A species is a population of organisms in which interbreeding takes place; these organisms are reproductively isolated from other populations. In order to comprehend how the characteristics of a species may change in time, we can study the variation in the relative frequencies of alleles for a particular trait in a population from one generation to the next. If the expression of a trait has survival and/or reproductive value for an organism, we would expect that most of the individuals within a population would possess the allele(s) for the expression of this trait. On the other hand, if an allele hinders reproduction, we would expect that natural selection would reduce the frequency of this allele in a population. Also, some traits may have little influence on the survival of an organism and would play little or no role in the process of natural selection. The purpose of this week's laboratory exercise is to calculate allelic frequencies of some human traits and to examine how factors such as selection affect gene frequencies.

**IMPORTANT BIOLOGICAL QUESTIONS ADDRESSED IN THIS LABORATORY**

* How is the frequency of an allele in a population estimated?
* Are dominant alleles always most frequent in a population?
* What conditions must be met for the Hardy-Weinberg law of equilibrium to hold true?
* How does selection against homozygous individuals affect allelic frequencies?
* How does selection against heterozygous individuals affect allelic frequencies?

**FREQUENCIES OF ALLELES IN A POPULATION**

The purpose of this exercise is to determine the frequencies of alleles in a population. We will study human traits, so please bring all of your body to class. Several human traits are thought to be influenced by pairs of alleles. Individuals with a dominant phenotype like dimples, for example, may be homozygous dominant (DD) or heterozygous (Dd), whereas those with the recessive phenotype (no dimples) must have a homozygous recessive genotype (dd). Because individuals with the dominant phenotype have two possible genotypes, we will direct our attention to recessive individuals. A Punnett-square will be used to understand the computation procedure below. In the example presented, we want to know the recessive and dominant allele frequencies when we only know the recessive phenotype frequencies in the population. To determine the dominant and recessive allele frequencies, use the following procedure:

1. **Count the dominant and recessive phenotypes in the population.**
   
   For example, count the dimpled (dominant) and non-dimpled (recessive) individuals: 
   
   36 Dimpled and 64 Non-dimpled

2. **Calculate the recessive phenotype frequency:**

   \[
   \text{RECESSIVE PHENOTYPE FREQUENCY} = \frac{\text{Number of Recessive Phenotypes}}{\text{Total}}
   \]

   For example, Non-dimpled Phenotype Frequency = $\frac{64}{100} = 0.64$ (64%). The probability of finding a recessive phenotype, therefore, is 0.64. Probability and frequency are the same thing in population genetics. We will use certain mathematical rules in probability to help solve frequency questions.
3. **Calculate the recessive genotype frequency:**
   Since the only way a recessive phenotype can exist is with a recessive genotype, then:

   \[ \text{RECESSIVE GENOTYPE FREQUENCY} = \text{Recessive Phenotype Frequency} \]

   For example, Non-dimpled Genotype (dd) Frequency \( f(\text{dd}) = 0.64 \) (64%). Thus, the probability of finding a recessive genotype is 0.64. Find this frequency in the Punnett-square below.

<table>
<thead>
<tr>
<th>Frequencies of Male Gametes (Alleles)</th>
<th>D</th>
<th>d</th>
</tr>
</thead>
<tbody>
<tr>
<td>D</td>
<td>DD</td>
<td>Dd</td>
</tr>
<tr>
<td></td>
<td>(dimpled)</td>
<td>(dimpled)</td>
</tr>
<tr>
<td>d</td>
<td>Dd</td>
<td>dd</td>
</tr>
<tr>
<td></td>
<td>(dimpled)</td>
<td>(non-dimpled)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>0.64</td>
</tr>
</tbody>
</table>

4. **Take the square root of the recessive genotype frequency to obtain the recessive allele frequency:**
   The frequency (probability) of a recessive genotype is the product of the equal frequency (probability) of a recessive male gamete and that of the recessive female gamete; therefore we can determine the recessive allelic frequency by taking the square root of the recessive genotype (dd) frequency (0.64).

   \[ \text{RECESSIVE ALLELE FREQUENCY} = (\text{Recessive Genotype Frequency})^{0.5} \]

   For example, Recessive Allele (d) Frequency \( f(d) = (0.64)^{0.5} = 0.80 \). In other words, 80% of the alleles in this population are recessive (d). More of the Punnett-square may now be filled in.

