



MICROEVOLUTION

NOTES

This activity is an adaptation of an exercise originally published by L. A. Welch. 1993. A model of microevolution in action. *The American Biology Teacher*. 55(6), 362-365. It has been adapted multiple times and used in several contexts at the University of Colorado at Boulder. This new version, while incorporating the concept of genotypic frequencies, borrows extensively from the work of numerous undergraduate teaching faculty at UCB who have perfected its use over the years.

MATERIALS

- Small paper drinking cups (1 per student)
- Plastic spoons, knives, and forks (i.e. “prey capturing devices”)
- Dry beans, rice, pasta (4-5 different types, e.g. dry kidney beans, green split peas, yellow split peas, elbow macaroni, rice) (i.e. “prey”)
- Colored beads (purple and green or two other colors)
- Colored dot labels or permanent markers in the same colors as the beads
- Calculators or computers
- Graph paper
- String and stakes or tape to mark boundaries of “habitat”

TEACHER INSTRUCTIONS FOR BASIC ACTIVITY

Predators

In this activity, there is one predator species with three distinct prey-capturing device phenotypes – the fork, the knife and the spoon. These phenotypes are expressions of genotypes resulting from the different combinations of two alleles.

alleles:

P (purple)

G (green)

genotypes	PP	PG	GG
phenotypes	spoon	fork	knife

In this activity, neither allele is completely dominant. The heterozygote has a phenotype intermediate to the two homozygotes.

Habitat:

Measure and mark a square area 20' by 20'. The area may be outside or inside. This area will be the "habitat" for the activity. Use tape or stakes and string to mark the boundaries of the habitat. The characteristics of your habitat will almost certainly have an impact on the outcome of the activity as "prey" may be difficult to find in grass or hard to scoop up from slippery surfaces. Hence you may wish to try the activity more than once in different habitats or to experiment with variation within the habitat (part grass, part pavement for example). If you are working with an indoor habitat, you may alter the surface by adding Easter basket grass, or shredded paper, or different colored and/or textured carpets.

Materials assembly and set-up:

1.) Assemble the prey items and place in a re-sealable plastic bag or other container. The success rate of different prey capturing devices will vary depending on the type proportion of prey items as well as on habitat type (see Table 1). You may want to try several different mixtures.

Have additional prey items on hand to replenish food supply as the activity goes on.

2.) Place one green bead for each student in the class and one purple bead for each student in the class into a bag or hat, which will be designated the "gene pool".

3.) Mark plastic cutlery by placing round colored labels or stripes with a permanent marker on the handle to indicate genotype.

Spoon = two purple labels

Fork = one purple and one green

Knife = two green labels

NOTE: The student instructions accompanying this activity are written to demonstrate the change in predator populations over time. One may easily also model the changes in prey populations by noting the number of each type of prey remaining at the end of each round, and doubling the number of survivors. An additional data table for recording information about prey types is included for your convenience.



INTRODUCTION TO CONCEPTS IN MICROEVOLUTION

This activity models the changes in *genotypes* and *phenotypes* and *allele* frequencies of a “predator” and its “prey” species over several generations in response to *natural selection*. This process is often referred to as “microevolution” because it involves subtle changes in the characteristics of a species as opposed to the significant change resulting in the emergence of new species, which is often referred to as “macroevolution”. Before continuing with this activity, it would be wise to review the following terms and concepts.

Allele

Definition: alternative form of a gene (Campbell, 1996)

As an example consider the ABO blood group in humans. A person’s blood type is determined by the genes which code for this blood group. There are three alternate forms of the gene or *alleles*. The alleles are I^A , I^B , and I^O .

Genotype

Definition: genetic make-up of an organism (Campbell, 1996)

To continue our example using the ABO blood group, any one person would have two copies of the ABO blood type gene, these copies could be of the same allele or different alleles. The possible *genotypes* that a person could have for the ABO blood group include: $I^A I^A$, $I^A I^B$, $I^B I^B$, $I^B I^O$, $I^O I^O$, $I^A I^O$.

