. (See track pattern, upper right, p. 3. Source: California Department of Fish and Wildlife. Patterns by Karen Converse.)

As part of this activity, students examine a diagram that shows the relationships among species in the dog family (Canidae) based on molecular genetic information. It is important to note that diagrams of this type are not family trees or genealogies.

Instead, they represent similarities or differences among living (extant) groups based on their genetic information. Groups that are found on the same branches (or clades) of the tree share unique genetic information and are descendants of the same founding or ancestral population.



In the diagram above, species A and B are more closely related to each other more than to any other species or cluster of species on the diagram. Similarly, species C and D are more closely related to each other than to a member of any other group. Of the species on the diagram, species E is the least related to any of the other groups.

This type of diagram, in which groups are defined by shared inherited characteristics, usually is called a phylogeny or phylogenetic tree. The term phylogeny comes from the Greek words, *phylon* (tribe or clan) and *genesis* (origin).

MATERIALS

- Complex Traits slide set (slides 2–10), available at <http://www.bioedonline.org/slides/classroom-slides/genetics-and-inheritance/complex-traits/>
- Computer and projector, or interactive whiteboard
- Copies of “The Domestic Dog and Related Species” (one per student or group)
- *Optional:* Copies of “Examples of the Dog and Related Species”

PROCEDURE

1. Share with students that they will be starting a unit on modern genetic information, using examples from dogs. Project Slide 2 as an introduction to the unit, then show Slide 3 and ask students, *Would you have this animal as a pet?*



MACKENZIE GRAY WOLF

Allow a few minutes for students to respond to your questions.

2. Project Slide 4 to students, and ask, *What about this animal? Is it suitable as a pet? Why or why not?* Tell students that the slide depicts a common dog breed, an English springer spaniel.



ENGLISH SPRINGER SPANIEL

3. After students have discussed characteristics of the dog, present Slide 5, which shows the gray wolf and dog, side by side.
4. Create a table at the front of the class and present Slide 6, which provides samples of characters and traits of the wolf and dog shown in the previous slides. Have students work in groups of two or four to create similar charts that list at least five characters that differ between the wolf and dog. OR conduct a discussion and create a class chart.

Character (Category)	Wolf Trait (<i>Canis lupus</i>)	Dog Trait (<i>Canis lupus familiaris</i>)
1. Ear shape	Pointed	Rounded
2. Eye color	Yellow	Brown
3.		

Note: You may want to clarify for students that “character” refers to a feature that can vary from one individual or group to another. “Trait” refers to a specific variation or form of a given feature. For example, hair texture is a character. Curly hair and straight hair are two different traits.

5. Show students Slide 7, and explain that scientists now can use genetic information to estimate the relationships among different groups of species. Species that are more closely related share more genetic information. In the slide, the numbers represent similar versions of genes. Ask, *Which numbers are shared by all of the groups?* [1,2,3]. *Which numbers distinguish the branch containing Species A, B, C and D, from the branch with Species E?* [4]. *How are the branches with Species A and B, and C and D different?*

One also can say that Species A and B share a common ancestor, as do

Species C and D. The entire group of Species shares a more distant common ancestor, which was characterized only by genes 1, 2 and 3.

6. Give each student or group of students a copy of the page, “Dogs and Related Species” (see page 4 and Slide 8).

Explain to students that this diagram was created using real genetic information from the different species. Have students interpret the diagram to answer the questions at the bottom of the student page.

Optional: Project photos of the dog and some related species for students to see unique genetic variations (see page 5, and Slides 9–10.

An “Answer Key” is provided on page 6.

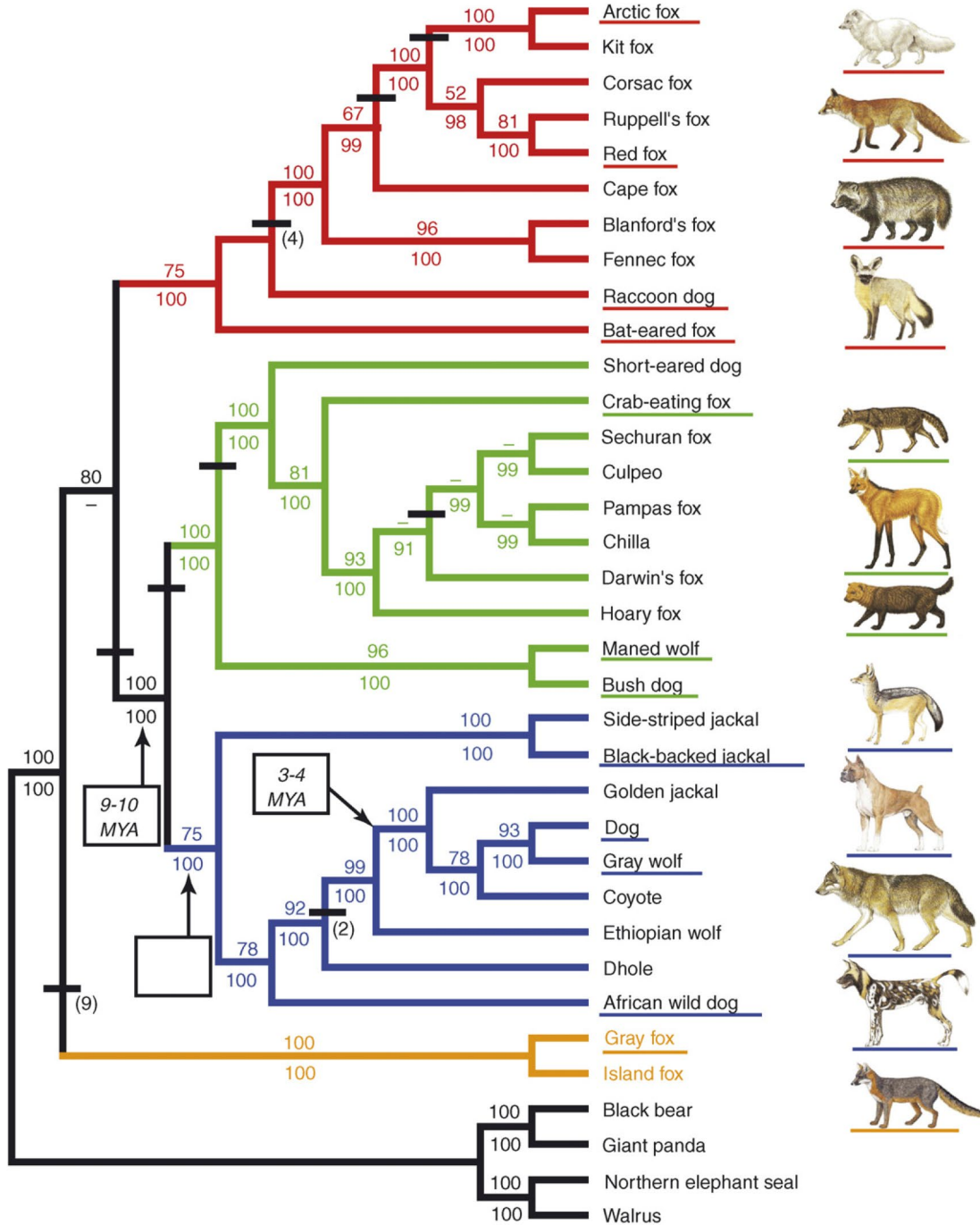
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The Domestic Dog and Related Species



This diagram shows genetic similarities among 31 species of the dog family (Canidae). Each branch represents a group that shares the same ancestral genetic information. Study the chart, then answer the questions below on the back of this sheet.



1. The diagram has a reference group of other mammals. Find this group and list the members.
2. Find the four main groups of dog relatives, and list the members of each group.
3. Which species is the closest relative to the Dog? Explain your answer.
4. Which species or branch of species can be considered the least related to the Dog? Explain your answer.

Examples of the Dog and Related Canids



AFRICAN WILD DOG



ARCTIC FOX



BAT-EARED FOX



BLACK-BACKED JACKAL



BUSH DOG



CRAB-EATING FOX



DOG



GRAY FOX



GRAY WOLF



MANED WOLF



RACCOON DOG



RED FOX

African wild dog © Michael Gäbler, Wikimedia Commons CC-BY-SA 3.0, Dog (boxer) © Artman, licensed for use, Gray wolf © MacNeil Lyons, courtesy of the U.S. National Park Service, Arctic fox © Jason Burrows; Bat-eared fox © Mike Cilliers; Black-backed jackal © Ray Morris; Bush dog © Josh Moore; Crab-eating fox and Raccoon Dog © Tambako the jaguar, Gray fox © Cary Robertson; Maned wolf © Pascal Voystekker; and Red fox © Peter Trimming, CC-BY-SA 2.0, flicker.com

Answer Key



1. The diagram has a reference group of other mammals. Find this group and list the members.

Black Bear

Giant Panda

Northern Elephant Seal

Walrus

2. Find the four main groups of dog relatives, and list the members of each group.

Red fox-like Canids

Arctic fox

Bat-eared fox

Blanford's fox

Cape fox

Corsac fox

Fennec fox

Kit fox

Raccoon dog

Red fox

Ruppell's fox

South American Canids

Bush dog

Chilla

Crab-eating fox

Culpeo

Darwin's fox

Hoary fox

Maned wolf

Pampas fox

Sechuran fox

Short-eared dog

Wolf-like Canids

African wild dog

Black-backed jackal

Coyote

Golden jackal

Dhole

Dog

Ethiopian wolf

Gray wolf

Side-striped jackal

North American Gray Canids

Gray fox

Island fox

3. Which species is the closest relative to the Dog? Explain your answer.

The Gray wolf, because it shares the most recent branching point with the Dog.

