

Genetic Equilibrium: Human Diversity

Student Version

Key Concepts:

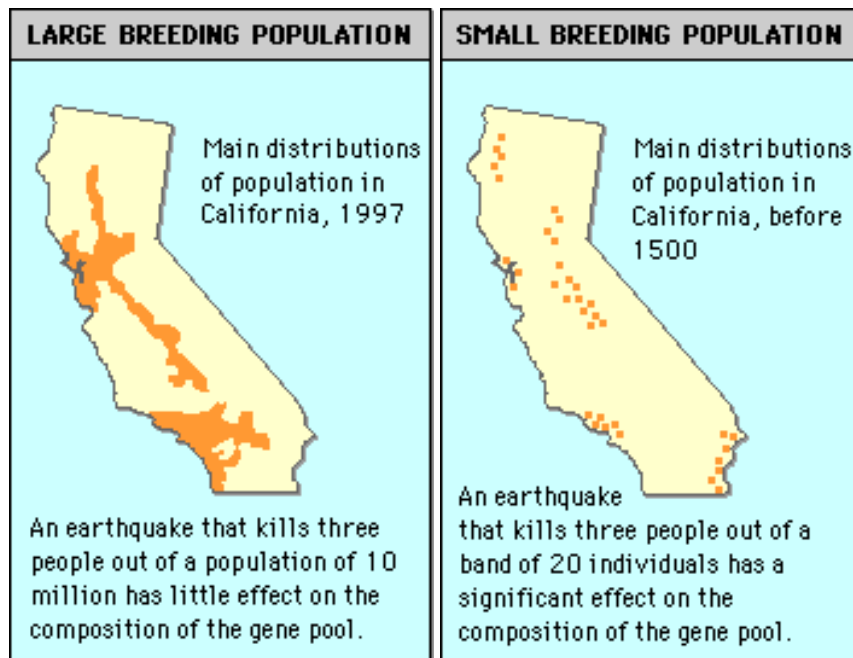
- A **population** is a group of organisms of the same species that live and breed in the same area.
- **Alleles** are alternate forms of genes. In standard Mendelian genetics, two alleles—one from each parent—control an inherited trait or characteristic (e.g. seed pod color).
- A **gene pool** is the collective term representing all the genes, including all the different alleles, found in a population.
- The written expression of the DNA code, called the **genotype**, is normally represented using two letters, each letter representing one allele (e.g. AA).
- **Dominant** alleles are represented by capital (uppercase) letters.
- **Recessive** alleles are represented by lowercase letters.
- Genotypes with two dominant alleles (e.g. AA) are referred to as **homozygous dominant**.
- Genotypes with two recessive alleles (e.g. aa) are referred to as **homozygous recessive**.
- Genotypes with one dominant and one recessive allele (e.g. Aa) are referred to as **heterozygous**.
- The physical expression of the genotype (e.g. brown hair, blue eyes) is called the **phenotype**.
- In standard Mendelian genetics, the heterozygous condition (e.g. Aa) retains the homozygous dominant phenotype because the dominant allele masks the phenotype of the recessive allele. An example of this in humans would be a heterozygote for brown eye color. The person would carry both a dominant brown allele “A” and a recessive blue allele “a” yet have brown eyes. The dominant brown allele masks the recessive blue allele.
- **Genetic equilibrium** is the state in which allele frequencies remain constant.
- The **Hardy-Weinberg Principle**, named for English mathematician G.H. Hardy and German physician W. Weinberg, is a model used to help clarify evolutionary change by determining what happens if *no* change occurs. When no change occurs and an environment is stable, genetic equilibrium is maintained.
- The **Hardy-Weinberg Principle** states that for genetic equilibrium to be maintained from one generation to the next, five conditions must be met:
 - Random mating – all individuals in a population have equal opportunity to pass on their alleles to offspring.
 - Large populations – **genetic drift**, or random changes in allele frequency, has less effect on large populations than small populations.
 - No mutations - if genes randomly mutate, new alleles may be introduced into the population and allele frequencies will change.
 - No migration – individuals cannot move into or out of the population.
 - No natural selection - all genotypes must have equal probabilities of reproduction.

