Topic 6: Evolution – 6d. Hardy-Weinberg Lab

Resources:	Miller, K., Levine, J. (2004). *Biology.* Boston, MA: Pearson Prentice Hall.
	The Ernest Hemingway Home and Museum [Internet]. Key West, FL. 2002. Available from: http://www.hemingwayhome.com/HTML/our_cats.htm
Building on:	Microevolution is the study of the change in the frequency of an allele in a population from one generation to the next. Mathematicians Hardy and Weinberg explained how an allele could change in a population by first showing how it would not change, the Hardy-Weinberg principle.
	The Hardy-Weinberg principle states that the frequency of an allele in a population should not change from one generation to the next. This depends on five conditions:

1. No mutation
2. No natural selection
3. No immigration or emigration
4. No mating selection
5. It must be a large population to avoid the affect to genetic drift.

They developed the following equations for a single locus two allele trait:

$$P^2 + 2pq + q^2 = 100\% \ (1.0) \qquad\qquad p + q = 100\% \ (1.0)$$

These formulas can be used to calculate the frequency of an allele if the number of homozygous dominant, heterozygous, and homozygous recessives are none. They can also be used to estimate allele frequency when only the number of the dominant phenotype and the recessive phenotype are known.

Links to Chemistry and Physics:	Probability Prediction
Stories:	Students often think that if a trait is dominant, it will have a high frequency. In other words, if the trait is dominant, it should be more common in the population. This is not necessarily true, and a good example of this is polydactyly, having extra fingers. Polydactyly is a dominant trait in humans and can be expressed as an extra functional finger or a small vestigial stub.
	Polydactyly is also dominant in cats. Ernest Hemingway adopted a stray cat while he was living in Key West. The cat had extra toes. That cat mated with another local cat and many of the offspring had extra toes.

After Hemingway's death, a fund was established to preserve his Key West home as a historical site. The fund stipulated that the cats would have to be provided for and would have full run of the house and grounds. If you visit the Hemingway home in Key West, you will see the cats wandering the grounds, laying on display cases, and waiting for tourist attention. Many of the cats have especially big feet because they have extra toes.

Materials for the Lab:
- Index cards (1/2 labeled with A, and 1/2 labeled with a)
- Calculators

Instructions for the Teacher:
This lab is pretty easy and straightforward. Many students will have trouble with the math at first. The problem students have is knowing when they can calculate the actual frequency of an allele and when they can only estimate the frequency of an allele.

Simulation 3 is designed to illustrate genetic drift (being in the wrong place at the wrong time). You might want to tape a small dot under the desk top of five to ten desks in your room (depending on the size of your class). When you get to the end of Simulation 3, you can ask students to look under their desks, and if the dot is there, sadly, they did not survive the "great earthquake." Note, this was not selection; it was random.

Hardy-Weinberg Lab

Introduction: In 1908, G. H. Hardy and W. Weinberg suggested a scheme whereby evolution could be viewed as changes in the frequency of alleles in a population of organisms. They established what is now known as the Hardy-Weinberg principle. The Hardy-Weinberg principle states: *The frequency of an allele in a population will remain constant from generation to generation.*

The frequency of an allele is equal to the # of that allele divided by the total # of all alleles in the population for that specific gene. **Frequency = # of specific allele/# of total alleles.** When confronted by critics, they explained that their principle would hold true if five conditions were met. What are those five conditions? When you complete this lab, you will be asked to list and explain those conditions.

Procedure: Assume that you are dealing with a single gene that has two allele alternatives, A and a. "A" is dominant to "a," and the gene is autosomal.

To begin each simulation, each member of the class must have two cards representing the diploid state for that gene. Each member of the class will be heterozygous (one A and one a).

Simulation 1: Begin by counting the number of students in the class and counting the genotypes in the class and then calculate the frequency of the alleles, A and a. Record this information on the Evidence Table.

Each member will mate (exchange a card) with another member of the class. After the exchange, each class member will now represent the newest generation and will be ready to "mate" with another member of the class.

You must mate with a different person each time, and you must mate five times.

After everyone in the class has mated five times, count the number of each type of genotype in the class and calculate the frequency of the alleles, A and a. Record this information on the Evidence Table.

Simulation 2: Everyone begins as a heterozygote again. Count the number of different genotypes and the frequency of the alleles, A and a. Record this information on the Evidence Table.

Now mate as you did before, however, if you should receive "aa" the homozygous recessive condition, then you die and you must sit down. Everyone that is living will mate a total of three times. The genotypes of the survivors and

the frequency of the alleles, A and a, should be determined. Record this information on the Evidence Table.

Simulation 3: Everyone begins as a heterozygote again. Count the number of different genotypes and the frequency of the alleles, A and a. Record this information on the Evidence Table. Now mate as you did in Simulation 1. At the end of five matings, sit down and your teacher will tell you if you survive or not. You see, you may have been in the wrong place at the wrong time and chance alone determined that you did not survive. The remaining students survive. Count the different genotypes of the survivors and calculate the frequency of the alleles, A and a. Record this information on the Evidence Table.

Evidence Table

Simulation 1	Beginning number of homozygous dominants	Beginning number of heterozygotes	Beginning number of homozygous recessives	Total number of alleles	Beginning frequency of A	Beginning frequency of a
	Ending number of homozygous dominants	Ending number of heterozygotes	Ending number of homozygous recessives	Total number of surviving alleles	Ending frequency of A	Ending frequency of a
Simulation 2	Beginning number of homozygous dominants	Beginning number of heterozygotes	Beginning number of homozygous recessives	Total number of alleles	Beginning frequency of A	Beginning frequency of a
	Ending number of homozygous dominants	Ending number of heterozygotes	Ending number of homozygous recessives	Total number of surviving alleles	Ending frequency of A	Ending frequency of a
Simulation 3	Beginning number of homozygous dominants	Beginning number of heterozygotes	Beginning number of homozygous recessives	Total number of alleles	Beginning frequency of A	Beginning frequency of a
	Ending number of homozygous dominants	Ending number of heterozygotes	Ending number of homozygous recessives	Total number of surviving alleles	Ending frequency of A	Ending frequency of a

Analysis Questions:

1. Explain why the frequency of the alleles in Simulation 1 did not change although the number of different phenotypes did change.

2. Why did the frequency of the alleles change in Simulation 2?

3. In Simulation 3, the frequency of the alleles should have changed due to the random event that removed a portion of the population.
   a. How was Simulation 3 different from Simulation 2?

   b. If the class size had been 1,000 students instead of your actual class size, and the same students were randomly removed, do you think the change in allele frequency would have been as different as the change your class experienced?

4. Discuss four other factors that you think might interfere with the Hardy-Weinberg principle.

5. If you know that a population is 75% the dominant phenotype and 25% is the recessive phenotype, can you determine approximately how many of the dominant phenotype are homozygous dominant and how many are heterozygous dominant? Try this mathematically.

6. Tall is dominant over short in pea plants. In a population of pea plants, 60 were tall and 40 were short.
   a. What is the frequency (%) of short plants in the population?

   b. Using your answer to part a, calculate the frequency of the short gene.

7. What is the frequency of the tall gene?

8. If the all of the pea plants in question 6 reproduce and the next generation is 200 plants, how many of those plants will be:
   a. Homozygous dominant = _____
   b. Heterozygous = _____
   c. Homozygous recessive = _____

9. If all of the short (homozygous recessive) plants in question 7 die, what will be the new frequency of:
   a. The allele for tall = _____
   b. The allele for short = _____

10. If the short plants continue to die generation after generation, will the frequency of t (the recessive allele) ever reach zero? Defend your answer.