Evolution

Natural Selection and Morphological Change in Green Algae

Learning Objectives

By the end of this exercise you should be able to:

1. Give a working definition of evolution, fitness, selection pressure, and natural selection.
2. Determine the genotypic and phenotypic frequency of a population while properly using the terms allele, dominant, recessive, homozygous, and heterozygous.
3. Explain the Hardy-Weinberg Principle and use it to demonstrate negative selection pressures on a population.
4. Describe the significance of the Volvocine line, particularly in the areas of cellular specialization and colonial complexity.
5. Describe examples of how a mutation affecting the plane of cellular division could result in the evolution of morphologically different body plans.

Please visit connect.mheducation.com to review online resources tailored to this lab.

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Figure 18.1 Mutations produce new alleles and genetic combinations. This child has a streak of white hair, caused by a somatic mutation in a single cell during embryonic development. This cell continued to divide to produce a streak of white hair.

The theory of **evolution** broadly describes genetic change in populations. The existence of genetic change (and therefore evolution) is universally accepted by biologists. We know that many mechanisms can change the genetic makeup of populations, but the relative importance of each mechanism remains to be fully described. Events such as **mutations** (changes in the genetic message of a cell, fig. 18.1) and catastrophes (e.g., meteor showers, ice ages) can produce genetic change. However, Charles Darwin (fig. 18.2) formulated a theory that explains a major force behind genetic change that produces adaptation: natural selection.

Darwin postulated that organisms that survive and reproduce successfully have genetic traits aiding survival and reproduction. These traits enhance an organism's **fitness,** which is its tendency to produce more offspring than competing individuals, and therefore contribute more genes to the next generation. Darwin noticed that fit individuals (that is, ones that reproduce the most) produce more offspring because their traits are better adapted for survival and reproduction than the traits of their competitors. He further reasoned that if the traits of the more fit individuals are transmitted to the next generation more often, then more of these traits will be found in the next generation. After many generations, the frequency of these traits will increase in the population, and the nature of the population will gradually change. Darwin called this process **natural selection** and proposed it as a major force that guides genetic change while producing adaptations and forming new species. Review in your textbook the theories of evolution and the mechanism of natural selection.

Showing the effects of natural selection in living populations is usually time-consuming and tedious. Therefore, in this exercise you will simulate reproducing populations with nonliving, colored beads representing organisms and their gametes. With this artificial population you can quickly follow genetic change over many generations. Before you begin work, review the previous exercise on genetics, especially the terms **gene, allele, dominant alleles, recessive alleles, homozygous,** and **heterozygous.**

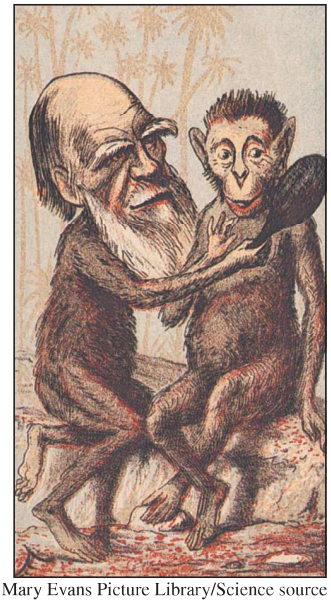

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Figure 18.2 Darwin greets his "monkey ancestor." In his time, Darwin was often portrayed unsympathetically, as in this drawing from an 1874 publication.

You will begin your experiments using a "stock population" of organisms consisting of a container of beads. Each bead represents a haploid (having one set of chromosomes) gamete, and the color of the "gamete" (colored or white) represents an allele it is carrying. Individual organisms from this population are diploid (having two sets of chromosomes) and therefore are represented by two beads.

UNDERSTANDING ALLELIC AND GENOTYPIC FREQUENCIES

Frequency is the proportion of individuals in a certain category relative to the total number of individuals considered. The frequency of an allele or genotype is expressed as a decimal proportion of the total alleles or genotypes in a population. For example, if 1/4 of the individuals of a population are genotype *Bb,* then the frequency of *Bb* is 0.25. If 3/4 of all alleles in a population are *B,* then the frequency of *B* is 0.75.

In this exercise you will simulate evolutionary changes in allelic and genotypic frequencies in an artificial population. The trait you will work with is fur color. A colored bead is a gamete with a dominant allele (complete dominance) for black fur (*B*), and a white bead is a gamete with a recessive allele for white fur (*b*). An individual is represented by two gametes (beads). Individuals with genotypes *BB* and *Bb* have black fur, and those with *bb* have white fur.

