

# Cat Genetics Activity

This activity is adapted from Christensen, A. C. (2000). Cats as an aid to teaching genetics. *Genetics*, 155, 999-1004.

In cats coat colour, pattern, and length are controlled by several genes. In this lab you will learn about several of the different genes and then make observations of local cats. You will use your observations to predict potential offspring. Finally, you'll analyze some population statistics.

## Cat coat genetics background



### Hair length

Fur length is controlled by a single gene with two alleles. The two alleles are long hair and short hair. Short hair (L) is dominant to long hair (l).

Photo from @Cat\_Cafe\_on\_Whyte on Instagram

### Coat colour



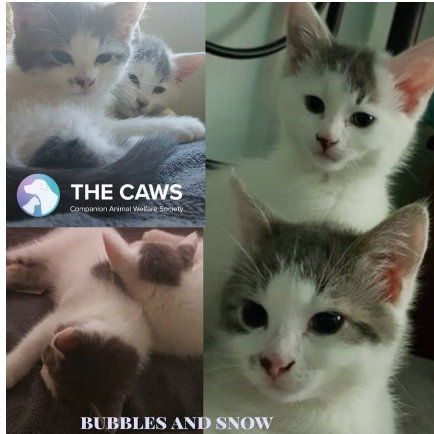
### White or non-white

The allele for white is **completely dominant** to non-white. This means that a cat that has the genotypes WW or Ww will be completely white. This will mask the effects of all of the other coat colour and pattern genes. If you find a completely white cat you can fill out W\_ in the table and that's it. Cats with the genotype ww will have at least some non-white fur. As kittens, dominant white cats may have small pigmented spots on their forehead but these tend to fade by adulthood.

Photo from @scars\_care on Instagram

## White spotting (Piebald spotting)

**Incomplete dominance** is when the heterozygous genotype results in an intermediate phenotype between the two homozygous genotypes.



**Variable expressivity** refers to how much of a particular phenotype is expressed by individuals with a particular genotype. In humans, this can be seen in some diseases where different individuals may experience differences in the severity of symptoms, age of onset, or other characteristics. White spotting, which is the presence of some white fur in cats, demonstrates both incomplete dominance and variable expressivity. (Remember if the cat is totally white it has the genotype  $W\_$  and you can't determine any of the other genes.)

Photo from @cawsab on Instagram

We are going to use the following system to determine the genotype at the White spotting locus:

$S_1S_1$  - more than 50% white

$S_1S_2$  - less than 50% white

$S_2S_2$  - no white fur



## Dilute modifier

Another gene, the dilute modifier gene will affect the intensity of the colour of the fur. The dominant allele ( $D\_$ ) results in full colour expression (Black or orange) While the recessive genotype ( $dd$ ) will dilute the colour so that black becomes gray and orange becomes cream.

Photo by Tai Munro



## Orange and not-orange

Orange hair is a **sex-linked trait**. The gene is on the X chromosome.  $X^O$  codes for orange and  $X^B$  for not orange. An orange cat will be  $X^O X^O$  (female) or  $X^O Y$  (male).

Photo by @cat\_cafe\_on\_whyte on Instagram

A non-orange cat will be  $X^B X^B$  (female) or  $X^B Y$  (male).



A female cat can also be heterozygous ( $X^O X^B$ ) and show both orange and another colour of fur.

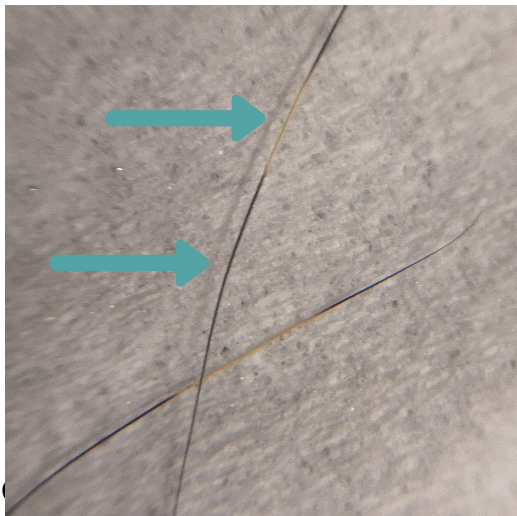
For our purposes these are co-dominant.

Photo by @ehs\_adoptable\_animals on Instagram

## Agouti and tabby

The agouti allele, A, results in single hairs having variable colour along the hair shaft.