<table>
<thead>
<tr>
<th>Frequencies of Female Gametes (Alleles)</th>
<th>D</th>
<th>d 0.80</th>
</tr>
</thead>
<tbody>
<tr>
<td>D</td>
<td>DD</td>
<td>Dd</td>
</tr>
<tr>
<td></td>
<td>(dimpled)</td>
<td>(dimpled)</td>
</tr>
<tr>
<td>d 0.80</td>
<td>Dd</td>
<td>dd</td>
</tr>
<tr>
<td></td>
<td>(dimpled)</td>
<td>(non-dimpled)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>0.64</td>
</tr>
</tbody>
</table>
5. **Calculate the dominant allele frequency:**
Since the alleles are either dominant or recessive, the frequencies (probabilities) of dominant and recessive alleles must add to one: 1 = \( f(\text{Dominant allele}) + f(\text{Recessive allele}) \). With this information we will be able to calculate the frequency of the dominant allele.

**DOMINANT ALELE FREQUENCY = 1.00 - Recessive Allele Frequency**

For example, Dominant Allele (D) Frequency = \( f(D) = 1.00 - 0.80 = 0.20 \). The Punnett-square now shows:

\[
\begin{array}{c|c|c|c|c}
\text{Frequencies of Female Gametes (Alleles)} & D & 0.20 & d & 0.80 \\
\hline
D & 0.20 & DD & (dimpled) & Dd & (dimpled) \\
\hline
d & 0.80 & Dd & (dimpled) & dd & (non-dimpled) \\
\hline
& & & & 0.64 \\
\end{array}
\]

6. **Calculate the dominant genotype frequencies:**
Remember, the probability of finding a homozygous or heterozygous genotype is the product of the probabilities of the male-gamete and female-gamete alleles.

**HOMOZYGOUS DOMINANT GENOTYPE (DD) FREQUENCY = f(DD)**
\( = [f(\text{Dominant Allele})]^2 = (0.20)^2 = 0.04 \) (4%)

**HETEROZYGOUS GENOTYPE (Dd) = f(Dd) (two ways to get the Dd combination) =**
\( = f(\text{Dominant Allele}) \times f(\text{Recessive Allele}) \times 2 = \)
\( = 0.20 \times 0.80 \times 2 = 0.16 \) (16%) \( \times 2 = 0.32 \) (32%)

The Punnett-square may now be completed:

\[
\begin{array}{c|c|c|c|c}
\text{Frequencies of Female Gametes (Alleles)} & D & 0.20 & d & 0.80 \\
\hline
D & 0.20 & DD & (dimpled) & Dd & (dimpled) \\
\hline
& & & & 0.04 & 0.16 \\
\hline
d & 0.80 & Dd & (dimpled) & dd & (non-dimpled) \\
\hline
& & & & 0.16 & 0.64 \\
\end{array}
\]
(Note that the numbers within the square sum to one.) Thus, 64% of this population have no dimples and have a dd genotype. On the other hand, of the 36% who have dimples, we estimate that 4% have a DD genotype and 32% (16% x 2) have a heterozygous (Dd) genotype. The estimates of dominant and recessive allele frequencies as determined above depend upon the assumptions underlying the Hardy-Weinberg Law of Equilibrium, which are described in your text.

The calculations shown above are derived from basic rules of probability and concepts of Mendelian genetics. Hardy and Weinberg summarized the calculations of allelic and genotypic frequencies using two equations:

\[
\begin{align*}
(1) \quad p + q &= 1 \\
(2) \quad p^2 + 2pq + q^2 &= 1,
\end{align*}
\]

where \( p = f(\text{dominant allele}) \), \( q = f(\text{recessive allele}) \), \( p^2 = f(\text{homozygous dominant genotype}) \), \( 2pq = f(\text{heterozygous genotype}) \), and \( q^2 = f(\text{homozygous recessive genotype}) \).