Procedure 18.1 Establish a parental population

1. Obtain a "stock population" of organisms consisting of a container of colored and white beads.
2. Obtain an empty container marked "Parental Population."
3. From the stock population, select 25 homozygous dominant individuals (*BB*) and place them in the container marked "Parental Population." Each individual is represented by two colored beads.
4. From the stock population, select 50 heterozygous individuals (*Bb*) and place them in the container marked "Parental Population." Each individual is represented by a colored and a white bead.
5. From the stock population, select 25 homozygous recessive individuals (*bb*) and place them in the container marked "Parental Population." Each individual is represented by two white beads.
6. Calculate the total number of individuals and the total number of alleles in your newly established parental population. Use this information to calculate and record in table 18.1 the correct genotypic frequencies for your parental population.
7. Complete table 18.1 with the number and frequency of each of the two alleles.

Question 1

a. How many alleles are present for this particular trait?

b. How many of the total beads are colored and how many are white?

TABLE 18.1

FREQUENCIES OF GENOTYPES AND ALLELES OF THE PARENTAL POPULATION

GENOTYPES	FREQUENCY	ALLELES	FREQUENCY
BB ●●	_____	*B* ●	_____
Bb ●○	_____	*b* ○	_____
bb ○○	0.25		

c. What color fur do *Bb* individuals have?

d. How many beads represent the population?

THE HARDY-WEINBERG PRINCIPLE

The **Hardy-Weinberg Principle** enables us to calculate and predict allelic and genotypic frequencies. We can compare these predictions with actual changes that we observe in natural populations and learn about factors that influence gene frequencies. Deviations of observed frequencies from frequencies predicted by the Hardy-Weinberg Principle indicate evolution.

This predictive model includes two simple equations first described for stable populations by Godfrey Hardy and Wilhelm Weinberg. Hardy-Weinberg equations (1) predict allelic and genotypic frequencies based on data for only one or two frequencies, and (2) provide a set of theoretical frequencies that we can compare to frequencies from natural populations. For example, if we know the frequency of *B* or *BB,* we can calculate the frequency of *b, Bb,* and *bb.* Then we can compare these frequencies with those of a natural population that we might be studying. If our observed data vary from our predictions, we can study the reasons for this genetic change. This comparison is important because biological characteristics of natural populations rarely correspond exactly to theoretical calculations. Furthermore, deviations are important because they often reveal unknown factors influencing the population being studied.

According to the Hardy-Weinberg Principle, the frequency of the dominant allele of a pair is represented by the letter *p,* and that of the recessive allele by the letter *q.* Also, the genotypic frequencies of *BB* (homozygous dominant), *Bb* (heterozygous), and *bb* (homozygous recessive) are represented by p^2, $2pq$, and q^2, respectively. Examine the frequencies in table 18.1 and verify the Hardy-Weinberg equations:

$$p = \text{frequency of dominant allele}$$
$$q = \text{frequency of recessive allele}$$
$$p + q = 1$$
$$p^2 + 2pq + q^2 = 1$$

The Hardy-Weinberg Principle and its equations predict that frequencies of alleles and genotypes will remain constant from generation to generation in stable populations. Therefore, these equations can be used to predict genetic frequencies through time. However, the Hardy-Weinberg prediction assumes that

- The population is large enough to overcome random events.
- Choice of mates is random.
- Mutation does not occur.
- Individuals do not migrate into or out of the population.
- There is no selection pressure.

Question 2

a. Consider the Hardy-Weinberg equations. If the frequency of a recessive allele is 0.3, what is the frequency of the dominant allele?

b. If the frequency of the homozygous dominant genotype is 0.49, what is the frequency of the dominant allele?

c. If the frequency of the homozygous recessive genotype is 0.36, what is the frequency of the dominant allele?

d. If the frequency of the homozygous dominant genotype is 0.49, what is the frequency of the homozygous recessive genotype?

e. Which Hardy-Weinberg equation relates the frequencies of the alleles at a particular gene locus?

f. Which Hardy-Weinberg equation relates the frequencies of the genotypes for a particular gene locus?

g. Which Hardy-Weinberg equation relates the frequencies of the phenotypes for a gene?

Additional problems to test your understanding of the Hardy-Weinberg Principle are at the end of this exercise.