4. Which species or branch of species can be considered the least related to the dog? Explain your answer.

The branch containing the Gray fox and Island fox is the least related (most distant branch from the Dog).

OVERVIEW

Students follow the case study of a “mutt,” whose breed identity is uncovered by its owners through commercial genotyping. In addition, students learn about variation within and among dog breeds, and the origins of common breed clusters.



Genotyping a Mixed-breed Dog

As described in the previous activity, all dogs are members of the same species (*Canis familiaris*). Even though members of different dog breeds vary physically and even behave in different ways, all domestic dogs can interbreed and produce viable offspring. The variation among (i.e., “between”) dog breeds is the result of selective breeding over time. In many cases, distinctive traits of a particular breed is the result of the crosses between close relatives. Unfortunately, inbreeding also will consolidate undesirable traits, such as hereditary diseases. Thus, breeders and owners have considerable interest in knowing about the genetic makeup of their dogs. Breeders, for example, would like to avoid breeding dogs that can pass on genetic diseases, such as von Willebrand’s disease (an inherited bleeding disorder), to their offspring.



DOVEKIE AS A PUPPY

Several companies now provide genetic tests for many disease-causing mutations and common physical characteristics, such as coat color. In addition, genetic testing can provide insights into the ancestry of mixed breed dogs. This information is useful to owners, who would like to know if their dog has hidden disease tendencies or has ancestors with specific behaviors (such as herding or barking).

Genetic testing does not examine the entire genome of an individual. Instead, it looks for irregularities in the chromosomes themselves, changes in specific sections of DNA or even proteins that are associated with a specific trait or disease. The dog genome is divided into 78 chromosomes, with 38 pairs of non-sex chromosomes and a pair of sex chromosomes. Sex in dogs is determined the same way as

in humans: females have two “X” chromosomes (one from each parent) and males have one “X” and one “Y” chromosome. The DNA in chromosomes stays in a tightly wound or bunched state, until a section is “unwound,” to enable the DNA to be read.

In this activity, students will learn how one family used genetic testing to uncover the ancestry of an unusual puppy. In addition, they will examine the relationships

BETWEEN VS. AMONG

Geneticists often refer to variation or differences “among” groups. This is equivalent to saying that there are differences “between” two groups, but the word, “among,” is used when more than two groups are being considered. In other words, we can talk about differences “between” two groups, and “among” three groups.



Pictured above is a set of unmatched dog chromosomes, and the same chromosomes matched into pairs. The paired depiction of chromosomes is called a karyotype. Chromosomes are found within the nucleus of a cell.



among common clusters of dog breeds, and investigate the characteristics of different breeds.

MATERIALS

- Complex Traits slide set (slides 11–15), available at <http://www.bioedonline.org/slides/classroom-slides/genetics-and-inheritance/complex-traits/>
- Computer and projector, or interactive whiteboard
- Copies of student page, “Dog Breeds Diagram” (one per student or one per group)

PROCEDURE

1. Play the NPR radio story, *Hounded by Doubt, Dogged Owners Probe a Mystery*, which may be found at the link below. Or download the transcript and have students read the story. Photographs of Dovekie and a purebred golden retriever are provided on Slide 11.

<http://www.npr.org/templates/story/story.php?storyId=127484075>
2. Encourage a discussion by asking students, *Have you heard about genetic testing before? What does genetic testing examine? Do you think they will be able to figure out who Dovekie’s parents are?* Tell students that genetic tests can be developed to identify unique hereditary information, and that genetic information often is used to understand relationships among different families or groups. Remind students that most organisms (including humans and dogs) have two sets of genetic information, with a single set coming from each of the individual’s two parents. This information is carried on DNA molecules (students will learn more about this process in the activity, “Mapping a Mutation”).
3. Display Slide 12 showing a litter of puppies and their parent (or print copies of the slide for students to share). Ask students, *What do you observe about the puppies in this photograph?* Students should notice that several different



CATAHOULA LEOPARD DOGS

- coat colors and patterns of markings are present. In addition, none of the puppies has the same markings as the mother. Ask, *Where did this variation come from?* Invite student responses—they should identify the parents (through genetic information, genes, DNA etc.) as the sources of the observed variations in the puppies.
4. Next, show Slide 13, which shows several different dog breeds. Ask students to identify the ways in which the different kinds of dogs differ in appearance [body size and shape; head shape; coat length, color and curliness]. Tell students that modern dogs provide an interesting model for learning genetics, because humans selected desirable dogs to breed—based on the parent dogs’ appearance or behaviors. This process over many generations, and many crosses, led to the different kinds of dog breeds.
 5. Have students work in teams of two, and give each team a copy of the “Dog Breed Diagram” page, and display Slide 14. Tell students that the diagram represents the complex genetic relationships among different dog breeds and was developed using information similar to that used for genetic tests ordered for Dovekie. Clarify for students that the circular diagram was created

from a linear branching diagram like the one in the activity, “Dogs—A Model for Modern Genetics.”

Have students answer the questions on their student sheet and discuss as a group. (Answers are provided below.)

- What is the closest ancestor to dogs? [Wolves]
- How many major clusters of dog breeds have been identified? [10]
- What is the closest branch to the retriever group? [Newfoundland]
- Why are Mastiff-like dogs shown in several different branches of the tree. [They contain genetic similarities to several other groups, probably because of crosses between groups.]
- Which breed clusters might be represented in Dovekie based on his appearance?



DOVEKIE AND HENRY: WIRE-HAIRED POINTING GRIFFONS

6. Play the radio story, The Case of the Mystery Puppy Solved! (Sort Of). The story can be found at the link below. Tell students that they should be prepared to discuss the following questions after listening to the story. Alternatively, you may download and print the transcript and have student read the story.

<http://www.npr.org/templates/story/story.php?storyId=127563468>

7. Have students work in groups to answer the following questions (Slide 15). Afterward, conduct a class discussion about the story and guiding questions, such as the following.

- What did his owners learn about Dovekie?
- What kind of dog is Dovekie?
- What does this story tell us about the commercial applications of genetic testing?

Dovekie is a mixed breed dog with an unusual appearance. After genetic testing by three different companies, his owners learned that he had a mix of genetic material from a rare breed (purebred wirehaired pointed griffon) and almost purebred golden retriever, or golden retriever mix. The somewhat different results from each lab demonstrate that genetic testing techniques still are being refined, and that results, while informative, may need interpretation.

8. To conclude, have each team of students select a dog breed from the diagram, and use resources on the website of the American Kennel Club (www.akc.org) to learn more about their assigned or selected breed. Each team should prepare a written description of the origin, original purpose, physical characteristics and unique attributes of their selected breed. Have students report their findings during the next class period.