The following is a list of some human traits, the inheritance of which has been studied using genealogical or pedigree analysis, since controlled breeding experiments cannot be done for obvious reasons. You should not infer from this list that each trait is exclusively controlled by a single gene. Other genes and perhaps environmental factors could contribute to the phenotypic expression of each trait (Barnes and Mertens, 1976).

1. Record, by filling in the appropriate column in Table 1, the frequencies of phenotypes in your class for the traits described below.
2. Calculate the allelic frequencies for each trait.
3. Name a trait whose dominant allele frequency is less than its recessive allele frequency.

**HUMAN TRAITS**

**Attached Ear Lobe (ee):** In many people, the ear lobes hang free, but when a person is homozygous recessive for an allele (ee), the ear lobes are attached directly on to the side of the head so that there is no lobe hanging freely.

**Widow's Peak (W):** If the hairline drops downward and forms a distinct point in the center of the forehead, one is said to have a "widow's peak." This is due to the action of a dominant allele (W). Note: if a gene for baldness has been expressed, it will not be possible to score this trait.

**Tongue Rolling (T):** A dominant allele (T) gives one the ability to roll the tongue into a distinct U-shape when it is extended from the mouth.

**Interlocking Fingers (I):** Fold your hands together and interlock the fingers. Notice which thumb is on top. Left over right is dominant (I).

**Hitch-Hiker's Thumb (hh):** Bend your thumb tip back as far as it will go. If the angle created by the outside of your thumb approaches 90° rather than 45°, you are homozygous for a recessive allele called hitch-hiker's thumb.

**Bent Phalanx (B):** Hold your hands in front of you with your palms toward you. Place the little fingers of each hand side-by-side and press them together. Are they parallel over their entire length or do the terminal digits flare out away from each other? If they flare out, you possess at least one dominant allele; if they are straight you are homozygous recessive (bb).
**Left Handedness (rr):** Left handedness is recessive (rr) to right handedness which is associated with the presence of a dominant allele (R).

**Short Stature (S):** Short stature (S) is dominant to tall stature (ss). Males taller than 70 inches (5' 10") and females taller than 67 inches (5' 7") are considered to be tall.

**Long Palmar Muscle (ll):** A long palmar muscle (ll) can be detected by examining the tendons that run over the inside of the wrist. Clench your fist tightly, flex your hand, and feel your tendons. If there are three, you have a long palmar muscle (ll). If there are two, since the large middle one will be missing, you do not have this muscle (L). Examine both wrists since it may be present in one arm only.

**Pigmented Iris in Eyes (F):** The presence of a dominant allele (F) causes the formation of pigment in the iris of eyes. Other genes determine the exact nature and density of this pigment, and hence we have eyes that are brown, hazel, violet and green. Unpigmented irises (ff) result in eyes that are blue or gray in color. Be careful of pseudo phenotypes generated by contact lenses.

**Mid-Digital Hair (H):** Some people have hair on the middle joints of their fingers, while others do not. The complete absence of hair from the fingers is due to recessive alleles (hh) and its presence is due to a dominant (H) allele. Other genes may determine which fingers produce hair. This hair may be very fine so you should look very carefully on all fingers before deciding whether this hair is absent from your fingers.

**Curly, Wavy, and Straight Hair:** Curly (CC) hair is incompletely dominant over straight (cc) hair; heterozygotes (Cc) have wavy hair. Again, be ready to recognize pseudo phenotypes with this trait.

**Dimples (D):** The presence of facial dimples is due to the presence of a dominant allele (D). Perhaps dimples are evident on one cheek only, or there may be more than one dimple per cheek. Have your laboratory partner smile for an assessment of this trait.

**Freckles (F):** Freckles (F) are dominant to no freckles (ff). Note that freckles are most evident in the summer when skin is exposed to sunlight.

**Dark Hair (H):** Dark hair color (H) is dominant to blond or tawny hair color (hh). Pseudo phenotypes should report their true hair color.

**Non-Red Hair (R):** Non-red hair (R) is dominant to red hair (hh) color. If an individual has dark hair (H) and also red alleles (rr), then the phenotype will be dark hair with reddish highlights. These two genes for hair color are assorted independently.

