Hardy Har Har
Investigating the Hardy-Weinberg Principle

About this Lesson

This activity involves a fun way for students to experience a population undergoing genotypic frequency change (evolution) and measure this change using the Hardy-Weinberg principle. This is an essential lesson because it allows students practice Algebra I concepts and see their real-world applications in nature. It also provides a context for past evolutionary content in the middle grades and sets the foundation for all future learning of how populations change over time.

Objective

Students will calculate the allelic, genotypic, and phenotypic frequencies of populations by utilizing the Hardy-Weinberg principle.

Level

Biology I

Common Core State Standards for Science Content

LTF Science lessons will be aligned with the next generation of multi-state science standards that are currently in development. These standards are said to be developed around the anchor document, *A Framework for K–12 Science Education*, which was produced by the National Research Council. Where applicable, the LTF Science lessons are also aligned to the Common Core Standards for Mathematical Content as well as the Common Core Literacy Standards for Science and Technical Subjects.

Explicitly addressed in this lesson:

Code	Standard	Level of Thinking	Depth of Knowledge
N-RN.2	Extend the properties of exponents to rational exponents. Rewrite expressions involving radicals and rational exponents using the properties of exponents.	Apply	II
A-CED.1	Create equations that describe numbers or relationship. Create equations and inequalities in one variable and use them to solve problems. Include equations arising from linear and quadratic functions, and simple rational and exponential functions.*	Apply	II

S-IC.1	Understand and evaluate random processes underlying statistical experiments. Understand statistics as a process for making inferences about population parameters based on a random sample from that population.*	Apply	II
S-ID.4	Make inferences and justify conclusions from sample surveys, experiments, and observational studies. Use data from a sample survey to estimate a population mean or proportion; develop a margin of error through the use of simulation models for random sampling.*	Apply	II
S-IC.6	Make inferences and justify conclusions from sample surveys, experiments, and observational studies. Evaluate reports based on data.*	Apply	II
S-MD.4	Calculate expected values and use them to solve problems. Develop a probability distribution for a random variable defined for a sample space in which probabilities are assigned empirically; find the expected value. For example, find a current data distribution on the number of TV sets per household in the United States, and calculate the expected number of sets per household. How many TV sets would you expect to find in 100 randomly selected households?*	Apply	II
S-MD.6	Use probability to evaluate outcomes of decisions. Use probabilities to make fair decisions (e.g., drawing by lots, using a random number generator).*	Apply	II

Connections to AP*

AP Biology: II. Heredity and evolution C. Evolutionary biology 3. Mechanisms of evolution

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Materials and Resources

- 1 Memo note for each student
- Graphing calculator

Assessments

The following types of formative assessments are embedded in this lesson:

- Assessment of prior knowledge (Pre-Lab)

- Class discussion of complete dominance and genotype/phenotype characteristics.
- Class discussion of percentage calculations.
- Class discussion of Analysis questions.

The following additional assessments are located on the LTF website:

- Biology – LTF Diagnostic Test: Evolution and Taxonomy free response question.

Teaching Suggestions

Preparing for the Activity

1. Have the students answer Question 1 and Question 2 in the Pre-Lab section on their student answer page.
2. Depending on what you have done with calculations previously in the school year, you must decide how to handle the small values students will get while solving these problems.
    a. Option 1 is to have students keep all numbers to the right of the decimal. Because these numbers are considered counted numbers, each number to the right of the decimal is of value. In this case, you would have students round their final answers to include four significant figures. This method will yield the most accurate results.
    b. Option 2 is to have the students set their FLOAT value to 4. This will cause the calculator to automatically round the values for the students to four places past the decimal. To do this, the students should press MODE, arrow down to FLOAT, arrow over to “4” and hit ENTER twice.
    c. Option 3 is to just have the students round the value that is calculated to four places after the decimal or to include two significant figures. Again, this option is the mathematically least accurate but could be completed using a scientific calculator.
3. Before you start with the Hardy-Weinberg equations, have the students complete the simple calculations in the Pre-Lab on their student answer page.
    a. This will provide a review for students on how to calculate percentages, take the square root of a number, and square a number.
    b. Because students will be using very small numbers, the graphing calculators will represent values like 0.00045 as “4.5E−4” if they are set to display scientific notation.
    c. It is very helpful for the students to employ the “copy answer” shortcut in the TI graphing calculators. Consider the following example:

        Ex: Solve for a when $a^2 = 1/12000$.