- Two equations are used to model the **Hardy-Weinberg Principle**.
 - $p + q = 1$; where p represents the dominant allele, “A,” and q represents the recessive allele, “a.” This equation, used to calculate **allele frequency**, equals 1 or 100% of the population.
 - $p^2 + 2pq + q^2 = 1$; where p^2 represents the homozygous dominant genotype, $2pq$ represents the heterozygous genotype, and q^2 represents the homozygous recessive genotype. This equation, used to calculate **genotype frequency**, equals 1 or 100% of the population.

Part I – Introduction

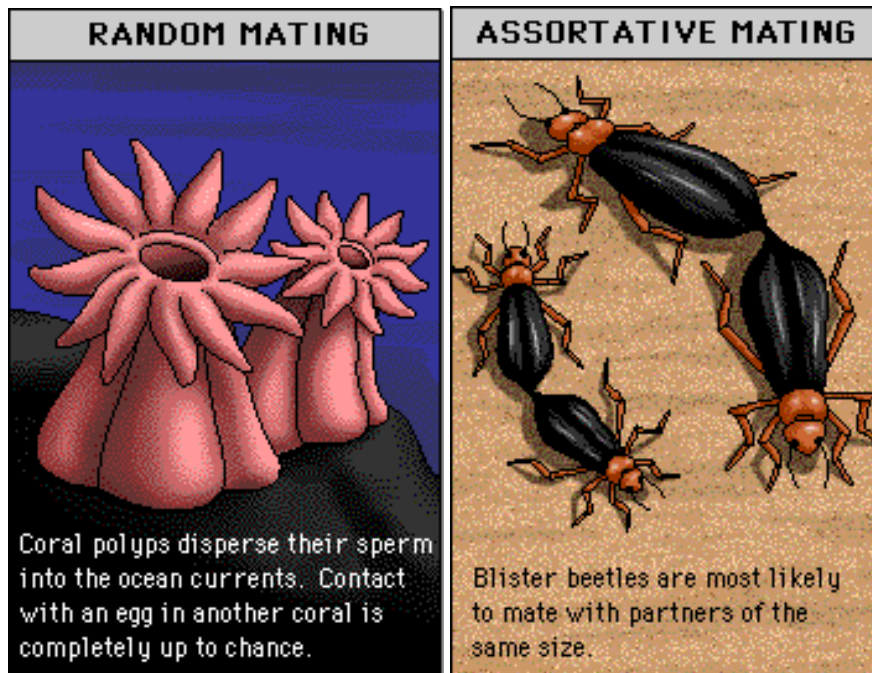
Procedure:

- If computers with Internet access are available, view the animation on the following website before moving on with parts II-IV below:
http://www.phschool.com/science/biology_place/labbench/lab8/intro.html
- Alternatively, you may view the animation as a group from the teacher’s computer if available or simply interpret the still pictures included below.
 - According to the Hardy-Weinberg Principle, there are five conditions required in order for a population to remain genetic equilibrium.
 - 1.) Large populations:



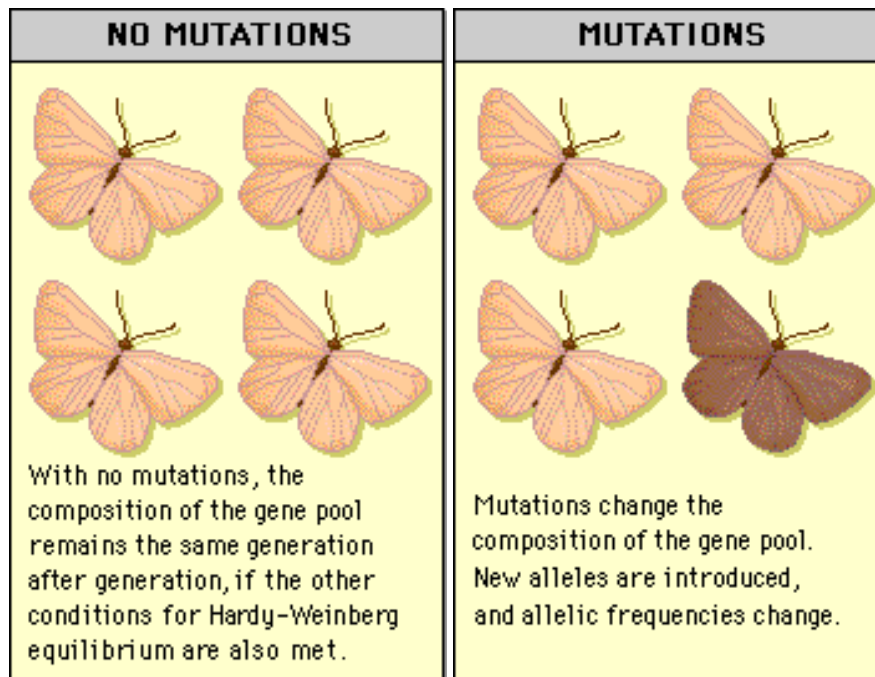
http://www.phschool.com/science/biology_place/labbench/lab8/breedpop.html