EXTENSION

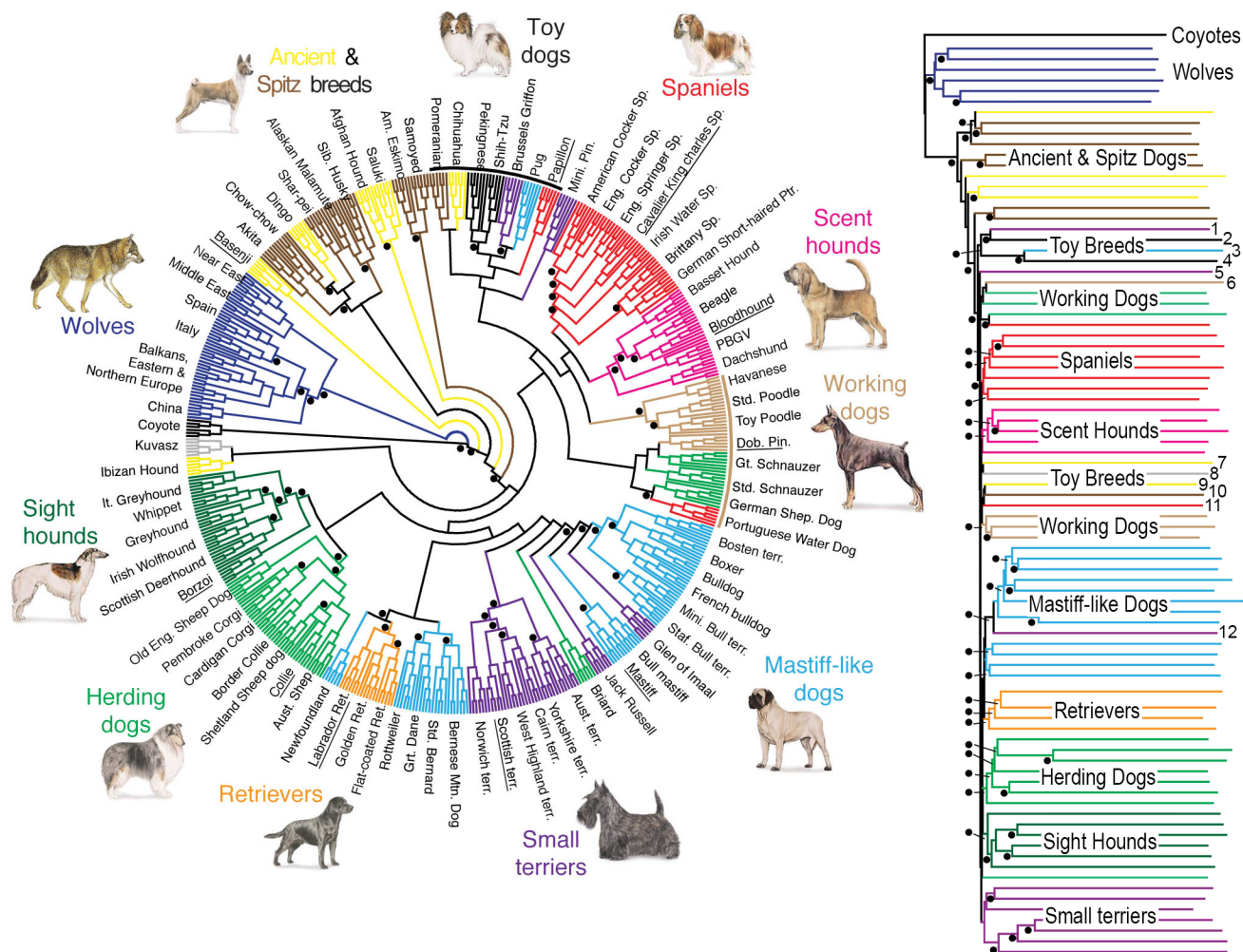
If students have immediate questions about DNA and genes, have them complete the online Tour of the Basics found at the Learn Genetics website (<http://learn.genetics.utah.edu/content/begin/tour/>). The tutorial will introduce and explain key concepts and terms related to genetics, which also will be introduced as they move through this unit.



Dog Breed Diagram



This diagram shows complex genetic relationships among different dog breeds, and was similar to that used for genetic tests ordered for Dovekie. Study the chart, then answer the questions below on the back of this sheet.



1. What is the closest ancestor to dogs?
2. How many major clusters of dog breeds have been identified?
3. What is the closest branch to the retriever group?
4. Why are Mastiff-like dogs shown in several different branches of the tree.
5. Which breed clusters might be represented in Dovekie based on his appearance?

Wayne, R. © UCLA Department of Ecology and Evolutionary Biology. Used with permission. Text modified by M.S. Young for clarity. <http://newsroom.ucla.edu/releases/dogs-likely-originated-in-the-15101>

OVERVIEW

Students learn about the genetic code, and how small substitutions within the code can lead to physical changes in individuals. Students use authentic data to uncover the single nucleotide polymorphism (SNP) responsible for long hair in dogs.

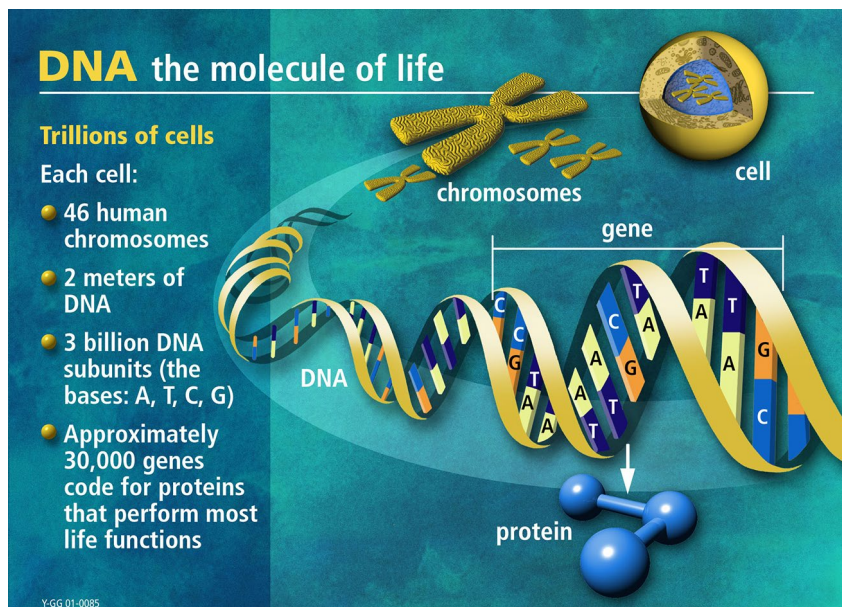


Mapping a Mutation

In the activity, “Genotyping a Mixed-breed Dog,” students were introduced to the variety of characteristics found across breeds of dogs. They used information produced by modern genetics research to learn which breeds of dogs were most related and how genetics information is used commercially to help people figure the history and possible parentage of mixed breed dogs. These examples represent applications of genomics—a field that offers a new way of thinking about genes and heredity.

Traditionally, genetics researchers have focused on identifying single genes, their variant forms (alleles) and their functions. Genes are hereditary units that occupy a fixed location on a chromosome or DNA

molecule. Each gene has a specific influence on the characteristics of an individual (phenotype) and provides the instructions for creating proteins (technically, certain sections of genes code for strings of amino acids or polypeptides). Usually a single gene has various forms, known as alleles. Since every individual has two sets of chromosome, each individual also has two versions or alleles for each gene. The interaction between the two alleles, and of a particular gene with other genes and the environment, determines the phenotype of the individual.



Genes are encoded along a pair of twisted DNA (deoxyribonucleic acid) strands, known as a double helix. Each strand is made of a sequence of four much smaller molecules, adenine (A), guanine (G), cytosine (C) and thymine (T). The strands are complementary, so that an A on one strand is matched by a T on the other strand, and a C is matched by a G (see graphic, above). The human genome consists of more than 3 billion of these pairs, called base pairs, packaged into 23 pairs of chromosomes. A small amount of DNA also is found in the mitochondria (where energy is processed inside cells).

Humans have about 20,000–25,000 genes. The average human gene consists of about 3,000 bases. Dogs have 39 pairs of chromosomes, which contain approximately 2.5 billion base pairs, and about 19,000 genes.

The “central dogma” of genetics explains that DNA codes for RNA (ribonucleic acids, another class of long chain molecules), which in turn, encodes and manufactures all of the proteins needed by an organism. The process of creating RNA from DNA is called transcription. Even though DNA has two strands, only one strand is read during transcription of a given sequence (genes can be located on either strand). The other



strand serves as a template to produce a molecule of RNA with the same sequence as the “coding” or “non-template” strand. We now know that 80% of human DNA does not code for proteins. These noncoding regions have other functions, including preserving important gene sequences and regulation of gene functions.

The relatively new field of genomics looks at an organism’s entire complement of DNA, including all of its genes. The nucleus of every cell (except for red blood cells) contains a copy of the entire genome of the organism. The human genome was sequenced for the first time in 2003. In 2005, a complete dog genome was sequenced using DNA from a female boxer named Tasha.



TASHA

Mutations provide the raw material for genetic variation, and come about through mistakes when DNA is copied or environmental factors, such as ultraviolet radiation from the sun. A mutation is a permanent change in the sequence of DNA. Mutations range in size from a change in a single DNA base (point mutation) to a change in a large segment of a

chromosome. When a single nucleotide at the same location differs between individuals, the variation is called a “snip” (short for single nucleotide polymorphism or SNP).

In this activity, students are introduced to genetic variation by looking at recent research results on hair length in dogs. Short hair is the ancestral (original) condition in dogs. Long-haired dog breeds were found to have a mutation in the gene that signals for the termination of hair growth. The mutation causes a loss of function in hair growth regulation, presumably leading to longer hair.

The researchers began by studying a gene that was known to contribute to hair growth in other species (called *FGF5*, named for the “fibroblast growth factor 5” protein). By comparing sequence data from different dog breeds, they found that a single mutation (from C to T) at one location consistently correlated with the presence of long hair. The mutation causes an amino acid change (cysteine to phenylalanine). Only dogs that are homozygous (have two copies) for the mutation have long hair. Students will use some of the original published data to find the location and nature of the mutation.