**Long Eyelashes (L):** If your eyelashes are 3/8 inch (1.0 cm) long or longer, you possess a dominant allele (L) for long eyelashes.

**Taste of Sodium Benzoate (S):** If you possess a dominant allele (S) you will be able to taste sodium benzoate; non-tasters are homozygous recessive.

**Taste of Phenylthiocarbamate (PTC) (P):** If you can taste PTC, you possess a dominant (P) allele. Should you question your ability to taste this chemical, which is completely harmless to humans, you are a non-taster.
<table>
<thead>
<tr>
<th>Trait</th>
<th>Phenotypic Counts</th>
<th># with recessive phenotype</th>
<th>Total #</th>
<th>Recessive Phenotype Frequency $f(aa) = q^2$</th>
<th>Allele Frequencies</th>
</tr>
</thead>
<tbody>
<tr>
<td>Attached Ear Lobe (ee)</td>
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<td>Widow's Peak (W)</td>
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<td>Tongue Rolling (T)</td>
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<td>Interlocking Fingers (I)</td>
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<tr>
<td>Hitch-Hiker's Thumb (hh)</td>
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<td>Bent Phalanx (B)</td>
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<td>Left Handedness (rr)</td>
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<tr>
<td>Short Stature (S)</td>
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<tr>
<td>Long Palmar Muscle (ll)</td>
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<tr>
<td>Pigmented Eyes (F)</td>
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<tr>
<td>Mid-Digital Hair (H)</td>
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<tr>
<td>Curly Hair (K)</td>
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<td></td>
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<tr>
<td>Dimples (D)</td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Freckles (F)</td>
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<td></td>
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</tr>
<tr>
<td>Dark Hair (H)</td>
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<td></td>
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<tr>
<td>Non-Red Hair (R)</td>
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<td></td>
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<tr>
<td>Long Eyelashes (L)</td>
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<td></td>
</tr>
<tr>
<td>Taste Sodium Benzoate (S)</td>
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<td></td>
</tr>
<tr>
<td>Taste PTC (P)</td>
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<td></td>
</tr>
</tbody>
</table>

**TABLE 1.**
In this simulation, beads will represent genes; alleles will be depicted by beads of different colors, red or yellow. Beads in a beaker will represent the gene pool of a "population." Pairs of beads, selected at random, will represent individuals of the next generation. The frequencies of alleles (i.e., the frequencies of the colored beads) of these "offspring" will be used to construct a new gene pool, (i.e., beaker of beads). Pairs of beads will be selected again to make another generation, etc. Using this procedure, you will have an opportunity to see how allele frequencies change from one generation to the next. For the following procedures, use the worksheets provided in Figure 3 (no natural selection) and Figure 4 (with natural selection).

**Procedure for No Natural Selection**

The following procedure should be used to simulate the flow of alleles from one generation to the next without natural selection.

1. **Construct an initial population of 100 diploid individuals:** each individual carries two alleles (beads). To start, set up the dominant and recessive allele frequencies to be 0.5 (50%).

   **INITIAL GENERATION GENE POOL:**
   Dominant Allele Frequency $\times$ 200 = 0.5 $\times$ 200 = 100 R's or red beads
   Recessive Allele Frequency $\times$ 200 = 0.5 $\times$ 200 = 100 r's or yellow beads
   Note that the dominant and recessive alleles (beads) in the gene pool will always sum to 200 (i.e., 100 individuals).

   For 100 individuals (200 alleles) place 100 red (R) beads + 100 yellow (r) beads in the gene pool (beaker) and mix them up.

2. **Produce 20 Offspring:** Select 20 pairs of alleles (beads) at random; each pair of alleles (beads) represents an individual and should be maintained as such: i.e., 20 pairs of beads (40 alleles altogether) should be selected a pair at a time keeping the pairs together.

   In the sample shown in Figure 1, 8 RR (homozygous dominant, both red), 8 Rr (heterozygotes, one red and one yellow) and 4 rr (homozygous recessive, both yellow) were chosen. The offspring were 20 individuals or 40 alleles altogether. Use worksheets in Figure 3.