To verify the predictions of the Hardy-Weinberg Principle, use the following procedure to produce a generation

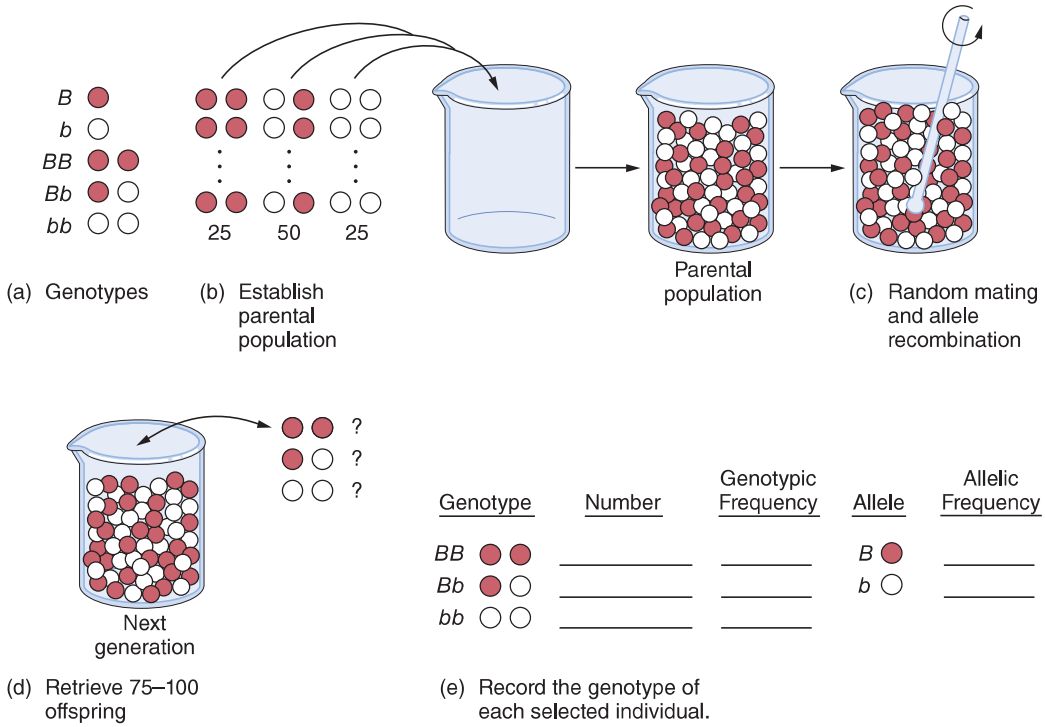

Figure 18.3 Verification of the Hardy-Weinberg Principle. See procedure 18.2 for an explanation of each step.

of offspring from the parental population you created in the previous procedure.

Procedure 18.2 Verify the Hardy-Weinberg Principle

1. Examine figure 18.3 for an overview of the steps of this procedure.
2. Establish the parental population from procedure 18.1 (fig. 18.3*a*, 18.3*b*).
3. Simulate the random mating of individuals by mixing the population (fig. 18.3*c*).
4. Reach into the parental container (without looking) and randomly select two gametes. Determine their genotype (fig. 18.3*d*). This pair of gametes with colored or white alleles represents an individual offspring.
5. Record the occurrence of the genotype in figure 18.3*e* as a mark under the heading "Number" or temporarily on a second sheet of paper and return the beads to the container.
6. Repeat steps 4 and 5 (100 times) to simulate the production of 100 offspring.
7. Calculate the frequency of each genotype and allele, and record the frequencies in figure 18.3*e*. Beside each of these new-generation frequencies write (in parentheses) the original frequency of that specific genotype or allele from table 18.1.

Question 3

a. The Hardy-Weinberg Principle predicts that genotypic frequencies of offspring will be the same as those of the parental generation. Were they the same in your simulation?

b. If the frequencies were different, then one of the assumptions of the Hardy-Weinberg Principle was probably violated. Which one?

EFFECT OF A SELECTION PRESSURE

Selection is the differential reproduction of phenotypes (fig. 18.4); that is, some phenotypes (and their associated genotypes) are passed to the next generation more often than others. In positive selection, genotypes representing adaptive traits in an environment increase in frequency because their bearers are more likely to survive and reproduce. In negative selection, genotypes representing nonadaptive traits in an environment decrease in frequency because their bearers are less likely to survive and reproduce.