MATERIALS

- Complex Traits slide set (slides 16–23), available at <http://www.bioedonline.org/slides/classroom-slides/genetics-and-inheritance/complex-traits/>
- Computer and projector, or interactive whiteboard
- Copies of the student page (one per student)

FAST FACTS

The nucleus of every cell (except for red blood cells) contains DNA, which is the hereditary material in organisms.

A gene is DNA material that occupies a fixed location (section) on a chromosome or strand of DNA.

A DNA strand containing a single gene also contains various forms of that gene, known as alleles.

Each gene has a specific influence on the characteristics an individual or organism (phenotype).

A genome is an organism’s complete set of DNA.

PROCEDURE

1. Introduce the topic of genes and genomes by showing Slide 16. Write on the board or project the following conversation for students to see (Slide 17).

Person 1: hru?

Person 2: hv hw

Person 1: cul8r?

Person 2: gr8 ttys

Ask students, *When would you write something like this?* [text message on a smart phone] Follow by asking, *Does the message use symbols that everyone can read?* [Only people who know how to send text messages in English can understand the code.] Have one or more students translate the text messages into full sentences.

Person 1: How are you?

Person 2: Have homework.

Person 1: Call you later?

Person 2: Great. Talk to you soon.

Ask students to share other examples of text messaging codes. Ask, *What are the advantages of using a code?* [A code conveys information in a compact way, but the receiver has to know how to make sense of the code.]

2. Tell students that living cells also use a code, which contains all of the instructions for a living organism. This information, which is contained on long DNA molecules, is packaged inside the nucleus of every cell and are found on chromosomes (Slide 18). Show the following three-minute video created by the BBC (Knowledge Explainer DNA), which provides a general explanation of the genetic code in DNA.

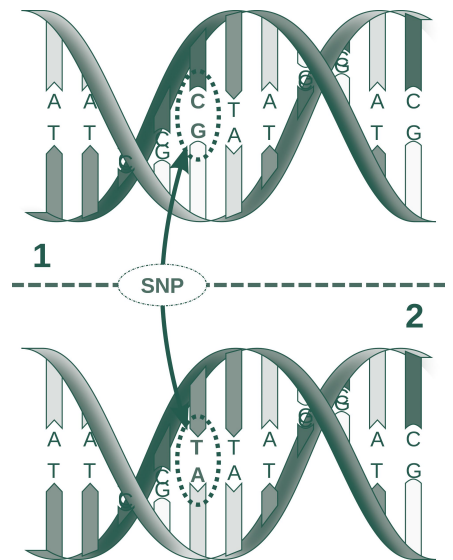
<http://vimeo.com/60747882#>

3. Help students understand that DNA contains a unique code that directs all of the

functions of a living organism (Slide 19). Further, all living organisms use the same code. This code was unlocked about 60 years ago by researchers James Watson and Francis Crick. Show students the video below, in which James Watson describes how they figured out the paired, helical structure of DNA.

<http://www.youtube.com/watch?v=PDexLx-oL75M>

4. Discuss the concepts covered in the video with students: DNA consists of sequences of four molecules or nucleotide bases: adenine (A), guanine (G), cytosine (C) and thymine (T). DNA always has two complementary strands, in which an A on one strand is matched by a T on the other strand, and a G is always matched with a C. The A-T and G-C combinations are called base pairs. Since the strands are complementary, only the sequence on one of the strands is used as a template for the first step in producing a protein molecule.



5. Use Slide 20 to further explain the DNA molecule. Tell students that biologists now can identify the sequence of nucleotides in a section of DNA. Usually, there are many differences in the DNA from one individual organism to another member of the same species. Most differences do not cause any observable changes or diseases. However, sometimes a mutation (change in the DNA sequence) causes some individuals to be



different. By comparing the DNA sequences of two different groups, biologists sometimes can find the genetic change responsible for variation among individuals.

6. Show students Slide 21, which asks, *Is there a genetic explanation for long hair in dogs?* Have students discuss the information. They should conclude that genetics must be involved, because long hair can be inherited by offspring.



DACHSHUNDS (L-R): WIRE HAIR, SHORT HAIR, LONG HAIR

7. Have students work in teams of two or four persons, and give each group a copy of the student sheet (Slide 22), “Understanding Long Hair in Dogs.” Refer back to slide Slide 20 to explain SNPs if students have questions.
8. Have students read the instructions carefully, and work to find the location of the change in the genetic code that correlates to long vs. short hair. Students will examine the sequence data to find the location (row) with a pattern of nucleotides that best matches the phenotypes of the individuals (long vs. short hair).

You may need to guide students with questions, such as, *Which rows do not show any changes from one individual to the next? Can you eliminate these rows from further consideration? Why or why not?* [The rows may be eliminated because they do not help discriminate between the short- and long-haired dogs.]

Remind students, to think about patterns within each pair of nucleotides, because each individual has two copies at every location. When the two nucleotides are the same within a pair, the condition is called homozygous. When the two nucleotides in a pair are different, the condition is called heterozygous.

9. Have each team present its results and the rationale for the selected location, or write a paragraph describing their findings.

Students will find that only one row (location 20) completely matches the pattern of long vs. short hair. Dogs with two copies of the T nucleotide at this location exhibit long hair.

10. Discuss students’ findings in class. Help them to understand that the single substitution of a “T” for a “C” led to the formation of a defective protein, which in turn, altered the signal for telling individual hairs to stop growing. In other words, the mutation causes a loss of function in hair growth regulation, presumably leading to longer hair. Only dogs with two copies of the mutation have long hair. It is likely that dogs with one copy of the short-hair allele produce enough of the hair termination protein to keep the hair from growing excessively.
11. Remind students of the text messages used to begin the activity. Project Slide 23. Ask, *What would happen if the message were changed in the following way?*

Person 1: hru?

Person 2: hv hw

Person 1: cul8r?

Person 2: gr8 ttys changes to gr8 ttyl

“Talk to you soon” becomes “Talk to you later.” The change probably would not affect the overall message, although one word was changed. This is similar to the many mutations in DNA that do

not change characteristics (phenotype) of the individual.

12. Next, ask about the following changes.

Person 2: gr8 ttys changes to gr8 tty**t**

“Talk to you soon” becomes “Talk to you tomorrow.”

Person 2: gr8 ttys changes to g**2g** tty**t**

“Great” becomes to “Got to Go”; and “Talk to you soon” becomes “Talk to you tomorrow.”

These changes not only change the words

designated by the code, but also alter the meaning of the messages.

13. Help students understand that mutations in DNA act in similar ways. Most mutations lead to no detectable changes in phenotype. Other mutations cause variations that are helpful or harmful, or have neutral effects. Variations at a single location along a DNA strand are called “single nucleotide polymorphisms.”

Note: The mutation for long hair causes a loss of function in dogs that receive two copies of the allele.



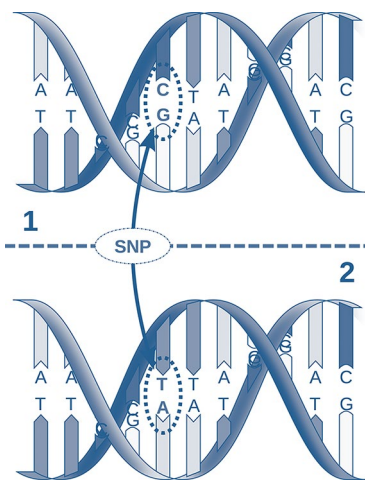
Understanding Long Hair in Dogs



The table to the right presents sequence data from a gene that controls hair growth in dogs. The gene is found on dog chromosome number 32, and contains about 70,000 nucleotides (or “letters”).

Certain sections of the gene appeared to be more variable, and those sections were sequenced in 10 individual dogs of different breeds. The investigators found a number of locations where individual dogs had different nucleotides at the same spot along the DNA strand. These locations are given in the table.

The columns in the table represent the 10 sampled dogs. Each row corresponds to a single location where the nucleotides (letters) were different. Biologists refer to a mutation at a single nucleotide position as a SNP, pronounced “snip” (which stands for single nucleotide polymorphism). Many times, these tiny mutations do not cause any differences between individuals. Remember that each dog has two versions of the nucleotide (one on each chromosome).



When a single nucleotide at the same location differs between individuals, the variation is called a “snip” (SNP).

Your challenge is to find the SNP location that explains the differences between the dogs that were sequenced. In other words, which SNP location best matches the pattern of long vs. short hair?

