NAME ____________________ AP BIOLOGY - POPULATION GENETICS

Natural Selection and the fate of the Teddy Graham Bear

INTRODUCTION

Many think that Charles Darwin "discovered evolution", when in fact it was a mechanism for evolutionary change - **NATURAL SELECTION** - that he proposed. In the *On the Origin of Species,* he published in 1859, Darwin described natural selection, provided evidence in support of evolution. He defined evolution as a change in populations over time. By 1900, geneticists and naturalists still disagreed about the role of natural selection and the importance of small variations in natural populations. It took the advent of population genetics to allow natural selection to be widely accepted.

Ayala (1982-close to the time you were born) defined evolution as "*changes in the genetic constitution of populations.* A **population** is defined as a group of organisms of the SAME species that occur in the SAME area and interbreed or share a common **gene pool**, all the alleles at all gene loci of all individuals in the population. The population is considered to be the basic unit of evolution. Therefore, POPULATIONS EVOLVE, not individuals.

In 1908, G.H. Hardy (an English mathematician) and W. Weinberg (a German physician) developed models of population genetics. They worked independently, but both showed that the process of heredity by itself did not affect the genetic structure of a population. Today we call their theorem (for all you mathematicians who like theorems, this should be fun) the **Hardy-Weinberg theorem**. It states that the frequency of alleles in the population will remain the same regardless of the starting frequencies. Furthermore, the equilibrium genotypic frequencies will be established after one generation of random mating. What does this mean?

If **A** and **a** are alleles for a particular gene locus and each diploid individual has two such loci, then **p** can be designated as the frequency of the **A** allele and **q** as the frequency of the **a** allele.

Therefore if you have a population of 100 individuals (each with 2 loci) in which 40% of the alleles are **A**, then **p** = 0.40. The rest of the alleles (60%) would be **a** and **q** would equal 0.60 (**p + q = 1.0**). These are referred to as **allele frequencies**. The frequency of the possible diploid combinations of these alleles (AA, Aa, aa) is $p^2 + 2pq + q^2 = 1$.

Don't forget that this theorem is valid only if certain conditions are met:

1. **The population is very large.** (This reduces the effect of chance on changes in allele frequencies.) - (NO GENETIC DRIFT)
2. **Matings are random**
3. **There are no net changes in the gene pool due to mutation, that is, mutation from A to a must be qual to mutation from a to A.**
4. **There is no migration of individuals into and out of the population.** (NO GENE FLOW)
5. **There is no selection; all genotypes are equal in reproductive success.**

Basically, the Hardy-Weinberg theorem provides a baseline model in which gene frequencies do not change and evolution does not occur. By testing the fundamental hypothesis of the Hardy Weinberg theorem, evolutionists have investigated the roles of mutation, migration, population size, nonrandom mating, and natural selection in effecting evolutionary change in natural populations. Although some populations maintain genetic equilibrium, the exceptions are still providing scientists with something to talk about.

Activity: Natural Selection and Evolution in Teddy Grahams

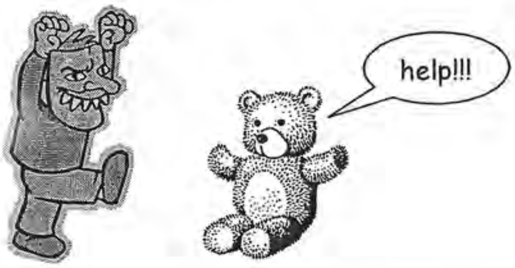
Purpose: To demonstrate that evolution occurs through Natural selection

Materials: Happy and Sad Bears, graph paper

Procedure:

Read the following story:

You are a bear-eating monster. There are two kinds of bears: Happy Bears and Sad Bears. You can tell the difference between them by the way they hold their hands. Happy Bears hold their hands high in the air, and Sad Bears hold their hands down low. Happy Bears taste sweet and are easy to catch. Sad Bears taste bitter, are sneaky, and are hard to catch. Because of this, you eat **only Happy Bears**. New bears are born every 'year' (during hibernation) and the birth rate is one new bear for every old bear left from the last year.



1. Obtain a population of 10 bears from the cave, and record in Table 1 the number of each: total population, happy bears, and sad bears. Using the equations for H-W equilibrium, calculate the frequencies of both the dominant and recessive alleles and the genotypes that are represented in the population.