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Figure 18.4 Reproduction. These birds hatching from eggs may or may not survive to reproduce. On average, birds with characteristics best adapted to their environment will survive and reproduce more than those with less adaptive characteristics. As a result, the frequencies of adaptive traits (and their alleles) in the population will increase from generation to generation. This change in frequencies of alleles over time is evolution.

Selection pressures are factors such as temperature and predation that affect organisms and result in selective reproduction of phenotypes. Some pressures may elicit 100% negative selection against a characteristic and eliminate any successful reproduction of individuals having that characteristic. For example, mice with white fur may be easy prey for a fox if they live on a black lava field. This dark environment is a negative selection pressure against white fur. If survival and reproduction of mice with white fur were eliminated (i.e., if there is 100% negative selection), would the frequency of white mice in the population decrease with subsequent generations? To test this, use the following procedure to randomly mate members of the original parental population to produce 100 offspring (fig. 18.5).

Procedure 18.3 Simulate 100% negative selection pressure

1. Establish the same parental population that you used to test the Hardy-Weinberg prediction.
2. Simulate the production of an offspring from this population by randomly withdrawing two gametes to represent an individual offspring.
3. If the offspring is *BB* or *Bb,* place it in a container for the accumulation of the "Next Generation." Record the occurrence of this genotype on a separate sheet of paper.
4. If the offspring is *bb,* place this individual in a container for those that "Cannot Reproduce." Individuals in this container should not be used to produce subsequent generations. Record the occurrence of this genotype on a sheet of paper.
5. Repeat steps 2–4 until the parental population is depleted, thus completing the first generation.

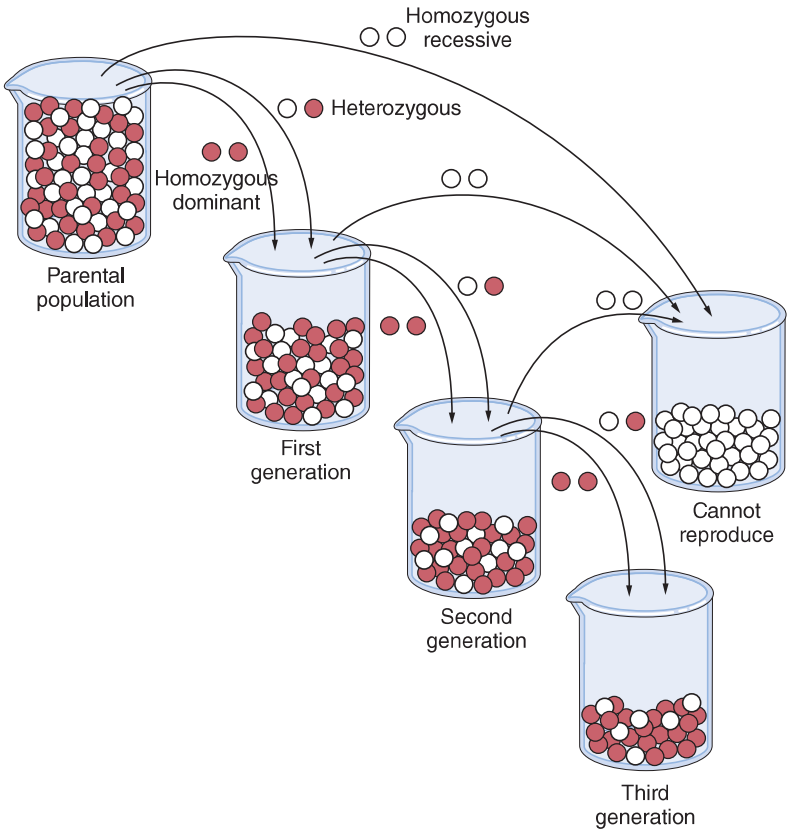

Figure 18.5 Demonstrating the effect of 100% selection pressure on genotypic and phenotypic frequencies across three generations. In this example, selection is against the homozygous recessive genotype. Random mating within the parental population is simulated by mixing the gametes (beads), and the parental population is sampled by removing two alleles (i.e., one individual) and placing them in the next generation. Homozygous recessive individuals are removed (selected against) from the population. The genotypic and phenotypic frequencies are recorded after the production of each generation. The production of each generation depletes the beads in the previous generation in this simulation.

TABLE 18.2

GENOTYPIC FREQUENCIES FOR 100% NEGATIVE SELECTION

	GENERATION				
GENOTYPE	FIRST	SECOND	THIRD	FOURTH	FIFTH
BB ●●	_____	_____	_____	_____	_____
Bb ●○	_____	_____	_____	_____	_____
bb ○○	_____	_____	_____	_____	_____
Total*	1.0	1.0	1.0	1.0	1.0

*Note: The total of frequencies for each generation must equal 1.0.