3. **Determine the dominant and recessive allele frequencies:**

   **DOMINANT ALLELE FREQUENCY** = Number of Dominant (R) Alleles / Total Number of Alleles
   For example, there are 24 red beads (R alleles) in the sample (Fig. 1). Thus, the Dominant Allele Frequency = 24/40 = 0.6 (60%). Use worksheets in Figure 3.

   **RECESSIVE ALLELE FREQUENCY** = 1 - Dominant Allele Frequency
   For example, Recessive Allele Frequency = 1 - 0.6 = 0.4 (40%)

4. **Construct the next generation with a total of 100 individuals** (200 beads) using the allele frequencies of the "offspring" computed above.

   **NEXT GENERATION GENE POOL:**
   Dominant Allele Frequency $\times$ 200 = 0.6 $\times$ 200 = 120 R's or red beads
   Recessive Allele Frequency $\times$ 200 = 0.4 $\times$ 200 = 80 r's or yellow beads

   Note that the dominant and recessive alleles in the gene pool will always sum to 200 (i.e., 100 individuals). You will save a lot of time counting beads if you return all the beads (100 red and 100 yellow) to the beaker and then adjust the numbers to construct the new generation by adding (in this example) 20 red beads and removing 20 yellow beads from the gene pool. Use worksheets in Figure 3.

5. **Select the next generation of "offspring" by returning to step 2.**

   After 5 generations, make a graph illustrating Recessive Allele Frequency as a function of generation.
Compare these results with what the Hardy-Weinberg Law would predict. Do the allele frequencies vary much between generations? Are the frequencies very different* in later generations from what they were in generation 1?

*You may test how closely matched your allelic frequencies are with those predicted in a population in H-W equilibrium by performing a chi square analysis on the number of each allele you counted in the offspring of the last generation (observed) compared with the number of each allele predicted for the offspring of the population if it were in H-W equilibrium (expected). See Table 2 (pg. 125) for a chi square worksheet and pgs. 5-7 and pgs. 97-99 for more information on chi square analysis.

**Figure 1.** An example of the computations required by the physical simulation of a breeding population without natural selection.

**SAMPLE COMPUTATIONS WITHOUT NATURAL SELECTION**

Generation __1___
Allele Frequencies:
Dominant/Red beads (R) __0.50___  Recessive/Yellow beads (r) ___0.50___

Offspring Selected:

\[
\begin{array}{cccccccccc}
    & Rr & RR & RR & rr & Rr & Rr & rr & rr & Rr & Rr \\
rr & Rr & Rr & RR & RR & RR & RR & Rr & RR & RR & RR \\
\end{array}
\]

Count the number of dominant (R) and recessive (r) alleles in offspring; compute allele frequencies.

Dominant/Red (R) Count __24__  Frequency __0.60__
Recessive/Yellow (r) Count __16__  Frequency __0.40__

Next generation gene pool will be __120__ Red alleles (R) and __80__ Yellow alleles (r).

Note:
NEXT GENERATION GENE POOL:
Dominant Allele Frequency x 200 = 0.6 x 200 = 120 R's or red beads
Recessive Allele Frequency x 200 = 0.4 x 200 = 80 r's or yellow beads
**Procedure for Natural Selection**

The following procedure should be used to simulate the flow of alleles from one generation to the next with natural selection. Prior to establishing an initial gene pool, decide which phenotype or genotype will be subjected to selection: dominant phenotype (RR and Rr individuals), recessive phenotype (rr individuals) or genotypes: homozygous dominant (RR), heterozygous (Rr), or homozygous recessive (rr). You will also have to decide on the degree of selection: for example, you may want to prevent 50 percent of a particular phenotype or genotype from reproducing.

1. **Construct an initial population of 100 diploid individuals:** each individual carries two alleles (beads). To start, set up the dominant and recessive allele frequencies to be 0.5 (50%).