        » In the calculator, type “1/12000” to determine the decimal value for a^2.

        » To solve for a, you must take the square root of this value by pressing $\boxed{\text{2nd}}\boxed{x^2}$. Rather than retyping this long number, press $\boxed{\text{2nd}}\boxed{(-)}$. This will automatically copy the last answer behind the active cursor to memory.

Starting the Activity

1. On the board, draw a circle that looks like a pond and label it “Gene Pool.” Tear 10 memo notes in half. On 10 of the memo note halves, write the capital letter “L”. On the other 10,

write the lower-case letter "l". Place the notes in the pond, or into the "gene pool."

2. On the board, draw the data table shown as Table A.

Table A: Sea Legs

	Homozygous Dominant	Heterozygous	Homozygous Recessive
P1			
F1			
F2			

3. Give each student a blank memo note. Explain that they will be investigating how alleles or genes change in populations over several generations. For this activity, the allele that will be investigated is a newly discovered trait in a population of pirates that exist around the Weinberg Islands. This population is unique for two reasons: it has large number of female pirates, and the population has been determined to have a gene (L) that enables them to maintain balance in a rocking ship and climb ropes atop the highest masts. The population describes people with this trait as having "sea legs."
4. Discuss with the students that this "sea legs" gene exhibits complete dominance like free earlobes, straight thumbs, or widow's peak. Those individuals that are homozygous dominant or heterozygous will have sea legs. An individual that has a homozygous recessive genotype will have not have sea legs.
5. Split the class into three groups. Assign 25% of the students to start off homozygous dominant, 50% to start heterozygous recessive, and the remaining 25% to start homozygous recessive. LL or Ll = sea legs, ll = lacks sea legs.
6. Instruct the students to write their genotype on their note as large as they can. If the class consists of an odd number of students, you may also complete a note. If you are uncomfortable doing this, you can use a stand-in like Mr. Bones, the skeleton, so that each student will have a partner during the activity.
7. Record the total number of students in class that have this genotype and write this value in the table on the board. The following chart is based on a class of 24 students.

Table A: Sea Legs

	Homozygous Dominant	Heterozygous	Homozygous Recessive
P1	6	12	6

F1			
F2			

8. Ask the students to assist you in calculating the percentage of each genotype and record it on the board. Homozygous dominant = 6/24 = 0.2500, which tells us that 25% of the population is homozygous dominant.

Table A: Sea Legs

	Homozygous Dominant	Heterozygous	Homozygous Recessive
P1	6	12	6
	0.2500	0.5000	0.2500
F1			
F2			

9. Have each student tear their memo notes in half while at the same time splitting the genotypes in half. Remind them that during the process of meiosis, alleles are segregated. Each gamete will only contain one of the parent's alleles. (This same concept was addressed by Gregor Mendel's law of segregation.)
10. Now that each student has two separate alleles, they will need to find a partner. They should randomly pair up as well. Each pair of students represents a mating pair.
11. Have each pair of students stand facing each other with their alleles behind their back. On the count of three, each partner should randomly select one of the alleles to share with their partner. This represents fertilization of the gametes. By combining each of the alleles, the students will have their first offspring.
12. Each mating pair should now have two offspring. Afterward, they should record their number of offspring of each genotype on the board with tally marks.

Table A: Sea Legs

	Homozygous Dominant	Heterozygous	Homozygous Recessive
P1	6	12	6
	0.2500	0.5000	0.2500

F1	8	11	5
F2			

13. After each group has recorded their offspring, they are to switch alleles to become their offspring. In many situations, students will be able to switch notes to become their children's genotypes. In the event that the pair cannot utilize their own alleles, they may return to the gene pool to get the correct alleles to become their offspring.

