OBJECTIVES

- Investigate a genetically inherited trait and apply the Hardy-Weinberg Principle to a population
- Compare allele frequencies within the classroom to North American averages
- Demonstrate the stability of allele frequencies over five generations in an ideal Hardy-Weinberg population
- Examine the effects of selection, heterozygous advantage, and genetic drift on allele frequencies in a simulated mating exercise

MATERIALS

MATERIALS NEEDED PER STUDENT

PTC paper
Control paper
4 Index cards
1 Coin

DID YOU KNOW?

The population geneticists, Fisher, Haldane, Wright, and others, made major advances in theory during the 1920s and 1930s using the Hardy-Weinberg Equilibrium as a starting point.

PROCEDURE

A. Calculating Allele Frequencies Using the Hardy–Weinberg Principle

Testing different individuals' ability to taste PTC (phenylthiocarbamide) is a good way to demonstrate the Hardy–Weinberg principle. Homozygous-dominant (AA) and heterozygous (Aa) individuals can taste this bitter chemical, although homozygous-recessive (aa) individuals cannot. Use your class as a representative population to calculate the frequencies of the two alleles with the Hardy–Weinberg equation.

Use each strip of PTC and control test paper only once. Do not share test papers with other students in your class.

1. Obtain a piece of PTC test paper.
2. Place it on your tongue and note whether you can detect a bitter taste.

3. Obtain a piece of control paper and place it on your tongue. Comparing the control paper with the PTC paper will help determine whether you detected a taste on the PTC paper.

4. Record your results in Table 1 in the Analysis section of the lab.

5. Tally the results for the entire class and enter the results in Table 2. Calculate the frequencies for each allele, using the Hardy-Weinberg equation, in the Analysis section. Be sure to show your work.

Used test papers may be disposed of with general waste.

B. Testing the Hardy–Weinberg Principle

Case 1: Testing an Ideal Population

The entire class will be used as a representative population. The four cards each student uses, two "A" and two "a", represent haploid chromosomes contributed by parents in a simulated breeding exercise. Each parent begins with the genotype Aa, providing initial genotype frequencies of 0.25 AA, 0.50 Aa, and 0.25 aa. Record these initial frequencies in the Analysis section of the lab.

1. Obtain four index cards. Label two "A" and two "a". These will be your haploid chromosomes.

2. Randomly pair off with another student for "breeding". Choose any other student; your gender, and your partner's, doesn't matter in the simulation.

3. Turn your cards upside down and shuffle them. Turn over the top card in your pile. Pair this card with your partner's card; this will be the genotype of your first offspring. Record this in the Analysis section.

4. Turn over the next card in your pile. Pair this card with your partner's card; this will be the genotype of your second offspring.

5. Now you and your partner must take on the genotypes of the two offspring that you produced. For example, if you produced offspring with the genotypes AA and Aa, one member will begin the next generation with four A cards, and the other member will begin the next generation with two "A" cards and two "a" cards. Record the genotype in the Analysis section of the lab.

DID YOU KNOW?

In 1908, R.C. Punnett (of Punnett square fame) was asked at a lecture to explain "if brown eyes were dominant, why wasn't the whole country becoming brown-eyed?" Punnett in turn asked his friend G.H. Hardy, a conversation which sparked the Hardy-Weinberg Law.

6. Randomly seek out another class member to pair off with for the next generation of "breeding".

7. Repeat the above procedure for the second generation. Record the genotypes in the Analysis section.

8. Repeat Steps 3-7 for three more generations, for a total of five generations. Record the genotypes for each subsequent generation.

9. Combine the genotype of your fifth generation results with the rest of the students' fifth generation results and enter the totals in the Analysis section.

10. Below Case 1 in the Analysis section, calculate the allele frequencies after five generations of random mating.

Case 2: Selection

The previous exercise was conducted with ideal parameters. For a more realistic situation, selection must be used. There is 100% selection against homozygous-recessive offspring. If offspring are recessive (if they receive two mutated alleles), they will never live long enough to reach a reproductive age; offspring that are either heterozygous or homozygous dominant will survive long enough to reproduce.

Because selection can lead to the elimination of certain alleles, it will be necessary to have extra alleles (index cards) in the event of death of an offspring.

1. Follow the same procedure as the previous exercise, with one difference: If offspring is produced with the genotype aa, this offspring will not survive; eliminate the alleles from the population. To maintain population size, you must produce two surviving offspring. If two alleles are eliminated, draw two new alleles from the extra cards.

2. Repeat the procedure for a total of five generations, selecting against homozygous-recessive offspring in each generation. Record the genotypes after every generation in the Analysis section.

3. Combine your fifth generation results with the rest of the students' fifth generation results and record in the Analysis section.

4. Below Case 2 in the Analysis section, calculate the allele frequencies after five generations of random mating.

DID YOU KNOW?
The Hardy-Weinberg Law is able to tell us whether or not evolution is occurring as well as the factors that cause it.

Case 3: Heterozygote Advantage

The previous exercise showed how selection against homozygous-recessive individuals clearly alters the allelic frequencies in a population. Another form of selection that operates within a gene pool is diseases, such as a deadly form of malaria, that affect homozygous-dominant individuals more severely than heterozygous individuals. The heterozygote is therefore favored in a population.

Since selection can lead to the elimination of certain alleles, it will be necessary to have extra alleles (index cards) in the event of death of an offspring.

