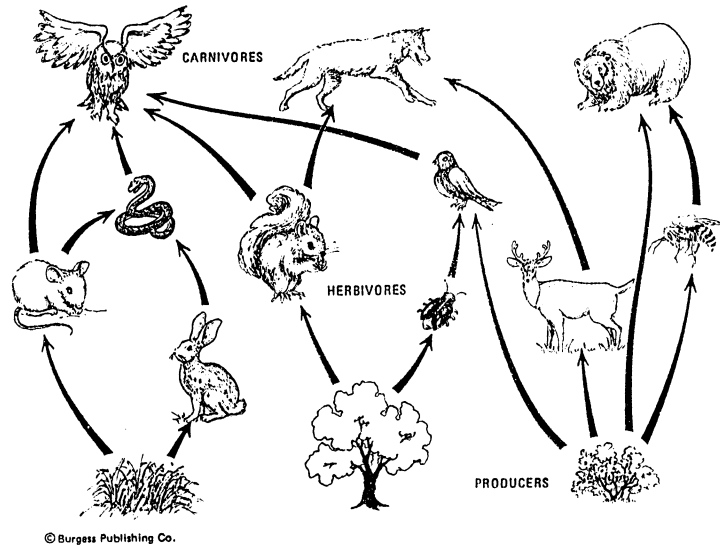


Genetic Changes in Populations: The Consequences of Selection



THINGS TO DO BEFORE LAB

1. Read the first two sections of this lab text ("TODAY'S LAB" and "COLLECTING YOUR DATA") **before** coming to lab. Your GSI will assume that you already understand how population geneticists study selection.
2. Make sure that you're familiar with the terms and concepts listed below. Consult your lecture notes, textbook, or this lab manual about any item that is new or unclear to you before coming to lab. Your T.A. may ask you to define or explain some of them to the class.

allele
C. Darwin
diploid
dominant
evolution
fertilization
gamete
gene pool

genetic drift
genotype
Hardy-Weinberg Principle
heterozygote
homozygote
locus
migration
mutation

nonrandom mating
phenotype
polymorphic
population
recessive
selection
A. R. Wallace

3. Use your lecture notes and textbook to complete the Worksheet (page 3). Your GSI will post the answers to this exercise or briefly review it at the beginning of lab.

THINGS TO BRING TO LAB

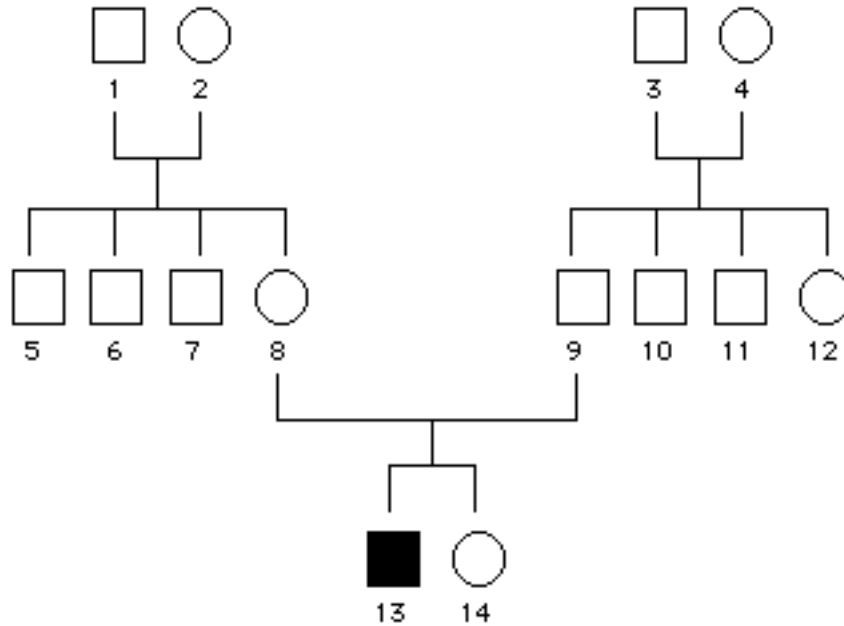
Calculator

WORKSHEET

Name: _____

A REVIEW OF MENDELIAN GENETICS AND THE HARDY-WEINBERG PRINCIPLE

Friedreich's ataxia is a human disorder that involves degeneration of the cerebellum, spinal cord, and peripheral nerves. A recessive allele (f) is responsible for the ataxic condition. Only recessive homozygotes express the disease. The following family pedigree illustrates the inheritance of ataxia. A square represents a male, a circle indicates a female, and a filled symbol denotes an ataxic individual.