LOCATION	LONG HAIR				SHORT HAIR					
	1	2	3	4	5	6	7	8	9	10
	Havanese	American Eskimo	Standard Poodle	Dachshund (long hair)	Entlebucher Mountain Dog	Dachshund (short hair)	Dachshund (short hair)	Collie	Border Terrier	Pug
1	CC	CC	TC	CC	CC	CC	CC	CC	CC	CC
2	GG	GG	GG	GT	GG	GT	GG	GG	TT	TT
3	AA	AA	AA	AG	AA	AG	AA	AA	GG	GG
4	CC	CC	CC	CT	CC	CT	CC	CC	TT	TT
5	GG	GG	GG	GG	GT	GG	GG	GG	GG	GG
6	TT	TT	TT	CT	TT	CT	TT	TT	CC	CC
7	AA	AA	AA	AT	AA	AT	AA	AA	TT	TT
8	AA	AA	AA	GA	GA	GA	AA	AA	GG	GG
9	TT	TT	TT	GT	TT	GT	TT	TT	GG	GG
10	CC	CC	CT	CT	CT	CT	CC	CC	GG	GG
11	TT	CT	CT	CT	TT	TT	TT	TT	TT	TT
12	GG	GA	GA	GA	GA	GG	GG	GG	GG	GG
13	GG	GA	GA	GA	GA	GG	GG	GG	GG	GG
14	CC	CT	CT	CT	CC	CC	CC	CC	CC	CC
15	CC	CC	CT	CC	CC	TT	TT	TT	TT	TT
16	GG	AA	AA	AA	AA	GG	GG	GG	GG	GG
17	AA	AA	AA	AA	GG	AA	AA	AA	AA	AA
18	CC	CC	CC	CT	TT	CC	CC	CC	CC	CC
19	GG	GG	GG	GG	GG	AA	AA	AA	AA	AA
20	TT	TT	TT	TT	GG	GG	GG	GG	GG	GG
21	GG	GG	GT	GT	TT	TT	TT	TT	GG	GG
22	TT	TT	CT	CT	CT	CC	CC	CC	TT	TT
23	AA	AA	AA	AA	AA	CC	CC	CC	AA	AA
24	GG	GG	GG	GG	GG	GG	GG	GG	GG	GG
25	CC	CC	CT	CT	CC	TT	TT	TT	CC	CC

Graphic courtesy of NIH/David Hall

OVERVIEW

Using short- and long-haired dachshunds as examples, students learn about how a change in the nucleotide sequence affects phenotype. They predict the outcomes of crosses between short- and long-haired dachshunds.



Genotypes and Phenotypes

Traditionally, biology books have begun the section on genetics with a discussion of the experimental findings of Gregor Mendel (1822–1884). Mendel was an Austrian friar, who studied variation in plants to answer questions about heredity. He created lines of pea plants that were pure-breeding for specific traits, such as flower color (purple or white) and seed surface texture (smooth or wrinkled). He tracked the inheritance of

these traits through multiple generations of pea plants, and conducted many crosses of plants with different characteristics. Mendel concluded that hereditary information is transmitted from parents to offspring in the form of discreet “particles,” which we now refer to as genes and alleles.

Beginning with the discovery of DNA, biologists are learning that genetics is much more complex than the particulate model of inheritance proposed by Mendel. In fact, most characteristics (phenotypes) are shaped by the actions of multiple genes, rather than the “one gene—one trait” model that so often is taught to biology students. Traits that are influenced by more than one gene, and often also by behavioral and environmental factors, are referred to as complex traits. Many common human illnesses and conditions, such as cardiovascular disease, diabetes or asthma, are the result of many genes acting in concert with environmental conditions.

To identify genetic changes associated with a particular characteristic or disease, biologists survey large sections of DNA from many different individuals to find areas where changes in the sequence of bases

occurs consistently in affected individuals. Because new technologies make it possible to determine the exact order of the nucleotide bases—adenine (A), thymine (T), guanine (G), and cytosine (C)—in a segment or multiple segments of DNA, sections of the genomes of many different individuals can be compared to find changes in the DNA sequence that might be related to particular traits. These traits may include genetic changes that promote or prevent diseases. This type of survey approach was used to find the mutation responsible for long hair in dogs that students explored in the previous activity.

DNA sequence changes can be simple substitutions at a single location. Other kinds of changes include the insertion of extra bases, the deletion of sections of DNA, and the repetition of one or more sequences. Changes in the sequence of bases are called mutations, and they occur as mistakes when DNA is copied. However, mutations are not always detrimental. In fact, many



TIBETAN TERRIER

Phenotype is the physical appearance and characteristics of an individual.



Genotype is the genetic information of an individual.



mutations have no apparent effect on the organism, and in some cases, are beneficial.

As shown in the activity, “Mapping a Mutation,” changes in the DNA sequence can (but do not always) affect the proteins that are produced.

Overall, the effects of these changes might be neutral, detrimental (leading to death, disease or reduced ability to survive and reproduce) or advantageous (such as conferring disease resistance or a competitive advantage over other individuals).

MATERIALS

- Complex Traits slide set (Slides 24–26), available at <http://www.bioedonline.org/slides/classroom-slides/genetics-and-inheritance/complex-traits/>
- Computer and projector, or interactive whiteboard
- Copies of the student sheets (one set per student)

PROCEDURE

1. Remind students of the previous activity, “Mapping a Mutation.” Ask, *What caused some dogs to grow long hair rather than short hair?* [substitution of a single base pair, which changed the protein responsible for ending hair growth; the new protein is defective and does not stop growth of the hair shaft.] Next ask, *Was this mutation (or substitution) harmful, neutral or beneficial?* Give students opportunities to discuss the ways in which long hair might be helpful or detrimental to different kinds of dogs, depending on where they live or their activities.
2. Now, ask students, *Do you think we could use genetic information to predict which puppies might end up with long or short hair?* Allow students time to discuss the idea. Clarify for students the differences between phenotype and genotype (Slide 24). Genotype is an individual’s set of genes; phenotype is all of its observable characteristics. These two concepts are related: The genotype is expressed when the information encoded in the genes’ DNA is used to RNA and protein molecules. The expression of the geno-

type contributes to the individual’s observable traits, called the phenotype. Phenotype includes body characteristics, developmental patterns, biochemical properties and even behaviors. Environment (all of the external factors that influence an organism) also contributes to phenotype.

3. Prompt student thinking by asking the following questions. *What was the nucleotide at location 20 that resulted in long hair?* [T] *How many copies of the nucleotide substitution were necessary for a dog to have long hair?* [two] *Thus, what is genotype at location 20 of a dog with long hair?* [TT; tell students that when both chromosomes have the same information, the condition is called “homozygous.”]
4. Follow by asking, *Can you determine the genotype of a dog with short hair?* [In this case, the answer is no, because a short-haired dog could be homozygous for the original form of the gene that codes for short hair; or it could carry one copy of the substitution. Tell students that when an individual carries two different versions (alleles) of a gene, the condition is described as “heterozygous.”]



DACHSHUND PUPPIES

5. Project Slide 25, shortly followed by Slide 26 (for use with question 6 on the student sheet). Divide students into groups and have them work through the examples on the “Dachshunds: Predict the Puppies” student sheets. Or, work through most of the questions with the class as a group. Assign question 7 (student sheet, p. 20) as homework or as an exercise for students to conduct in small groups.

Dachshunds: Predict the Puppies



MALE PARENT: FIDO

FEMALE PARENT: FLUFFY

Take a careful look at the two parent dachshund dogs in the photo, then answer the questions below on the back of this sheet.

1. Which dog has the mutation that leads to long hair? Does the dog you identified have one or two copies of the mutation? Explain your answer.
2. Look at the other dog. Can you tell whether this dog also has the mutation for long hair? Explain your answer.
3. Which term refers to the appearance of each of the dogs; for example, the presence of long or short hair (phenotype or genotype)? Which term refers to the DNA variations that are present in each of the dogs (phenotype or genotype)?
4. Just like they use letters to refer to nucleotides (A, C, T, G), biologists also assign letters to specific characters and traits that they observe. For example, the letter “L” can stand for hair length. However, an upper-case “L” is used when only one copy of an allele enables the trait to be seen. A lower-case “l” is used when two copies of an allele are necessary for the trait to be present.

Based on this information, how would you write the possible genotype or genotypes of Fido? How would you write the possible genotype or genotypes of Fluffy?

5. If you know the genotype of each parent, is it possible to predict the genotypes *and* phenotypes (appearance) of each of the offspring? Explain your answer.

(Continued on page 20.)

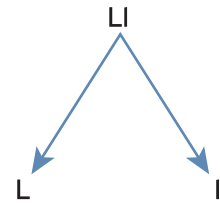
Dachshunds: Predict the Puppies



(Continued from page 19.)

- During reproduction, every offspring receives a single copy of each gene from each parent. Logically, since every offspring has two parents—in the end, each puppy once again will have two copies of each gene.

Thus, if a parent has the genotype, Ll, half of the offspring will receive an “L” version of the gene, and the other half will receive an “l” version of the gene.



