

# Bean Bunny Evolution

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

### About this Lesson

This is an excellent lesson that models evolution by natural selection of the gene frequency of two alleles in a population of wild rabbits represented by dried beans. Students are asked to calculate the gene frequency of the alleles for each generation and then graph the frequency of the two alleles over 10 generations

This lesson is included in the LTF Middle Grades Module 7.

### Objectives

Students will:

- Model evolution by natural selection of the gene frequency of two alleles in a population of organisms.
- Calculate the gene frequency of the alleles for each generation
- Generate a graph of the frequency of the two alleles over 10 generations

### Level

Middle Grades: Life Science

### Common Core State Standards for Science Content

LTF Science lessons will be aligned with the next generation of multi-state science standards that are currently in development. These standards are said to be developed around the anchor document, A Framework for K–12 Science Education, which was produced by the National Research Council. Where applicable, the LTF Science lessons are also aligned to the Common Core Standards for Mathematical Content as well as the Common Core Literacy Standards for Science and Technical Subjects.

Code	Standard	Level of Thinking	Depth of Knowledge
(LITERACY) RST.9-10.3	Follow precisely a multistep procedure when carrying out experiments, taking measurements, or performing technical tasks, attending to special cases or exceptions defined in the text.	Apply	II
(MATH) A-CED.2	Create equations in two or more variables to represent relationships between quantities; graph equations on coordinate axes with labels and scales.	Apply	II

### **Connections to AP\***

AP Biology: This lesson addresses concepts contained in Big Idea 1 in the revised AP Biology curriculum under the following section: 1.C.2 and 1.C.3

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### **Materials**

*Each lab group will need the following:*

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

### **Assessments**

The following type of formative assessment is embedded in this lesson:

- Visual assessment of student generated graphs

The following assessments are located on the LTF website

- Middle Grades Life: Evolution Assessment
- 2007 7<sup>th</sup> grade Posttest, Free Response Question 2

## Teaching Suggestions

*Bean Bunny Evolution* provides a straight forward and simple exploration of a natural selection evolutionary model using only different colored beans, a bag and some Petri dishes!

This activity should be done only after students have had a good introduction to genetics, Punnett squares and alleles. Also, the students should have a thorough understanding of natural selection and evolution.

In *Bean Bunny Evolution*, there are several simplifications. We have assumed that rabbits mate once and do not reenter the breeding pool. (Of course, this is not true with real rabbits.) For this reason, the population declines at an artificially rapid rate. The activity helps show the change in frequency of a lethal recessive allele over time, but is not intended to represent exactly what would happen with a population of real rabbits.

Dried small pinto beans and dried small lima beans can be found at any grocery store at minimal cost. The beans should be as close to the same size as possible so the students cannot feel or detect a difference between the beans when they are in the paper bag. Students may try, after a few generations, to “kill off” the recessive alleles once they begin to figure out the pattern.

To help students begin, it is recommended that you model for students how to select the beans from the bag and how to mark the data table. Also, an explanation of how to calculate the gene frequency on the overhead or the chalkboard is recommended. The text of the student lab procedure explains how to calculate the frequency:

*“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 sample data came from two real student lab groups. It demonstrates that students can possibly eliminate all *f* alleles in a few generations or they might continue on through 10 generations with a few recessive alleles remaining in the population.

When the students start the lab, carefully and vigilantly monitor the students as they perform the 1<sup>st</sup> generation to make sure that they are following the procedure correctly. Once they finish the 1<sup>st</sup> generation, they can (and probably will) work independently.

This activity, used with permission, was only slightly modified from the original activity, *Breeding Bunnies*, written by Joseph Lapiana and displayed at the PBS (<http://www.pbs.org>) website.

## SAMPLE DATA

Here are two examples of student generated results.