1. Identify the two alleles that can occur at the ataxia locus.
2. What is the genotype of an ataxic individual?
3. What is the genotype of a carrier of the ataxia gene?
4. What are the two possible genotypes of a phenotypically normal individual?
5. The genotypes of only three individuals in the pedigree shown above are certain. Identify these individuals by number and give their genotypes.
6. Each of the other individuals has one of only two possible genotypes. What are they?
7. The frequency of Friedreich's ataxia in the American population is $1/50,000$ ($= 2 \times 10^{-5}$). Assuming that this population is at Hardy-Weinberg equilibrium, calculate the frequency of the ataxia allele among Americans.
8. Again, assuming that the American population is at Hardy-Weinberg equilibrium, determine the frequency of carriers of the heterozygotic ataxia allele in the population.
9. Is the assumption that the American population is at Hardy-Weinberg equilibrium valid? Why or why not?

TODAY'S LAB

Many wild **populations** of deer mice (*Peromyscus maniculatus*) in southwestern New Mexico are **polymorphic** for coat color: Some individuals possess dark reddish-brown fur, others have a pale gray pelage. Population geneticists have discovered that coat color in deer mice is determined by a single **locus** with two **alleles**, where dark is **dominant** (*D*) and pale is **recessive** (*d*).

Deer mice represent important sources of food for North American barn owls (*Tyto alba* ssp. *pratincola*). A barn owl is a visual predator that hunts in the dim evening light. It is likely to pursue, capture, and eat any deer mouse that it can see in dim light. A deer mouse's coat color determines, in large part, a barn owl's ability to see it. A deer mouse is virtually invisible, and therefore safe from barn owls, if its color matches that of the substrate upon which it is foraging. On the other hand, a deer mouse is highly vulnerable to predation by barn owls if the color of its surroundings contrasts sharply with its coat color. Large, dense shrubs and accumulations of dead vegetation cast enough shade during twilight hours that a deer mouse, regardless of its coat color, effectively escapes the attentions of hungry barn owls in their dark shadows.

A few populations of deer mice are endemic to extensive outcrops of black lava in southwestern New Mexico. Owls almost never spot deer mice having dark colored coats in this habitat. However, barn owls readily detect deer mice with pale fur against the black substrate, unless they remain in shady microsites.

Clearly, the barn owl exerts a **selective** force on populations of deer mice occupying black lava outcrops in southwestern New Mexico. How does such selection affect the **genotype** and allele frequencies of wild populations of deer mice? Can selection cause a deer mouse population to **evolve**, as claimed by **Darwin** and **Wallace**? Does the strength of selection influence its ability to bring about evolutionary change?

A population geneticist might attempt to answer these questions by monitoring the changes in allele and genotype frequencies over several generations in isolated populations of deer mice subjected to different levels of selection by barn owls. Obviously, you cannot conduct this sort of study in a single laboratory period (or even in a semester). However, you can quickly *simulate* the behavior of deer mouse populations for various selective regimes using the classical "bean-bag" model of population genetics. Under this model, a bag of colored beans represents a population's **gene pool**. Each bean corresponds to a **gamete** (sperm or egg) produced by one of the population's members. The color of a bean (a gamete) indicates the particular allele that it carries. By randomly drawing a pair of beans out of the bag, you can simulate the random mating of **diploid** parents. The pair of beans represents two gametes that have become united through **fertilization** to form a new individual. What do data provided by the bean-bag model tell you about the effects of selection by barn owls upon the genetic makeup of populations of deer mice?

The **Hardy-Weinberg Principle** provides a basis for evaluating your observed genotype and allele frequencies by specifying the genetic behavior of an ideal population, i.e., a randomly mating population of infinite size in which no **mutation**, **migration**, or selection occurs. The Hardy-Weinberg Principle makes two important predictions about future generations when ideal conditions prevail:

1. Genotype frequencies assume the values p^2 (dominant **homozygotes**), $2pq$ (**heterozygotes**), and q^2 (recessive homozygotes) after a single generation of random mating, and remain constant thereafter.
2. The frequency of the dominant allele p as well as the frequency of the recessive allele q remain constant (evolution does not occur).

A population that exhibits stability in both genotype and allele frequencies from generation to generation is said to be in Hardy-Weinberg equilibrium. The failure of one or both predictions indicates that the population has departed from the equilibrium state, and that **nonrandom mating**, **genetic drift**, mutation, migration, or selection is occurring.

Nonrandom mating in a population that otherwise meets all of the conditions for Hardy-Weinberg equilibrium causes a failure of the first prediction, but allele frequencies remain unchanged from one generation to the next. Thus, nonrandom mating alone cannot produce evolutionary change. It is important to remember that fixation of a selective advantageous allele must result in a character or feature that increases the organism's chance of survival and reproduction compared to organisms that lack this allele.

The occurrence of genetic drift, mutation, migration, or selection causes a failure of both predictions, i.e., genotype and allele frequencies differ from those expected for an equilibrium population. These forces disrupt Hardy-Weinberg equilibrium and they bring about evolutionary change.

