

Baker's Dozen Lab 2: Hardy-Weinberg Equilibrium

Objectives

Before doing this lab you should understand the Hardy-Weinberg equation and its use in determining the frequency of alleles in a population.

After doing this lab you should be able to calculate the frequencies of alleles and genotypes in the gene pool of a population using the Hardy-Weinberg formula.

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 organism 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 in which 40% of the alleles are A , p would be 0.40. 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 **allele frequencies**. 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 allele and genotype frequencies will remain constant from generation to generation, indicating that no evolution is occurring. These five 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 mating preference for a particular phenotype.)
3. **There is no mutation of alleles.** (No alteration in the DNA sequence of alleles.)
4. **No differential migration occurs.** (No immigration or emigration; gene flow or genetic drift).
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 allele or genotype frequencies in the population. Of what value is such a rule? It provides a yardstick 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 activity is to test some of the basic tenets of population genetics and evolutionary biology.

Case Studies: Case #1: A Test of an Ideal Hardy-Weinberg Population

The class will simulate a population of randomly mating heterozygous individuals. To ensure random mating, **choose another student AT RANDOM**. We will assume that gender and genotype are irrelevant to mate selection. The population begins with an **initial gene frequency of 0.5 for the dominant allele A and the recessive allele a and genotype frequencies of 0.25 AA , 0.50 Aa , and 0.25 aa . Your initial genotype is Aa** . Record this on the data page (5).

Each student will receive four cards, two with an A written on them and two with an a . These cards represent the products of meiosis in an heterozygous individual. Each "parent" contributes one card to the next generation.

Procedure:

1. Find a partner with whom to RANDOMLY mate.
2. Turn the four cards over so the letters do not show. Shuffle the cards and take the card on the top to contribute to the production of your first offspring. Your partner should do the same. The two cards represent the alleles of the first offspring.

Evolution

Big Idea 1

3. One of you should record the genotype of your first offspring in the Case #1 section on the data page.
4. Repeat steps 2 and 3 so your partner can record the genotype of his/her first offspring on his/her data page.
5. Now you and your partner assume the genotypes of your offspring respectively and become the second generation of the population. Each of you should obtain the correct index cards to accurately represent the sex cells generated by your new genotype.
6. Each of you RANDOMLY seek out another person with whom to mate and repeat the process, each contributing one allele, recording the genotype of one person's data page and repeating it for the other partner.
7. Be sure to assume your new genotype for each successive generation.
8. Class data will be collected by your teacher at the end of five generations.
9. Calculate the allele frequencies in the population AFTER THE FIFTH GENERATION using the equations below.

Number of offspring with genotype AA _____ x 2 = _____ A alleles

Number of offspring with genotype Aa _____ x 1 = _____ A alleles

Total = _____ A alleles

$$p = \frac{\text{TOTAL \# of A alleles}}{\text{TOTAL \# of alleles in the population}} = \underline{\hspace{2cm}}$$

In this case, the total number of alleles in the population is equal to the number of students in the class x2.

Number of offspring with genotype aa _____ x 2 = _____ a alleles

Number of offspring with genotype Aa _____ x 1 = _____ a alleles

Total = _____ a alleles

$$q = \frac{\text{TOTAL \# of a alleles}}{\text{TOTAL \# of alleles in the population}} = \underline{\hspace{2cm}}$$

Questions

1. What does the Hardy-Weinberg equation predict the new p and q should be after the fifth generation?

2. Do the results you obtained in this simulation agree with the prediction above? If not, why?

3. What major assumption(s) were NOT strictly followed in this simulation?



Case #2: Selection

Now 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 favor 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 case study, you will assume that the homozygous recessive individuals never survive (100% selection against) and that heterozygous and homozygous dominant individuals survive 100% of the time.

Procedure (similar to that of Case #1)

1. Start again with your initial genotype and produce your “offspring” as you did for Case #1. This time, however, there is ONE IMPORTANT DIFFERENCE: Every 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.
2. Proceed through five generations, selecting against the homozygous recessive offspring 100% of the time. Then add up the genotype frequencies that exist in the population and calculate the new p and q frequencies in the same way you did for Case #1.
3. Record this data on the data page.