- 2.) Random mating:



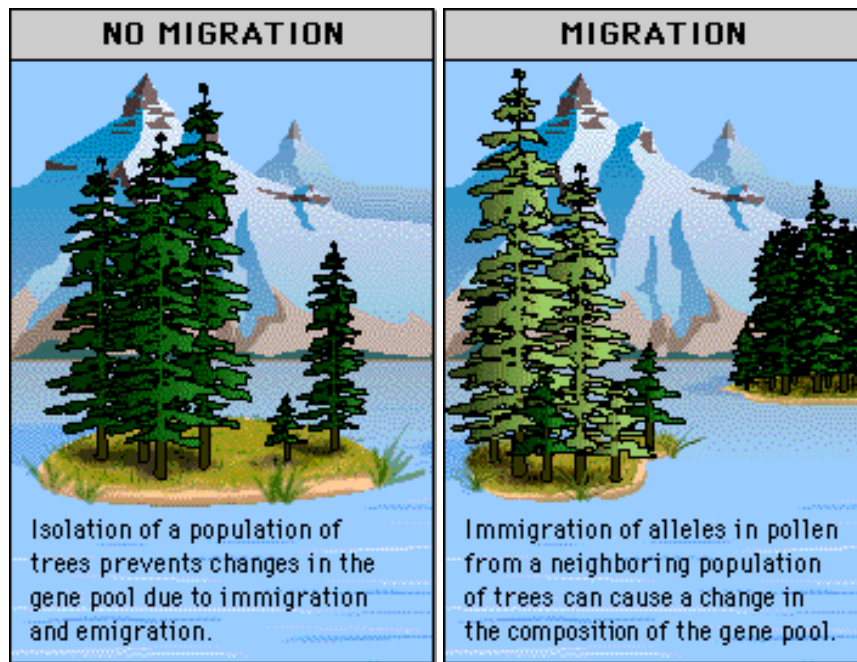
http://www.phschool.com/science/biology_place/labbench/lab8/mating.html

- 3.) No mutations:



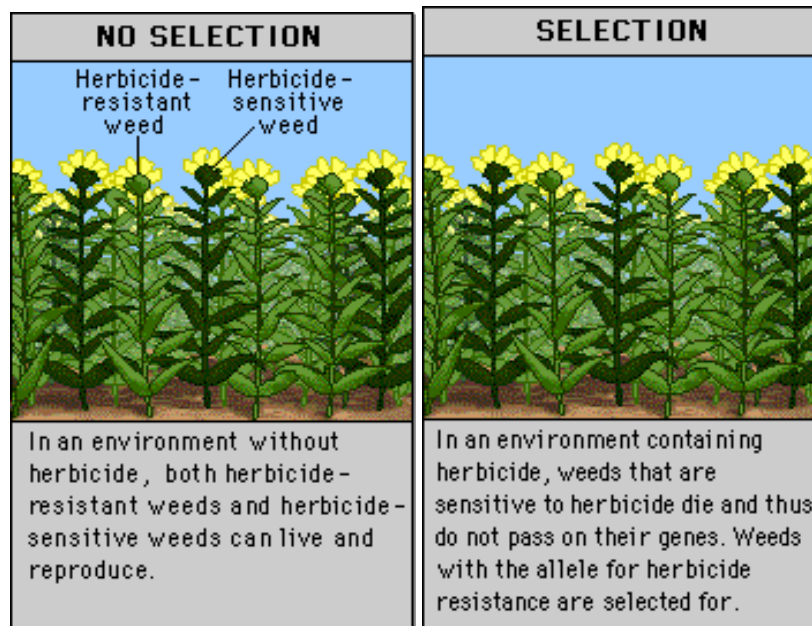
http://www.phschool.com/science/biology_place/labbench/lab8/mutation.html