This process can be represented using a simple table that allows you to plot the outcomes of any possible cross between two parents with known genotypes. The genotype of one parent is written across the top. The genotype of the other parent is written along the left side. The example below has the genetic contribution of one parent already written across the top, and the contribution of another parent along the side. It is using a hypothetical example of floppy ears (f) vs. straight ears (F).

		Straight ears (F)	
		F	F
Floppy ears (f)	f	↓ F f	
	f		

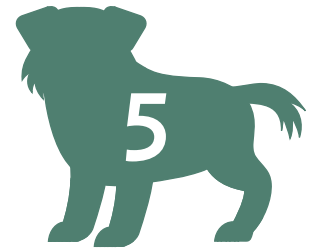
Next, fill in the boxes by copying the row and column-head letters into each square. An example with the first square is completed for you. Create a similar table and fill in the remaining squares. Each of the squares represents the genotype of a single possible offspring.

Assume that capital letter “F” refers to a fictitious gene for ear type, and signifies straight ears, while lower case “f” leads to floppy ears. When two copies of “f” are present are present, a dog will have floppy ears. What are the phenotypes of the offspring?

- Now, based on what you know about the phenotypes and genotypes of Fido and Fluffy, make one or more tables to estimate what their puppies might look like. If you do not know the genotype of one of the parents, make a separate table for each of the possible genotypes.

OVERVIEW

Students explore phenotypic differences in hair types found in the coats of different dog breeds, as they begin to learn about complex traits. Based on information provided, students also predict the genotypes of different dog breeds.



Categorizing Hair Types in Dogs

Most characteristics, such as height, body shape and disease susceptibility, in living organisms are controlled by more than one gene. Coat type in dogs is an example. Variations in three genes determine the patterns of hair length, curl and presence of “furnishing” (beard and bushy eyebrows, combined with wiry hair) that are observable in about 95% of all dog breeds. In this activity, students will categorize the coat phenotypes of eight different dog breeds, and then will connect the phenotypes to possible genotypes.

The dog breeds that are included in this activity are the Bassett Hound, Bichon Frise, Border Terrier, English Cocker Spaniel, Golden Retriever, Havanese, Irish Water Spaniel, and Kerry Blue Terrier. These breeds display the complete range and combinations of coat types: long vs. short hair, curly vs. straight hair, and presence or absence of furnishings. The ancestors of modern dogs all had coats with short, straight hair without furnishings. The other characteristics have arisen because of mutations in genes related to hair growth and development. Mutations are changes in the DNA sequence, usually as a result of mistakes when DNA is copied. If the mutation is present in the egg or sperm cell of a parent, it is passed onto the offspring. In dogs, selective breeding has consolidated and increased the frequency of many mutations that affect appearance or behavior.



In 2016, 190 dog breeds were recognized by the American Kennel Club; 199 by the Westminster Kennel Club.

Three different genes regulate hair type in dogs. Hair length (L), as described previously, can be long or short. The ancestral condition in dogs is short hair. Long-haired dogs have inherited a mutation involving the substitution of a single nucleotide in the gene responsible for terminating hair growth. Dogs with one or two copies of the mutation have long hair. Thus, dogs with the genotype “ll” and “LL” have short hair. Dogs with the genotype “ll” have long hair.

Curl (C) is governed by a change in one of the genes responsible for a structural protein in hair (keratin). The mutation again involves the substitution of a single nucleotide—this time, a T (thymine) is substituted for a C (cytosine). The substitution is believed to affect folding of the completed protein, leading to curled or wavy hair. Dogs with straight hair have two copies of the straight form of the gene (cc); dogs with wavy hair have one copy of the straight form of the gene and one copy of the curly form (Cc); dogs with curly hair are homozygous for the curly mutation (CC).

Wiry hair is an interesting characteristic in dogs. Dogs that possess hair that is coarse and bristly like wire, always also have a beard (longer hair on the chin and muzzle and bushy eyebrows). Dog experts refer to the



additional facial hair features as “furnishings.” All of these physical changes are due to the same mutation in a single gene. The gene is responsible for producing a signaling protein important for keratin development and initiation of hair growth. Importantly, in this case, one mutation in a single gene leads to multiple changes in the phenotype. The Irish terrier, shown at right, provides a good example of furnishing and wiry coat. The mutation leading to wiry hair and furnishings consists of the insertion of 167 base pairs within the signaling protein gene called *RSPO2*. This means that extra DNA was added into the existing sequence that comprised the gene. The extra section of DNA appears to change the levels and actions of the proteins produced by the gene.



TYPICAL IRISH SETTER

Only one copy of the “furnishings” (F) mutation is necessary for the characteristic to be present. A dog with the genotype “ff” will not have furnishings. However, a dog with Ff or FF will present the furnishings phenotype.

When only one copy of an allele is necessary for a trait to be present, inheritance of the trait is described as “dominant.” Furnishings is an example of a dominant trait. Dogs with only one copy of the furnishings allele (genotype of Ff) will have wiry hair and a bearded face. Conversely, absence of furnishings is a recessive trait, because two copies of the allele (ff) are necessary for furnishings to be absent.

MATERIALS

- Complex Traits slide set (slides 27–41), available at <http://www.bioedonline.org/slides/classroom-slides/genetics-and-inheritance/complex-traits/>
- Computer and projector, or interactive whiteboard
- Set of eight Dog Breed cards copied onto cardstock (see p. 25–26; one set per group)
- Copy of “Genetics of Dog Coats” (p. 27, one per student)
- Copy of “Confirmed Hair Genotypes” to be distributed after students have completed Part 2, item 6 (one per student, p. 28)

PROCEDURE

Part 1: Hair phenotypes

1. Remind students about the activity, “Genotypes and Phenotypes.” Ask, *Is short or long hair the only distinguishing characteristic of dog’s coats?* Students might mention curly vs. straight hair or coat color. Explain, *Coat color and patterns of color, for example, are governed by interactions among many different genes.* Show students Slide 27, with two different coat patterns. Mention, for example, that several different genes can be responsible for something that appears simple, such as a black coat.



GIANT SCHNAUZER

BASENJI

2. Show Slide 28 and tell students that they will

be investigating hair length and texture in eight different dog breeds. Give each group of students one set of Dog Breed cards. Direct the members of each group to discuss the different kinds of fur or hair that can be observed on the dogs. Use the term “phenotype” when referring to the different observable features of hair.

3. Next, direct the groups to sort the eight cards into different categories of fur or hair. They should not use color as a criterion for sorting.
4. After the groups have sorted their cards, allow each group to present or describe the different coat categories they used.

Part 2: Hair genotypes

1. Remind students about what they already have learned about the gene mutation that determines whether a dog has long or short hair. (If necessary, revisit Slide 24.) Discuss the other characteristics that contribute to hair type in dogs. Show Slide 29 and explain that three genes govern the hair type in most breeds of dogs. The gene for hair length is one of the three genes. Curl is affected by a gene that codes for one of the structural proteins in hair. Like the gene for hair length, a single point mutation is responsible for the curly allele. In this case, however, one inherited copy of the mutation (Cc) causes soft, wavy hair and two copies (CC) cause soft, curly hair. A dog must have two copies of the original (“ancestral”) version of the allele (cc) to have straight hair.
2. Display Slide 30 showing a photo of an Irish terrier with furnishing and wiry hair. Ask if any of the students have a dog with similar facial and coat hair. Mention that the eyebrows and beard are called “furnishings.” Tell students that the coat hair is stiff like wire. In the case of the gene for furnishing, extra DNA (167 base pairs) has been inserted into the original gene. The protein produced by the gene is involved in switching on

other genes, and the additional DNA changes how that protein regulates hair growth. Mention that this is an example of how a single gene can have effects in many different parts of the body.

3. Give each group of students the sheet entitled “Genetics of Dog Coats” (Slide 31). Tell students that they will decide on the phenotype and genotype of each dog, based on what they have learned about the genetics of hair type.
4. Display Slide 32. Point out that photos of a dog’s coat may be misleading because of breed standards in dog competitions.



The Bichon frise on the left has curly hair that looks short. On the right is a Bichon Frise with its hair combed out, which reveals the coat’s length.

5. Project Slide 33 showing the Bichon Frise by itself. Tell students, *Let’s figure out what the genotype of the dog must be, based on the traits that we have observed and recorded.*
 - *Since the Bichon has long hair, which combination of alleles is possible? [“ll” is the only possible genotype.]*
 - *We determined that the hair is curly. What genotypes are possible? [Since the Bichon is clearly “curly,” and not wavy or straight, the genotype is CC].*
 - *Since the dog has furnishing, what are the*



possible genotypes? [It is not possible to know if the individual pictured is homozygous, FF, or heterozygous, Ff. However, since the trait appears consistently within members of the breed, it is reasonable to assume that most individuals of this breed are homozygous for the furnishings allele, FF].