In this lab, you will use the bean-bag model to determine allele and genotype frequencies for three generations of deer mice under each of three selective regimes. Then, you will employ the Hardy-Weinberg Principle as a tool to assess the impact of selection by barn owls on the evolution of deer mice.

COLLECTING YOUR DATA

Set-up

1. Form a team with three other students. Each team of four students will perform three simulations.
2. Obtain the following items for your team:

1 large bag of beans ("Wild Population's Gene Pool")
 1 container labelled "Parental Gene Pool"
 1 die

Procedure for establishing the First Parental Gene Pool

Each of three simulations will generate data about the genetic variability of three generations of offspring under a different selective regime. You'll begin each simulation with the same sample of 100 alleles drawn at random from a wild population of deer mice. This sample is the First Parental Gene Pool.

1. Pick 100 beans out of the Wild Population's Gene Pool without looking, and place them in the container marked "Parental Gene Pool". This is the First Parental Gene Pool.

The First Parental Gene Pool should represent a random sample of the Wild Population's Gene Pool (the proportion of red to white beans should be about the same in both gene pools). Try to avoid biasing your sample by selecting beans on the basis of feel (or color).

2. Determine the allele frequencies in the First Parental Gene Pool. Record your results in the Data Table for each of the three simulations (pages 18-19).

A red bean corresponds to a dominant allele for dark coat color (*D*), while a white bean corresponds to a recessive allele for pale coat color (*d*).

Example:

Allele frequencies in the First Parental Gene Pool		Offspring generation	Offspring population size	Observed genotype numbers --- frequencies			Observed allele frequencies		Expected genotype frequencies			Expected allele frequencies	
<i>D</i>	<i>d</i>			<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>	<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>
.56	.44	1		---	---	---							

Procedure for Simulation 1 (0% selection against pale coat color)

To identify the effects of selection on deer mouse populations, you first need to determine how a population behaves without selection (or other disturbing forces such as genetic drift, mutation, migration, and nonrandom mating). This simulation allows you to assess the genetic variability of three generations of offspring in the absence of selection against pale coat color. This simulation is equivalent to a field experiment in which you raise a large, isolated population of deer mice on a black lava outcrop that is completely shaded by old, massive creosote bushes. In performing your calculations, carry all numbers to at least two decimal places.

1. Without looking, draw two beans out of the Parental Gene Pool.

All three simulations assume that mating is random (the probability of drawing a red bean equals the probability of drawing a white bean). Avoid biasing your results by selecting beans on the basis of feel (or color).

2. Determine the genotype of the newborn deer mouse, and score this result on the Tally Sheet (page 19).

A newborn deer mouse can belong to one of three possible genotypic classes: *DD*, *Dd*, or *dd*. However, it can have one of only two possible **phenotypes**. Two genotypes specify a dark coat color: *DD* and *Dd*. One genotype specifies a pale coat color: *dd*. Of course, in nature, you couldn't distinguish dominant homozygotes from heterozygotes.

Example:

You have drawn two red beans out of the Parental Gene Pool

Simulation 1			
	<i>DD</i>	<i>Dd</i>	<i>dd</i>
Offspring generation 1			

3. **Return the two beans to the Parental Gene Pool.**

This step ensures that the probability of drawing a particular allele (a red or white bean) remains close to its frequency in the Parental Gene Pool.

4. Repeat steps 1-3 until you have produced 50 newborn deer mice.

50 replications should give you a statistically representative sample of the offspring genotype frequencies produced by random mating among the parents.

5. Enter the offspring population size (50) as well as the number of offspring belonging to each genotypic class (observed offspring genotype numbers) in the appropriate Data Table. Example:

Allele frequencies in the First Parental Gene Pool				Observed genotype numbers --- frequencies			Observed allele frequencies		Expected genotype frequencies			Expected allele frequencies	
<i>D</i>	<i>d</i>	Offspring generation	Offspring population size	<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>	<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>
.56	.44	1	50	18	22	10							
				---	---	---							

6. Convert your observed genotype numbers to frequencies. Add your results to the Data Table.

In the example below,

$$\text{frequency of } DD = (\text{observed number of } DD \div \text{offspring population size})$$

$$.36 = (18 \div 50).$$

Allele frequencies in the First Parental Gene Pool				Observed genotype numbers --- frequencies			Observed allele frequencies		Expected genotype frequencies			Expected allele frequencies	
<i>D</i>	<i>d</i>	Offspring generation	Offspring population size	<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>	<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>
.56	.44	1	50	18	22	10							
				---	---	---							
				.36	.44	.20							

7. Calculate the frequencies of alleles *D* and *d* from your observed genotype frequencies. Add your results to the Data Table.

All of the alleles possessed by dominant homozygotes (*DD*) and half of the alleles belonging to heterozygotes (*Dd*) are dominant alleles (*D*). Likewise, all of the alleles contained in recessive homozygotes (*dd*) and half of the alleles held by heterozygotes are recessive alleles (*d*).