    For example, two heterozygotes cross and produce a child with LL and ll. This pair can mix up their alleles to become their children. If those same parents had produced children that were both homozygous dominant (LL), there would not be enough dominant alleles between the pair for them to become their children. They would need to go to the gene pool to get those extra dominant alleles while placing their recessive alleles back into the pool.

14. Instruct the students to calculate the genotypic percentages of each genotype.

Table A: Sea Legs

	Homozygous Dominant	Heterozygous	Homozygous Recessive
P1	6	12	6
	0.2500	0.5000	0.2500
F1	8	11	5
	0.3333	0.4583	0.2083
F2			

15. Have the students answer Questions 1, 2, and 3 in the Analysis section. Discuss their responses as a class, and guide the class through the following questions.

16. Have the students mate again and produce two offspring. After they record their data on the board, have them place their alleles into the gene pool.

Table A: Sea Legs

	Homozygous Dominant	Heterozygous	Homozygous Recessive
P1	6	12	6
	0.2500	0.5000	0.2500

F1	8	11	5
	0.3333	0.4583	0.2083
F2	7	12	5
	0.2917	0.5000	0.2083

17. Have students assist in calculating the percentages. Instruct the students to create a graph of the data on their student answer page.
18. Facilitate a discussion answering the remaining questions in the Analysis section.
19. Calculate the percentages in the gene pool.
20. On the last question in the Analysis section, begin relating the activity to the Hardy-Weinberg principle. Explain the purpose of the Hardy-Weinberg principle. Introduce the two equations and explain what each variable in the equation represents.
21. Model with the students how to calculate all of the variables using the four Practice Problems.
22. Have the students complete the remaining practice problems as well as answer the Conclusion Questions.

Answers

Pre-Lab

1. A carrier's genotype would be Hh and therefore the cross would be Hh × Hh, which would yield 75% of offspring with normal thumbs and 25% with hitchhiker's thumbs.
2. Allele pairs separate during gamete formation and then randomly re-form pairs during the fusion of gametes at fertilization.
3. a. $x = 4$
   b. a = 21.213
   c. $p = 0.01$
   d. $r^2 = 25$
   e. $s^2 = 2.5 \times 10^{-5}$
   f. $y = 0.45$
   g. $b = 0.15$
   h. $2pq = 2(0.3560)(0.6440) = 0.4585$

Data and Observations

Table 2: Sea Legs

	Homozygous Dominant	Heterozygous	Homozygous Recessive
P1	6	12	6
	0.2500	0.5000	0.2500
F1	8	11	5
	0.3340	0.4583	0.2083
F2	7	12	5
	0.2917	0.5000	0.2083

Answers will vary depending on student data.

Graph

Answers will vary depending on student data, but the results should look similar to Figure A.

