

Ap biology lab report for population genetics and microbiology essay sample

[Science](#), [Genetics](#)



Abstract

The study of microevolution was tested in this laboratory experiment through the examination, observation, and analysis of various population conditions, some under the Hardy-Weinberg Theory of Genetic Equilibrium, which would advance the student scientists' understanding of both microevolution and the mathematical aspects of microevolution known as population genetics. The students first predicted the result of each of the 6 cases. The data was found using a program called PopCycle (Herron 2002), which picked genotypes randomly, and showed the results after particular conditions were entered. Students took these numbers and visually displayed them in charts.

They configured the predicted amount of adults for each genotype by using the Hardy-Weinberg mathematical equation $p^2 + 2pq + q^2$ to figure out the expected adults for the genotypes AA, Aa, and aa. The students also produced graphs showing allelic frequencies and genotype frequencies. They concluded that their original hypotheses were indeed correct. Therefore, there was support that the Hardy-Weinberg Theory and the 5 cases for evolution were indeed accurate in their own particular cases (170 words).

Introduction

In this report, students conduct a laboratory procedure that exemplifies certain occurrences of genetics among populations. In other words, the students predict and observe the results in a population from generation-to-generation due to certain specific conditions, also known as a study called

microevolution (Pearson Education, Inc. 2002). In some cases, evidence supports evolution. Evolution is defined as the changes that have transformed life on Earth from its earliest beginnings to the diversity that characterizes it today (Pearson Education, Inc. 2002). There are five known cases for evolution, known as selection, migration, non-random mating, genetic drift, and mutations. Selection is best described by the alteration of survival rates. For example, if a specific genotype (eg. AA, or homozygous dominant) is lethal, there will be no (0) adults in the population. Or perhaps there are limiting factors that limit a particular genotype to 50%, that case too is also selection. Migration is also known as gene flow.

When members of a population migrate or move away from their habitat, various genes enter different communities and other populations. Migration rates are originally 100% if there is no net movement. Non-random mating means that mates are selected individually, and that perhaps two organisms mate so that their offspring will have beneficial features, also changing the species' possible features. Genetic drift occurs in small populations, and it is the change of the population's gene pool due to chance (Pearson Education, Inc. 2002). Due to small numbers in the population, results are inconsistent and therefore change is frequent. Lastly, mutations are a case for evolution in that the rare changes in DNA cause genetic diversity (Pearson Education, Inc. 2002).

One of the reoccurring themes in the laboratory procedure is the Hardy-Weinberg Equilibrium Theory. Under this theory by these two popular scientists, they stated that gene pool frequencies are inherently stable, but

that evolution should be expected in all populations all the time; they resolved this apparent paradox by analyzing the probable net effects of evolutionary mechanisms (O'Neil 2002). The particular conditions that had to exist for this to apply were that the population had no mutation, had no natural selection, was a large population, had only random mating, and had no migration. For the cases to follow later in the lab, Cases 1 and 2 exemplify Hardy-Weinberg conditions. All of the others either have selection or not enough members in the population, which will be the most-closely observed conditions.

In this lab, there are also mathematical aspects. Population genetics is known as the branch of biology that provides the mathematical structure for the study of the process of microevolution (Wikipedia 2004). An equation exists under the Hardy-Weinberg Equilibrium Theory. The equation $(p^2 + 2pq + q^2)$ helps to determine the predicted amount of adults of a particular genotype under particular conditions. In the equation, p represents the dominant allele, noted by a capital letter, A for instance. Also, q in the equation represents the recessive allele, noted by a lowercase letter. And, as suspected, pq represents heterozygous. The equation was derived from when two alleles come to produce a genotype from p and q (UVa 1996). Since the allele frequencies must add up to 1, q must equal $1 - p$ and p must equal $1 - q$. Therefore an individual is represented by $p + q$, and the offspring could be found by $(p + q)^2$, which comes out to $p^2 + 2pq + q^2$ (UVa 1996). Essentially, the allele frequencies could be multiplied by 100%

to find the chance that that particular allele will show up in the next generation, given that the conditions are of Hardy-Weinberg.

The students next hypothesized what would happen in the 6 cases that follows. They concluded that Case 1 was the control group and that there would only be small fluctuations in the allele frequencies. This is supported best by the fact that the conditions are under those described by Hardy and Weinberg. In Case 2, the students also hypothesized that there would be a small fluctuation in the allele frequencies, however they were different numbers due to the initial allele A frequency change. In Case 3, with the addition of selection, the students hypothesized that there would be no (0) adults with genotype aa, and that therefore, the allele frequencies would have greater fluctuations. In Case 4, the students hypothesized that due to the selection rates, there would ultimately be a heterozygote advantage.

