

## Lab: Breeding Bunnies

In this activity, you will examine natural selection in a small population of wild rabbits. Evolution, on a genetic level, is a change in the frequency of alleles in a population over a period of time. Breeders of rabbits have long been familiar with a variety of genetic traits that affect the survivability of rabbits 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 a definite selective force against it.

### Learning Goals:

1. Students observe the impact that genetics has on the evolution of a population of organisms.
2. Students observe the influence that the environment has on organisms that are selected

**Key Vocabulary Terms:** dominant, recessive, evolution, allele frequency, genotypic frequency, homozygous recessive, homozygous dominant, heterozygous dominant, natural selection, Hardy-Weinberg equilibrium, mutation, random mating, population size, allele, emigration, immigration, generation

**Textbook Reference:** 14.8-14.9

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

### Materials:

- 50 purple beads
- 50 black beads
- 1 container
- 3 cups labeled  $FF$ ,  $Ff$ ,  $ff$
- 1 plastic bag

### Procedure Part I:

1. **Create a hypothesis** to address the following question: How does natural selection affect gene frequency over several generations?
2. Given the  $F$  and  $f$  alleles in bunnies, **state your prediction** of what would happen to the frequency of  $F$  alleles and  $f$  alleles in the population of rabbits after 10 generations, where  $ff$  bunnies are selected against (do not survive).
3. The purple beads represent the allele for fur, and the black beads represent the allele for no fur. The container represents the English countryside, where the rabbits randomly mate.
4. Label one dish  $FF$  for the homozygous dominant genotype. Label a second dish  $Ff$  for the heterozygous condition. Label the third dish  $ff$  for those rabbits with the homozygous recessive genotype.
5. Place the 50 purple and 50 black beads (alleles) in the container and shake up (mate) the rabbits. (Please note that these frequencies have been chosen arbitrarily for this activity.)
6. Without looking at the beads, 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 black bead, place a mark in the chart (see Table 1 at end of lab) under "Number of  $Ff$  individuals." Continue drawing pairs of beads and recording the results in your chart until all beads 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 beads because each rabbit requires two alleles.)
7. 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 in the plastic bag before beginning the next generation.

8. Count the  $F$  and  $f$  alleles (beads) that were placed in each of the "furred rabbit" dishes in the first generation 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."
9. 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.
10. Repeat steps five through nine to obtain generations two through ten. If working as a team, make sure everyone in your group has a chance to either select the beads or record the results.
11. 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.
12. **Graph your frequencies.** Prepare a graph with the horizontal axis as the generation and the vertical axis as the frequency in decimals. Plot all frequencies on one graph. Use a solid line for  $F$  and a dashed line for  $f$ . Plot the class totals.

**Discussion Questions:** (*write out questions and answers*)

1. Based on your lab data, is your hypothesis supported or not supported? Explain citing data from the simulation.
2. How do the number of alleles for the dominant characteristic compare with the number of alleles for the recessive characteristic?
3. What are the frequencies of the dominant and recessive alleles and how do they compare to one another?
4. In a natural environment, how might emigration and immigration affect the gene frequency of  $F$  and  $f$  in this population of rabbits? Make sure to identify what would happen in a natural population with regards to emigration and immigration.
5. What are the five conditions necessary for Hardy-Weinberg?
6. How does this simulation relate to Hardy-Weinberg?

**Table 1:**

Generation	# $FF$ Individuals	# $Ff$ Individuals	# of $ff$ Individuals	# $F$ Alleles	# $f$ Alleles	Gene Frequency of $F$	Gene Frequency of $f$
0	---	---	---	50	50	0.50	0.50
1							
2							
3							
4							
5							
6							
7							
8							
9							
10							