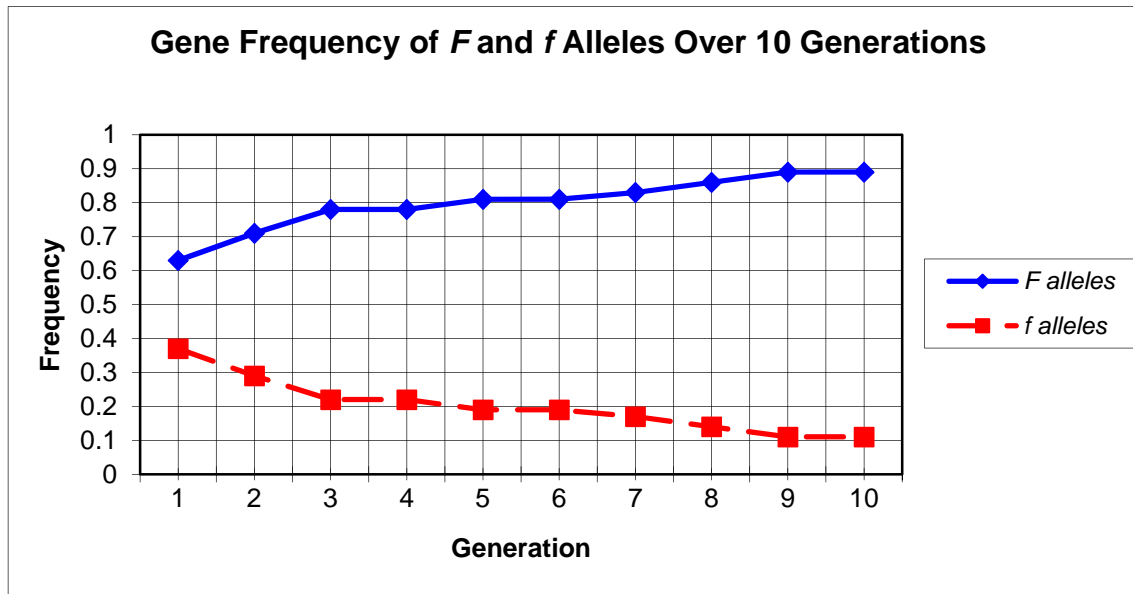
### Student Data Table #1

Generation	Number of <i>FF</i> Bunnies	Number of <i>Ff</i> Bunnies	Number of <i>ff</i> Bunnies	Number of <i>F</i> Alleles	Number of <i>f</i> Alleles	Total Number of Alleles	Gene Frequency of <i>F</i>	Gene Frequency of <i>f</i>
1	12	26	12	50	26	76	0.66	0.34
2	19	12	7	50	12	62	0.81	0.19
3	22	6	3	50	6	56	0.89	0.11
4	23	4	1	50	4	54	0.93	0.07
5	25	0	2	50	0	50	1	0
6	25	0	0	50	0	50	1	0
7	25	0	0	50	0	50	1	0
8	25	0	0	50	0	50	1	0
9	25	0	0	50	0	50	1	0
10	25	0	0	50	0	50	1	0

### Student Data Table #2

Generation	Number of <i>FF</i> Bunnies	Number of <i>Ff</i> Bunnies	Number of <i>ff</i> bunnies	Number of <i>F</i> alleles	Number of <i>f</i> alleles	Total Number of Alleles	Gene Frequency of <i>F</i>	Gene Frequency of <i>f</i>
1	10	30	10	50	30	80	0.63	0.37
2	15	20	10	50	20	70	0.71	0.29
3	18	14	3	50	14	64	0.78	0.22
4	18	14	0	50	14	64	0.78	0.22
5	19	12	1	50	12	62	0.81	0.19
6	19	12	0	50	12	62	0.81	0.19
7	21	8	1	50	10	60	0.83	0.17
8	21	8	1	50	8	58	0.86	0.14
9	22	6	2	50	6	56	0.89	0.11
10	22	6	0	50	6	56	0.89	0.11

## Example of Typical Graph, Using Data from Student Data Table #2



### POSSIBLE ANSWERS TO THE CONCLUSION QUESTIONS

1. Based on your lab data, do you need to modify your hypothesis? Explain.
  - Answers will vary. Most students will correctly hypothesize, however, that the gene frequency of the alleles will change over time.
2. What was the original gene frequency of the  $F$  and the  $f$  alleles before selection occurred?
  - The original gene frequency of  $F$  and  $f$  was 0.5 each. There were 50 red beans, representing  $F$  alleles, and 50 white beans, representing  $f$  alleles, for a total of 100 beans, or alleles.
3. How did the gene frequency of the  $F$  and  $f$  alleles change by the 10th generation?
  - By the 10th generation, most groups of students will have selected out all of the white beans, or  $f$  alleles. If they have not selected them all out, by the 10th generation, the frequency of  $F$  will probably be approximately 0.9 or more while the frequency of  $f$  will be approximately 0.1.
4. How do you explain that both alleles,  $F$  and  $f$ , changed in frequency over time in the lab?
  - The  $f$  allele, coding for the furless phenotype, is a lethal allele. When two  $f$  alleles are combined in a rabbit as a homozygous recessive genotype, and expressed as the hairless phenotype, the rabbit will die, and the lethal condition is naturally selected against. This rabbit can no longer pass along its genes to the next generation. Over time and after multiple generations, the number of rabbits passing along  $f$  alleles will decrease. Concurrently, the  $F$  alleles will increase in the population. This causes the  $f$  alleles to decrease in frequency and the  $F$  alleles to increase in frequency.
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?

- Immigration and emigration will change the gene frequencies of both  $F$  and  $f$ , depending on what types of alleles migrate in or out of the population.
  - To simulate this effect in the modeling lab, students could add or take away beans from the bag, representing new alleles coming in or out of the population.
6. How do your group's results compare with the class data? If significantly different, why are they different?
- Each group's  $F$  alleles will increase in frequency and each group's  $f$  alleles will decrease in frequency. The number of generations it takes to decrease is what varies from group to group. Some groups might eliminate the  $f$  alleles within 4 generations or less, but other groups will still have a few  $f$  alleles even after 10 generations.
7. How is this simulation an example of evolution by natural selection?
- Evolution can be defined as biological change over time. As the  $ff$  (furless) individuals die off, the gene frequency of both the  $F$  and  $f$  alleles changes, as there are more  $F$  alleles in the population. As the genotypic frequency within the population changes over time, the phenotypic variation also changes. Genotypic and phenotypic change is "biological change". As biological characteristics of a population change over the generations, the population evolves.
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?
- The fact that all genotypes are represented by two alleles (one from each parent) means that when a recessive lethal allele is in combination with a dominant normal or wild type allele, the recessive condition will not be expressed. This allows the "silent killer" recessive genes to be passed down through the generations.

# 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<sup>®</sup>  
 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 dish  $ff$  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 red 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.



# Bean Bunny Evolution

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

**HYPOTHESIS**

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**DATA TABLE**

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

**DATA ANALYSIS**

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## **CONCLUSION QUESTIONS**

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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?