Phenotype

Definition: physical and physiological traits of an organism (Campbell, 1996)

Again to continue our example, people have four possible phenotypes for the ABO blood group. The phenotype in this case is their blood type: Type A, Type B, Type AB, and Type O. In this case, an individual’s phenotype is determined by their genotype. Someone with the genotype $I^A I^A$ or $I^A I^O$ will be Type A. Someone with the genotype $I^B I^B$ or $I^B I^O$ will be Type B. Someone with the genotype $I^A I^B$ will be Type AB. Someone with the genotype $I^O I^O$ will be Type O. However, for other traits such as height, an individual’s phenotype is usually the result of both their genotype and their environment.

Natural selection

Definition: Differential success in the reproduction of different phenotypes resulting from the interaction of organisms with their environment. Evolution occurs when natural

selection causes changes in relative frequencies of alleles in the gene pool. (Campbell, 1996)

As an example, if, hypothetically speaking, people with Type A blood were able to produce more offspring every generation than people with Type B, AB, or O blood because they were more resistant to a particular disease, this would be an example of natural selection.

Hardy-Weinberg equilibrium

Definition: axiom maintaining that sexual shuffling of genes alone cannot alter the overall genetic makeup of a population (Campbell, 1996)

Understanding Hardy-Weinberg equilibrium requires that we think of the gene pool of a population of organisms in which the frequency of each allele in the population is expressed as follows:

p = frequency of allele 1 (A_1)

q = frequency of allele 2 (A_2)

Consider a population of dogs in which there are two alleles of the gene that codes for coat color, A_1 and A_2 . The A_2 allele codes for black fur. The A_1 allele codes for yellow fur. The possible genotypes are $A_1 A_1$, $A_1 A_2$, and $A_2 A_2$. A_1 and A_2 have incomplete dominance; therefore the phenotypes are as follows: $A_1 A_1$ = yellow coat, $A_1 A_2$ = brown coat, $A_2 A_2$ = black coat.

We would calculate p and q by first calculating the frequency of each genotype:

$f(YY) = \# A_1 A_1$'s in the population / total number of individuals in the population

$f(YB) = \# A_1 A_2$'s in the population / total number of individuals in the population

$f(BB) = \# A_2 A_2$'s in the population / total number of individuals in the population

The frequency of allele 1 (A_1) or “ p ” can be calculated by the following formula:

$$p = f(A_1A_1) + 1/2 f(A_1A_2)$$

The frequency of allele 2 (A_2) or “ q ” can hence be calculated by the following similar formula:

$$q = f(A_2A_2) + 1/2 f(A_1A_2)$$

The following relationship should always hold true when there are only two alleles involved in a system:

$$p + q = 1$$

Under the theorem of Hardy-Weinberg Equilibrium, genotypic frequencies are related to allelic frequencies according to the following statements:

$$p^2 = f(A_1A_1)$$

$$2pq = f(A_1A_2)$$

$$q^2 = f(A_2A_2)$$

Hardy-Weinberg Equilibrium also states that the allelic frequencies, p and q, will not change over successive generations unless one or more of the following is true:

- There is migration from or immigration to the population.
- There is non-random mating.
- There is natural selection acting on the alleles in question or on linked alleles.
- There is mutation of either or both alleles.
- The population is not infinitely large.



MICROEVOLUTION ACTIVITY STUDENT INSTRUCTIONS AND RULES

- 1.) Distribute “prey” items from one bag throughout the “habitat”.
- 2.) Students choose genotypes at random.
 - Each student will receive a safety pin.
 - Each student selects two beads at random from the “gene pool” and places them on her/his safety pin.
 - Each student notes her/his genotype (PP, PG, or GG).
 - Record the number of each genotype in the population in the data table.
- 3.) Each student obtains a prey-capturing device to match her/his genotype:
PP – spoon, PG – fork, GG– knife.
- 4.) When the instructor gives the signal, “predators” will begin capturing prey, adhering to the following rules:
 - Predators may use only their prey capturing device to capture prey. They may not use any part of their body (hands, feet, tongue, etc.)
 - Predators must successfully transfer the prey into their cup in order for it to be considered captured. They may not use the cup to help capture the prey. The cup may not touch the ground.
 - Predators will be allowed to search for prey for exactly one minute. At the end of the minute, the instructor will give the signal to stop and all predators must stop capturing prey immediately. Only prey already in the cup at this time may be counted.
 - Take care not to collide with other predators.
- 5.) At the beginning of each one minute round:
 - Record the number of each predator phenotype/genotype under “# Predators at Beginning of Round” in the data table.
 - Record the number of each allele present in the population in the data table under “# Alleles at beginning of Round”.

