**Population Genetics and Evolution**

**Introduction**

In 1908 G. H. Hardy and W. Weinberg independently suggested a scheme whereby evolution could be viewed as changes in the frequency of alleles in a population of organisms. In this scheme, if A and a are alleles for a particular gene locus and each diploid individual has two such loci, then $p$ can be designated as the frequency of the A allele and $q$ as the frequency of the a allele. Thus, in a population of 100 individuals (each with two loci) in which 40% of the alleles are A, $p$ would be 0.4. The rest of the alleles (60%) would be a, and $q$ would equal 0.60 (*i.e.*, $p + q = 1.0$). These are referred to as the **allele frequency**. The frequency of the possible diploid combinations of these alleles (AA, Aa, aa) is expressed as $p^2 + 2pq + q^2 = 1.0$. Hardy and Weinberg also argued that if five conditions are met, the population's alleles and genotype frequencies will remain constant from generation to generation. These conditions are as follows:

1. **The breeding population is large**. (The effect of chance on changes in allele frequencies is thereby greatly reduced.)
2. **Mating is random**. (Individuals show no preference for a particular phenotype.)
3. **There is no mutation**. (No alteration in the DNA sequence of alleles.)
4. **No differential migration occurs**. (No immigration or emigration.)
5. **There is no selection**. (All genotypes have an equal chance of surviving and reproducing.)

The Hardy-Weinberg equation describes an existing situation. If the five conditions are met, then no change will occur in either the allele or genotype frequencies in the population. Of what value is such a rule? It provides a benchmark by which changes in allele frequency, and therefore evolution, can be measured. One can look at a population and ask: Is evolution occurring with respect to a particular gene locus? Since evolution is difficult (if not impossible) to observe in most natural populations, we will model the evolutionary process using the class as a simulated population. The purpose of this simulation is to provide an opportunity to test some of the basic tenets of population genetics and evolutionary biology.

**Exercise 8A: Estimating Allele Frequencies for a Specific Trait within a Sample Population**

Using the class as a sample population, the allele frequency of a gene controlling the ability to taste the chemical PTC (phenylthiocarbamide) could be estimated. A bitter-taste reaction to PTC is evidence of the presence of a dominant allele in either the homozygous (AA) or heterozygous (Aa) condition. The inability to taste the chemical at all depends on the presence of homozygous recessive alleles (aa). To estimate the frequency of the PTC-tasting allele in the population, one must find $p$. To find $p$, one must first determine $q$, (the frequency of the non-tasting PTC allele), because only the genotype of the homozygous recessive individuals is known for sure (*i.e.*, those that show the dominant trait could be AA or Aa).

**Procedure**

1. Using PTC taste-test papers provided, tear off a short strip and press it to the tip of your tongue. PTC tasters will sense a bitter taste. For the purposes of this exercise these individuals are considered to be tasters.
2. A decimal number representing the frequency of tasters ($p^2 + 2pq$) should be calculated by dividing the number of tasters in the class by the total number of students in the class. A decimal number representing the frequency of non-tasters ($q^2$) can be obtained by dividing the number of non-tasters by the total number of students. Record these in Table 1.
3. Use the Hardy-Weinberg equation to determine the frequencies ($p$ and $q$) of the two alleles. Record these in Table 1. Also, calculate and record the values for $p$ and $q$ for the North American population.

| | Phenotypes | | | | Allele frequency based on H-W Equation | |
|---|---|---|---|---|---|---|
| | Tasters ($p^2 + 2pq$) | | Non-tasters ($q2$) | | p | q |
| Class Population | # | % | # | % | | |
| | | | | | | |
| North American Population | 0.55 | | 0.45 | | | |

**Questions:**

1. What was the percentage of heterozygous tasters in the class? How does this compare with the North American population?

**Exercise 8B**

**Case 1 - A Test of an Ideal Hardy-Weinberg Population**

In this exercise, the entire class will represent a breeding population. In order to ensure random mating, choose another student at random. In this simulation, we will assume that gender and genotype are irrelevant to mate selection.