Thus, the observed frequency of *D* equals the frequency of dominant homozygotes plus one-half the frequency of heterozygotes, and the observed frequency of *d* is the frequency of recessive homozygotes plus one-half the frequency of heterozygotes.

As only two alleles (*D* and *d*) occur at the coat color locus, the sum of the observed frequencies of these two alleles must equal one. Expressed mathematically,

$$p + q = 1$$

where *p* = the frequency of *D*, and *q* = the frequency of *d*.

In the following example,

frequency of *D* = (frequency of *DD*) + (half the frequency of *Dd*)

$$.58 = (.36) + (.44 \div 2),$$

frequency of *d* = (frequency of *dd*) + (half the frequency of *Dd*)

$$.42 = (.20) + (.44 \div 2).$$

Allele frequencies in the First Parental Gene Pool		Offspring generation	Offspring population size	Observed genotype numbers --- frequencies			Observed allele frequencies		Expected genotype frequencies			Expected allele frequencies	
<i>D</i>	<i>d</i>			<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>	<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>
.56	.44	1	50	18 --- .36	22 --- .44	10 --- .20	.58	.42					

8. Using parental allele frequencies (*Caution: It's tricky to figure out which pair of allele frequencies belongs to the parents of the current generation of offspring.*) and Hardy-Weinberg expectations, determine the expected genotype frequency for each genotypic class. Enter the results in the Data Table.

Remember, the Hardy-Weinberg Principle states that, at equilibrium, the following equation specifies the expected genotype frequencies within the population:

$$p^2 + 2pq + q^2 = 1$$

Example:

frequency of *DD* = p^2

$$.31 = (.56) \times (.56),$$

frequency of *Dd* = $2pq$

$$.49 = (2) \times (.56) \times (.44),$$

frequency of *dd* = q^2

$$.19 = (.44) \times (.44).$$

Allele frequencies in the First Parental Gene Pool		Offspring generation	Offspring population size	Observed genotype numbers --- frequencies			Observed allele frequencies		Expected genotype frequencies			Expected allele frequencies	
<i>D</i>	<i>d</i>			<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>	<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>
.56	.44	1	50	18 --- .36	22 --- .44	10 --- .20	.58	.42	.31	.49	.19		

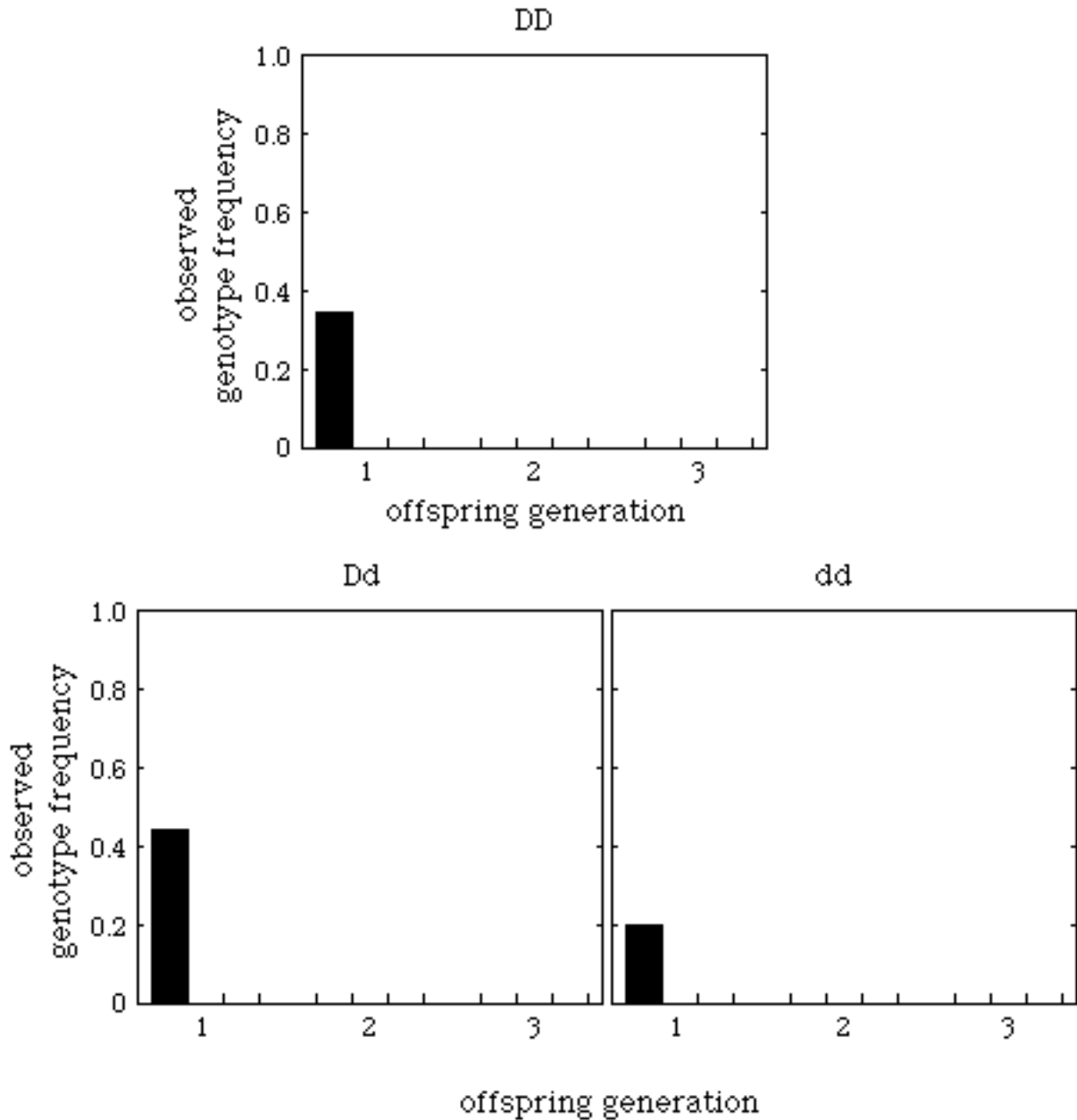
9. Using expected genotype frequencies and Hardy-Weinberg expectations, determine the expected allele frequencies (calculate them like you did in step 7). Enter the results in the Data Table. Example:

Allele frequencies in the First Parental Gene Pool		Offspring generation	Offspring population size	Observed genotype numbers --- frequencies			Observed allele frequencies		Expected genotype frequencies			Expected allele frequencies	
<i>D</i>	<i>d</i>			<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>	<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>
.56	.44	1	50	18 --- .36	22 --- .44	10 --- .20	.58	.42	.31	.49	.19	.56	.44

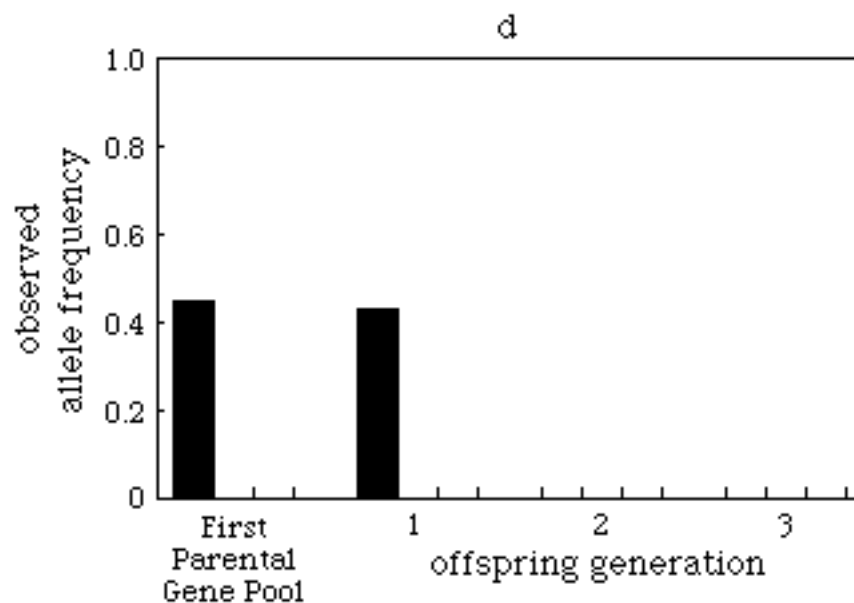
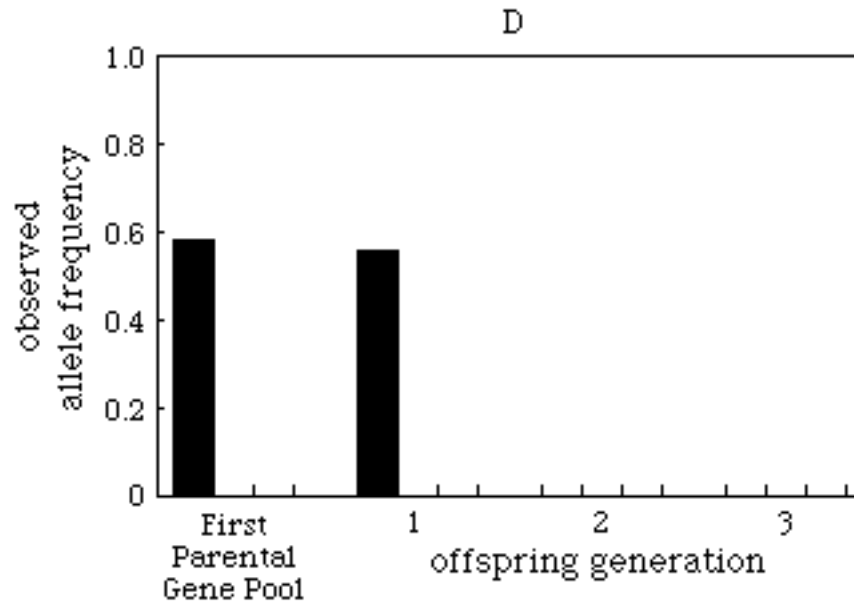
10. Adjust the numbers of red and white beans in the Parental Gene Pool. The frequencies of the beans must correspond to the observed frequencies of alleles *D* and *d* in the offspring population (.58 and .42 in the preceding example). Be sure to maintain a total of 100 beans in the Parental Gene Pool. Obtain extra beans of the needed color from the Wild Population's Gene Pool.