- 4.) No immigration or emigration



http://www.phschool.com/science/biology_place/labbench/lab8/migrate.html

- 5.) No natural selection



http://www.phschool.com/science/biology_place/labbench/lab8/select.html

Part II – Testing the Hardy-Weinberg Principle using a Bean Model

Procedure:

Working in pairs, you will be testing the Hardy-Weinberg Principle by simulating a population using beans, beads, or similar materials. The bag of beans represents the gene pool for the population. Each individual bean represents one allele, whereas a pair of beans—either both dark, one dark and one light, or both light—represent the genotype for a single genetic characteristic or trait. Each bag should contain 100 beans of the two colors: 70 dark beans and 30 light beans.

The allele frequency is found by dividing the beans of one color by the total number of beans.

Ex. Allele frequency for dark beans = Number of dark beans / Total number of beans

B = _____ *color and* _____ *allele frequency*

b = _____ *color and* _____ *allele frequency*

Q1. How many diploid individuals are represented in this population?

Q2. What would be the color of the beans for a homozygous dominant individual?

Q3. What would be the color of the beans for a homozygous recessive individual?

Q4. What would be the color of the beans for a heterozygous individual?

- Place all 100 beans in the bag and shake. Without looking into the bag, randomly remove two beans from the bag. These two beans represent the genotype of one diploid individual in the next generation.
- Record the genotype of the individual (BB, Bb, or bb) in the data table below.
- **Return the beans to the bag and shake.** Replacing the beans to the bag each time maintains the size of the gene pool and the probability of selecting any allele should remain equal to its frequency.
- Select another two beans and record the genotype of this individual in the data table below. **Return the beans to the bag and shake.** Repeat selecting and replacing steps as outlined above until you have recorded the genotypes of 50 individuals who will form the next generation of the population.

Q5. Using the five conditions outlined in the Hardy-Weinberg Principle write a reasonable/logical hypothesis for this experiment.

What is the expected genotype rank (BB, Bb, and bb) from most to least number of times drawn?

Data Table: Genotypes of Next Generation (alleles in population = 100)

(1)	(2)	(3)	(4)	(5)
(6)	(7)	(8)	(9)	(10)
(11)	(12)	(13)	(14)	(15)
(16)	(17)	(18)	(19)	(20)
(21)	(22)	(23)	(24)	(25)
(26)	(27)	(28)	(29)	(30)
(31)	(32)	(33)	(34)	(35)
(36)	(37)	(38)	(39)	(40)
(41)	(42)	(43)	(44)	(45)
(46)	(47)	(48)	(49)	(50)

- **Before calculating the results of your experiment**, determine the *expected* frequencies of alleles and genotypes for the new population and record in the table below.
- Use the original allele frequencies for the population provided above. Recall that the frequency of the dominant allele is p and the frequency of the recessive allele is q .
- Calculate the expected genotype frequencies using the H-W equation $p^2 + 2pq + q^2 = 1$.
- Next, calculate the number of individuals expected for each genotype by multiplying 50 (total diploid number) by the expected genotype frequencies.
- The dominant and recessive allele frequencies for the new population can be found by taking the square root of the homozygous dominant and homozygous recessive genotype frequencies, respectively.

Expected Allele/Genotype Frequencies for the Next Generation (alleles in population = 100)

Parent Population		New Populations				
Allele Frequency		Genotype Frequency (number of individuals with specific genotype)			Allele Frequency	
“B” (p)	“b” (q)	“BB” (p^2)	“Bb” ($2pq$)	“bb” (q^2)	“B” (p)	“b” (q)

- Next, **using the results of your experiment**, calculate the *observed* frequencies in the new population that was created as you removed and replaced beans from the bag and record in the table below.
- For the parent population, use the same allele frequencies as before since you began with the same gene pool prior to selecting out and replacing individuals.
- Calculate the expected allele frequencies, genotype frequencies, and the number of individuals with specific genotypes for the new population as was done for the expected outcomes. Above

Observed Allele/Genotype Frequencies for the Next Generation (alleles in population = 100)

Parent Population		New Populations				
Allele Frequency		Genotype Frequency (number of individuals with specific genotype)			Allele Frequency	
“B” (p)	“b” (q)	“BB” (p^2)	“Bb” ($2pq$)	“bb” (q^2)	“B” (p)	“b” (q)

Q6. Were your observed results consistent with the expected results based on your statistical analysis? If not, can you suggest an explanation?

