**AP Biology AP Lab 8 – Population Genetics**

 **Using the Computer Simulation Allele A1**

Name \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Block \_\_\_\_\_\_\_ # \_\_\_\_\_\_\_\_

**PRE-LAB**

1. Explain what is meant by a population being in Hardy-Weinberg equilibrium.

1. List and briefly explain the 5 conditions that need to be met to maintain a population in Hardy-Weinberg equilibrium.

(1)

(2)

(3)

(4)

(5)

In 1908, G.H. Hardy and W. Weinberg independently suggested a mathematical approach to study evolution. In this approach, evolution is viewed as changes in the frequency of alleles in a population of organisms. The Hardy-Weinberg theorem can be used to predict the frequencies that one would expect of different genotypes in a population. Of what value is such a prediction? It provides a yardstick by which changes in a population — changes in allele frequency, and thereby evolution — can be measured. One can study a population and ask: Is evolution occurring for a specific gene? Then one can hypothesize and further investigate: What force(s) is acting on this population to cause this change over time?

**INTRODUCTION**

The purpose of this case study is to help you develop an intuition about how selection and mutation cause evolution. You will use a software simulation of an evolving population to analyze the examples discussed in AP Lab 8, and to answer a variety questions concerning changes in the frequencies of alleles. Once you are familiar with the simulation program, you can use it to answer questions of your own.

To complete this case study you will need the application program AlleleA1. At school, access this from your student drive folder. At home, you can download AlleleA1 from the Evolutionary Analysis website (<http://faculty.washington.edu/herronjc/SoftwareFolder/AlleleA1.html>). Versions are provided that run under MacOS and Windows. AlleleA1 simulates evolution at a single locus in an ideal population. The locus has 2 alleles: *A1* and *A2.* AlleleA1 allows you to enter parameters controlling selection, mutation, migration, drift, and inbreeding. The program then plots a graph showing the frequency of allele *A1* over time. Each generation's frequency is calculated from the previous generation's frequency, according to the Hardy-Weinberg equations.

AlleleA1 is easy to use. Small boxes in the lower portion of the AlleleA1 window allow you to enter and change the parameters for the simulation. The tool palette has buttons that allow you to run the simulation, clear the graph, reset all parameters to their default values, print your graph, and quit. More details on using AlleleA1 can be found in the manual, available both as a separate PDF file and online under the Help menu.

**CASE 1: A TEST OF AN “IDEAL” HARDY-WEINBERG POPULATION**

After fiddling with the simulation program to see how it works, restore all parameters to their default settings. The default settings encompass initial frequencies of 0.5 for both alleles, and the assumptions of no selection, no mutation, no migration, no genetic drift, and random mating.

Run the simulation to investigate what happens to the frequency of the genes under the conditions described above.

1. Change the values for the starting frequency of allele *A1.*
	1. Click in the box next to the parameter “Starting frequency of allele A1” and enter a value between 0 and 1.
	2. In the bottom right, under “Graph lines” click the option – “Auto”, this will graph each trial on the same graph using different colors.
	3. After you enter each gene frequency, click the “Run” button.
	4. Enter the final frequency after 500 generations for both A1 and A2 in the table below.

|  |  |  |
| --- | --- | --- |
| **Frequency of A1** | **Final Frequency of A1****after 500 Generations** | **Final Frequency of A2****after 500 Generations** |
| 0.1 |  |  |
| 0.25 |  |  |
| 0.4 |  |  |
| 0.5 |  |  |
| 0.6 |  |  |
| 0.75 |  |  |
| 0.9 |  |  |

1. Copy the results for each frequency on the graph below. Clearly label each line on your graph.



**QUESTION -** Based on your results, how does the beginning frequency of a gene effect the frequency of the genes after 500 generations when a population is in Hardy-Weinberg equilibrium? Explain why.

