

Name



Breeding Bunnies

Background Information: Sometimes the frequency of alleles changes in a population over a period of time. This means that how often you will see a particular trait will change also.

Breeders of rabbits have long been familiar with a variety of genetic traits that affect the ability of rabbits to survive in the wild, as well as in breeding populations. One such trait is the trait for furless rabbits (naked bunnies). This trait was first discovered in England by W.E. Castle in 1933. The furless rabbit is rarely found in the wild because the cold English winters are too harsh for the rabbits; if the rabbits cannot survive the cold, they cannot survive to reproduce.

Vocabulary to know:

Allele: One of the alternative forms of a gene. For example, if a gene determines the seed color of peas, one allele of that gene may produce green seeds and another allele produce yellow seeds. In a diploid cell there are usually two alleles of any one gene (one from each parent).

Dominant: Describes a trait that covers over, or dominates, another form of that trait. An allele that is almost always expressed, even if only one copy is present.

Recessive: describes a trait that is covered over, or dominated, by another form of that trait and seems to disappear. An allele that is expressed only when two copies are present.

Homozygous: Having identical alleles for a particular trait.

Heterozygous: Having two different alleles for a particular trait.

Genotype: The set of two genes possessed by an individual at a given spot on a chromosome.

Gene frequency: The frequency in the population of a particular gene relative to other genes. . Expressed as a proportion (between 0 and 1) or percentage (between 0 and 100 percent).

Purpose: To model the changes in gene frequency over several generations.

Materials:

50 orange beads	50 purple beads	1 paper bag
3 cups		

Procedure:

Note: In this lab, the dominant allele for normal fur is represented by F(purple bead) and the recessive allele for no fur is represented by f (orange bead). Bunnies that inherit two F alleles or one F and one f allele have fur, while bunnies that inherit two fs have no fur.

- 1. Label one cup *FF* for the homozygous dominant genotype.
- 2. Label a second dish *Ff* for the heterozygous condition.
- 3. Label the third dish *ff* for those rabbits with the homozygous recessive genotype.
- 4. Place the 50 orange and 50 purple beans (alleles) in the container and shake up (mate) the rabbits.
- 5. Without looking at the beans, select two at a time, and record the results on the data form next to "Generation 1." For instance, if you draw one purple and one orange bead, place a mark in the chart under "Number of *Ff* individuals." Continue drawing pairs of beads and recording the results in your chart until all beans have been selected and sorted. Place the "rabbits" into the appropriate dish: *FF, Ff,* or *ff.* (Please note that the total number of individuals will be half the total number of beans because each rabbit requires two alleles.)
- 6. The *ff* bunnies are born furless. The cold weather kills them before they reach reproductive age, so they can't pass on their genes. Place the beads from the *ff* container aside before beginning the next round.
- 7. Count the F and f alleles (beads) that were placed in each of the "furred rabbit" dishes in the first round and record the number in the chart in the columns labeled "Number of F Alleles" and "Number of f Alleles." (This time you are really counting each bead, but don't count the alleles of the *ff* bunnies because they are dead.) Total the number of F alleles and f alleles for the first generation and record this number in the column labeled "Total Number of Alleles."
- 8. Place the alleles of the surviving rabbits (which have grown, survived and reached reproductive age) back into the container and mate them again to get the next generation.
- 9. Repeat steps five through nine to obtain generations two through ten.
- 10. Determine the gene frequency of *F* and *f* for each generation and record them in the chart in the columns labeled "Gene Frequency *F*" and "Gene Frequency *f*." To find the gene frequency of *F*, divide the number of *F* by the total, and to find the gene frequency of *f*, divide the number of *f* by the total. Express results in decimal form. The sum of the frequency of *F* and *f* should equal one for each generation.

Data:

Generation	# of FF individuals	# of F <i>f</i> individuals	# of <i>ff</i> individuals	# of F alleles	# of <i>f</i> alleles	Total # of alleles	Gene frequency of F	Gene frequency of f	
1									
2									
3									
4									
5									
6									
7									
8									
9									
10									

What is the best type of graph to show change?

What is the independent variable in this investigation?

What is the dependent variable in this investigation?

Graph your data. Remember TAILS and DRY MIX.

Conclusions:

1. Compare the number of alleles for the dominant characteristic with the number of alleles for the recessive characteristic.

2. Compare the frequencies of the dominant allele to the frequencies of the recessive allele.

3. In a real rabbit habitat new animals often come into the habitat (immigrate), and others leave the area (emigrate). How might emigration and immigration affect the gene frequency of F and f in this population of rabbits? How might you simulate this effect if you were to repeat this activity?

4. How do your results compare with the class data? If significantly different, why are they different?

5. What are some limitations of this type of model?