

Evolution of Populations**Modeling a Gene Pool****Introduction**

A population is a group of organisms of the same species that live together in a particular location. Each population is normally isolated from other populations of the same species. Populations can be observed for many characteristics.

Population genetics is the study of genes in a population of organisms. Biologists who study population genetics are interested in how frequently alleles of a gene appear in a population. Biologists are also interested in any changes in gene frequencies that may be occurring.

In this investigation beans will be used to represent individuals in a simulated population of organisms. Red beans will be symbols for homozygous dominant individuals RR . Pink (pinto) beans will be symbols for heterozygous individuals Rr . White beans will be symbols for homozygous recessive individuals rr . You will study various crosses using the beans and analyze frequencies and frequency changes as they appear in a simulated population in which a harmful phenotype occurs. In addition to this, you will be able to see how a potentially lethal genetic disorder affects allele frequency in the population over generations.

Problem

How does gene frequency change in a population of organisms?

Pre-Lab Discussion

Read the entire investigation. Then work with a partner to answer the following questions.

1. Why are you asked to set aside and not use some of the white beans at the start of the experiment?

2. If the initial breeding population (the parent generation) is composed of 16 RR individuals, 32 Rr individuals, and 8 rr individuals, how many R alleles are present in the parent generation? How many r alleles are present in the parent generation?

3. For the individuals in this lab, can the genotype of each be determined from the phenotype? Explain your answer.

4. Is the population represented by this lab in genetic equilibrium?
Why or why not?
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5. **Predicting** How would you expect the gene pool of this population to change over time?
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Materials (per group)

paper bag pink (pinto) beans
red beans white beans

Procedure

1. Work in pairs. Obtain an opaque container such as a paper bag. Place into it 16 red beans (RR), 32 pink beans (Rr), and 16 white beans (rr). The white beans represent individuals having the potentially lethal phenotype (rr). To represent the early deaths in the parent generation, remove half of the white beans and set them aside.
2. Mix the beans. Then, without looking into the container, remove the beans in pairs. Each pair will be one of the six possible combinations, as shown in Figure 1. Count the number of pairs of each of the six combinations. These six combinations will represent the parent pairs that will produce the first generation of offspring. To help count the pairs, you may wish to divide a sheet of paper into six columns with labels. See Figure 2 A and B on page 139. **Note:** *You will not necessarily have a pair of each type.*

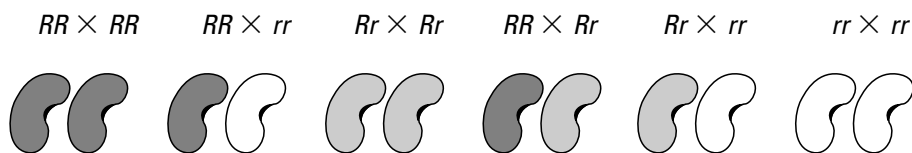


Figure 1

3. Record the number of parent pairs for each combination in Data Table 1 on p. 140.
4. Assume that each pair of parents will have four offspring. Calculate the expected number of offspring for each category of parent pairs. Record these numbers in Data Table 1. For example, if you counted six $Rr \times Rr$ parent pairs, and each pair has four offspring, there will be 24 offspring for that combination. Recall from your study of genetics that the expected ratio of genotypes for the cross of two heterozygous parents is 1 RR : 2 Rr : 1 rr . The expected ratio of genotypes for 24 offspring would be 6 RR : 12 Rr : 6 rr . Record the numbers that reflect your data in Data Table 1.
5. Calculate the total of each expected genotype from this first generation of offspring and record the totals in Data Table 1.