The offspring in one generation represent the parents of the next generation. Therefore, you must change the constitution of the Parental Gene Pool to reflect the new parental allele frequencies before proceeding.

- Repeat steps 1-10 to produce a total of three generations of offspring.
- Draw nine solid bars on the three Observed Genotype Frequency Graphs on page 23. Construct three solid bars for each genotypic class. For a given genotypic class, each bar corresponds to the observed genotype frequency for a single offspring generation. The three bars below were drawn using data from the preceding example (.36, .44, .20):



13. Draw eight solid bars on the two Observed Allele Frequency Graphs on page 24. For each allele, construct one solid bar for the allele frequency in the First Parental Gene Pool, and one solid bar for the observed allele frequency in each offspring generation. The four bars below were drawn using data from the preceding example (.56, .58, .44, .42):



Procedure for Simulation 2 (50% selection against pale coat color)

This simulation permits you to observe the genetic changes brought about by moderate (50%) selection against pale coat color over three generations of offspring. This simulation is comparable to a field experiment in which you rear a large, isolated population of deer mice on a black lava outcrop only half of which is shaded by creosote bushes. In performing your calculations, carry all numbers to at least two decimal places.

1. Adjust the numbers of red and white beans in the Parental Gene Pool so that their frequencies match those in the First Parental Gene Pool, but maintain a total of 100 beans in the Parental Gene Pool. Obtain extra beans of the needed color from the Wild Population's Gene Pool.

2. Without looking, draw two beans out of the Parental Gene Pool.
3. Determine the genotype of the newborn deer mouse.

•If the newborn's genotype is DD or Dd , then the newborn survives. Score the genotype on your Tally Sheet (page 19).

We're assuming that selection does not operate against dark newborns, and that all of them survive.

•If the newborn's genotype is dd , then roll the die.

••If the number on the die is 1, 2, or 3, then the newborn survives. Score the genotype on your Tally Sheet.

••If the number on the die is 4, 5, or 6, then the newborn dies. Record the death in the proper column of your Tally Sheet.

We're assuming that selection acts against pale newborns (barn owls eat them), but only 1/2, or 50%, of the time.

4. Return the two beans to the Parental Gene Pool.

5. Repeat steps 2-4 until 50 births have occurred (whether a newborn ultimately survives or dies is irrelevant here).
6. Enter the total number of surviving offspring (offspring population size), and the number of surviving offspring belonging to each genotypic class (observed offspring genotype numbers) in the appropriate Data Table (pages 21-22).

For example, consider part of a Tally Sheet:

DD	Dd	dd	Deaths

These tally marks translate into the numbers shown in the appropriate boxes below:

Allele frequencies in the First Parental Gene Pool		Offspring generation	Offspring population size	Observed genotype numbers --- frequencies			Observed allele frequencies		Expected genotype frequencies			Expected allele frequencies	
<i>D</i>	<i>d</i>			<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>	<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>
.56	.44	1	46	10 ---	31 ---	5 ---							

7. Convert your observed genotype numbers to frequencies. Add your results to the Data Table.
8. Compute the observed frequencies of alleles *D* and *d* from your observed genotype frequencies. Add your results to the Data Table.
9. Using parental allele frequencies and Hardy-Weinberg expectations, determine the expected genotype frequency for each genotypic class. Enter the results in the Data Table.
10. Using expected genotype frequencies and Hardy-Weinberg expectations, determine the expected allele frequencies. Enter the results in the Data Table.
11. Adjust the numbers of red and white beans in the Parental Gene Pool. The frequencies of the beans must correspond to the observed frequencies of alleles *D* and *d* in the offspring population. Be sure to maintain a total of 100 beans in the Parental Gene Pool. Obtain extra beans of the needed color from the Wild Population's Gene Pool.
12. Repeat steps 2-11 to produce a total of three generations of offspring.
13. Draw nine striped bars on the three Observed Genotype Frequency Graphs on page 23. Construct three striped bars for each genotypic class. For a given genotypic class, each bar corresponds to the observed genotype frequency for a single offspring generation.
14. Draw eight striped bars on the two Observed Allele Frequency Graphs on page 24. For each allele, construct one striped bar for the allele frequency in the First Parental Gene Pool, and one striped bar for the observed allele frequency in each offspring generation.