6. Let each group work through the remaining dog breeds. (Slides 33–40 contain enlarged images all eight dogs for use as needed.) Tell students to determine the phenotypes of all the dogs, before proceeding to the genotypes. If you have Internet access in your classroom, students may want to access additional photographs of the different breeds to look for characteristics, such as furnishings.
7. Have the groups report on their conclusions regarding the genotype and phenotypes of each breed, by asking each group to present the findings for a different breed. Or, have each group submit a written explanation of the decisions they made regarding each breed.
8. Distribute the student sheet, “Confirmed Hair Genotypes,” which summarizes typical genotypes for each breed (Slide 41) for a discussion with the class. Students may notice that in most cases, the breeds are homozygous for dominant traits. Based on phenotype, it is not possible to know if an individual has a single or both alleles

for a trait that shows a dominant pattern of inheritance. However, because dog breeds have been selected over generations to “breed true,” most of the variant alleles have been eliminated over time. In other words, dogs with undesirable characteristics themselves (or whose offspring had undesirable characteristics) were not bred to produce additional offspring.

EXTENSIONS

- If students have questions about dog coat color, access one of the commercial dog testing websites to find a summary of the many different genes (and genetic tests) that are involved in determining color and patterns. Simply search, “dog coat color genetic testing.”
- Much of the research on the Dog Genome has been led by Dr. Elaine Ostrander of the National Human Genome Research Institute of the National Institutes of Health. The following video summarizes much of the work to date on the dog genome, including examples used in this set of activities. In addition, she describes the relevance of studying dog genetics to understanding human diseases.

<https://www.youtube.com/watch?v=sxtX1pfSUec>

- More information about the Dog Genome project can be found at the URL below.

http://research.nhgri.nih.gov/dog_genome/

Dog Breed Cards



1. Bichon Frise



2. Border Terrier



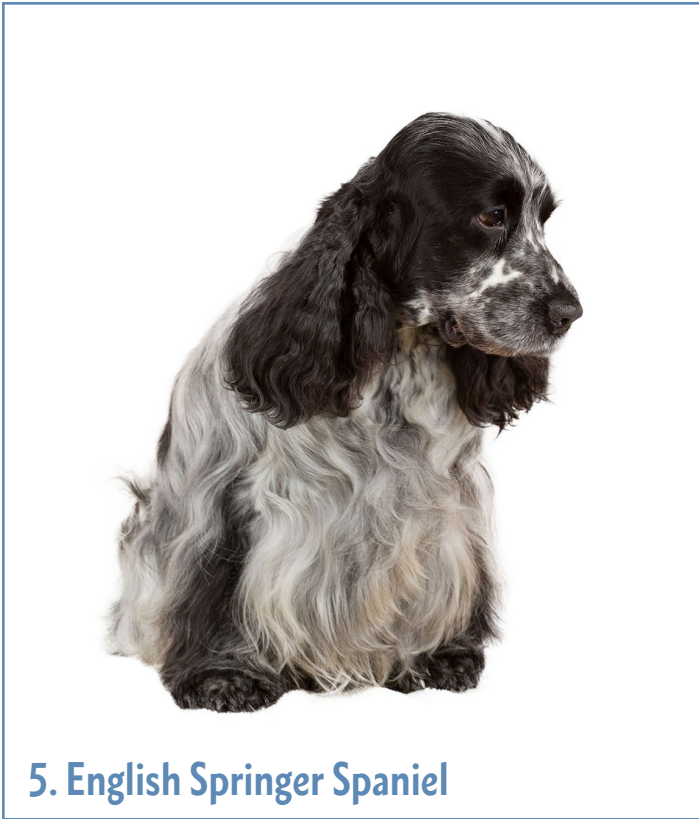
3. Havanese



4. Basset Hound

Basset Hound © Bonzami Emmanuelle. Bichon Frise © Violel Sima. Border Terrier © Eric Iselee. Havanese © Mdorothy. Licensed for use.

Dog Breed Cards (cont.)



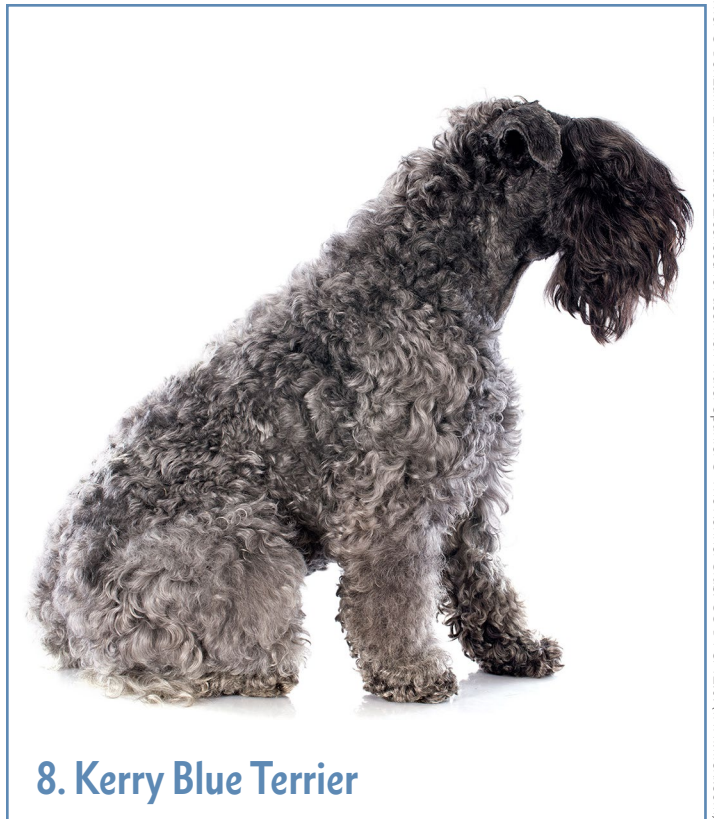
5. English Springer Spaniel



6. Irish Water Spaniel



7. Golden Retriever



8. Kerry Blue Terrier

English Cocker Spaniel © Zdenek Malý, Golden Retriever © Eric Isselee, Kerry Blue Terrier © Bonzani Emmanuelle, Licensed for use, Irish Water Spaniel © The Kennel Club CC-BY-SA 2.0 (www.flickr.com)

Genetics of Dog Coats



DOG BREED	PHENOTYPE			GENOTYPE		
	Describe the hair type using the phenotype traits listed below.			Fill in the genotype that corresponds to each phenotype you identified.		
	Short or Long	Curly, Wavy, or Straight	With or Without Furnishings	LL = short LI = short II = long	CC = curly Cc = wavy cc = straight	FF = furnishings Ff = furnishings ff = no furnishings
1.						
2.						
3.						
4.						
5.						
6.						
7.						
8.						

Confirmed Hair Genotypes




1.



Bichon Frise
II, CC, FF

2.



Border Terrier
LL, cc, FF

3.



Havanese
II, cc, FF

4.



Basset Hound
LL, cc, ff

5.



English Cocker Spaniel
II, cc, ff

6.



Irish Water Spaniel
II, CC, ff

7.



Golden Retriever
II, cc, ff

8.



Kerry Blue Terrier
II or II, CC or Cc, FF

Basset Hound and Kerry Blue Terrier © Bonzani Emmanuelle; Bichon Frise © Vorel Sima; Border Terrier and Golden Retriever © Eric Isselee; English Cocker Spaniel © Zdenek Malý; Havanese © Mdorothy; Licensed for use: Irish Water Spaniel © The Kennel Club CC-BY-SA 2.0 (www.flickr.com)

OVERVIEW

Students learn about three examples where genetic mutations are related both to desirable characteristics and to harmful effects in certain dog breeds. Students place themselves in the roles of different individuals involved with dog breeding, health and care, and report on the relevance of canine genetic testing for each of the roles.



Genetic Testing and Designer Dogs

More than 1,000 tests have been developed to look for desirable or harmful gene alleles in dogs. Once a researcher has found a particular gene mutation or biochemical marker for a mutation, university-based or commercial laboratories develop tests for different versions of the gene. In the case of coat color, breeders use genetic testing to produce offspring with certain coat colors or patterns of markings. Many canine genetic tests screen for alleles that cause diseases, either immediately or as a dog becomes older. In some cases, genetic tests identify alleles that convey increased risk of developing a disease—depending on diet and other environmental factors. Of course, these technologies and approaches are based on the growing range of genetic tests available for humans.



WHIPPET

In this activity, students learn about three mutations that can be harmful in dogs. The first mutation is found in whippets and other breeds of dogs. The mutation affects a muscle protein (myostatin), such that dogs with one copy of the mutated allele are able to run faster (genotype Bb). Dogs with two copies of the mutation (BB), however, have an unusual body shape, bulky muscles, an overbite, shorter legs and thicker tails. This is another example of a single gene influencing many physical traits—because of its roles in different body systems. Bully whippets are not valuable as racing or as show dogs. Thus, one copy of the mutated allele produces dogs with an advantage in racing. However, dogs with two copies are undesirable as racing or show dogs.



