Notes to Instructors

Chapter 21 Genomes and Their Evolution

What is the focus of this activity?

While the Sanger method for sequencing DNA and the modifications that follow are conceptually fairly simple, most students don't understand them. As noted previously, in order for most students to understand unfamiliar processes, they need to build models for themselves to discover what it is they understand and, more important, what they don't.

What is this particular activity designed to do?

Activity 21.1 How can we discover the sequence of an organism's DNA?
This activity allows students to interpret the results of a classic Sanger method for sequencing a DNA molecule only 20 bp long. It then asks them to translate these results into the results they would expect using more modern fluorescently tagged ddNTP methods.

What misconceptions or difficulties can this activity reveal?

Because much of the methodology and information in this area is relatively new, students tend to lack conceptions in this area rather than have misconceptions. Walking them through how sequencing is done and how it is interpreted should overcome this.

Answers

Activity 21.1 How can we discover the sequence of an organism's DNA?

Bacterial genomes have between 1 million and 6 million base pairs (Mb). Most plants and animals have about 100 Mb; humans have approximately 2,900 Mb. Individual chromosomes may therefore contain millions of base pairs. It is difficult to work with DNA sequences this large, so for study purposes the DNA is broken into smaller pieces (approximately 500 to 1,000 bp each). These pieces are sequenced and then the sequenced pieces are examined and aligned based on overlapping sequence homology at their ends.

By comparing the DNA sequences among organisms, scientists can determine

- what parts of the genomes are most similar among organisms and are therefore likely to have evolved earliest,
- what key differences exist in the genomes that may account for variations among related species, and
- what differences within species exist that may account for development of specific types of disease.

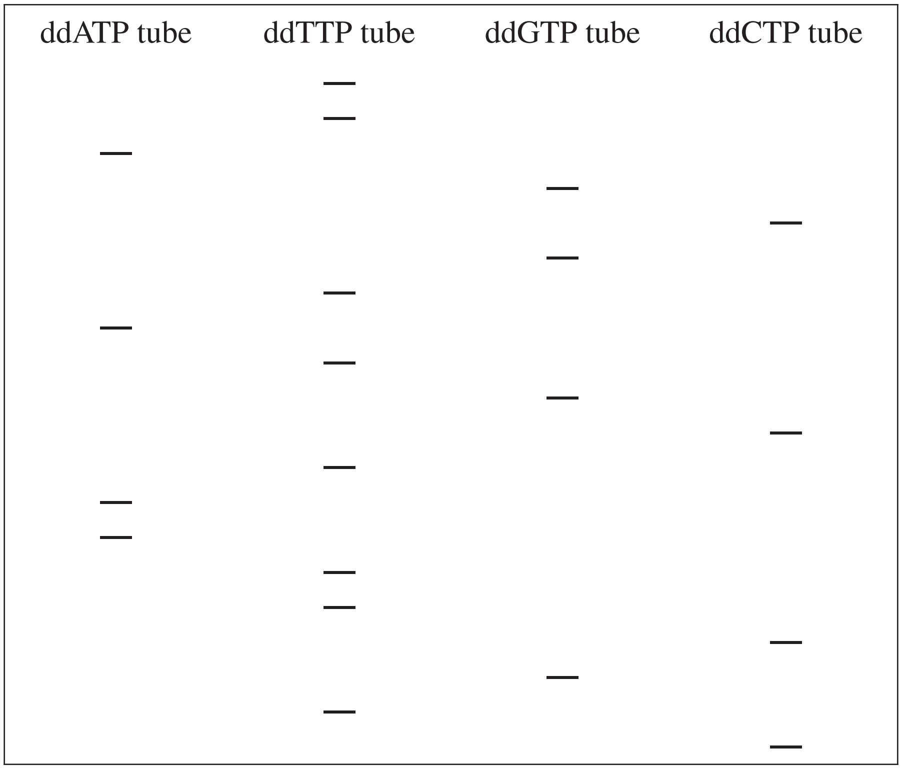
The following activity has been designed to help you understand how genomes are sequenced and how the sequence information may be used.

1. In 1980, Frederick Sanger was awarded the Nobel Prize for inventing the dideoxy method (or Sanger method) of DNA sequencing. A double-stranded DNA segment approximately 700 bp in length is heated (or treated chemically) to separate the two strands. The single-stranded DNA that results is placed into a test tube that contains a 9-to-1 ratio of normal deoxynucleotides to dideoxynucleotides. A dideoxynucleotide has no $-$OH group at either $2'$ or $3'$ carbon. As a result, whenever any dideoxynucleotide (abbreviated ddNTP) is added to the growing DNA strand, synthesis stops at that point. If the ratio of normal to dideoxynucleotides is high enough, where the dideoxynucleotide (rather than the normal deoxynucleotide) will be included in the sequence is random.