1. Change the number of generations. In this case, does it make a difference if the number of generations is smaller or larger? Why?
	1. Click the “Reset” button to return the program to its default settings and to clear the previous test.
	2. Click in scroll box next at the end of the X-axis to change the number of generations.
	3. In the bottom right, under “Graph lines” click the option – “Auto”, this will graph each trial on the same graph using different colors.
	4. After you select the generation size the previous graph will clear, so make note of your graph before you change the generation number.
	5. Click the “Run” button and note the graph.
	6. Enter the final frequency after each run for both A1 and A2 in the table below.

|  |  |  |
| --- | --- | --- |
| **Number of Generations** | **Final Frequency of A1** | **Final Frequency of A2** |
| 15 |  |  |
| 25 |  |  |
| 50 |  |  |
| 500 |  |  |
| 1,000 |  |  |
| 10,000 |  |  |
| 100,000 |  |  |

1. Copy the results of the graph for the effects of the size of each of the selected generation size.



**QUESTION –** Based on your results, how does the number of generations effect the frequency of the genes when a population is in Hardy-Weinberg equilibrium? Explain why.

**QUESTION -** Does your experimentation verify that *any* starting frequencies are in equilibrium so long as there is no selection, no mutation, no migration, and no drift?

**CASE 2: SELECTION AGAINST HOMOZYGOUS RECESSIVE**

In the natural world, not all genotypes have the same rates of survival. The environment mayfavor some genotypes while selecting against others. In Case 2, we will create a more realisticsimulation by applying a selection pressure to the population. In this Case, you will assume thatthe homozygous recessive individuals never survive (100% selection against), and thatheterozygous and homozygous dominant individuals survive 100% of the time.

To mimic this case using our computer simulation we will change the “Fitness” values for each genotype. We will set homozygous dominant (A1, A1) to 1.0, heterozygous (A1, A2) to 1.0, and homozygous recessive (A2, A2) to 0.0. This is telling the computer that for every 100 homozygous dominant individuals that survive, 100 heterozygous individuals would also survive, but 0 homozygous individuals would survive.

1. Run this simulation using the following number of generations:

|  |  |  |
| --- | --- | --- |
| **Number of Generations** | **Final Frequency of A1** | **Final Frequency of A2** |
| 15 |  |  |

1. Record the final phenotype frequencies for the 15 generations run.

|  |  |  |  |
| --- | --- | --- | --- |
| Number of Generations | Homozygous dominant (A1, A1) | Heterozygous(A1, A2) | Homozygous recessive(A2, A2) |
| 25 |  |  |  |

**QUESTION -** Predict what would happen to the p and q frequencies if you simulated another 10 generations?

**QUESTION -** Since homozygous recessives are strongly selected against, would you expect the recessive (A2) allele to be completely removed from the population? In other words, in a large population would it be possible to completely eliminate a deleterious (or even lethal) recessive allele. Explain.

1. Continue to run this simulation using the following number of generations:

|  |  |  |
| --- | --- | --- |
| **Number of Generations** | **Final Frequency of A1** | **Final Frequency of A2** |
| 25 |  |  |
| 50 |  |  |
| 500 |  |  |
| 1,000 |  |  |

1. Record the final genotype frequencies for the 1,000 generations run.

|  |  |  |  |
| --- | --- | --- | --- |
| **Number of Generations** | **Homozygous dominant (A1, A1)** | **Heterozygous****(A1, A2)** | **Homozygous recessive****(A2, A2)** |
| 1,000 |  |  |  |

1. Copy the results of the graph you generated using 1,000 generations.



**QUESTION -** Describe a real-life example of selection against a homozygous recessive genotype.

**CASE 3: HETEROZYGOUS ADVANTAGE**

From Case 2, it is easy to see what happens to the lethal recessive allele in a population.However, data from human populations, sometimes show an unexpected high frequency of adeleterious allele in some populations. Sometimes there is a slight advantage to beingheterozygous for a trait rather than homozygous dominant. So the situation is now morecomplicated: homozygous recessives are still strongly selected against and do not survive toreproduce, but now, in addition, homozygous dominants have a lower reproductive rate than heterozygotes. We will incorporate this fact into our simulation.

To mimic this case using our computer simulation we will change the “Fitness” values for each genotype. We will set homozygous dominant (A1, A1) to 0.8, heterozygous (A1, A2) to 1.0, and homozygous recessive (A2, A2) to 0.0. This is telling the computer that for every 100 heterozygous individuals that survive, 80 homozygous dominant individuals would also survive, but 0 homozygous individuals would survive.