6. Calculate the frequencies of each of the three genotypes recorded on the separate sheet and record these frequencies for the first generation in table 18.2. Individuals in the next generation will serve as the parental population for each subsequent generation.
7. Repeat steps 2–5 to produce a second, third, fourth, and fifth generation. After the production of each generation, record your results in table 18.2.
8. Graph your data from table 18.2 using the graph paper at the end of this exercise. *Generation* is the independent variable on the *x*-axis and *Genotype* is the dependent variable on the *y*-axis. Graph three curves, one for each genotype.

Because some members (i.e., the *bb* individuals that you removed) of each generation cannot reproduce, the number of offspring from each successive generation of your population will decrease. However, the frequency of each genotype, not the number of offspring, is the most important value.

Question 4

a. Did the frequency of white individuals decrease with successive generations? Explain your answer.

b. Was the decrease of white individuals from the first to second generation the same as the decrease from the second to the third generation? From the third to the fourth generation? Why or why not?

c. How many generations would be necessary to eliminate the allele for white fur?

Most naturally occurring selective pressures do not eliminate reproduction by the affected individuals. Instead, their reproductive capacity is reduced by a small proportion. To show this, use procedure 18.4 to eliminate only 20% of the *bb* offspring from the reproducing population.

Procedure 18.4 Simulate 20% negative selection pressure

1. Establish the same parental population that you used to test the Hardy-Weinberg prediction.
2. Simulate the production of an offspring from this population by randomly withdrawing two gametes to represent an individual offspring.
3. If the offspring is *BB* or *Bb,* place it in a container for production of the "Next Generation." Record the occurrence of this genotype on a separate sheet of paper.
4. If the offspring is *bb,* place every fifth individual (20%) in a separate container for those that "Cannot Reproduce." Individuals in this container should not be used to produce subsequent generations. Place the other 80% of the homozygous recessives in the container for production of the "Next Generation." Record the occurrence of this genotype on a sheet of paper.
5. Repeat steps 2–4 until the parental population is depleted, thus completing the first generation.
6. Calculate the frequencies of each of the three genotypes recorded on the separate sheet and record these frequencies for the first generation in table 18.3.
7. Repeat steps 2–5 to produce a second, third, fourth, and fifth generation. Individuals in the "Next Generation" will serve as the parental population for each subsequent generation. After the production of each generation, record your results in table 18.3.
8. Graph your data from table 18.3 using the graph paper at the end of this exercise. *Generation* is the independent variable on the *x*-axis and *Genotype* is the dependent variable on the *y*-axis. Graph three curves, one for each genotype.

Because some members of each generation cannot reproduce, the number of offspring from each generation of your

TABLE 18.3

GENOTYPIC FREQUENCIES FOR 20% NEGATIVE SELECTION

	GENERATION				
GENOTYPE	FIRST	SECOND	THIRD	FOURTH	FIFTH
BB ●●	_____	_____	_____	_____	_____
Bb ●○	_____	_____	_____	_____	_____
bb ○○	_____	_____	_____	_____	_____
Total*	1.0	1.0	1.0	1.0	1.0

*Note: The total of frequencies for each generation must equal 1.0.

population will decrease. However, the frequency of each genotype, not the number of offspring, is the most important value.

Question 5

a. Did the frequency of white individuals decrease with successive generations?

b. Consult your graphs and compare the rate of selection for procedures in 18.3 and 18.4. Was the rate of decrease for 20% negative selection similar to the rate for 100% negative selection? If not, how did the rates differ?

c. How many generations would be necessary to eliminate the allele for white fur?

AN EXAMPLE OF EVOLUTION: THE VOLVOCINE LINE

The evolution of most species is too slow to witness in the lab, but we can examine modern species to learn about changes that likely occurred over evolutionary time. Researchers might ask which characteristics are conserved throughout an evolutionary lineage of species and which ones evolve rapidly and consistently. Are more complex species always more successful?

The **Volvocine line** of algae is a group of modern species that reflects an easily recognized sequence of changes

INVESTIGATION

The Effect of Selection against Heterozygotes

Observations: Natural selection can change allelic frequencies in populations. Negative selection pressure (i.e., an environment that reduces reproduction by a particular phenotype) against a homozygous genotype can reduce allelic frequencies in only a few generations. The results of selection against heterozygotes may differ.