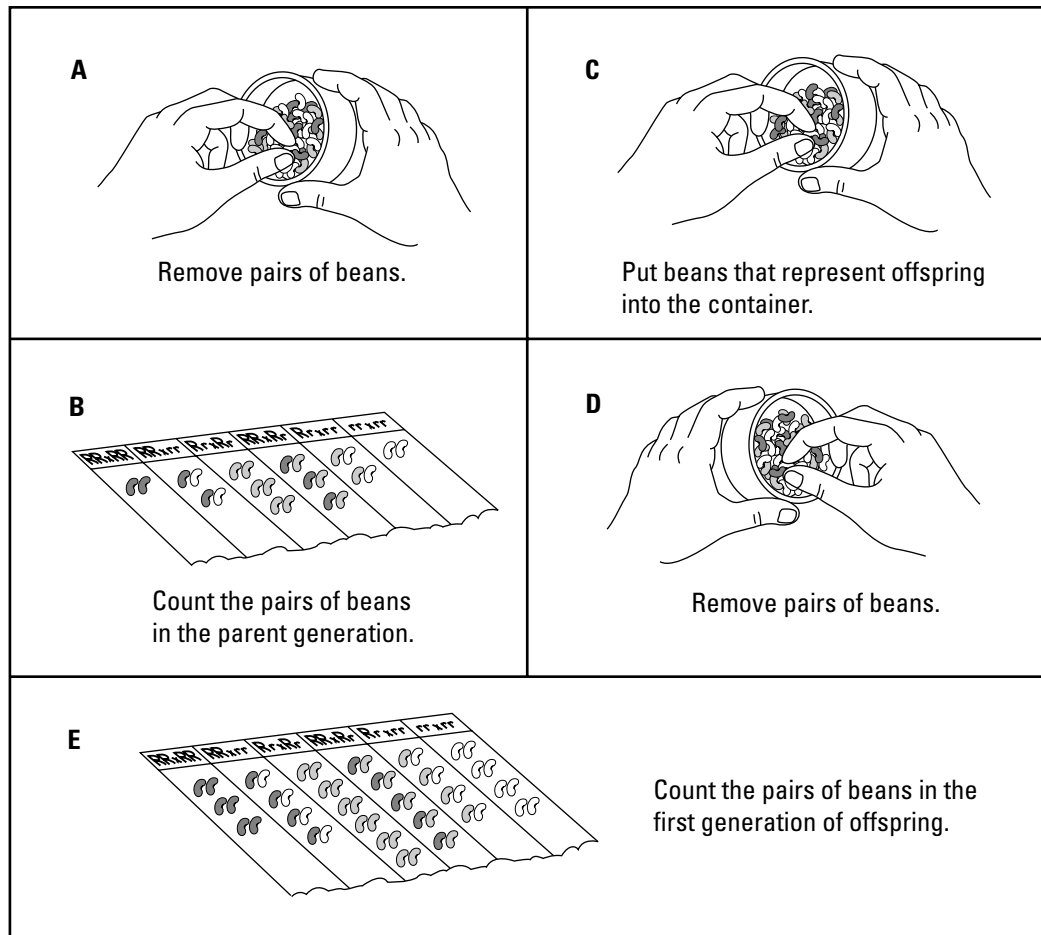


Figure 2

6. Using these totals, count the total number of *R*'s and *r*'s in the offspring population. Remember that each *RR* individual has 2 *R*'s, and each *Rr* individual has 1 *R* and 1 *r*. Record the data in the bottom row of Data Table 1. Then calculate the frequency of each allele by using the following formulas:

$$\text{Frequency of } R = \frac{\text{Total } R}{\text{Total } R + \text{Total } r}$$

$$\text{Frequency of } r = 1 - \text{Frequency of } R$$

Record your calculated gene frequencies in Data Table 1.

7. Based on the totals in Data Table 1, put enough beans to represent all the first generation offspring into your container. You will need to obtain more beans since each parent pair had four offspring. As before, remove one-half of the total number of white beans (*rr* offspring) to represent individuals that die before reproducing.
8. Mix the beans. Then, without looking into the container, pull out pairs of beans until you have removed all the beans. Arrange these pairs into the six possible combinations as you did in Figure 2 E. These six combinations will represent the first generation parents that will produce the second generation of offspring.

9. On a separate sheet of paper, draw two data tables in the same format as the Data Table below. Label them Data Table 2 and Data Table 3. Record the number of counted parent pairs in Data Table 2.
10. Assume that each parent pair will have four offspring. Calculate the expected number of offspring for each category of the parent pairs and record in Data Table 2.
11. Repeat the same calculations you did in step 6 for this second generation. Record your results in Data Table 2.
12. Repeat Steps 7 through 11 for a second generation of offspring. Record your data in Data Table 3.
13. Compare your results with other groups in your class as your teacher instructs.

Data Table 1

Parent pairs	Number of parent pairs	Number of offspring with genotypes		
		<i>RR</i>	<i>Rr</i>	<i>rr</i>
<i>RR</i> × <i>RR</i>				
<i>RR</i> × <i>rr</i>				
<i>Rr</i> × <i>Rr</i>				
<i>RR</i> × <i>Rr</i>				
<i>Rr</i> × <i>rr</i>				
<i>rr</i> × <i>rr</i>				
	Totals:			
Total of <i>R</i> 's ____ in offspring		Total of <i>r</i> 's ____ in offspring		
Frequency of <i>R</i> = ____		Frequency of <i>r</i> = ____		

Analysis and Conclusions

1. **Calculating** Which of the six parent pairs of the first parent set (*RR* × *RR*, *RR* × *rr*, *Rr* × *Rr*, *RR* × *Rr*, *Rr* × *rr*, or *rr* × *rr*) is least likely to occur? Why is this so?

2. **Predicting** Would you predict that another group of students in your class would have data identical to yours? Explain your answer.

3. Drawing Conclusions Can a single factor that affects the reproductive success of only some individuals in a population result in evolution? Explain your answer.

4. Using Models Can you use this activity as it is to model all patterns of inheritance in a population? Explain your answer.

5. Forming Operational Definitions Evolution is change of a population over generations. Form an operational definition of evolution as it occurs in this model.

Going Further

Sometimes the relationship between a certain phenotype and overall reproductive success is not a simple one. Using library or Internet resources, research the incidence of sickle cell anemia, an inherited disorder, and its relationship to malaria, a disease due to a pathogen. Use this example to explain how natural selection can work to keep a harmful allele in a population.