1. Follow the same procedure, eliminating homozygous-recessive individuals as before. In addition, if a homozygous-dominant individual is produced, flip a coin. If the result is heads, the offspring dies; if it is tails, the offspring survives.

2. Repeat the procedure for a total of five generations. Record the genotypes after every generation in the Analysis section.

3. Combine your fifth generation results with the rest of the students' fifth generation results and record in the Analysis section.

4. Continue the procedure for five more generations, for a total of ten generations, this time starting with the genotypes from the end of the fifth generation. Record the genotypes in the Analysis section.

5. Below Case 3 in the Analysis section, calculate the allele frequencies after ten generations of random mating.

DID YOU KNOW?
The three main results of genetic drift are: a loss of genetic variation within populations, genetic divergence between populations, and evolution.

Case 4: Genetic Drift

Genetic drift is a phenomenon where an allele is lost solely from chance instead of through selection. The most important factor in genetic drift is population size; smaller populations have a much greater potential for genetic drift.

1. Your instructor will divide the class into several smaller populations. Within your smaller population, follow the mating procedure, as in the first exercise, for a total of five generations. Record the genotypes after every generation in the Analysis section.

2. Combine your group's fifth generation results with those of the other small populations and calculate the new allele frequencies below case 4 in the Analysis section.

Name:_____
Group: _____
Date: _____

ANALYSIS

Part A
Table 1

	Taster	Nontaster
PTC		
Control		

Table 2

	Phenotypes				Allele Frequency Based on the Hardy-Weinberg Equation	
	Tasters (p^2+2pq)		Nontasters (q^2)		p	q
	#	%	#	%		
Class population						

Part B
Case 1
Testing an Ideal Population

Initial Class Frequencies: AA:_____ Aa:_____ aa:_____

My Initial Genotype: _____

F_1 Genotype: _____

F_2 Genotype: _____

F_3 Genotype: _____

F_4 Genotype: _____

F_5 Genotype: _____

Final Class Frequencies: AA:_____ Aa:_____ aa:_____

p:_____ q:_____

Number of A alleles present at the fifth generation

Number of offspring with genotype AA _____ X 2 = _____ A alleles

Number of offspring with genotype Aa _____ X 1 = _____ A alleles

Total = _____ A alleles

$$p = \frac{\text{TOTAL number of A alleles}}{\text{TOTAL number of alleles in the population}} = \_\_\_\_\_$$

Number of a alleles present at the fifth generation

Number of offspring with genotype aa _____ X 2 = _____ a alleles

Number of offspring with genotype Aa _____ X 1 = _____ a alleles

Total = _____ a alleles

$$q = \frac{\text{TOTAL number of a alleles}}{\text{TOTAL number of alleles in the population}} = \_\_\_\_\_$$

Case 2
Selection

Initial Class Frequencies: AA:_____ Aa:_____ aa:_____

My Initial Genotype: _____

F_1 Genotype: _____

F_2 Genotype: _____

F_3 Genotype: _____

F_4 Genotype: _____

F_5 Genotype: _____

Final Class Frequencies: AA:_____ Aa:_____ aa:_____

p:_____ q:_____

Case 3
Heterozygote Advantage

Initial Class Frequencies: AA:_____ Aa:_____ aa:_____

My Initial Genotype: _____

F_1 Genotype: _____

F_2 Genotype: _____

F_3 Genotype: _____

F_4 Genotype: _____

F_5 Genotype: _____

Final Class Frequencies: (After five generations) AA:_____ Aa:_____ aa:_____

p:_____ q:_____

F_6 Genotype: _____

F_7 Genotype: _____

F_8 Genotype: _____

F_9 Genotype: _____

F_{10} Genotype: _____

Final Class Frequencies: (After ten generations) AA:_____ Aa:_____ aa:_____

p:_____ q:_____

Case 4
Genetic Drift

Initial Class Frequencies: AA:_____ Aa:_____ aa:_____

p:_____ q:_____

My Initial Genotype: _____

F_1 Genotype: _____

F_2 Genotype: _____

F_3 Genotype: _____

F_4 Genotype: _____

F_5 Genotype: _____

Final Class Frequencies: AA:_____ Aa:_____ aa:_____

p:_____ q:_____

Name:_____
Group: _____
Date: _____

ASSESSMENT

1. Using the PTC tasting results for the entire class, how close were the frequencies of each phenotype (taster vs. non-taster) to those found in the North American population (approximately 70% tasters)? If there was variation, what could have accounted for this?

2. In the first exercise in Part B, 'Testing an Ideal Population', what would be the expected values of p and q after the five generations?

3. How close were your class results to an ideal population?

4. What do you think would happen if you carried this simulation out for ten more generations?

5. How do the frequencies of p and q compare after the factor of selection was added to the simulation?

6. What do you think would happen if you carried this simulation out for another ten generations?

7. Do you think that the a allele would ever be totally eliminated from the population? Why or why not?

8. Suppose there was a medical advance that allowed most individuals with the double recessive condition to survive and reach reproductive age. How would this affect the allele frequencies?

9. Explain the difference in the results of the simulation showing selection to the simulation favoring heterozygotes.

10. Why is the heterozygous condition important in maintaining genetic variation within a population?

11. In the simulation demonstrating genetic drift, what do the resulting allele frequencies suggest about population size as an evolutionary force?