Question: How would selection against heterozygous individuals over many generations affect allelic frequencies in a population?

a. Establish a working lab group and obtain Investigation Worksheet 18 from your instructor.
b. Discuss with your group a well-defined question relevant to the preceding observation and question. Record it on Worksheet 18.
c. Translate your question into a testable hypothesis and record it.
d. Review procedures 18.3 and 18.4. Outline on Worksheet 18 your experimental design and supplies needed to test your hypothesis. Ask your instructor to review your proposed investigation.
e. Conduct your procedures, record your data, answer your question, and make relevant comments.
f. Discuss with your instructor any revisions to your questions, hypothesis, or procedures. Repeat your work as needed.

as their common ancestors evolved. In this example, the changes were in colony complexity.

Studies of morphology and molecular genetics indicate that an ancient species similar to today's flagellated *Chlamydomonas* (fig. 18.6) was probably the original and most ancient common ancestor to the Volvocine line. The probable sequence of events was that an ancestor of unicellular *Chlamydomonas* evolved a novel colonial morphology that was successful and gave rise to *Gonium* (figs. 18.7 and 18.8). In turn that ancestor evolved greater colonial complexity to give rise to today's *Pandorina* (fig. 18.9) and then *Eudorina* (fig. 18.10). That colonial ancestor later gave rise to *Volvox* (fig. 18.11), the most complex alga of the Volvocine line. These five genera are modern representatives of a lineage of species that evolved along a path of colonial complexity.

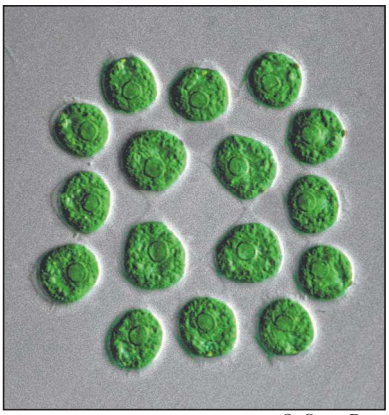

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Figure 18.8 *Gonium,* a colonial green alga composed of 16 cells (400×).

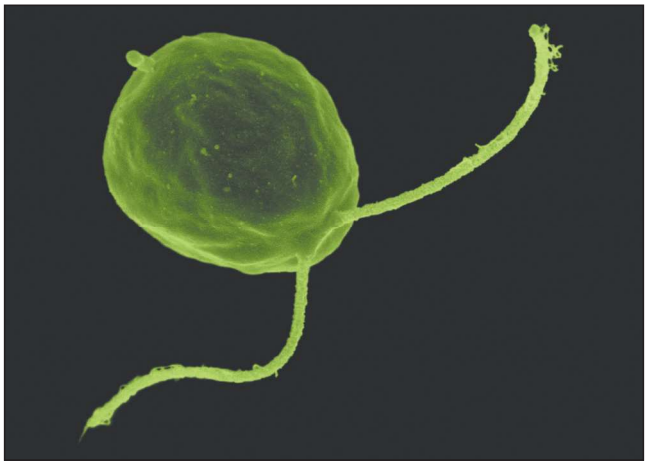

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Figure 18.6 *Chlamydomonas,* a unicellular green alga (1700×). *Chlamydomonas* has two flagella.

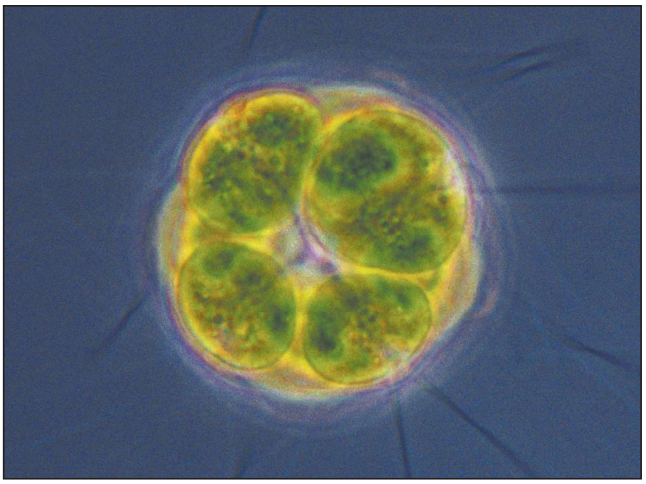

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Figure 18.9 *Pandorina,* a colony of 16 or 32 flagellated green algal cells (890×).

