Genetic Equilibrium and Natural Selection

Introduction: If different forms of a gene (alleles) are present in a large randomly breeding population, the gene frequencies will remain in equilibrium from generation to generation if other factors, such as migration, mutation, and selection, are not functioning. If one or more of these factors is functioning within a population, the equilibrium may be disturbed and the gene frequencies may change. The gene frequencies may be altered in a direct manner and evolution will occur if there is continued selection for a particular phenotype (actually selection against an unfavorable phenotype). Genetic equilibrium with respect to all combinations of genes in a population rarely, if ever occurs. However, an equilibrium concept can be used as a basic model against which we can measure genetic change. This is a basic law of population genetics and is known as the Hardy-Weinberg Equilibrium and is based on probabilities.

I. The Hardy-Weinberg Equilibrium

Background:
Each team of students should have one packet of 100 plastic ‘alleles’ and a shaker. Colors represent alleles of a gene. Each packet should contain 60 dark colored alleles (A) and 40 light colored alleles (a). The 100 represent all such alleles in the gene pool of a population. The allele frequencies are therefore expressed as $A = 0.6 = p$ and $a = 0.4 = q$. Since only two alleles are being considered, the mathematical expression can be written as $p + q = 1$. When mating is taken into account, this becomes $p^2 + 2pq + q^2 = 1$. Where $p^2$ is the proportion of AA individuals, $2pq$ the Aa individuals, and $q^2$ the aa individuals in a population.

Procedure:
1. Place 100 alleles in the shaker, cover with your hand and shake it to randomly mix. Without looking, remove 2 alleles from the shaker. This pair simulates the diploid combination of alleles in an individual of the next generation.
2. Record the genotype (‘A’ for dark and ‘a’ for light) in Data Table II. Replace the alleles in the shaker and repeat #1 – 100 times. Record the results EACH time.

Data and Calculations:
1. Using the gene frequencies given in the background do the following and record in Data Table I:
   a. Record the allele frequency.
   b. Calculate the genotype frequency that is expected according to the Hardy-Weinberg equilibrium $p^2 + 2pq + q^2 = 1$.
   c. Calculate the phenotype frequency (dominant vs. recessive), assuming that ‘a’ is the recessive trait, remember that dominant would be $(p^2 + 2pq)$ and the recessive would be $q^2$.
2. Using the data that was collected during the experiment do the following:
   a. Calculate the genotype frequencies from the genotypes recorded in the chart, using the following equations. Record results in Data Table II.

\[
\text{Frequency of AA} = \frac{\text{Total AA}}{\text{Total AA} + \text{Total Aa} + \text{Total aa}}
\]

\[
\text{Frequency of Aa} = \frac{\text{Total Aa}}{\text{Total AA} + \text{Total Aa} + \text{Total aa}}
\]
Genetic Equilibrium and Natural Selection

Frequency of aa = \( \frac{\text{Total } aa}{\text{Total } AA + \text{Total } Aa + \text{Total } aa} \)

b. Using the equation \( p^2 + 2pq + q^2 = 1 \), and \( p + q = 1 \), calculate the experimental frequency of each allele (A, a). Record the results in Data Table II.

c. Calculate the phenotype frequency (dominant vs. recessive), assuming that ‘a’ is the recessive trait, remembering that dominant would be \( (p^2 + 2pq) \) and the recessive would be \( q^2 \).

II. Natural Selection

1. Place all of the alleles in shaker as in Part I. Remove two at a time as before and record a total of 100 resulting genotypes in Data Table III.

2. When complete, report the results to the instructor for recording. Record this information and complete the information for this generation using the same equations as the previous example.

3. Natural selection operates only on the phenotype, therefore the less favorable genes must be expressed in order for selection to occur. Thus if A is dominant to a and aa produces an unfavorable phenotype, selection will eliminate a greater proportion of the aa individuals than AA or Aa individuals. Selection will be simulated against \( \frac{1}{2} \) of the aa phenotypes by removing \( \frac{1}{2} \) of the light alleles (a) present in the percent of aa individuals based on the class total.

4. Remove the alleles in pairs as before to obtain a total of 100 offspring and record the number of each genotype for the second generation in Data Table II.

5. Report your second generation results to the instructor. Record the class results for the 2nd generation and complete the data chart for the rest of the information for this generation.

6. Repeat the experiment for a third generation following the same instructions as above.
III. Data Tables

Data Table I – Expected Results

<table>
<thead>
<tr>
<th>Genotype Frequency</th>
<th>Allele Frequency</th>
<th>Phenotype Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>AA</td>
<td>Aa</td>
<td>AA and Aa</td>
</tr>
<tr>
<td></td>
<td>aa</td>
<td>aa</td>
</tr>
</tbody>
</table>

Data Table II – Experimental Results

<table>
<thead>
<tr>
<th>Number of each Genotype (alleles picked)</th>
<th>Genotype Frequency</th>
<th>Allele Frequency</th>
<th>Phenotype Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>AA</td>
<td>Aa</td>
<td>A</td>
<td></td>
</tr>
<tr>
<td></td>
<td>aa</td>
<td>a</td>
<td></td>
</tr>
</tbody>
</table>

Conclusion Questions Part I.
1. How do the experimental results compare with the expected results? Does it appear that evolution is taking place? Justify your answer.

2. Why does the allele frequency remain constant between the expected and experimental results?
Data Table III

<table>
<thead>
<tr>
<th>Generation</th>
<th>Team Results</th>
<th>Class Results</th>
<th>Class Results</th>
<th>Class Results</th>
<th>Class Results</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Number of each Genotype</td>
<td>Number of each Genotype</td>
<td>Genotype Frequency</td>
<td>Allele Frequency</td>
<td>Phenotype Frequency</td>
</tr>
<tr>
<td>1st</td>
<td>AA Aa aa</td>
<td>AA Aa aa</td>
<td>AA Aa aa</td>
<td>A a</td>
<td>AA + Aa aa</td>
</tr>
<tr>
<td>2nd</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3rd</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Conclusion Questions Part II.
1. What is happening to the frequencies of the two alleles as selection against ‘aa’ individuals continues to operate through successive generations?

2. If this selection continues, will all of the ‘a’ genes eventually be eliminated from the population? Why or why not?