The class will simulate a population of randomly mating heterozygous individuals with an initial gene frequency of 0.5 for the dominant allele A and 0.5 for the recessive allele a, and genotype frequencies of 0.25 AA, 0.5 Aa, and 0.25 aa. For simplicity, all individuals will have the initial genotype Aa. Record this in Table 2. Each member of the class will receive four cards. Two of the cards will have "A" written on them and two will have "a." The four cards represent the products of meiosis and each "parent" contributes a haploid set of chromosomes to the next generation.

**Procedure**

1. Turn the four cards over so that the letters do not show, shuffle them, and take the card on top to contribute to the production of the first offspring. Your partner should do the same. Put the two cards together to represent the alleles of your first offspring. On of you should record the genotype of this offspring in Table 2. Each student pair must produce two offspring, so all four cards must be reshuffled and the process repeated to produce a second offspring.
2. The other partner should record the genotype of the second offspring in Table 2. The very short reproductive career of this generation is over. How sad **: ~ (** You and your partner now become the next generation by assuming the genotypes of the two offspring. That is, one student assumes the genotype of the first offspring while the other students assumes the genotype of the second offspring.
3. Each student should obtain, if necessary, new cards representing the alleles in his or her respective gametes following meiosis. For example, Student 1 becomes genotype Aa and obtains cards A, A, a, a; Student 2 becomes aa and obtains cards a, a, a, a. Each participant should randomly select another individual with whom to mate in order to produce the offspring of the next generation. Remember, the sex of your mate does not matter, nor does the genotype. Follow the same mating procedure as before and record the new genotype after each generation. Collect class data after each generation.
4. **Allele frequency**: The allele frequencies, $p$ and $q$, should be calculated for the population after five generations of simulated random mating.

Number of A alleles present at fifth generation:
(# AA offspring x 2) + # Aa offspring = _____ A alleles

$$p = \frac{\text{total \# A alleles}}{\text{total alleles in population}}$$

Number of a alleles present at fifth generation:
(# aa offspring x 2) + # Aa offspring = _____ a alleles

$$q = \frac{\text{total \# a alleles}}{\text{total alleles in population}}$$

**Table 2 - Hardy-Weinberg Equilibrium**

| | |
|---|---|
| Initial Class Frequencies | AA _____ Aa _____ aa _____ |
| My initial genotype | _____ |
| $F_1$ genotype | _____ |
| $F_2$ genotype | _____ |
| $F_3$ genotype | _____ |
| $F_4$ genotype | _____ |
| $F_5$ genotype | _____ |

| | |
|---|---|
| Final class frequencies | AA _____ Aa _____ aa _____<br>*p* _____ *q* _____ |

**Questions**

1. What does the Hardy-Weinberg equation predict for the new *p* and *q*?
2. Do the results you obtained in this simulation agree? If not, why?
3. What major assumption(s) were not strictly followed in this simulation?

**Case 2 - Selection**

In this exercise, you will modify the simulation to make it more realistic. In the natural environment, not all genotypes have the same rate of survival; that is, the environment might favour some genotypes while selecting against others. An example is the human condition of sickle-cell anemia. This is a disease caused by a mutation on one allele, and individuals who are homozygous recessive often do not survive to reach reproductive maturity. For this simulation, you will assume that the homozygous recessive individuals never reach reproductive age, while homozygous dominant and heterozygous individuals always do.

**Procedure**

1. The procedure is similar to that for Case 1. Start again with your initial genotype and produce your "offspring" as before. Any time your offspring is aa it does not reproduce. Since we want to maintain a constant population size, the same two parents must try again until they produce two surviving offspring. You may need to get new allele cards from the pool, allowing each individual to complete the activity.
2. Proceed through five generations, always selecting against the homozygous recessive offspring. Record all your data in Table 3 and calculate the new frequencies, *p* and *q*.