   You set up each of four test tubes as noted below:

Tube number	Deoxynucleotides	Dideoxynucleotide
1	dATP, dTTP, dGTP, dCTP	ddATP
2	dATP, dTTP, dGTP, dCTP	ddTTP
3	dATP, dTTP, dGTP, dCTP	ddGTP
4	dATP, dTTP, dGTP, dCTP	ddCTP

All tubes contain the same single-stranded DNA molecules and the same primers. All other components required for DNA replication, such as enzymes, are present in each tube. You allow the replication to continue for the same length of time in each tube. At the end of the time period, you extract the DNA from each tube and run it on an agarose gel. You dye the gel with ethidium bromide and observe the following banding patterns on the gel. (*Note*: For this demonstration, we are using a DNA strand that is only 20 bases in length.)



a. Which band in the gel contains the shortest DNA strand? What is the identity of its terminal ddNTP?

The last band in the ddCTP column contains the shortest DNA strand. (Remember, the shorter the DNA the faster it moves in the gel.) The terminal ddNTP is C.

b. Which band contains the next shortest DNA strand? What is the identity of its terminal ddNTP?

The last band in the ddTTP column is the next shortest. The terminal ddNTP here is T.

c. Continue reading the terminal ddNTP of each band from shortest to longest to determine the linear sequence of nucleotides in the DNA strand complement. What is the sequence?

The sequence (reading from shortest to longest) would be: CTGCTTAATCGTATGCGATT.

2. The Sanger method has been modified so that each ddNTP used is now flagged with an identifying fluorescent tag.

Assume that you run the same experiment that you did earlier. However, this time you combine all of the different nucleotides (both dNTPs and ddNTPs) in the same test tube. You run the products of the reaction on an agarose gel. Indicate the bands you would see on the gel below using the appropriate colors: ddTTP fluoresces red; ddGTP, yellow; ddCTP, blue and ddATP, green.

Band sequence for combined experiment
T red
T red
A green
G yellow
C blue
G yellow
T red
A green
T red
G yellow
C blue
T red
A green
A green
T red
T red
C blue
G yellow
T red
C blue

3. To help determine evolutionary relationships among different groups of organisms, scientists compare gene sequences of highly conserved genes. What are "highly conserved genes"? Give examples and indicate what is "highly conserved" and why.

   Highly conserved genes are genes that have experienced little change throughout evolution. Highly conserved genes are essential for the survival of organisms. For example, the genes coding for enzymes involved in glycolysis and the genes for ribosomal RNA are both highly conserved. Most changes in the sequence of these genes would result in a nonfunctional gene product. As a result, the organism would be unable to survive. Therefore, over time, only mutations that did not significantly alter the function or end product of these genes were retained or conserved. Many of these types of alterations may have occurred in the "wobble" site of codons. The greater the number of these differences in sequence, the more distantly related the organisms are; the fewer the differences, the more closely related.

4. What types of DNA do scientists use to determine individual identities of organisms within the same species? Why do they use this type of DNA?

   Repetitive D—for example, simple sequence DNA or short tandem repeat DNA—is used for identifying individuals of the same species. This DNA is noncoding and as a result can be highly variable from individual to individual.

Notes to Instructors

Chapter 22 Descent with Modification: A Darwinian View of Life

What is the focus of these activities?

Campbell Biology, 9th edition, defines natural selection as "differential success in the reproduction of different phenotypes resulting from the interaction of organisms with their environment." The text goes on to state that "evolution occurs when natural selection causes changes in relative frequencies of alleles in the gene pool." Taken at face value, these two sentences are unambiguous, direct statements of fact. Then why do so many students have difficulty understanding what evolution is and how it can operate to change species over time? Often their previous experiences in life and education have left them with preexisting alternate conceptions (or misconceptions) about how biology and life work.

How can we change students' misconceptions? It would be easy if all we had to do was tell them what the current evidence indicates. However, the vast majority of students don't learn new concepts and ideas simply by hearing about them in lecture. To learn new concepts and modify their existing ideas, students have to work with the evidence, test it, and prove to themselves that their new understanding works and has value. For this to happen, we need to address these questions:

- Where do student misconceptions and problems about evolution originate?
- How can we determine what misconceptions our students have?
- How can we help students alter their misconceptions?
- How can we evaluate our students' levels of understanding? What diagnostics can we use?

What are the particular activities designed to do?

Activity 22.1 How did Darwin view evolution via natural selection?
Activity 22.2 How do Darwin's and Lamarck's ideas about evolution differ?
Activity 22.3 How would you evaluate these explanations of Darwin's ideas?
These activities are designed to help students understand the logic Darwin used to develop his theory of evolution via natural selection. They focus on how Darwin's theory for the mechanism behind evolution differs from other theories—in particular, Lamarck's.