6.) At the end of each one minute round:

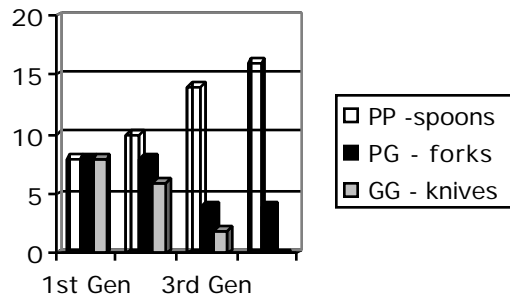
- For each predator, count the total number of prey captured. Compute the mean number of prey captured per predator and record this in the data table under “Mean # Prey Captured”.
- Every predator that has successfully captured the mean number of prey or greater for that round “survives”. Record the number of each type of predator surviving under “#Predators Surviving at End of Round” .
- Record the number of surviving alleles of each type under “# Alleles at end of Round”.
- Assume that every surviving predator will have three offspring. Hence, every predator that survives (*i.e.* has successfully captured the mean number of prey or greater) removes their beads from their pins. They then obtain four more identical beads and place all six back in the gene pool. For example: if a predator with a spoon phenotype that captured more than the mean number of prey during a given round, she/he would place six purple beads into the gene pool. A fork phenotype that captured more than the mean number of prey during a given round would place three purple beads and three green beads into the gene pool. A knife phenotype that captured more than the mean number of prey during a given round would place six green beads into the gene pool. Every predator who did not capture at least the mean number of prey would place their beads into a pool of “extras”. Every student then draws two beads at random from the “gene pool” and obtains the appropriate matching phenotype before beginning the next round.

7.) Perform as many rounds as time allows. Each round represents one generation.

8.) Construct two graphs using your data.

Graph one: x-axis = generations (rounds)
y-axis = number of predators at beginning of round (plot each predator type using a different symbol)

Graph two: x-axis = generations (rounds)
y-axis = number of alleles at beginning of round (plot each allele type using a different symbol)



Example Graph 1: Number of genotypes/phenotypes at beginning of round over four generations.



DEMONSTRATING HARDY-WEINBERG EQUILIBRIUM

After completing the basic microevolution activity, calculate the frequency of each allele and each genotype in the population.

$$f(\text{PP}) = \frac{\# \text{PP genotypes}}{\# \text{PP genotypes} + \# \text{PG genotypes} + \# \text{GG genotypes}}$$

$$f(\text{PG}) = \frac{\# \text{PG genotypes}}{\# \text{PP genotypes} + \# \text{PG genotypes} + \# \text{GG genotypes}}$$

$$f(\text{GG}) = \frac{\# \text{GG genotypes}}{\# \text{PP genotypes} + \# \text{PG genotypes} + \# \text{GG genotypes}}$$

$$f(\text{P}) = p = f(\text{PP}) + \frac{1}{2} f(\text{PG})$$

$$f(\text{G}) = q = f(\text{GG}) + \frac{1}{2} f(\text{PG})$$

Generation	f(PP)	f(PG)	f(GG)	p	q

Using the values for p and q in the last generation, compute the expected values of the frequency of each genotype according to the Hardy-Weinberg theory:

Expected frequency of PP = p^2 =

Expected frequency of PG = $2pq$ =

Expected frequency of GG = q^2 =

How do these values compare with the observed genotypic frequencies in the last generation? Use the table below to compare the observed and expected frequencies.

