**Eukaryotic Natural Selection Activity Handout**

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**Introduction**

This activity is a simulation of the classic example of color change due to natural selection in the Peppered Moth (*Biston betularia*) in England which was studied by Kettlewell. Initially the Peppered Moth had a light brown color which provided them camouflage on most trees. With the advent of the industrial revolution, the bark of the trees became covered in soot and thus was darker. As a result the light brown coloration was no longer cryptic. The darker forms of the moth were harder to see on the dark bark and thus survived better and reproduced more.

In this activity there are two colors of moths (phenotypes) black and brown. There are three genotypes. The black moths have two possible genotypes: homozygous dominant (BB) and heterozygous (Bb). The brown moths are all the homozygous recessive (bb) genotype. The frequency of the dominant allele (B) in the population is given by p and the frequency of the recessive allele (b) in the population is given by q. The sum of p and q equals 1. The Hardy Weinberg Equation allows us to use p and q to calculate the frequency of the three genotypes. This equation is written as p2 + 2pq + q2 = 1. The frequency of the homozygous dominant genotype (BB) is given by p2. The frequency of the heterozygous genotype (Bb) is given by 2pq. The frequency of the homozygous recessive genotype is given by q2. Because all the homozygous recessive moths are brown and the other genotypes are black, q2 can be calculated by simply dividing the number of brown moths by the number of total moths. For example, if there were 10 brown moths out of a total of 40 moths, then q2 would equal 10/40 or 0.25. Take the square root of q2 to calculate q. In our example above, the square root of 0.25 is 0.5. If q equals 0.5, then p equals 1 – q or 0.5. The homozygous dominant frequency (p2) equals 0.52 or 0.25. The heterozygous frequency is 2\*p\*q (2\*0.5\*0.5) which equals 0.5.

By knowing the total population size (total moths) and the number of individuals with the recessive phenotype (brown moths) one can calculate q and p as well as the frequency for the three different genotypes. In this activity you will make these calculations at different times over a ten minute period for black and brown moths and on three different colored backgrounds: green, brown, and black. Robins will be eating the moths. On the green background the two colors of moths are consumed equally. On the brown background more black than brown moths are consumed by the robins. On the black background more brown than black moths are consumed by the robins.

**Activity**

Walk up to the large disk at the far end of the rectangular area for eukaryotic natural selection. You are going to need to be able to move your view up close to the disk and to the small sphere in front of the disk. To do this left click on the word Avatar on the far left of the top toolbar. In the drop down box that appears, left click on Camera Controls (5th item from the bottom). You will now see a rectangle with two boxes inside of it. The arrows in the left box allow you to spin your view, while the arrows in the right box allow you move up and down as well as left and right. You can drag the rectangle to other parts of your screen if you find it is in the way. I tend to leave it in the top right corner. To zoom in on this the disk or sphere, hold down the ALT key on your keyboard and left click on the disk or sphere. You can now use the wheel on your mouse to zoom in and out.

Left click on the disk and you will see a blue box that allows you to set the initial settings for the activity. There should be 5 robins, 40 moths, and the p value is set to 0.5. If you need to change a number, left click on the appropriate button along the bottom of the blue box and you can type in the correct number. Once you have set these numbers correctly, they should stay the same for all three trials. Now click on the button labeled Bark and select the green background.

Before you click on Run, go to the questions page (a separate handout) and look at table 1. This is the table you will be entering data into for the green bark trial. You will pause the run at specific times and count the number of brown moths. With the parameters you entered in the blue box, your initial total number of moths is 40 and the initial number of brown moths is 10. Enter those numbers in the first line of the first two open columns in table 1.

To monitor the time, you want to look closely at the small yellow-brown sphere in front of the disk. Zoom in on this sphere and you will see text in yellow above it. The top text is a timer and tells you how long the trial has been running. The next text down tells you how many moths are there. It should be 40 except just after a moth is eaten. The next two lines of text tell you the genotype of the last moth eaten and the last moth born.

*Collecting Data*

First off you need to obtain the tables and questions page and the Excel worksheet required to complete this activity. The tables and question page is available at:

<http://wiki.bio-se.info/lib/exe/fetch.php?media=wiki:handout_for_eukaryotic_natural_selection_question_sheet_-_tables.docx>

If your instructor gave you an Excel sheet to use, then use that. If no Excel sheet has been provided, thenthe Excel worksheet with tables and graphs is available at:

<http://wiki.bio-se.info/lib/exe/fetch.php?media=wiki:handout_for_eukaryotic_natural_selection_excel_sheet.xlsx>

Now you are ready to start the first trial. Click on run in the blue box. The blue box will disappear and on the green disk you will see that robins and moths start to appear. After about 30 seconds, the robins will start to move, eating moths, and the trial has begun. When the timer gets to 30 seconds, left click on the disk and from the blue box that appears, select Pause. The green background on the disk will go white and you can count the brown moths (they appear grey). Return to table 1 and enter the total number of moths and the number of brown moths in the row for 0.5 minutes (30 seconds). Return to the blue box and click on Unpause. The robins start to fly again eating the moths. Pause the run and count the brown moths at 1 minute as well as at 1.5, 2, 4, 6, 8, and 10 minutes. This should have allowed you to fill in the first two blank columns in table 1.

After you have collected all the brown moth data for table 1 (10 minutes) click on the disk and in the blue box, select Stop. This stops the run and removes all the robins and moths. Click on Bark again and this time select the Brown Bark. You are ready to start trail 2 and to enter data into Table 2. Repeat the steps for trail one, only using a brown background. Often all the black moths are consumed by the robins, in which case the dominant allele (B) is gone. In this case, all the homozygous dominant (BB) and heterozygous (Bb) moths are consumed and only the brown homozygous recessive (bb) moths remain. After 10 minutes, stop the run and change the background to black.

The black run is different because when all the brown moths (bb) are consumed, the recessive allele (b) is still found in the heterozygous (Bb) moths. Thus, rather than recording the number of brown moths alive at each time interval, you will record the frequency (q) of the recessive allele (b). To do this, click on the sphere after the run has started and you will get the advanced mode on the sphere. This mode gives you a lot more information, including q which is the frequency of the recessive allele. At each time interval record the q value in the appropriate column of Table 3. Once you have reached 10 minutes, stop the run. You are now done with the disk and sphere. Before you leave, take a photo of your avatar standing in front of the disk and send it to your instructor. To do this, set the view you want and use your camera icon on the toolbar at the bottom of your SL screen to take a photo. Do not save the photo (that cost money) but select the email option and email the photo to your professor. Be sure to type your real name in the title of the email so your professor can give you credit for this part of the assignment.

*Completing the Tables.*

Complete the tables as your instructor has advised you. Your instructor might ask you to complete the tables yourself, or might provide an Excel program that completes some or all of the tables for you once you have entered the data you collected. Once you have completed tables 1, 2 and 3, you can transfer some of this data to the table 4. Table 4 shows phenotype frequency from brown moths from the green (GR), brown (BR), and black (BL) background trials. Similarly it shows the dominant (B) allele frequency for all three trials and the heterozygous genotype (Bb) frequency for all three trials. You will use the data on table 4 to make graphs showing how phenotype, allele, and genotype frequency changed over time on the three different backgrounds. Your instructor might ask you to make the graphs directly on paper, or might ask you to go to the Excel sheet. Enter the data in table 4 in the Excel sheet and the graphs will be made for you.

Completing the Questions

At the bottom of the question page, below the tables, there are some questions. Answer these questions and then you are done. Save the question page and the Excel sheet with your name in the filename. Attach both the question page and the Excel sheet to an email, and send the email to your instructor.