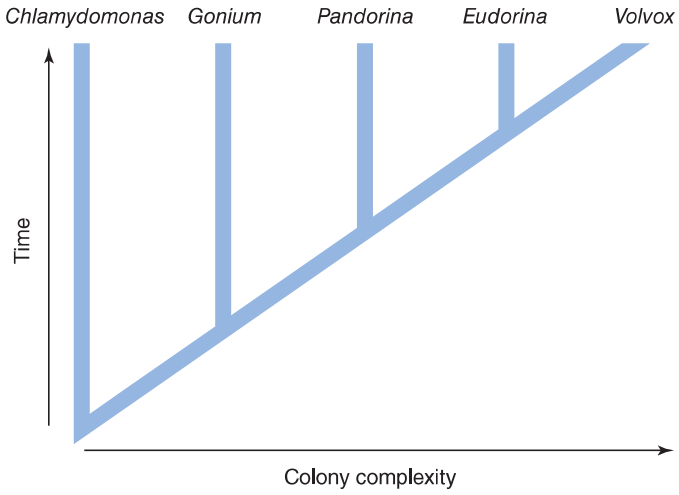

Figure 18.7 A cladogram representing the simplified phylogeny (family tree) of the Volvocine line. Proposed common ancestors are represented by the branching points called nodes.

Courtesy EPA

Figure 18.10 *Eudorina,* a colony of 32 flagellated green algal cells (420×).

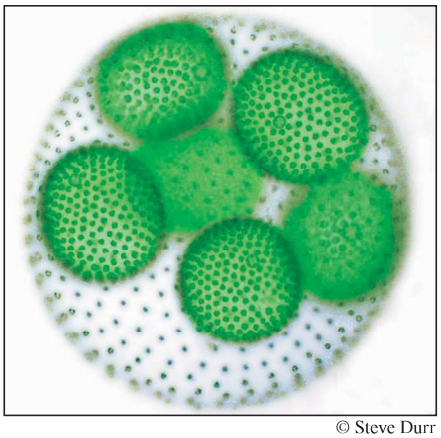

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Figure 18.11 *Volvox,* a common green alga (200×). Colonies of *Volvox* often consist of hundreds of cells. Daughter colonies are visible within the larger parent colony.

Procedure 18.5 Examine members of the Volvocine line of algae

1. Follow steps 2–6 to sequentially examine each of the organisms with your microscope. When preparing each of the colonial specimens, try both a standard microscope slide and a deep-well or depression slide. Determine which works best for colonies of cells.
2. *Chlamydomonas* is among the most primitive and widespread of the green algae. It is a unicellular biflagellate alga (fig. 18.6). All species of the Volvocine line consist of cells similar to *Chlamydomonas,* but the cells are in different configurations.
3. *Gonium* is the simplest colonial member of the Volvocine line (fig. 18.8). A *Gonium* colony consists of 4, 8, 16, or 32 *Chlamydomonas*-like cells held together in the shape of a disk by a gelatinous matrix. Each cell in the *Gonium* colony can divide to produce cells that produce new colonies. Like *Chlamydomonas, Gonium* is isogamous.

Question 6
Why do colonies of *Gonium* consist of only 4, 8, 16, or 32 cells? Why are there no 23-cell colonies?

4. *Pandorina* consists of 16 or 32 *Chlamydomonas*-like cells held together by a gelatinous matrix (fig. 18.9). Examine how *Pandorina* moves. Flagella on *Pandorina* move the ellipsoidal alga through the water like a ball. After attaining its maximum size, each cell of the colony divides to form a new colony. The parent matrix then breaks open like Pandora's box (hence the name *Pandorina*) and releases the newly formed colonies. *Pandorina* is isogamous.

Question 7
What is the significance of a specialization at one end of the colony?

5. *Eudorina* is a spherical colony composed of 32, 64, or 128 cells (fig. 18.10). Cells in a colony of *Eudorina* differ in size; smaller cells are located at the anterior part of the colony. The anterior surface is determined by the direction of movement.

Question 8
What is the significance of these structural and functional specializations of *Eudorina?*

6. *Volvox* is the largest and most spectacular organism of the Volvocine line. *Volvox* is a spherical colony made of thousands of vegetative cells and a few reproductive cells (fig. 18.11). Flagella spin the colony on its axis. In some species of *Volvox* and *Gonium,* cytoplasmic strands form a conspicuous network among the cells.