**Table 3 - Selection**

| | |
|---|---|
| Initial Class Frequencies | AA _____ Aa _____ aa _____ |
| My initial genotype | _____ |
| $F_1$ genotype | _____ |
| $F_2$ genotype | _____ |
| $F_3$ genotype | _____ |
| $F_4$ genotype | _____ |
| $F_5$ genotype | _____ |
| Final class frequencies | AA _____ Aa _____ aa _____<br>*p* _____ *q* _____ |

**Questions**

1. How do the new frequencies of *p* and *q* compare to the initial frequencies in Case 1?
2. What major assumption(s) were not strictly followed in this simulation?
3. Predict what would happen to the frequencies of *p* and *q* if you simulated another five generations.
4. In a large population would it be possible to completely eliminate a deleterious recessive allele? Explain.

**Case 3 - Heterozygote Advantage**

From Case 2 it is easy to see what happens to the lethal recessive allele in the population. However, data from many human populations show an unexpectedly high frequency of the sickle-cell allele in some population. Thus, our simulation does not accurately reflect the real situation; this is because individuals who are heterozygous are slightly more resistant to a deadly form of malaria than homozygous dominant individuals. In other words, there is a slight selection against homozygous dominant individuals as compared to heterozygotes. This fact will now be incorporated into the simulation.

**Table 4 - Heterozygote Advantage**

| | | |
|---|---|---|
| Initial Class Frequencies | AA _____ Aa _____ aa _____ | |
| My initial genotype | _____ | |
| $F_1$ genotype _____ | $F_6$ genotype _____ | $F_{11}$ genotype _____ |
| $F_2$ genotype _____ | $F_7$ genotype _____ | $F_{12}$ genotype _____ |
| $F_3$ genotype _____ | $F_8$ genotype _____ | $F_{13}$ genotype _____ |
| $F_4$ genotype _____ | $F_9$ genotype _____ | $F_{14}$ genotype _____ |
| $F_5$ genotype _____ | $F_{10}$ genotype _____ | $F_{15}$ genotype _____ |
| Final class frequencies (after 5) | AA _____ Aa _____ aa _____<br>*p* _____ *q* _____ | |
| Final class frequencies (after 10) | AA _____ Aa _____ aa _____<br>*p* _____ *q* _____ | |
| Final class frequencies (after 15) | AA _____ Aa _____ aa _____<br>*p* _____ *q* _____ | |

**Procedure**

1. In this round, keep everything the same as it was in Case 2, except that if the offspring is AA, flip a coin. If the coin lands heads up, the individual survives; if tails, the individual does not.
2. Simulate five generations, starting with the initial genotype from Case 1. The genotype aa never survives, and homozygous dominant individuals survive only if the coin lands heads up. To maintain a constant population size, the same two parents must try again until they produce twp surviving offspring. Get the new allele cards form the pool as needed. Record all your data in Table 4 and calculate the new frequencies *p* and *q*.
3. Starting with the $F_5$ genotype, proceed through five more generations, and again total the genotypes and calculate the new frequencies *p* and *q*.
4. Repeat the procedure and calculations for five more generations.

**Questions**

1. Explain how the changes in the frequencies of *p* and *q* in Case 2 compare with Case 1 and Case 3.
2. Do you think the recessive allele will be completely eliminated in either Case 2 or Case 3?
3. What is the importance of heterozygotes (the heterozygote advantage) in maintaining genetic variation in populations?

**Case 4 - Genetic Drift**

The simulation will now be changed once again to examine the phenomenon of genetic drift.

**Procedure**

1. Divide the class into several smaller populations so that individuals from one isolated population do not interact with those from other populations.

2. Simulate five generations as was done in Case 1. Record the new genotypic frequencies in Table 5 and calculate the new frequencies of *p* and *q* for each population.

**Table 5 - Genetic Drift**

| | |
|---|---|
| Initial Class Frequencies | AA _____ Aa _____ aa _____<br>*p* _____ *q* _____ |
| My initial genotype | _____ |
| $F_1$ genotype | _____ |
| $F_2$ genotype | _____ |
| $F_3$ genotype | _____ |
| $F_4$ genotype | _____ |
| $F_5$ genotype | _____ |
| Final class frequencies | AA _____ Aa _____ aa _____<br>*p* _____ *q* _____ |

**Questions**

1. Explain how the initial genotypic frequencies of the populations compare.
2. What do your results indicate about the importance of population size as an evolutionary force?