Procedure for Simulation 3 (100% selection against pale coat color)

This simulation offers you the opportunity to track the genetic changes induced in deer mouse populations by strong (100%) selection against pale coat color over three generations of offspring. This simulation is similar to a field experiment in which you monitor a large, isolated population of deer mice on a bare, black lava outcrop with no shade. In performing your calculations, carry all numbers to at least two decimal places.

1. Adjust the numbers of red and white beans in the Parental Gene Pool so that their frequencies match those in the First Parental Gene Pool, but maintain a total of 100 beans in the Parental Gene Pool. Obtain extra beans of the needed color from the Wild Population's Gene Pool.
2. Without looking, draw two beans out of the Parental Gene Pool.
3. Determine the genotype of the newborn deer mouse.
 - If the newborn's genotype is DD or Dd , then the newborn survives. Score the genotype on your Tally Sheet (page 19).

We're assuming that selection does not operate against dark newborns, and that all of them survive.

- If the newborn's genotype is dd , then the newborn dies. Record the death in the appropriate column of your Tally Sheet.

We're assuming that selection always acts against pale newborns (barn owls always eat them).

4. Return the two beans to the Parental Gene Pool.

5. Repeat steps 2-4 until 50 births have occurred (whether a newborn ultimately survives or dies is irrelevant here).
6. Enter the total number of surviving offspring (offspring population size), and the number of surviving offspring belonging to each genotypic class (observed offspring genotype numbers) in the appropriate Data Table (pages 21-22).
7. Convert your observed genotype numbers to frequencies. Add your results to the Data Table.
8. Compute the observed frequencies of alleles D and d from your observed genotype frequencies. Add your results to the Data Table.
9. Using parental allele frequencies and Hardy-Weinberg expectations, determine the expected genotype frequency for each genotypic class. Enter the results in the Data Table.
10. Using expected genotype frequencies and Hardy-Weinberg expectations, determine the expected allele frequencies. Enter the results in the Data Table.

11. Adjust the numbers of red and white beans in the Parental Gene Pool. The frequencies of the beans must correspond to the observed frequencies of alleles D and d in the offspring population. Be sure to maintain a total of 100 beans in the Parental Gene Pool. Obtain extra beans of the needed color from the Wild Population's Gene Pool.
12. Repeat steps 2-11 to produce a total of three generations of offspring.
13. Draw nine open bars on the three Observed Genotype Frequency Graphs on page 23. Construct three open bars for each genotypic class. For a given genotypic class, each bar corresponds to the observed genotype frequency for a single offspring generation.
14. Draw eight open bars on the two Observed Allele Frequency Graphs on page 24. For each allele, construct one open bar for the allele frequency in the First Parental Gene Pool, and one open bar for the observed allele frequency in each offspring generation.
15. **Return all beans to the Wild Population's Gene Pool.**

INTERPRETING YOUR DATA: YOUR TAKE-HOME ASSIGNMENT

To assess the impact of selection by barn owls upon the genetic constitution of deer mouse populations, you need to check your data for each generation (a total of nine generations) for discrepancies between observed genotype and allele frequencies and those expected for a population at Hardy-Weinberg equilibrium.

Chance almost always produces small deviations between observed genotype and allele frequencies and those predicted by the Hardy-Weinberg Principle, even if the population actually satisfies all of the conditions for equilibrium. How small do these deviations have to be to safely conclude that they are due only to chance? Conversely, how large do these deviations have to be to confidently conclude that they represent real differences between observed and expected frequencies? The chi-square statistical test helps you to make these decisions. However, we will not perform the chi-square tests due to the small number of simulations.

For a given generation, a difference between observed and expected genotype or allele frequencies indicates that the population deviates from Hardy-Weinberg equilibrium. The failure of both of the predictions for a population at Hardy-Weinberg equilibrium (see pages 3-4) tells you that selection (and/or some combination of genetic drift, mutation, and migration) is occurring.

Your assignment

Write four short essays about the effects of barn owls on wild populations of deer mice that inhabit black lava outcrops in southwestern New Mexico. Address each of the following questions in a 100-word essay (about half of a double-spaced, typed page):

- a. How did you study the impacts of selection on populations of deer mice?
- b. How does selection created by the predatory activities of barn owls affect the genotype and allele frequencies of populations of deer mice?
- c. Can selection cause a deer mouse population to evolve?
- d. Does the strength of selection influence its ability to bring about evolutionary change?