1. Run this simulation using the default settings, this represents Hardy-Weinberg equilibrium, and record the genotype and phenotype frequencies in the tables below.
2. Hit the “Reset” button.
3. Repeat the simulation, but this time change the “Fitness” settings as described above. Record the gene and genotype frequencies in the tables below.

|  |  |  |
| --- | --- | --- |
| **Number of Generations** | **Final Frequency of A1****after 500 generations** | **Final Frequency of A2****after 500 generations** |
| Hardy-Weinberg Equilibrium |  |  |
| Heterozygous Advantage |  |  |

Record the final genotype frequencies after each run.

|  |  |  |  |
| --- | --- | --- | --- |
| **Number of Generations** | **Homozygous dominant (A1, A1)** | **Heterozygous****(A1, A2)** | **Homozygous recessive****(A2, A2)** |
| Hardy-Weinberg Equilibrium |  |  |  |
| Heterozygous Advantage |  |  |  |

Copy the results for both graph lines you generated. Clearly label each line.



**QUESTION -** Explain how the changes in p and q frequencies in **Case 3** (Heterozygote Advantage) compare with the frequencies in **Case 1** (H-W Equilibrium) &**Case 2** (Selection)?

**QUESTION -** Do you think the recessive allele will be eliminated in Case 3? Explain.

**QUESTION -** What is the impact of heterozygote advantage to genetic variation in a population? Explain.

**QUESTION -** Describe a real-life example of heterozygote advantage.

**CASE 4: GENETIC DRIFT**

Remember that even though natural selection is creating adaptive change, it is not the onlyforce molding a population. Equally important are the forces of random chance that can cause changes over time in a population even though they are not adaptive. We will simulate this by creating smaller population in our simulation.

Change the size of the populations. Are smaller or larger populations more likely to experience genetic drift? Why?

1. Click the “Reset” button to return the program to its default settings and to clear the previous test.
2. Click in box next to “Population size”, which the default setting is *infinity*, and enter the number of your desired population size.
3. In the bottom right, under “Graph lines” click the option – “Auto”, this will graph each trial on the same graph using different colors.
4. Click the “Run” button after you enter each population size. **Run each size population several times!**
5. Enter the final frequency for each population size for both A1 and A2 and the final genotype frequencies in the table below for the **final run** of each population size.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Size of population** | **Final Frequency of A1** | **Final Frequency of A2** | **Homozygous dominant** **(A1, A1)** | **Heterozygous****(A1, A2)** | **Homozygous recessive****(A2, A2)** |
| 5 |  |  |  |  |  |
| 50 |  |  |  |  |  |
| 500 |  |  |  |  |  |
| 5,000 |  |  |  |  |  |
| 50,000 |  |  |  |  |  |

1. Copy the results of the graph for the effects of population size on gene frequency. Clearly label each line with the appropriate population size.



**QUESTION -** Compare the initial parental genotype and allele frequencies in the different sub-populations.

**QUESTION -** Compare the final genotype and allele frequencies in the different sub-populations.

**QUESTION -** What do these results indicate about the importance of population size as an evolutionary force?

**QUESTION -** How is this issue significant in conservation biology and endangered species conservation?

**QUESTION -** Describe a real-life example of genetic drift.

**CASE 5: THE EFFECTS OF MUTATIONS ON GENE FREQUENCY**

One of the five requirements for Hardy-Weinberg equilibrium is there can be no mutations occurring in the population. In this case study we will examine the effects mutations can have on gene frequency.

1. Hit the “Reset” button to restore the default settings.
2. The default settings are for Hardy-Weinberg equilibrium, which means the mutation rates are set at 0. Alter the mutation rates of the population by clicking in the box “Mutation rate from A1 to A2” and entering a value between 0 and 1.
3. In the bottom right, under “Graph lines” click the option – “Auto”, this will graph each trial on the same graph using different colors.
4. Click the “Run” button after you enter each mutation rate.
5. Enter the final frequency for each population size for both A1 and A2 and the final genotype frequencies in the table below.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Mutation Rates** | **Final Frequency of A1** | **Final Frequency of A2** | **Homozygous dominant** **(A1, A1)** | **Heterozygous****(A1, A2)** | **Homozygous recessive****(A2, A2)** |
| 0.001 (1/1000) |  |  |  |  |  |
| 0.01 (1/100) |  |  |  |  |  |
| 0.1 (1/10) |  |  |  |  |  |
| 0.5 (5/10) |  |  |  |  |  |

1. Copy the results of the graph for the effects of mutation rates on gene frequency. Clearly label each line with the appropriate mutation rate.