	OBSERVED	EXPECTED
f(PP)		
f(PG)		
f(GG)		

If your expected and observed frequencies differ dramatically, what could account for the difference?



DESIGNING AN EXPERIMENT IN MICROEVOLUTION

Design an experiment to test how altering some factor will affect the numbers of genotypes and alleles in the population.

1.) Form hypotheses about how changing some factor about the experimental ecosystem (prey, predators, habitat) would alter the frequency of genotypes and/or alleles in the predator population.

Remember that a hypothesis can be defined as an "educated guess" or a proposed pattern, cause, or explanation stated along with other alternatives to be tested and either falsified or supported. In almost all cases, there is more than one alternate hypothesis for any given scientific question. Hence, a truly rigorous examination of most questions involves testing each of these hypotheses and eliminating as many as possible through falsification. A null hypothesis for a given question refers to the hypothesis that there is no effect of the proposed cause or treatment or that there is no difference between control and experimental groups.

Some possible factors that could be changed in the microevolution scenario include:

Population size

Non-random mating

Habitat (surface on which prey items are placed)

Amount of prey items

Type of prey items

Other?

State your hypotheses to be tested:

2.) Make predictions. Once you have several alternate hypotheses to work with, the next step is to form predictions about what will happen under various test conditions if your original hypothesis is false or supported. The more specific you are able to make your predictions, the more direction they will provide in designing your experiments. As an example: For the hypothesis, "The pH of soil is higher on north facing slopes of

mountains", you could predict that "If the pH of soils is higher on north facing slopes than on south facing slopes, then the mean of repeated measurements of pH on slopes facing north will be significantly higher than the mean of repeated measurements of pH on slopes facing south.

State your predictions about your hypotheses. What do think will happen?

3.) Design an experiment to test your hypotheses. Identify you independent and dependent variables. *Independent variables* express the variables that we alter in an experiment or the variable that is the proposed cause or explanation. *Dependent variables* express the variables that we expect to respond to the change we make in the independent variable or the effect of the independent variable. Be sure to include an appropriate *control* or group of replicates in which we do not alter the independent variable.

Description of experimental design:

Control:

Independent variable:

Dependent variable(s):

4.) **Perform your experiment and record your results on a separate page.**

5.) **State your conclusions regarding your hypotheses.**



MICROEVOLUTION: SUMMARY DISCUSSION GUIDE

Questions to lead student discussion:

1.) Did all of the members of the predator population survive each generation? How many survived each generation?

Only half of the predator population survived each generation.

2.) What impact did survival have on an individual predator's ability to leave offspring?

Only survivors had offspring. Individual's who did not survive, did not leave any offspring.

3.) Was there any variation among the phenotype of the predators?

Yes – fork, knife, and spoon

4.) Did different phenotypes differ in their ability to leave offspring? Who was most successful? Least successful? Which phenotype would you say had the most advantage?

In most cases there will be differential success in reproduction among phenotypes.

5.) Are phenotypes inherited?

Yes, the phenotype of the predator (fork, knife, spoon) is directly related to the predator's genotype.

6.) What happened to the make-up of phenotypes in the population over time?

If there is differential reproductive success, the phenotype leaving the most offspring every generation will become the most prevalent.

What the activity has just demonstrated, therefor, is **natural selection**, which is based on the assumption that

If....

- Not all members of a population survive to reproduce.
- There is variation in the population, and certain forms are more successful at surviving and leaving offspring than others, and
- The characteristics leading to increased survival and reproduction are inherited.

Then....

The characteristics associated with increased reproduction will accumulate in the population.

Additional thought questions:

1.) You may have observed that even if no knives survived into the next generation, there will still be a few knives “born” in that generation. Explain how that could happen?

Because parents each contribute only one allele to the genotype of their offspring, it is possible that two surviving forks (PG) could mate, resulting in a 1/4 chance of their having an offspring with genotype GG – knife.

2.) What do you think would happen if the environment changed, and the prey items were most easily captured by the forks?

Most likely, the G allele would become more common, resulting in a larger number of forks and knives each generation until a new equilibrium was reached.