   **INITIAL GENERATION GENE POOL:**
   - Dominant Allele Frequency x 200 = 0.5 x 200 = 100 R's or red beads
   - Recessive Allele Frequency x 200 = 0.5 x 200 = 100 r's or yellow beads
   Note that the dominant and recessive alleles (beads) in the gene pool will always sum to 200 (i.e., 100 individuals).

   For 100 individuals (200 alleles) place 100 red (R) beads + 100 yellow (r) beads in the gene pool (beaker) and mix them up. (This is exactly as in step 2 of the previous procedure.)

2. **Produce 20 Offspring: Select 20 pairs of alleles (beads) at random:** each pair of alleles (beads) represents an individual and should be maintained as such: i.e., 20 pairs of beads (40 alleles altogether) should be selected a pair at a time keeping the pairs together. (This is exactly as in step 2 of the previous procedure and the offspring are the same as in Figure 1.)

   In the sample shown in Figure 2, 7 RR (homozygous dominant, both red), 9 Rr (heterozygotes, one red and one yellow) and 4 rr (homozygous recessive, both yellow) were chosen: 20 individuals or 40 alleles altogether. Use worksheets in Figure 4.

3. **Apply "natural selection" to the "offspring"** by eliminating a certain percentage (50%, for example) of a particular phenotype or genotype from the new population prior to reproduction.

   In the example shown in Figure 2, the selection was 50 percent against individuals with dominant phenotypes. Thus, 50% of the 16 RR and Rr individuals were eliminated, leaving 3 RR, 5 Rr, and 4 rr individuals or pairs of beads. There was a total of 12 individuals or 24 alleles after selection. Use worksheets in Figure 4.

4. **Determine the dominant and recessive allele frequencies:**

   **DOMINANT ALLELE FREQUENCY = Number of Dominant (R) Alleles / Total Number of Alleles**

   For example, there are 11 red beads (R alleles) in the sample (Fig. 2). Thus, the Dominant Allele Frequency = 11/24 = 0.46 (46%). Use worksheets in Figure 4.

   **RECESSIVE ALLELE FREQUENCY = 1 - Dominant Allele Frequency**

   For example, Recessive Allele Frequency = 1 - 0.46 = 0.54 (54%)
5. **Construct the next generation with a total of 100 individuals** (200 beads) using the allele frequencies of the "offspring" computed above.

**NEXT GENERATION GENE POOL :**
Dominant Allele Frequency x 200 = 0.46 x 200 = 92 R's or red beads
Recessive Allele Frequency x 200 = 0.54 x 200 = 108 r's or yellow beads

Note that the dominant and recessive alleles (beads) in the gene pool will always sum to 200 (i.e., 100 individuals). You will save a lot of time counting beads if you return all the beads (100 red and 100 yellow) to the beaker and then adjust the numbers to construct the new generation by (in this example) removing 8 red beads and adding 8 yellow beads from the gene pool. Use worksheets in Figure 4.

6. **Select the next generation of "offspring" by returning to step 2.** Be sure to continue using the same selection parameters as you used for the first generation.

After 5 generations, make a **graph** illustrating Recessive Allele Frequency as a function of generation.

Compare these results with what the Hardy-Weinberg Law would predict. Do the allele frequencies vary much between generations? Are the frequencies very different* in later generations from what they were in generation 1? Do you think it would make a difference which genotype is selected against?

*You may test how closely matched your allelic frequencies are with those predicted in a population in H-W equilibrium by performing a chi square analysis on the number of each allele you counted in the offspring of the last generation (observed) compared with the number of each allele predicted for the offspring if the population was in H-W equilibrium (expected). See Table 3 (pg. 127) for a chi square worksheet and pgs. 5-7 and pgs. 97-99 for more information on chi square analysis.

**Figure 2.** An example of the computations required by the physical simulation of a breeding population with natural selection against half (50%) of the dominant phenotype.