They believed that all homozygous recessive genotypes would be lethal and that all homozygous dominant genotypes would have a 50% survival rate. Therefore, there were reasonable fluctuations in the allele frequencies, and the heterozygote had the advantage. In Case 5, the students predicted that genetic drift would prevail. Due to a small population, one small change in the population would bring a great change in the allele frequencies. In Case 6, given the original conditions that the initial value of A is 0.5 and the survival rates of all genotypes is 0.5, the students hypothesized that essentially only 50% of the population would survive, while the allele frequencies were rather consistent.

Materials

Personal Computer

Internet Access or PopCycle v1. 0 program (Cited John C. Herron ©2002)

Calculator

Methods

Methods below apply to all 6 cases in Table I below. The particular settings such as the initial value for allele A's frequency, mutation rates, survival rates, and migration rates must be set to the required value before doing the methods listed below.

Case # Initial A Rates of Survival Migration Mutation Amt of Gen Zygotes

1 0.5 ALL 1.0 ALL 0 ALL 0.5 \rightarrow 100

2 0.9 ALL 1.0 ALL 0 ALL 0.5 \rightarrow 100

3 0.5 AA= 1 Aa= 1 aa= 0 ALL 0 ALL 0.5 \rightarrow 100

4 0.5 AA= 0.5 Aa= 1 aa= 0 ALL 0 ALL 0.10 \rightarrow 100

5 0.5 ALL 1.0 ALL 0 ALL 0.5 10 exact

6 0.5 ALL 0.5 ALL 0 ALL 0.5 \rightarrow 100

Table I

1. Using their knowledge of population genetics, students predicted the change in allelic frequency over time in each of the simulations and word as a hypothesis (If...then).
2. Randomly click in the Gene Pool area of PopCycle until the number of zygotes required is met
3. Click DONE in all categories of the window except the last one.
4. Record the number of adults of each genotype in your data table under the column Experimental.
5. Click DONE on the last category.
6. Record the ending allele frequency in the data table.
7. Using the Hardy-Weinberg Equation, calculate the expected (or hypothesized) number of adults for each genotype in each generation.

Results

The charts below represent the quantitative results for the 6 cases. Case 1 was more of a control group, in that all the settings for it were standard for Hardy-Weinberg conditions. As noticed in the Frequencies, there were only small fluctuations between the original 0.5 allele A frequency. Case 2 was just like Case 1 except the original allele A frequency is different. It is set to something other than 0.5, or 0.9 here. As noticed in the numerical data below, it too only had small fluctuations. In both Case 1 and Case 2, there is no selection; any deviations in data are due to genetic drift. In Case 3, the

survival rates were brought into effect, eliminating the existence of a Hardy-Weinberg situation.

The homozygous recessive genotype is made lethal; therefore no adults are listed in the chart for this case. Due to the use of Hardy-Weinberg equation without the actual conditions, there are larger fluctuations in the allele frequencies. This case demonstrates selection. In Case 4, the survival rates are changed again, this time giving the homozygous dominant genotype 50% chance of survival. There are large fluctuations again, as for the same reasons listed in Case 3. Case 4 demonstrates the heterozygote advantage. Case 5 is different in that the number of zygotes is lessened, therefore providing less accurate results and demonstrating genetic drift. There are few fluctuations in this case, but when there is a fluctuation, it's a large change. Case 6 is the made-up one, which in this case sets all survival rates to 0.5. As a result, half the population of the adults is eliminated, and there are only small fluctuations in the ending allele frequencies.