Photo by Tai Munro



The non-agouti allele, a, results in each hair being one single colour. In cats, the expression of the agouti allele is affected by the presence of tabby alleles at the tabby loci. This is called epistasis. Epistasis is when two or more genes affect a single phenotype and the effects don't just add together. In the case of the tabby alleles they affect when the agouti gene is expressed. There are multiple tabby alleles. For our purposes, we will use the presence of a tabby pattern to indicate the presence of the agouti gene. We won't be going into the different tabby alleles. So, a tabby



pattern can be recorded as  $A\_$  for agouti. No tabby pattern would be  $aa$  for non-agouti.

Please note that we are not going into the genetics of cats that are more likely to have been bred such as sphinx, Siamese, or Burmese.

## Putting it all together

Let's do a sample cat



Photo by Tai Munro

This cat is female.

Start with hair length. What are the two possible genotypes for this cat?  $LL$  or  $Ll$

Is the cat completely white? Then what is the genotype?  $ww$

Does it have more than 50% white fur, less than 50% white fur, or no white fur? Then what is the genotype?  $S_1S_2$

Does it have intense or dilute colours? Then what is the genotype?  $dd$

Does it have orange, non-orange, or both? Then what is the genotype?  $X^O X^B$

Does the cat have a tabby pattern? Then what are the possible genotypes for the agouti allele?  $AA$  or  $Aa$

# Activity 1: Genotyping cats

Use the following table to identify the different genotypes of at least three cats in the area you live. You can use your own cat, one from a friend or family member, or check out a local rescue organization. Some Edmonton area rescues that you could try are:

- [Edmonton Humane Society](#)
- [Arts Senior Animal Rescue](#)
- [Zoe's Animal Rescue Society](#)

Phenotypic guide to genotypes	Cat #1	Cat #2	Cat #3	Cat #4	Cat #5
Cat name					
Sex: m, f, unknown (don't guess)					
Long hair (H), short hair (L-)					
Dominant white W <sub>1</sub> , otherwise ww. If W <sub>1</sub> all other alleles are masked so leave the rest of the column blank					
White (Piebald) spotting: More than half white S <sub>1</sub> S <sub>1</sub> ; Less than half white S <sub>1</sub> S <sub>2</sub> ; No white S <sub>2</sub> S <sub>2</sub>					
Dilute: if black is changed to gray or orange is changed to light yellow or cream write dd, otherwise D <sub>1</sub>					
Orange: Male completely orange: X <sup>O</sup> Y Female completely orange: X <sup>O</sup> X <sup>O</sup> Calico (orange and other pigmented fur) female: X <sup>O</sup> X <sup>B</sup> Male with no orange fur X <sup>B</sup> Y Female with no orange fur X <sup>B</sup> X <sup>B</sup> Don't guess if you don't know the sex, just leave blank					
Agouti fur (indicated by tabby pattern): if present A <sub>1</sub> , if absent (each hair is a solid colour, aa.					

## Activity 2: Mendelian Genetics

For the next section, you need to know the complete genotypes for each of your cats. Since we can't tell what the genotype is for any of the individuals with the dominant phenotype we will make the arbitrary decision that any individual with the dominant phenotype has the heterozygous genotype. Again, remember that we can't actually know this, but it makes it possible for us to do some crosses.

1. Choose one of the Mendelian traits (hair length, all white, dilute).  
Perform a cross between two of the cats you identified. What is the probability that the cat will show the recessive genotype?
2. If you have an cat with the non-dilute phenotype, how could you determine the genotype? Illustrate your answer with a Punnett square.
3. Assuming that all of the traits are located on different chromosomes, what would the phenotypes of the offspring be if you crossed an individual that was LIWw with one of the cats you identified?

## Activity 3: Non-Mendelian Genetics

1. Look at the orange trait for one of your cats. If the cat is male, pair it with a female with the genotype XOXB. If the cat is female, pair it with a male that is XOY.  
Show the resulting cross using a Punnett Square. What is the probability that a male offspring would be black? What about a female offspring?
2. Look at the white-spotting trait for two of the cats you identified. What is the probability of having an offspring with more than 50% white from a cross between your two cats?
3. There are three different alleles that control for the tabby pattern in cats. What is this an example of?

## Activity 4: Hardy-Weinberg

Based on all the cats that are submitted, you can determine the number of individuals in the population that show the different traits.

Hair length and dilute colours are probably the easiest ones because these will be easier to track in the population. You can also calculate frequencies for White-spotting. Can you guess what  $2pq$  in the equation would be?

If you have any white cats you could also calculate the white allele and genotype frequencies. How would you be able to tell if this population of cats was in equilibrium or not?