Breeding Bunnies Lab

INTRODUCTION

In this activity, you will examine natural selection in a small population of wild rabbits. Evolution is a change in the frequency of alleles in a population over 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. This trait was discovered in England in 1933. The furless rabbit is rarely found because the cold English winters are a selective force against it.

Note: *FF/Ff = fur and ff = no fur*

The black beans represent the allele for fur (F), and the white beans represent the allele for no fur (f). The bag represents the English countryside, where the rabbits randomly mate.

HYPOTHESIS

Hypothesis 1: How does natural selection affect gene frequency over several generations?

Hypothesis 2: 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 (do not survive).

MATERIALS

1 paper bag with 50 red beans and 50 white beans   3 or 4 dishes/Dixie Cups

PROCEDURE

1. Label the dishes/cups: **FF** (homozygous dominant), **Ff** (heterozygous), and **ff** (homozygous recessive)
2. COUNT and place 50 black and 50 white beans (alleles) in a paper bag and shake up.
3. Without looking, select two beans and place in matching labeled cup from #1. Record the results on the data table next to "Generation 1."
4. Continue drawing pairs of beans and recording the results until all beans have been selected and sorted.
5. Place the beans from the *ff* container into the "dead bunny" dish before beginning the next round.
6. Count the *F* and *f* alleles (beans) that were placed in the *FF/Ff* dishes in the first round and record the number in the columns labeled "Number of *F* Alleles" and "Number of *f* Alleles." (You are really counting each bean).
   #### ****Don't count the alleles of the** ff **bunnies *because they are <u>dead.</u>* ****
7. 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** back into the container and shake them up.
9. Repeat steps 3 through 8 for ten generations.

Gene frequency

- To find the gene frequency of *F,* divide the number of *F* by the total alleles.
- To find the gene frequency of *f,* divide the number of *f* by the total alleles.
- Express results in decimal form. The sum of the frequency of *F* and *f* should equal one for each generation.

Data Table

Gener-ation	# of *FF* Individuals	# of *Ff* Individuals	# of *ff* Individuals	Total # of *F* Alleles (black beans)	Total # of *f* Alleles (white beans)	Total # of Alleles	Gene Frequency of *F*	Gene Frequency of *f*
0				50	50	100	0.5	0.5
1								
2								
3								
4								
5								
6								
7								
8								
9								
10								

ANALYSIS QUESTIONS:

1. Graph your frequencies within ONE graph. Create a line graph with generation as the independent and frequency (in decimals) as your dependent variable.

2. Explain your graph (*at least 3 sentences*). What is happening to the allele frequency of both the dominant and recessive? How do the number of alleles for the dominant trait compare with the number of alleles for the recessive trait.

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 in this population of rabbits? How might you simulate this effect if you were to repeat this activity?

4. How do your results compare to other groups in the class? If significantly different, why are they different?

5. How are the results of this simulation an example of **evolution**?