**QUESTION –** Summarize what the data tells us about the effects of mutations on gene frequency in a population.

**CASE 6: THE EFFECTS OF MIGRATION ON GENE FREQUENCY**

One of the five requirements for Hardy-Weinberg equilibrium is there can be no migration of new individuals into a population. In this case study we will examine the effects migration can have on gene frequency.

1. Hit the “Reset” button to restore the default settings.
2. The default settings are for Hardy-Weinberg equilibrium, which means the migration rates are set at 0. Alter the migration rates of the population by clicking in the box “Fraction migrants each generation” and entering a value between 0 and 1. This value represents the fraction of individuals in each generation that are migrants newly arrived from another population. For example setting the parameter to 0.1 means that each generation ten percent of the individuals in the population are new arrivals from another population.
3. You must also set the “Frequency of A1 in the source population” between 0 and 1. This establishes the frequency of the A1 gene in the source population that is providing the immigrants.
4. In the bottom right, under “Graph lines” click the option – “Auto”, this will graph each trial on the same graph using different colors.
5. Let us assume we are studying an island population and we will set the “***Starting Frequency of A1***” for the island to **0.2.** Let us also assume we have individuals migrating from the mainland to the island. The migrating individuals are coming from a mainland population with a higher frequency of A, so let us set the “***Frequency of A1 in the source population***” to **0.7**.

**PREDICTION**: What do you expect will happen to the frequency of A1 in the island population over 500 generations?

1. Click the “Run” button after you enter each migration rate.
2. Enter the final frequency for each population size for both A1 and A2 and the final genotype frequencies in the table below.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Fraction of Migration** | **Final Frequency of A1** | **Final Frequency of A2** | **Homozygous dominant** **(A1, A1)** | **Heterozygous****(A1, A2)** | **Homozygous recessive****(A2, A2)** |
| 0.001 (.01%) |  |  |  |  |  |
| 0.01 (1%) |  |  |  |  |  |
| 0.1 (10%) |  |  |  |  |  |
| 0.5 (50%) |  |  |  |  |  |

**QUESTION –** What happens to the frequency of A1 in the island population? Which genotype(s) becomes more common in the population? Explain why this happens.

1. Copy the results of the graph for the effects of mutation rates on gene frequency. Clearly label each line with the appropriate mutation rate.



**QUESTION –** What is the effect of the rate of migration on the change in gene frequency?

**QUESTION –** Why does the gene frequency level out at 0.7 for most of your trials?

1. Let us try the opposite scenario. This time let us assume we are studying an island population and we will set the “***Starting Frequency of A1***” for the island to **0.7.** Let us also assume we have individuals migrating from the mainland to the island. The migrating individuals are coming from a mainland population with a higher frequency of A, so let us set the “***Frequency of A1 in the source population***” to **0.2**.

**PREDICTION**: What do you expect will happen to the frequency of A1 in the island population over 500 generations?

1. Click the “Run” button after you enter each migration rate.

**QUESTION –** What happens to the frequency of A1 in the island population this time? Which genotype(s) becomes more common in the population this time? Explain why this happens.

  **HARDY-WEINBERG PROBLEM #1**

In fruit flies, *Drosophila melanogaster*, the allele for normal-length wing is dominant over theallele for vestigial wings (vestigial wings are stubby little curl that cannot be used for flight).In a population of 1,000 individuals, 360 show the recessive phenotype. How manyindividuals would you expect to be **homozygous dominant** and how many would be**heterozygous** for this trait?

1. Choose the letters you will use to represent the alleles & genotypes:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Dominant Allele |  |  | Homozygous dominant |  |
| Recessive Allele |  | Heterozygous |  |
| Homozygous recessive |  |

1. Translate to known frequencies:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| ***p***(Dominant Allele) |  |  | ***p2***(Homozygous dominant) |  |
| ***q***(Recessive Allele) |  | ***2pq***  (Heterozygous) |  |
| ***q2***(Homozygous recessive) |  |

1. Choose which Hardy-Weinberg formula you will primarily use:
2. Solve the problem using the appropriate equation(s). Neatly show your work below. Write your final answer in box.

**FINAL ANSWER**

**HARDY-WEINBERG PROBLEM #2**

The allele for unattached ear lobes is dominant over the allele for attached earlobes. In a population of 500 individuals, 25% show the recessive phenotype. How many individualswould you expect to be **homozygous dominant** and how many would be **heterozygous** forthis trait?