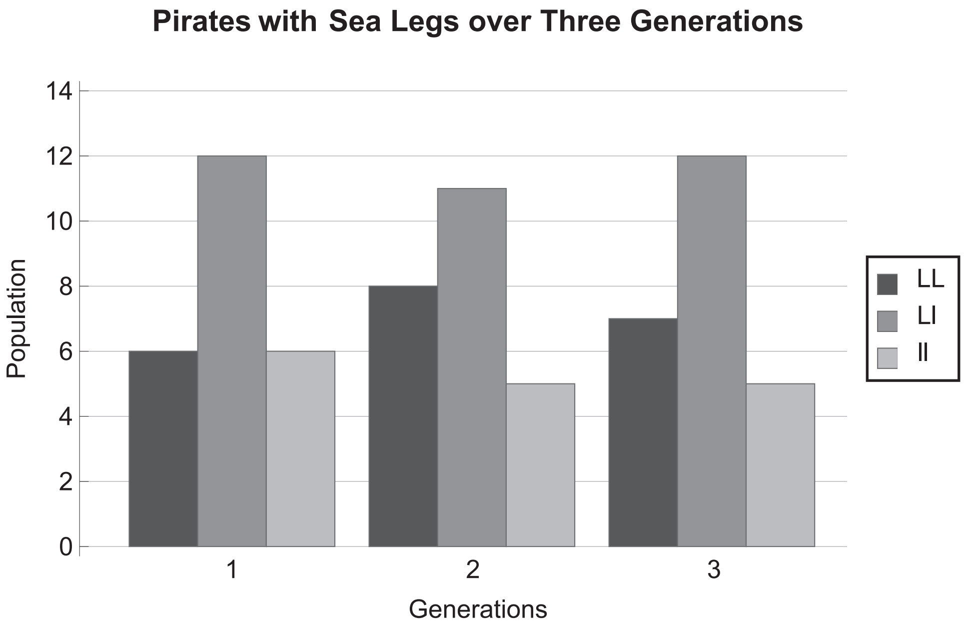

Figure A

Analysis

1. Answers will vary depending on student data.
2. Answers will vary depending on student data.
3. Answers will vary depending on student data; however, the number of organisms of each genotype should remain steady.
4. Answers will vary depending on student data.
5. Answers will vary depending on student data; however, students should predict that the percentages should remain constant.
6. Answers will vary depending on student data; however, students should understand that the gene pool has remained unchanged.
7. Students could mention any of the mechanisms of change that can cause a population to be out of Hardy-Weinberg equilibrium.

Practice Problems

1. a. 1:12 = 0.0833
   b. aa = 0.0833, so a = 0.2886
      $p + q = 1$
      $p = 1 - 0.2886 = 0.7114$
      $2pq = 2(0.7114)(0.2886) = 0.4106$, therefore Aa = 0.4106
   c. AA = $p^2 = 0.5061$
   d. $p = 0.7114$
   e. $q = 0.2886$
   f. $p^2 = 0.5061 = 50.61\%$
      $2pq = 0.4106 = 41.06\%$
      $q^2 = 0.0833 = 8.33\%$
2. a. $q^2 = 0.24$, therefore $q = 0.4899$ and $p = 0.5101$
   b. hh = 0.24, Hh = 0.4998, HH = 0.26
   c. The frequency of the recessive phenotype is 24%, and the frequency of the dominant phenotype is 76%
   d. 0.24 × 4000 = 960 people
   e. Students should predict that the population is not in equilibrium.
3. a. 1:1500 = 6.667×10^{-5}, which is q^2. Therefore, $q = 0.0082$ and $p = 0.9918$
   b. aa = 6.667×10^{-5}, Aa = 0.0162, AA = 0.9837
   c. 1.62%

Problems

1. a. The recessive characteristic is 30%, or equal to q^2. Therefore, bb = 0.30.

   b. bb = 0.30, so $q = 0.5477$

   $p + q = 1$

   $p = 1 - 0.5477 = 0.4523$

   $2pq = 2(0.4523)(0.5477) = 0.4954$, therefore Bb = 0.4954

   c. BB = $p^2 = 0.2046$

   d. $p = 0.4523$

   e. $q = 0.5477$

   f. $p^2 = 0.2046 = 20.46\%$

   g. $2pq = 0.4954 = 49.54\%$

   h. $q^2 = 30\%$, which was given in the problem

2. a. $1{:}2500 = q^2 = 0.0004$, so $q = 0.02$

   b. $p + q = 1$

   $p = 1 - 0.02 = 0.98$

   c. $2pq = 2(0.98)(0.02) = 0.0392$, or 3.92%

3. a. $345 + 755 = 1100$

   $345/1100 = q^2 = 0.3136$, so $q = 0.56$

   $p = 1 - 0.56 = 0.44$

   b. $q^2 = 0.3136$

   $2pq = 2(0.44)(0.56) = 0.4928$

   $p^2 = 0.1936$

   c. $(0.4928)(1100) = 542$

   d. Long-haired guinea pigs are recessive (q^2), therefore 0.3136 is the recessive phenotype frequency.

   Short-haired guinea pigs are dominant and so you must add p^2 and $2pq$, which equals a 0.6864 dominant phenotype frequency.

4. a. $(0.6864)(3500) = 2402.4$, or 2402

   b. $(0.3136)(3500) = 1097.6$, or 1098

   c. $(0.4928)(3500) = 1724.8$, or 1725

5. a. The total population on the cruise is 50. Two people are carriers, therefore there are a total of 2 recessive alleles.