SHETLAND SHEEPDOG

The second example focuses on the dappled or mottled coat pattern called merle, which is present in many dog breeds, including Shetland Sheepdogs. The allele that produces the desirable merle color markings is a version of a gene important for development of several systems during growth of the embryo. One copy of the merle allele leads to the observable color pattern, but few negative effects. Two copies, however, cause a variety of health problems, including vision and hearing problems, because these sensory systems do not develop properly. This situation creates a dilemma for breeders. If two merle dogs (genotype Mm) are bred, approximately 25% of the offspring will have two versions of the merle allele (MM) and will have hearing or eye defects. For this reason, many breeders insist on breeding a dog with a Merle coat (Mm) only to dogs with solid coats (mm). In this case, only half of the offspring will have the desirable merle markings—but all of the puppies will be healthy.



DALMATION

The third example involves the popular Dalmatian. Because of inbreeding over



many generations to develop a uniform set of physical characteristics—a disease trait also was incorporated into 100% of the bloodlines. All Dalmatians are homozygous for a disease mutation that predisposes dogs to develop painful stones in their bladders or kidneys (similar to human diseases). The disease, which is related to uric acid metabolism, can be managed through diet or medications, but sometimes surgery is necessary to remove the stones. In other words, all Dalmatians have two copies of the kidney stone (hyperuricemia) allele, which is recessive and involves a single nucleotide substitution. A breeding program was created to introduce the normal allele back into the breed. However, this action has generated considerable controversy among breeders, owners and Kennel Clubs, which register purebred dogs, and many organizations do not recognize the disease-free line of dogs as “pure” Dalmatians.

There are many perspectives on how genetic information should be used to manage disease risk, breed “better” dogs for competition or as companions, or even to generate a profit. This activity enables students to explore these questions as they place themselves in different roles related to dog health, breeding and care.

MATERIALS

- Complex Traits slide set (slides 42–45), available at <http://www.bioedonline.org/slides/classroom-slides/genetics-and-inheritance/complex-traits/>
- Computer and projector, or interactive whiteboard
- Set of “Job or Hobby Role Cards” copied onto cardstock (see p. 34; one card per student group)
- Copies of the student sheets (one set per student)
- Access to the Internet

PROCEDURE

1. Present Slide 42 and begin a class discussion about healthy and unhealthy mutations that can occur naturally in dogs, but some of which are caused by breeding practices.
2. Display Slide 43, which shows a purebred

whippet dog, a genetically modified whippet, and a “bully” whippet. Explain to students that bully whippets have a mutation in the gene for a muscle protein (myostatin). Dogs with one copy of the mutation run faster. Dogs with two copies of the mutation have an unusual body shape, bulky muscles, an overbite, shorter legs and thicker tails. These dogs are not valuable as racing or as show dogs. Thus, one copy of the mutated allele produces dogs with an advantage in racing. However, dogs with two copies are undesirable as racing or show dogs.

3. Follow with Slide 44, which illustrates the merle pattern of color distribution that is typical of Shetland sheepdogs and several other dog breeds. Explain that the allele that produces desirable merle color markings is a version of a gene important for development of several systems during growth of the embryo. One copy of the merle allele leads to the observable color pattern, but few negative effects. Two copies, however, cause a variety of health problems, including vision and hearing problems.
4. Display Slide 45, which describes a disease mutation in Dalmatians and other breeds, such as Bulldogs. The mutation predisposes dogs to developing painful stones in their bladders or kidneys, and is related to similar human diseases. The disease can be managed through diet or medications, but sometimes surgery is necessary to remove the stones. Because of selective breeding for desirable characteristics, the disease trait also was incorporated into 100% of Dalmatians. In other words, all Dalmatians have two copies (homozygous) of the kidney stone (hyperurcosuria) allele, which is recessive. A breeding program was created to introduce the normal allele back into the breed. However, this action has generated considerable controversy among breeders, owners and kennel clubs, which register purebred dogs, and many organizations do not recognize the dogs without

the disease allele as “pure” Dalmatians.

5. Students may have many questions about the implications of the genetic conditions shown in the slides. Tell students, *Gene mutations are common in all living organisms. Most of these mutations do not affect the health or appearance of the individual. In some cases, however, mutations confer a benefit—in other cases, they cause a deformity or increase the likelihood that the individual will develop an illness.*
6. Next, explain to students that they are going to learn more about how genome science is advancing the understanding of diseases, but also is creating new kinds of questions. More than 1,000 genetic tests are available for use with dogs—these tests identify gene alleles related to color, size, and disease traits, among many others, including the traits we have just seen. The availability of genetic testing provides opportunities to improve health, but also raises many ethical questions. We will examine these questions from different points of view.
7. Project Slide 46. Students will work in teams to investigate and play the roles of different people involved with dog care, health and breeding. These different kinds of roles are described on the Role cards. Each group of students should receive one card, which will refer to a specific role (see student sheet).
8. Each group will consider two questions related to the assigned role.
 - a) What does a person with this kind of job or hobby do?
 - b) What would be my viewpoint about possible uses of canine genetic testing information?
OR, How would I use genetic testing information?

Students should consider different aspects of

each person’s role. For example, does he or she need to earn money from the dog activities? Does profit overrule the importance of producing healthy dogs? Is it important to keep breeds genetically “pure?”

9. Have students conduct their own research to answer the questions. Be sure to have Internet-safe browsing software available for students if they will be working in class. Some places to begin include the following Web sites.

American Kennel Club Breeder

http://www.akc.org/enewsletter/akc_breeder/2011/summer/genetics.cfm

American Canine Association

<http://acacanines.com/>

University of California Davis Veterinary Genetics Laboratory

<http://www.vgl.ucdavis.edu/index.php>

American Kennel Club Canine Health Foundation. Gene for Merle Color Pattern Discovered

<http://www.akcchf.org/research/success-stories/gene-for-merle-color-pattern.html>

As Breeders Test DNA, Dogs Become Guinea Pigs

<http://www.nytimes.com/2007/06/12/science/12dog.html?pagewanted=all&r=0>

10. Have each group present its findings as a poster, oral presentation or slide show. After each group has made its presentation, allow the rest the class to ask questions. Students will discover that access to genetic information raises new ethical and moral questions, which do not have simple answers. Encourage students to discuss different viewpoints.



Designer Dogs: Bully Whippets



PUREBRED WHIPPET (bb)

MIXED ALLELES (Bb)

BULLY WHIPPET (BB)

“Bully” whippets have two copies of a gene mutation (BB) that causes bulky muscles and other changes in appearance. The mutation affects a muscle protein (myostatin), such that dogs with only one copy of the mutation (Bb) have greater muscle mass and are able to run faster than other whippets. Thus, one copy of the mutated allele produces dogs with an advantage in dog racing.

However, dogs with two copies of the mutation (BB), have significantly more muscle mass and are stronger than normal, with an unusual body shape, an overbite, shorter legs and thicker tails. Bully whippets are undesirable as racing or show dogs, and can have severe health problems

Mosher, D., Quignon, P., Bustamante, C., Sutter, N., Mellersh, C., Parker, H., et al. (2007) A Mutation in the Myostatin Gene Increases Muscle Mass and Enhances Racing Performance in Heterozygote Dogs. *PLoS Genet* 3(5): e79. doi:10.1371/journal.pgen.0030079. Public domain. <http://journals.plos.org/plosgenetics/article?id=info:doi/10.1371/journal.pgen.0030079>

Designer Dogs: A Merle Coat



PUREBRED SHETLAND SHEEPDOG (mm)



MIXED ALLELES RESULT IN MERLE PATTERN (Mm)



TWO MUTATIONS WITH MAJOR HEALTH ISSUES (MM)

A dappled or merle coat is considered desirable in many dog breeds. Merle coat pattern is controlled by an allele that also is important for normal eye and ear development.

The Shetland sheepdog shown at the top left is purebred, with no mutations (mm). The dog shown above has mixed alleles (Mm) which results in a desired merle pattern, with few negative health effects.

However, the sheepdog shown at the bottom left has two mutations of the merle allele (MM). Dogs with this mutation may be blind, deaf, or both, or have other health issues.

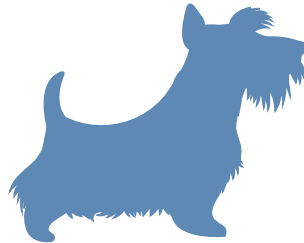
Job or Hobby Role Cars



**Breeder of
Racing Dogs**



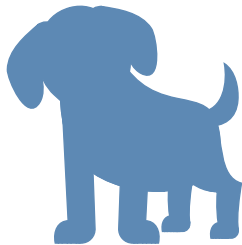
**Breeder of
Show Dogs**



**Canine Genetics
Testing Lab Owner**



**Kennel Club
Representative**



**Pet
Owner**



**Researcher of
Canine Genetics**



Veterinarian