Q7. Compare your results to those of other student groups. How variable are the results for each group? Explain.

Q8. Is this population evolving? Explain your response.

Part III – Introducing a Conditional Change to Alter Genetic Equilibrium

Procedure:

Once again, you will be working in pairs and testing the Hardy-Weinberg Principle by simulating a population using beans, beads, or similar materials. However, with this new experiment, you will be introducing one conditional change—using a small population rather than a large one—in the hopes of significantly altering genetic equilibrium. As with the previous experiment, the bag of beans represents the gene pool for the population. Each individual bean represents one allele, whereas a pair of beans—either both light, one light and one dark, or both light—represent the genotype for a single genetic characteristic or trait. Each bag should contain 10 beans of the two colors: 7 dark beans and 3 light beans.

$B =$ _____ color and _____ allele frequency

$b =$ _____ color and _____ allele frequency

Q9. How many diploid individuals are represented in this population?

- Place the 10 beans in the bag and shake. Without looking into the bag, randomly remove two beans from the bag. These two beans represent the genotype of one diploid individual in the next generation.

- Record the genotype of the individual (AA, Aa, or aa) in the data table below.
- **Return the beans to the bag and shake.** Replacing the beans to the bag each time maintains the size of the gene pool and the probability of selecting any allele should remain equal to its frequency.
- Select another two beans and record the genotype of this individual in the data table below. **Return the beans to the bag and shake.** Repeat selecting and replacing steps as outlined above until you have recorded the genotypes of 5 individuals who will form the next generation of the population.

Q10. Now that a conditional change is being included in the experiment, your initial hypothesis needs to be revised. Write a new, logical hypothesis that incorporates the change in the testing parameters.

Data Table: Genotypes of Next Generation (alleles in population = 10)

(1)	(2)	(3)	(4)	(5)
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- **Before calculating the results of your experiment,** determine the *expected* frequencies of alleles and genotypes for the new population and record in the table below.
- Use the original allele frequencies for the population provided above. Recall that the frequency of the dominant allele is p and the frequency of the recessive allele is q .
- Calculate the expected genotype frequencies using the H-W equation $p^2 + 2pq + q^2 = 1$.
- Next, calculate the number of individuals expected for each genotype by multiplying 10 (total diploid number) by the expected genotype frequencies.
- The dominant and recessive allele frequencies for the new population can be found by taking the square root of the homozygous dominant and homozygous recessive genotype frequencies, respectively.

Expected Allele/Genotype Frequencies for the Next Generation (alleles in population = 10)

Parent Population		New Populations				
Allele Frequency		Genotype Frequency (number of individuals with specific genotype)			Allele Frequency	
“B” (p)	“b” (q)	“BB” (p^2)	“Bb” ($2pq$)	“bb” (q^2)	“B” (p)	“b” (q)

- Next, **using the results of your experiment**, calculate the *observed* frequencies in the new population that was created as you removed and replaced beans from the bag and record in the table below.
- For the parent population, use the same allele frequencies as before since you began with the same gene pool prior to selecting out and replacing individuals.
- Calculate the expected allele frequencies, genotype frequencies, and the number of individuals with specific genotypes for the new population as was done for the expected outcomes. Above

Observed Allele/Genotype Frequencies for the Next Generation (alleles in population = 10)

Parent Population		New Populations				
Allele Frequency		Genotype Frequency (number of individuals with specific genotype)			Allele Frequency	
"B" (p)	"b" (q)	"BB" (p^2)	"Bb" ($2pq$)	"bb" (q^2)	"B" (p)	"b" (q)

Q11. Were your observed results consistent with the expected results based on your statistical analysis? If not, can you suggest an explanation?

Q12. Compare your results to those of other student groups. How variable are the results for each group? Explain.