Question 9
a. Does the *Volvox* colony spin clockwise or counterclockwise?

b. What is the significance of the cytoplasmic network in *Volvox?*

To organize your information and observations complete table 18.4.

Table 18.4

Evolutionary Specialization of Members of the Volvocine Line

Characteristic	*Chlamydomonas*	*Gonium*	*Pandorina*	*Eudorina*	*Volvox*
Number of cells					
Colony size					
Structural and functional specializations of cells					
Reproductive specialization (isogamy versus oogamy)					

Testing for Understanding: Solving Hardy-Weinberg Problems

1. Galactosemia is inherited as a homozygous recessive trait (i.e., *gg*). You have sampled a population in which 36% of people have galactosemia.

a. What is the frequency of the *g* allele?

b. What is the frequency of the *G* allele?

c. What is the frequency of the *GG* and *Gg* genotypes?

2. Suppose that in wasps, brown wings are dominant to white wings, and 40% of all wasps in a population you've sampled have white wings.

a. What percentage of the wasps is heterozygous?

b. What percentage of the wasps is homozygous dominant?

3. Suppose that you and 19 of your classmates (giving a final population of 10 males and 10 females) are on a cruise, and your ship sinks near a deserted island. You and all of your friends make it to shore and start a new population isolated from the rest of the world. Two of your friends carry the recessive allele (i.e., are heterozygous) for phenylketonuria. If the frequency of this allele does not change as the population on your island increases, what will be the incidence of phenylketonuria on your island?

4. Albinos produce very little of the pigment melanin in their skin and hair. Albinism is inherited as a homozygous recessive trait. In North America, about 1 in 20,000 people are albinos.

a. What is the frequency of the dominant allele for albinism?

b. What is the frequency of albinos?

c. What is the frequency of heterozygotes?

5. People who are heterozygous recessive for the sickle-cell trait have some sickling of their blood cells, but not enough to cause death. Malarial parasites cannot infect these individuals' blood cells. People who are homozygous dominant for the sickle-cell trait have normal blood cells, but these cells are easily infected with malarial parasites. As result, many of these individuals are killed by sickle-cell anemia. People who are homozygous recessive for the sickle-cell trait resist infections by malarial parasites, but their sickled blood cells collapse when oxygen levels drop, thereby killing the individuals. As a result, homozygous individuals—be they homozygous dominant or homozygous recessive—are less likely to survive than are heterozygous individuals. Suppose that 9% of a population in Africa is homozygous recessive for sickle-cell anemia. What percentage of the population will be heterozygous (i.e., more resistant to the disease)?

6. What would be the frequency of the recessive allele in a population that produces twice as many homozygous recessive individuals than heterozygotes?

Answers to Hardy-Weinberg Problems

1a. 60%
1b. 40%
1c. $GG = 16\%$; $Gg = 48\%$
2a. 47%
2b. 14%
3. 0.25%
4a. 99.3%
4b. 0.005%
4c. 1.4%
5. 42%
6. $q = 0.8$

Questions for Further Thought and Study

1. How would selection against heterozygous individuals over many generations affect the frequencies of homozygous individuals? Would the results of such selection depend on the initial frequencies of p and q? Could you test this experimentally? How?

2. How are genetic characteristics associated with nonreproductive activities such as feeding affected by natural selection?

3. Although Charles Darwin wasn't the first person to suggest that populations evolve, he was the first to describe a credible mechanism for the process. That mechanism is natural selection. What is natural selection, and how can it drive evolution?

4. Does evolutionary change always leads to greater complexity? Why or why not?

5. Is natural selection the only means of evolution? Explain.

6. Is natural selection the only means of evolution that produces adaptations? Explain.

7. What change in a population would you expect to see if a selection pressure was against the trait of the dominant allele?

8. The application of evolution to understanding disease is widespread and productive. What is the benefit of applying Darwinian principles to medical practice?

DOING BIOLOGY YOURSELF

Design an experiment to determine the phylogenetic relationships among members of the Volvocine line of algae. What information about their DNA sequences would be useful?

WRITING TO LEARN BIOLOGY

Summarize the most recent books and publications that review the benefits of applying Darwinian principles to medical practice.

WRITING TO LEARN BIOLOGY

The Hardy-Weinberg equilibrium assumes that pollination and subsequent fertilization must be random. Is that true for most wildflower populations? What characteristics of these plants influence pollination patterns?