**SAMPLE COMPUTATIONS WITH NATURAL SELECTION**

<table>
<thead>
<tr>
<th>Generation</th>
<th>Selection Rate is</th>
<th>Against</th>
<th>Allele Frequencies:</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>50%</td>
<td>Red (RR + Rr)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Dominant/Red beads (R) 0.50</td>
<td>Recessive/Yellow beads (r) 0.50</td>
</tr>
</tbody>
</table>

**Offspring Selected:**

- Rr
- RR*
- RR
- rr
- Rr
- rr
- Rr
- RR
- Rr
- RR
- RR
- RR
- RR
- RR

*The genotypes with a slash (ex., RR) are selected against. Then count the number of Dominant (R) and Recessive (r) alleles in offspring; compute allele frequencies.

- Dominant/Red (R) Count 11
- Frequency 0.46

- Recessive/Yellow (r) Count 13
- Frequency 0.54

Next generation gene pool will be 92 Red alleles (R) and 108 Yellow alleles (r).

**Note:**

**NEXT GENERATION GENE POOL :**
Dominant Allele Frequency x 200 = 0.46 x 200 = 92 R's or red beads
Recessive Allele Frequency x 200 = 0.54 x 200 = 108 r's or yellow beads
PROBLEMS

1. If beak length in Robins is controlled by a single pair of alleles with long beak associated with the presence of a dominant allele, what are the frequencies of dominant and recessive alleles if a population consists of 64 long beaked birds and 36 short beaked birds? Estimate the percentage of the population that is homozygous for the dominant (long beak) allele.

2. If red flower color in hawkweed is caused by the presence of a dominant allele and a population of hawkweed plants is 75 percent red flowered, what are the frequencies of the dominant and recessive alleles?

3. In mice, dark fur color is due to the presence of a dominant allele. If the frequency of recessive phenotype for fur color in a population of mice is 0.09, what is the dominant allele frequency?

4. If a population is large and there is natural selection against heterozygotes, how will the frequencies of dominant and recessive alleles change with time?

5. Would you expect the allele frequencies to change faster with selection against dominant phenotypes or recessive phenotypes? Explain your logic.

credits: This exercise was developed by G. Steucek and S. DiBartolomeis.

REFERENCES

Figure 3. A worksheet to aid your in your computations of allele frequencies for the simulated population without natural selection.

NO NATURAL SELECTION WORKSHEETS

Generation ______
Allele Frequencies:
Dominant/Red beads (R) _________  Recessive/Yellow beads (r) _________

Offspring Selected:

Count the number of Dominant (R) and Recessive (r) alleles in offspring; compute allele frequencies.

Dominant/Red (R) Count ______  Frequency _________
Recessive/Yellow (r) Count ______  Frequency _________

Next generation gene pool will be _______ Red alleles (R) and _______ Yellow alleles (r).

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Table 2. Statistical Analysis of Physical Simulation Without Natural Selection

<table>
<thead>
<tr>
<th># alleles in offspring</th>
<th>Observed # (O)</th>
<th>Expected # (E)</th>
<th>(O - E)^2/E</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dominant allele (R)</td>
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<td></td>
<td></td>
</tr>
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<tr>
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<td></td>
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Hypothesis/Model:

Calculated Chi Square Value ($\chi^2_{calc}$) =

Degrees of Freedom (# phenotypes – 1) =

Critical Chi Square Value =

Statistical Conclusion:

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<tr>
<th>Degrees of Freedom (DF)</th>
<th>Chi Square Critical</th>
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<tbody>
<tr>
<td>1</td>
<td>3.84</td>
</tr>
<tr>
<td>2</td>
<td>5.99</td>
</tr>
<tr>
<td>3</td>
<td>7.81</td>
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</table>
Figure 4. A worksheet to aid you in your computations of allele frequencies for the simulated population with natural selection.

**NATURAL SELECTION WORKSHEETS**

Generation ______ Selection Rate is ______ Against ______________________

Allele Frequencies:
Dominant/Red beads (R) _______ Recessive/Yellow beads (r) _______

Offspring Selected:

__________________________

Cross out genotypes selected against. Then count the number of Dominant (R) and Recessive (r) alleles in offspring; compute allele frequencies.

Dominant/Red (R) Count ______ Frequency ______

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Next generation gene pool will be _______ Red alleles (R) and _______ Yellow alleles (r).

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**Degrees of Freedom** (# phenotypes – 1) = 

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**Statistical Conclusion:**

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