Tally Sheet

	Simulation 1			Simulation 2				Simulation 3			
	<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>DD</i>	<i>Dd</i>	<i>dd</i>	Deaths	<i>DD</i>	<i>Dd</i>	<i>dd</i>	Deaths
Offspring generation 1											
Offspring generation 2											
Offspring generation 3											

DATA TABLES

Name: _____

Simulation 1 (0% selection against pale coat color)

Allele frequencies in Gene Pool		Offspring generation	Offspring population size	Observed genotype numbers --- frequencies			Observed allele frequencies		Expected genotype frequencies			Expected allele frequencies	
<i>D</i>	<i>d</i>			<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>	<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>
		1		---	---	---							
		2		---	---	---							
		3		---	---	---							

Simulation 2 (50% selection against pale coat color)

Allele frequencies in Gene Pool		Offspring generation	Offspring population size	Observed genotype numbers --- frequencies			Observed allele frequencies		Expected genotype frequencies			Expected allele frequencies	
<i>D</i>	<i>d</i>			<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>	<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>
		1		---	---	---							
		2		---	---	---							
		3		---	---	---							

DATA TABLES (CONTINUED)

Name: _____

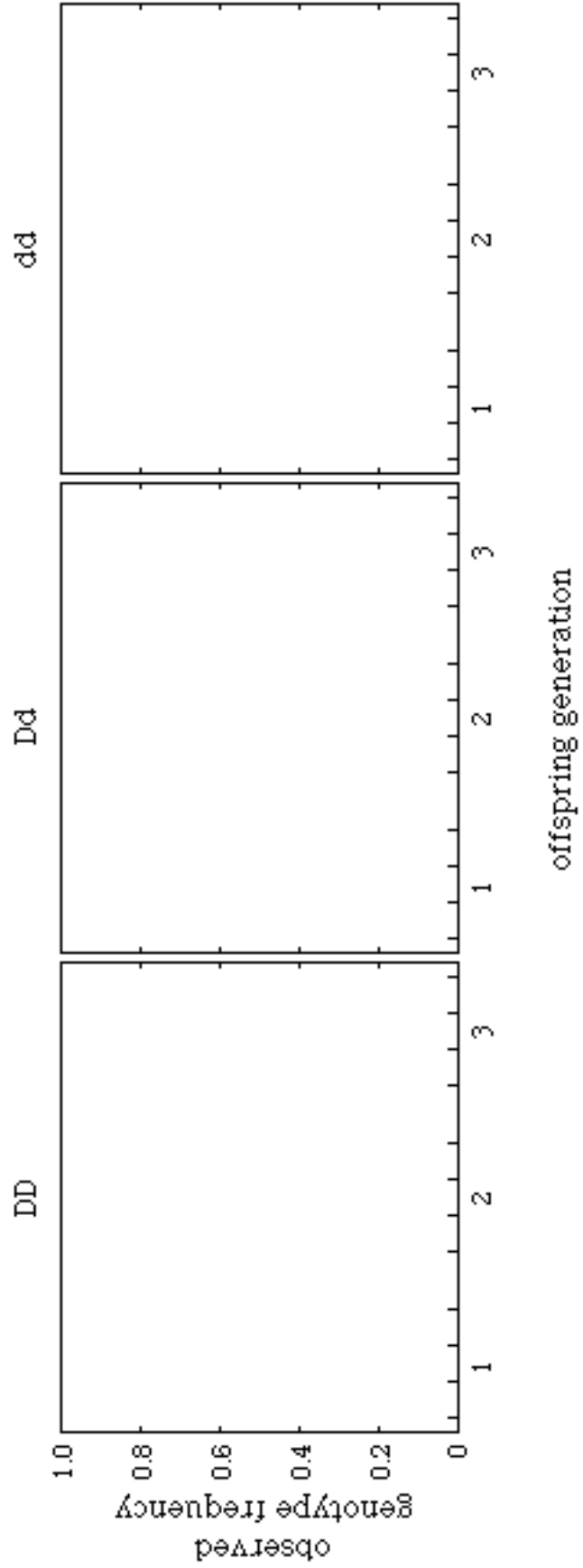
Simulation 3 (100% selection against pale coat color)

Allele frequencies in Gene Pool		Offspring generation	Offspring population size	Observed genotype numbers --- frequencies			Observed allele frequencies		Expected genotype frequencies			Expected allele frequencies	
<i>D</i>	<i>d</i>			<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>	<i>DD</i>	<i>Dd</i>	<i>dd</i>	<i>D</i>	<i>d</i>
		1		---	---	---							
		2		---	---	---							
		3		---	---	---							

OBSERVED GENOTYPE FREQUENCY GRAPHS

Name: _____

Observed genotype frequencies
at the coat color locus for simulated populations of deer mice



OBSERVED ALLELE FREQUENCY GRAPHS

Name: _____

Observed allele frequencies
at the coat color locus for simulated populations of deer mice

- Simulation 1
- ▨ Simulation 2
- Simulation 3

