Bean Bunny Evolution
Modeling Gene Frequency Change (Evolution) in a Population by Natural Selection

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 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.

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 (*FF* or *Ff*), while bunnies that inherit two *f* alleles have no fur (*ff*).

PURPOSE
In this activity you will model evolution by natural selection of the gene frequency of two alleles in a population of organisms. You will also calculate the gene frequency of the alleles for each generation and then graph the frequency of the two alleles over 10 generations.

MATERIALS

Each lab group will need the following:

bag, brown paper, small
50 beans, individual red
50 beans, individual white
marker, Vis-à-vis®
3 Petri dishes

PROCEDURE

1. Working with a partner, read the following problem question for today's lab:

   How does natural selection affect gene frequency over several generations?

2. From your previous knowledge about natural selection, evolution and genetics, answer the problem question on your student answer page in the space marked "Hypothesis." State your hypothesis in an "If…then…" format. Include your predictions regarding how you think natural selection will affect the gene frequency in a population. State what you would predict about the frequency of *F* alleles and *f* alleles in the population of rabbits after 10 generations, where *ff* bunnies are selected against and do not survive.

3. The red beans represent the *F* allele for fur, and the white beans represent the *f* allele for no fur. The paper bag represents the English countryside, where the rabbits randomly mate.

4. Using the overhead marking pen, label one Petri dish *FF* for the homozygous dominant genotype. Label a second Petri dish *Ff* for the heterozygous condition. Label the third Petri *ff* for those rabbits with the homozygous recessive genotype.

5. Place the 50 red and 50 white beans (alleles) in the paper bag and shake up (mate) the rabbits. (Please note that these frequencies have been chosen arbitrarily for this activity.)

6. Without looking at the beans, select two at a time; place the "rabbit," or bean pair, into the appropriate dish: *FF*, *Ff*, or *ff*. For example, if you draw out one white bean and one read bean place both beans into the *Ff* dish. Continue drawing out pairs until all beans have been placed in the appropriate dish. To determine the number of individual rabbits produced for each phenotype count the total number of beans in the appropriate Petri dish and divide this number by two since an individual is represented by a pair of beans. Record your results in the data table.

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 beans from the *ff* container aside before beginning the next round. You will not count these beans in the "Number of *f* Alleles" column.

8. Count the *F* and *f* alleles (beans) that were placed in each of the "furred rabbit" (*FF* and *Ff*) dishes in the first round and record the number in the data table under the columns labeled "Number of *F* Alleles" and "Number of *f* Alleles." 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 (*FF* and *Ff* dishes) back into the container and mate them again to get the next generation.

10. Repeat steps six through nine to obtain generations two through ten. Make sure to take turns so that each partner has a chance to select the beans and 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 number of alleles, and to find the gene frequency of *f*, divide the number of *f* by the total number of alleles. Express your results in decimal form. The sum of the frequency of *F* and *f* should equal one for each generation.

12. If there is time, your teacher may have you record your group's frequencies on the board so your classmates can see them.

13. Complete the conclusion questions on your student answer page.

14. Graph your frequencies of the *F* allele and the *f* allele on the graph paper provided. Prepare a line graph with the horizontal *x*-axis as the generation number and the vertical *y*-axis as the frequency in decimals. Plot all frequencies on one graph. Use a solid line for *F* and a dashed line for *f*.

15. If your teacher requests it, plot the class totals on the same graph. Use a different color for the lines representing the class data and make a legend illustrating which colors represent your individual data and which ones represent the class data.

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HYPOTHESIS

DATA TABLE

Generation	Number of *FF* Bunnies	Number of *Ff* Bunnies	Number of *ff* Bunnies	Number of *F* Alleles	Number of *f* Alleles	Total Number of Alleles	Gene Frequency of *F*	Gene Frequency of *f*
1								
2								
3								
4								
5								
6								
7								
8								
9								
10								

DATA ANALYSIS

CONCLUSION QUESTIONS

1. Based on your lab data, do you need to modify your hypothesis? Explain.

2. What was the original gene frequency of the *F* and the *f* alleles before selection occurred?

3. How did the gene frequency of the *F* and *f* alleles change by the 10th generation?

4. How do you explain that both alleles, *F* and *f*, changed in frequency over time in the lab?

5. 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?

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

7. How is this simulation an example of evolution by natural selection?

8. In nature, how is it that lethal alleles, like furlessness, are still passed along through the generations and not completely selected out of the population?