   $q = 2/100 = 0.02$ and $p = 1 – 0.02 = 0.98$

   b. $q = 0.02$, so $q^2 = 0.0004$

   $2pq = 2(0.98)(0.02) = 0.0392$

   $p = 0.98$, so $p^2 = 0.9604$

Conclusion Questions

1. The tearing in half of the memo note represents the process of meiosis. Students exchanging their notes represents fertilization.
2. Comparing the P1 and F1 generations, the percentages are not exact. It is possible to assume that the population is not in equilibrium because the percentages are not the same. The only way to truly determine equilibrium is to observe the population over many more generations or complete a chi-squared analysis on the population.
3. Genetic drift would be the most likely cause in the shift due to the fact that the population was very small.
4. Over time, the population would have an abundance of pirates with sea legs. Inheriting the gene for sea legs becomes an advantageous trait, which represents the mechanism of natural selection. Gene flow is also changing the population as pirates are exiled from the population.
5. Student #2 rounded the numbers to the hundredths place. It appears as if the frequencies are close and accurate; however, when calculating the number of carriers in the population, the error becomes magnified. By rounding the values, 18 carriers are not identified.

Extension Questions

1. a. Incomplete dominance is calculated differently as the heterozygous and homozygous dominant organisms are known.

   RR = 28 flowers × two alleles each = 56 alleles

   Rr = 45 flowers × two alleles each = 90 alleles

   rr = 27 flowers × two alleles each = 54 alleles

   56 dominant alleles + 45 heterozygous alleles = 101 total alleles that are dominant

   p = 101/200 (the total number of alleles) = 0.5050

   b. 54 recessive alleles + 45 heterozygotes alleles = equal 99 alleles that are recessive

   $q = 99/200 = 0.4950$

   c. $2pq = 2(0.5050)(0.4950) = 0.49995$, or 0.500

   d. $q^2 = 0.2450$

   e. $p^2 = 0.2550$

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Investigating the Hardy-Weinberg Principle

G.H. Hardy, an English mathematician, and W.R. Weinberg, a German physician, derived the **Hardy-Weinberg principle** in 1908. This principle states that the frequencies of alleles in a population's gene pool remain constant over the generations unless acted upon by agents other than sexual recombination.

When the allelic frequencies remain constant over many generations, the population is said to be in *Hardy-Weinberg equilibrium*. There are five qualitatively different ways that can cause a population to be out of Hardy-Weinberg equilibrium. Because each is considered an evolutionary process, the occurrence of one in a population will change the allelic or genotypic frequencies in the population. As a result, populations are rarely in Hardy-Weinberg equilibrium.

The five mechanisms or conditions that can cause a population to evolve and be out of Hardy-Weinberg equilibrium are listed in Table 1.

Table 1: Hardy-Weinberg Equilibrium

Mechanisms of Change		Conditions
1	*Gene flow* – Migration of an individual's alleles into or out of the population	Isolation from other populations
2	*Mutations* – Spontaneous change of alleles within a population	No net mutations
3	*Natural selection* – Differential success of one allele over another one	No natural selection
4	*Nonrandom mating* – Preferential mating of certain phenotypes or allele combinations over others	Random mating
5	*Genetic drift* – Random change in a small gene pool due to sampling errors in the propagation of alleles	Very large populations

The Hardy-Weinberg equation enables us to calculate theoretical frequencies of alleles in a gene pool if we know the frequencies of genotypes and vice versa. Following are the two equations that can be used together to calculate the frequencies.

Because there are only two alleles in our population, the frequency of these two alleles added together should represent 100 percent of the population, or equal to 1 when calculating frequency. For the sake of convenience, p can represent the frequency of the dominant allele and q can represent the frequency of the recessive allele. The first equation refers to the allelic frequency in a population.

$$p + q = 1 \tag{Eq. 1}$$

The second equation includes variables that represent the frequencies of the genotypes in a population. When an individual inherits a dominant allele from both parents, the variable representing this genotype is represented as p^2. In contrast, the variable q^2 represents the homozygous recessive genotype.

$$p^2 + 2pq + q^2 = 1 \tag{Eq. 2}$$

There are two different ways to inherit the heterozygous genotype. An individual can inherit L from the father and l from the mother, or they can inherit l from the father and L from the mother. As result, the cross-product term $2pq$ of the equation represents the frequency of the heterozygous genotype.