   Ex. If 5 of the 10 bears are happy, they 10 out of 20 alleles would be happy alleles. Therefore the q^2 number would be .5. You must then determine the q number by taking the square of .5.

   SO, HAPPY TRAIT IS RECESSIVE

2. **Now go hunting!!** Eat 3 of your Happy bears. (If you do not have 3 Happy bears, then eat the difference in sad bears.)
3. Once you have consumed the bears, obtain a new generation from the bears' cave (the box). You should only remove 7 additional bears from the den for a total of 14 bears. Remember: New bears are born at the rate of one new bear for every old bear left from the last year.
4. Repeat the procedures again, for 2 more generations (four generations total). Be sure to record the number of each type of bear and the total population. Use the

data from table 1 to determine the genotypic frequencies of the population. Record in table 2.

Construct a line graph for each genotype (AA, Aa, and aa) using the data from table 2.

Results:

Table 1: Phenotypic Frequencies

Generation	**# of Happy Bears**	**# of Sad Bears**	**Total # of Bears**
1			
2			
3			
4			

Table 2: Genotypic Frequencies

Generation	**P^2 AA**	**2pq Aa**	**q^2 aa**	**p**	**q**
1					
2					
3					
4					

Formulas:

1. $p + q = 1$ (allele frequency)

2. $p^2 + 2pq + q^2 = 1$ (genotypic frequency)

Graph:

Graph the frequencies of the 3 genotypes over the 4 generations. Try to graph it all on one graph.

What is your independent variable?

What is your dependent variable?

Key: Graph AA as : ------------

Graph Aa as: __________

Graph aa as: . . . .

You can also use 3 different colored lines.

Questions:

1. Explain which trait is not favorable.

2. Which phenotype is reduced in the population?

3. What specifically happens to each genotypic frequency from generation one to generation four?

4. What occurs when there is a change over time of the genotypic frequencies?

5. Explain what would happen if the selection pressure changed and the recessive gene was selected for.

6. What would happen if it were better to be heterozygous (Aa)? Will there be homozygous recessive bears? Explain your answer.

7. What happens to the recessive gene (a) over successive generations?

8. Explain why the recessive gene (a) does not disappear from the population.

TEACHER NOTES FOR TEDDY GRAHAM LAB

This lab requires 47 teddy grahams per student, and there are about 225 teddy grahams per box, so each box of teddy grahams has enough bears for four students.

Prior to lab, set up cups for each student by placing 50 teddy grahams in each cup.

NOTE: The information given in the student handout (Procedure, step 1) indicates that the **HAPPY ALLELE/TRAIT IS RECESSIVE!**

The procedure:

1) Students pull 10 random bears out of their cup and lay them down. They should enter total #happy and #sad in for Generation 1 in Table 1
2) Students then eat three HAPPY bears (if there aren't 3, they eat the difference in sad bears), leaving 7
3) Students then randomly pull a number of bears equal to what they have left (seven), which gives them a total of 14.
4) Students count #happy and #sad and enter totals for Generation 2 in Table 1
5) Students then eat three HAPPY bears (if there aren't 3, they eat the difference in sad bears), leaving 11
6) Students then randomly pull a number of bears equal to what they have left (seven), which gives them a total of 22
7) Students count #happy and #sad and enter totals for Generation 3 in Table 1
8) Students then eat three HAPPY bears (if there aren't 3, they eat the difference in sad bears), leaving 19
9) Students then randomly pull a number of bears equal to what they have left (seven), which gives them a total of 38
10) Students count #happy and #sad and enter totals for Generation 4 in Table 1

Students then must use info for each generation in Table 1 to calculate p^2, $2pq$, q^2, p, and q for each generation.

Easy way to calculate q^2:

- For each Generation 1 through 4, double the number of happy bears to determine **HAPPY** ALLELES in population.
- Also, double the number of bears in each generation to determine the **TOTAL** number of alleles in the population.
- Divide the number of HAPPY alleles by the total # of alleles in population to get a decimal number.....this number is the frequency of homozygous recessives, or q^2
- Now that you have q^2, you can now calculate q, which then gives you p, p^2, and $2pq$.