1. Choose the letters you will use to represent the alleles & genotypes:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Dominant Allele |  |  | Homozygous dominant |  |
| Recessive Allele |  | Heterozygous |  |
| Homozygous recessive |  |

1. Translate to known frequencies:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| ***p***(Dominant Allele) |  |  | ***p2***(Homozygous dominant) |  |
| ***q***(Recessive Allele) |  | ***2pq***  (Heterozygous) |  |
| ***q2***(Homozygous recessive) |  |

1. Choose which Hardy-Weinberg formula you will primarily use:
2. Solve the problem using the appropriate equation(s). Neatly show your work below. Write your final answer in box.

**FINAL ANSWER**

**HARDY-WEINBERG PROBLEM #3**

The allele for the hair pattern called “widow’s peak” is dominant over the allele for no“widow’s peak”. In a population of 1,000 individuals, 510 show the dominant phenotype.How many individuals would you expect of each of the three possible **genotypes** for thistrait?

1. Choose the letters you will use to represent the alleles & genotypes:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Dominant Allele |  |  | Homozygous dominant |  |
| Recessive Allele |  | Heterozygous |  |
| Homozygous recessive |  |

1. Translate to known frequencies:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| ***p***(Dominant Allele) |  |  | ***p2***(Homozygous dominant) |  |
| ***q***(Recessive Allele) |  | ***2pq***  (Heterozygous) |  |
| ***q2***(Homozygous recessive) |  |

1. Choose which Hardy-Weinberg formula you will primarily use:
2. Solve the problem using the appropriate equation(s). Neatly show your work below. Write your final answer in box.

**FINAL ANSWER**

**HARDY-WEINBERG PROBLEM #4**

Rh refers to a protein maker on red blood cells. In the United States about 16% of the population is Rh negative. The allele for Rh negative is recessive to the allele for Rh positive. If the student population of a high school in the U.S. is 2,000, how many studentswould you expect of each of the three possible **genotypes** for this trait?

1. Choose the letters you will use to represent the alleles & genotypes:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Dominant Allele |  |  | Homozygous dominant |  |
| Recessive Allele |  | Heterozygous |  |
| Homozygous recessive |  |

1. Translate to known frequencies:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| ***p***(Dominant Allele) |  |  | ***p2***(Homozygous dominant) |  |
| ***q***(Recessive Allele) |  | ***2pq***  (Heterozygous) |  |
| ***q2***(Homozygous recessive) |  |

1. Choose which Hardy-Weinberg formula you will primarily use:
2. Solve the problem using the appropriate equation(s). Neatly show your work below. Write your final answer in box.

**FINAL ANSWER**

**HARDY-WEINBERG PROBLEM #5**

In certain African countries 4% of the newborn babies have sickle-cell anemia, which is arecessive trait. Out of a random population of 1,000 newborn babies, how many would youexpect of each of the three possible **genotypes** for this trait?

1. Choose the letters you will use to represent the alleles & genotypes:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Dominant Allele |  |  | Homozygous dominant |  |
| Recessive Allele |  | Heterozygous |  |
| Homozygous recessive |  |

1. Translate to known frequencies:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| ***p***(Dominant Allele) |  |  | ***p2***(Homozygous dominant) |  |
| ***q***(Recessive Allele) |  | ***2pq***  (Heterozygous) |  |
| ***q2***(Homozygous recessive) |  |

1. Choose which Hardy-Weinberg formula you will primarily use:
2. Solve the problem using the appropriate equation(s). Neatly show your work below. Write your final answer in box.

**FINAL ANSWER**

**HARDY-WEINBERG PROBLEM #6**

In a population, the **dominant phenotype** of a certain trait occurs 91% of the time. What isthe frequency of the dominant allele?

1. Choose the letters you will use to represent the alleles & genotypes:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Dominant Allele |  |  | Homozygous dominant |  |
| Recessive Allele |  | Heterozygous |  |
| Homozygous recessive |  |

1. Translate to known frequencies:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| ***p***(Dominant Allele) |  |  | ***p2***(Homozygous dominant) |  |
| ***q***(Recessive Allele) |  | ***2pq***  (Heterozygous) |  |
| ***q2***(Homozygous recessive) |  |

1. Choose which Hardy-Weinberg formula you will primarily use:
2. Solve the problem using the appropriate equation(s). Neatly show your work below. Write your final answer in box.

**FINAL ANSWER**