After each of the allelic and genotypic frequencies is calculated, the percentages of each in the population can be determined. For example, when $q^2 = 0.7523$, it can be predicted that 75.23% of the population has the homozygous recessive genotype. If the percent of homozygous recessive individuals in a population is 95%, then one would know that the population was in fact not in Hardy-Weinberg equilibrium and must be experiencing evolution over many generations.

Purpose

In this activity you will calculate the allelic, genotypic, and phenotypic frequencies of a population using the Hardy-Weinberg principle.

Materials

1 memo note for each student
graphing calculator

Pre-Lab

1. Having a hitchhiker’s thumb is a trait passed on by inheriting a recessive allele, h, from both parents. The genotype of a person with hitchhiker’s thumb is hh. What is the chance that two carriers for hitchhiker’s thumb will have a child with a hitchhiker’s thumb?

2. State Mendel’s law of segregation.

3. Solve the following equations. Round each value to the ten-thousandths place.
    a. $x^2 = 16$. Solve for x.
    b. $a^2 = 450$. Solve for a.
    c. $p^2 = 1/10{,}000$. Solve for p.
    d. $r = 5$. Solve for r^2.
    e. $s = 0.005$. Solve for s^2.
    f. $x = 0.55$. If $x + y = 1$, solve for y.
    g. $a = 0.85$. If $a + b = 1$, solve for b.
    h. If $p = 0.3560$ and $q = 0.6440$, solve for $2pq$.

Procedure

1. Answer the Pre-Lab questions on the student answer page.
2. Get a memo note from your teacher.
3. Listen carefully as your teacher takes you through the introductory activity. During the activity, complete Table 2 on your student answer page as your teacher completes it on the board.
4. Complete the Practice Problems on the student answer pages.
5. Complete the Problems, Analysis, and Conclusion Questions on your student answer page.

Data and Observations

Table 2: Sea Legs			
	Homozygous Dominant	**Heterozygous**	**Homozygous Recessive**
P1			
F1			
F2			

Graph

Analysis

1. Do you see a tremendous change in the percentages of each genotype in the parental generation compared to the F1 generation?
2. Looking at the two existing generations, hypothesize what would happen to the genotypic percentages in the third generation.
3. Are there any observable trends?
4. Was your hypothesis for Question 2 correct?
5. If this population continued for 50 more generations, what would you predict to take place?
6. Why do you think these numbers remained consistent over the three generations?
7. What could we do to this population for there to be a more drastic change in the percentages of the genotypes?

Practice Problems

1. Sickle cell anemia is a condition caused by the inheritance of two recessive alleles, designated aa. Two million African-Americans, or 1 out of every 12, have the sickle cell trait. Calculate the following:
   a. The frequency of the aa genotype

   b. The frequency of the Aa genotype

   c. The frequency of the AA genotype

   d. The frequency of the dominant allele

   e. The frequency of the recessive allele

   f. The percentage of homozygous dominant

   g. The percentage of heterozygous

   h. The percentage of homozygous recessive

Practice Problems (continued)

2. You have sampled a population in which you know that 24% of the population has a hitchhiker's thumb, a recessive condition. In people with the dominant phenotype, they have straight thumbs. Calculate the following:
   a. The frequency of each allele
   b. The frequency of each genotype
   c. The frequency of each phenotype
   d. If the population consists of 4000 people, how many people have a hitchhiker's thumb?
   e. In the next generation, 60% of the population has a hitchhiker's thumb. What could you predict about this population?

3. A lethal recessive condition is responsible for the death of 1 out of every 15,000 babies in a population.
   a. Calculate the frequency of each allele.
   b. Calculate the frequency of each genotype.
   c. What percent of the population is heterozygous?