Questions

1. How do the new ending frequencies of p and q compare to the final frequencies from 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 this for another five generations.

4. In a large population would it be possible to completely eliminate a recessive allele when it is 100% selected against? 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 populations. 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.



Procedure

1. In this round, everything is the same as it was in Case #2, except that if your offspring is AA, flip a coin. If it is heads, the AA offspring does not survive; you have to draw letters again. If it is tails, the offspring does survive.
2. Simulate ten generations, starting again with the initial genotype from Case #1. The genotype aa NEVER survives and AA only survive if the coin lands on tails. Since we want to maintain a constant population size, the same two parents must try again until they produce two SURVIVING offspring.
3. Record your data on the data page and calculate the p and q frequencies for the class totals after five generations and again after all ten generations.

Questions

1. Explain how the changes in p and q frequencies in this case compare with Case #1 and #2.

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 in maintaining genetic variation in a population?

Case #4: Genetic Drift (Optional)

Divide the class into several smaller “populations” (for example, a class of 30 could be divided into three populations of ten each). Individuals from different populations CAN NOT interact or mate with individuals from another population. Now go through five generations just like in Case #1. Record the new genotypic frequencies and calculate the new frequencies of p and q .

Questions

1. Explain how the ending genotypic frequencies of the three population compare to each other.

2. What do your results indicate about the importance of population size as an evolutionary force?

Evolution

Big Idea 1

DATA PAGE

Case #1: Hardy-Weinberg Equilibrium

Initial Class Frequencies:

AA _____ Aa _____ aa _____

My Initial genotype: _____

F1 genotype: _____

F2 genotype: _____

F3 genotype: _____

F4 genotype: _____

F5 genotype: _____

Final Class Frequencies:

AA _____ Aa _____ aa _____

p _____ q _____

Case #3: Heterozygote Advantage

Initial Class Frequencies:

AA _____ Aa _____ aa _____

My Initial genotype: _____

F1 genotype: _____ F6 genotype: _____

F2 genotype: _____ F7 genotype: _____

F3 genotype: _____ F8: genotype: _____

F4 genotype: _____ F9 genotype: _____

F5 genotype: _____ F10 genotype: _____

Final Class Frequencies (after five generations)

AA _____ Aa _____ aa _____

p _____ q _____

Final Class Frequencies (after ten generations)

AA _____ Aa _____ aa _____

p _____ q _____

Case #2: Selection

Initial Class Frequencies:

AA _____ Aa _____ aa _____

My Initial genotype: _____

F1 genotype: _____

F2 genotype: _____

F3 genotype: _____

F4 genotype: _____

F5 genotype: _____

Final Class Frequencies:

AA _____ Aa _____ aa _____

p _____ q _____

Case #4: Genetic Drift

My Initial genotype: _____

F1 genotype: _____ F4 genotype: _____

F2 genotype: _____ F5 genotype: _____

F3 genotype: _____

Group 1 Final Frequencies:

AA _____ Aa _____ aa _____

p _____ q _____

Group 2 Final Frequencies:

AA _____ Aa _____ aa _____

p _____ q _____

Group 3 Final Frequencies:

AA _____ Aa _____ aa _____

p _____ q _____

Practice Hardy-Weinberg Problems:

1. In *Drosophila* the allele for normal-length wings is dominant over the allele for vestigial wings. In a population of 1,000 individuals, 360 show the recessive phenotype. How many individuals would you expect to be homozygous dominant? How many individuals would you expect to be heterozygous for this trait?
2. The allele for unattached earlobes is dominant over the allele for attached earlobes. In a population of 500 individuals, 25% show the recessive phenotype. How many individuals would you expect to be homozygous dominant? How many individuals would you expect to be heterozygous for this trait?
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 possible three genotypes for this trait?
4. 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 US is 2,000, how many students would you expect for each of the three possible genotypes?
5. In a certain population, the dominant phenotype of a certain trait occurs 91% of the time. What is the frequency of the dominant allele?