Part IV – Genetic Equilibrium Problem

Procedure:

Use your knowledge of the Hardy-Weinberg Principle to solve the following population dynamics problem.

Blue-footed Boobies



www.abrancoalmeida.com

Let “W” represent the allele for webbed feet and “w” represent the allele for non- webbed feet in Blue-footed Boobies. Birds with the “WW” or “Ww” genotype have webbed feet. Birds with the “ww” genotype have non-webbed feet. Below are the genotypes of 200 birds:

ww ww WW Ww ww WW ww Ww ww Ww ww ww WW
 ww ww WW ww ww Ww ww Ww ww ww ww Ww ww
 Ww ww ww Ww Ww WW ww ww Ww ww Ww ww ww
 Ww ww ww Ww ww Ww ww Ww ww Ww Ww Ww Ww
 ww WW Ww Ww ww Ww ww ww ww ww Ww ww ww
 Ww ww Ww ww ww Ww ww ww Ww WW ww ww
 Ww Ww ww WW ww Ww ww ww Ww ww ww Ww Ww
 ww Ww WW ww Ww ww Ww ww Ww ww Ww WW Ww Ww
 Ww ww Ww ww Ww ww Ww ww Ww Ww ww Ww ww
 Ww WW ww Ww ww Ww ww Ww ww Ww Ww Ww Ww
 ww Ww Ww ww Ww ww WW Ww ww Ww ww ww Ww
 ww Ww Ww ww Ww Ww ww ww ww ww WW ww
 WW Ww Ww WW WW

Calculate the frequency of the alleles in the population. Express your answer as a decimal.

$$\text{Frequency of allele "W"} = \frac{\text{Number of "W" alleles}}{\text{Total number of alleles ("W" + "w")}}$$

$$\text{Frequency of allele "W"} = \frac{\quad}{\quad} =$$

$$\text{Frequency of allele "w"} = \frac{\text{Number of "w" alleles}}{\text{Total number of alleles ("W" + "w")}}$$

$$\text{Frequency of allele "w"} = \text{-----} =$$

Q13. The sum of the two frequencies, if calculated correctly will add up to what number?

In the Hardy-Weinberg equations, the frequency of the dominant allele in a population is represented by the letter p, whereas the frequency of the recessive allele in a population is represented by the letter q.

In the next step, determine the relationship between the frequency of Blue-footed Boobies with non-webbed feet ("ww") and the frequency of the allele for non-webbed feet in the population ("w"). Use the following equation to calculate the frequency of non-webbed Blue-footed Boobies:

$$\begin{array}{l} \text{Frequency of Blue-footed Boobies} \\ \text{with non-webbed feet} \end{array} = \frac{\text{Number of Blue-footed} \\ \text{Boobies with non-webbed feet (ww)}}{\text{Total number of Blue-footed Boobies}}$$

$$\begin{array}{l} \text{Frequency of Blue-footed Boobies} \\ \text{with non-webbed feet} \end{array} = \text{-----}$$

$$\begin{array}{l} \text{Frequency of Blue-footed Boobies} \\ \text{with non-webbed feet} \end{array} =$$

Q14. Is this frequency greater or smaller than the frequency of the "w" allele?

Q15. If q = the frequency of "w" (the recessive allele) in the population, is the frequency of Blue-footed Boobies with non-webbed feet in the population equal to 2q or to q²?

Q16. $2pq$ represents the genotype frequency of what individual? Do you expect these individuals to have webbed or non-webbed feet? Why?

Q17. Match each of the following symbols with the phrase that defines it.

- p → _____ A. The frequency of homozygous dominant individuals in the population.
- q → _____ B. The frequency of the dominant allele.
- $p + q = 1$ → _____ C. The Hardy-Weinberg equation for genotype frequency.
- p^2 → _____ D. The frequency of heterozygotes in the population.
- $2pq$ → _____ E. The frequency of the recessive allele.
- q^2 → _____ F. The frequency of homozygous recessive individuals in the population.
- $p^2 + 2pq + q^2 = 1$ → _____ G. The Hardy-Weinberg equation for allele frequency.

G.H. Hardy



www.en.wikipedia.org

W. Weinberg



chsbowman.wordpress.com