Problems

1. Within a population of butterflies, the color brown allele, B, is dominant over the color white allele, b. The portion of all butterflies that are white is 30%. Calculate the following:
   a. The frequency of the bb genotype
   b. The frequency of the Bb genotype
   c. The frequency of the BB genotype
   d. The frequency of the dominant allele
   e. The frequency of the recessive allele
   f. The percentage of homozygous dominant
   g. The percentage of heterozygous
   h. The percentage of homozygous recessive

Problems (continued)

2. Cystic fibrosis is a recessive condition that affects about 1 in 2,500 babies in the Caucasian population of the United States. Calculate the following:
   a. The frequency of the recessive allele in the population

   b. The frequency of the dominant allele in the population

   c. The percentage of heterozygous individuals (carriers) in the population

3. A large population has 345 long-haired guinea pigs and 755 short-haired guinea pigs. Knowing that long hair is completely recessive to short hair in guinea pigs, calculate the following:
   a. The frequencies of each allele

   b. The expected genotype frequencies

   c. The number of heterozygous individuals in the population

   d. The expected phenotype frequencies

Problems (continued)

4. If the guinea pigs in Question 3 are left to their own devices, their population could increase to 3500 in a very short time. Assuming that the frequencies of the alleles remain the same, answer the following questions.
   a. How many guinea pigs in this population would you expect to have short hair?

   b. How many guinea pigs in this population would have long hair?

   c. How many guinea pigs would be carriers for the long hair trait?

5. For a senior trip, you and 49 of your closest friends take a cruise to the Bahamas. While on the trip, you discover that two people in your group are carriers for sickle cell anemia. Unfortunately, the ship wrecks on an island. Assuming that the frequency of this allele does not change as the population grows on the island, calculate the following:
   a. The frequency of each allele

   b. The frequency of each genotype

Conclusion Questions

1. In the Pre-Lab activity, what process in the activity represented meiosis? What process represented fertilization?

2. Using the P1 generation in Table 2, determine if the P1 generation was in Hardy-Weinberg equilibrium compared to the F1 generation. Explain.

3. After looking at the percentages in each of the generations, what is the most likely cause of shift in the allelic frequency?

4. In this activity, the participants inherited a gene for sea legs. Imagine that the activity had been completed with some different parameters. After the F1 generation was created, your teacher stated that inheriting the sea legs trait was advantageous. Those children that did not inherit sea legs would be exiled from the pirate population, leaving only those with sea legs to mate. Given this case, predict what would happen to our population of pirates over time and justify your answer by describing the mechanism of change taking place.

Conclusion Questions (continued)

5. Following are the calculations of two classmates used to solve the problem stated. Both students completed the calculations as instructed but their answers were different. Analyze both students' calculations and explain the cause of the difference.

A widow's peak is a trait that can be expressed when a single dominant allele is inherited. In a given population, 2491 people have a widow's peak whereas 522 do not have the trait. Calculate the number of people in the population that are carriers of the gene for a widow's peak.

Student #1	Student #2
$q^2 = 522/3013 = 0.1732$	$q^2 = 522/3013 = 0.17$
$q = 0.4162$	$q = 0.41$
$p = 0.5837$	$p = 0.59$
$p^2 = 0.3408$	$p^2 = 0.35$
$2pq = 0.4860$	$2pq = 0.48$
Ww = $2pq = (0.4860)(3013)$	Ww = $2pq = (0.48)(3013)$
Ww = 1464 carriers	Ww = 1446 carriers

Extension Questions

1. In snapdragons, R is dominant for red flowers and r is recessive for white flowers. Snapdragons exhibit incomplete dominance: when a red snapdragon is crossed with a white snapdragon, pink dragons are produced. When two snapdragons are crossed, 45 of the offspring have pink flowers and 27 have white flowers. The remaining offspring in the population of 100 are red. Calculate the following:
    a. The frequency of the dominant allele

    b. The frequency of the recessive allele

    c. The frequency of heterozygous individuals

    d. The frequency of homozygous recessive individuals

    e. The frequency of homozygous dominant individuals