Gen Total Adults Genotype for AA Genotype for Aa Genotype for aa Ending Freq

Pred Expect Pred Expect Pred Expect A a

1 100 25 28 50 49 25 23 . 53 . 47

2 100 28 38 50 41 22 21 . 59 . 41

3 100 35 31 48 52 17 17 . 57 . 43

4 100 33 34 49 49 19 17 . 59 . 41

5 101 35 35 49 46 17 20 . 57 . 43

Table II-Case 1

Gen Total Adults Genotype for AA Genotype for Aa Genotype for aa Ending
Freq

Pred Expect Pred Expect Pred Expect A a

1 100 81 77 18 21 1 2 . 88 . 12

2 100 77 79 21 20 1 1 . 89 . 11

3 100 79 77 20 22 1 1 . 88 . 12

4 100 77 78 21 21 1 1 . 89 . 11

5 100 79 77 20 21 1 2 . 88 . 12

Table III-Case 2

Gen Total Adults Genotype for AA Genotype for Aa Genotype for aa Ending
Freq

Pred Expect Pred Expect Pred Expect A a

1 75 19 36 38 39 19 0 . 74 26

2 96 53 61 37 35 6 0 . 82 . 18

3 95 64 69 28 26 3 0 . 86 . 14

4 99 73 82 24 17 2 0 . 91 . 09

5 99 82 85 16 14 1 0 . 93 . 07

Table IV-Case 3

Gen Total Adults Genotype for AA Genotype for Aa Genotype for aa Ending
Freq

Pred Expect Pred Expect Pred Expect A a

1 69 17 11 35 58 17 0 . 58 . 42

2 67 23 16 33 51 12 0 . 62 . 38

3 74 28 19 35 55 11 0 . 63 . 37

4 67 27 23 31 44 9 0 . 67 . 33

5 62 28 23 27 39 7 0 . 69 . 31

6 66 31 24 28 42 6 0 . 68 . 32

7 72 33 22 31 50 7 0 . 65 . 35

8 70 30 23 32 47 9 0 . 66 . 34

9 67 29 22 30 45 8 0 . 66 . 34

10 63 27 26 28 37 7 0 . 71 . 39

Table V-Case 4

Gen Total Adults Genotype for AA Genotype for Aa Genotype for aa Ending
Freq

Pred Expect Pred Expect Pred Expect A a

1 10 2/3 2 5 6 2/3 2 . 5 . 5

2 10 2/3 2 5 5 2/3 3 . 45 . 55

3 10 2 1 5 5 3 4 . 35 . 65

4 10 1 1 5 5 4 4 . 35 . 65

5 10 1 1 5 2 4 7 . 2 . 8

Table VI-Case 5

Gen Total Adults Genotype for AA Genotype for Aa Genotype for aa Ending
Freq

Pred Expect Pred Expect Pred Expect A a

1 51 13 8 25 28 13 15 . 43 . 57

2 50 9 6 25 25 16 19 . 37 . 63

3 51 7 6 24 24 20 21 . 35 . 65

4 50 6 7 23 20 21 23 . 34 . 66

5 51 6 9 23 21 22 21 . 38 . 62

Table VII-Case 6

Additionally, there are graphs attached at the end of the lab report. The first six graphs show the trend of the allele A frequency over generations. Keep in mind that the allele a frequency line would be opposite of the line shown, for there is no need to show the line. The value for the allele a can be found by doing $1 -$. The next set of 6 graphs shows the genotype frequencies at the first and last generation of the particular population.

Discussion

All hypotheses are evidently supported in the results. In Case 1, the students hypothesized that only little or no fluctuations in the allele frequencies would result. The original proportions for each genotype, as derived from the Hardy-Weinberg equation, are 1: 2: 1 to the genotypes AA: Aa: aa, respectively. Therefore, the students' hypothesis was indeed correct. In Case 2, the students predicted almost the same thing, saying that the frequency values would just not be around 0. 5, but rather around the figure that the student selected as the initial allele A value. Therefore, the students accurately predicted the results for the case. In Case 3, the students concluded that the homozygous recessive genotype was lethal and found this to be supported by the data. They predicted this would create a large fluctuation in the allele frequencies, and it indeed did. In Case 4, the students hypothesized that in addition to the lethal homozygous recessive

genotype, the homozygous dominant genotypes would have a 50% survival rate, eliminating half of them.

This, the students noted, would create an even large change in the ending allele frequencies. Since the heterozygous genotype was favored, the students noted it as having stabilizing selection. In Case 5, the students hypothesized that, due to a small population, there would be greater changes in the alleles because there are less chances of probability. For instance, if one flips a coin twice and gets heads both times, it does not mean that the coin is only heads on both sides. If they were to flip a coin 200 times, they would find that it would create an even 1: 1 ratio. In Case 6, the students hypothesized that, due to the 50% survival rates in all genotypes, half the population would be eliminated. This hypothesis was supported in that each time either 50 or 51 adults survived out of 100. The cases most effectively exemplified each of the following listed below:

Case # Overall Result

- 1 No Selection; considered the control group
- 2 No selection; different initial allele freq
- 3 Selection in lethal dominant recessive allele (aa)
- 4 Heterozygous advantage (stabilizing selection)
- 5 Genetic Drift due to small population
- 6 50% survival rate for all genotypes in population

Conclusion

In this laboratory experiment, students have learned very much, extending their knowledge especially on genetics. In the field of microevolution, the students observed various cases after hypothesizing what they think would happen. They found that they were right the entire time on all their hypotheses. The lab helped them to understand the Hardy-Weinberg Theory and their mathematical equation $[p^2 + 2pq + q^2]$, which are crucial parts to understanding population genetics. The lab was an excellent opportunity for the students to extend their knowledge on an issue that is addressed continually over and over. They have been provided with a valid argument for evolution, although it does not mean they must support it. It is best in today to be most informed with current issues, so not only was the lab an opportunity for students to understand microevolution and population genetics, but it also helped them to understand the argument for evolution when considering genetic variation causes.

Sources Cited

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