What misconceptions or difficulties can these activities reveal?

Activity 22.1
Activity 22.2
Activity 22.3
It should come as no surprise that some students' misconceptions come from our own teaching and lectures, textbooks, and popular videos and movies dealing with evolution.

For example, have you ever caught yourself saying, "In order to survive, this organism needed to evolve (some structure or capability)"? One slip of the tongue like this can undo volumes of evidence. As a result, we need to be very careful and very precise in how we express evolutionary ideas. If we find ourselves saying, "this organism needed to evolve . . . ," we must immediately correct ourselves.

We also have to be aware that certain key words used in explaining evolution may have very different meanings to our students. For example, the words *adaptation, fitness, primitive*, and *advanced* have very different meanings in common use compared to their meanings in the study of evolution. When I use the terms *primitive* and *advanced*, I make sure to let my students know that *primitive* is what came first and *advanced* is what came later; that is, in evolution, these are chronological terms, and no value is implied. For example, the chairs you're sitting in are advanced; the Louis the 14th chairs in museums are primitive. Which are better? In some environments, the more primitive have the advantage (are better), and in other situations, the more advanced have the advantage.

We also need to stop using the same examples of evolution over and over again. By the time students have reached college (if they've had any education in evolution), they've studied evolution at least three different times in both grade school and college. You can bet that each of those times, the key examples used were the peppered moth (*Biston betularia*) and Darwin's finches. Students start to think that these are the only examples, and this does not make a very convincing argument for evolution as a unifying principle of biology. We need to use many more and varied examples of evolution.

To uncover students' misconceptions and alter them, we need to find out what each individual student's understanding is. We also have to recognize that simply presenting students with the evidence one more time will not necessarily alter their existing understanding. For students to change their ideas, we need to provide them with the basic concepts and with novel examples, exercises, and problems that challenge their existing conceptions.

If you assign these activities, keep in mind that the best way to find out what students are really thinking is to have them answer some of the questions in class (lecture or discussion). Have students discuss them in small groups. Wander among the groups during their discussions to answer any questions they may have. Without appearing to do so, listen in on their discussions. You will learn more about possible misconceptions this way than if you collect activities as written assignments. What students write down is not necessarily what they are really thinking. Instead, they often write down what they think the instructor wants to hear.

The activities for Chapter 22 reveal some common misconceptions:

- Many students have a Lamarkian view that organisms are modified by their environment.
- Some think that evolution and natural selection lead directly to speciation.

- Some think that nature purposefully selects for traits that are beneficial for survival.
- Students may confuse physiological adaptations with evolutionary adaptations or be unable to distinguish between them.
- Many students think that evolution leads to perfection in organisms. In other words, they think that because organisms today all appear well suited to their environment, this must have been planned. Otherwise, they can't understand why we don't see organisms that aren't well suited.

Given these misconceptions, when we teach the basics of evolution and natural selection, we need to make sure that we include the following ideas:

1. ***Mutation is random***. Almost all mutations that could have occurred in the past probably did occur. This begs the question of why we don't see all these mutations in the fossil record or among organisms. Most were so deleterious that they died during development.

2. ***Variability exists in populations, and only the variability that is heritable can be acted upon by natural selection***. This variability includes some genes that are currently advantageous, some that are disadvantageous, and some that are neither; that is, some genes are neutral. Because students often think that a gene can be only one of these, I provide the following examples:

   - Currently eye color in humans is a neutral mutation. It is neither advantageous nor disadvantageous to survival and reproduction.
   - In chickens, the frizzle gene affects the feathers. Chickens with this trait have feathers that don't interlock and, as a result, the chickens can't control loft and insulation well. The feathers on these chickens stick up all over at odd angles from the body. In temperate zones, frizzle chickens can't maintain heat well in winter and tend to die. In other words, in temperate zones, this mutation is disadvantageous.

   Environmental conditions can and did change over the course of life's history on Earth. This means that some genes that were advantageous could have become disadvantageous, and vice versa. It also means that some genes that were previously neutral could have become either disadvantageous or advantageous. Here are two examples:

   - Consider the eye color trait. Assume that the hole in the ozone layer becomes even larger, and more ultraviolet light penetrates to Earth. People with blue eyes have no pigment in their iris, so UV light can penetrate much farther into their eyes and cause blindness. Blue-eyed people would find themselves at a disadvantage for survival compared to brown-eyed people.

- To use a real example, consider the frizzle chicken. Normal chickens sent to the tropics to be used in agriculture don't survive well in the heat. Frizzle chickens do very well, however. Ask your students, "So, is the frizzle gene advantageous or disadvantageous?"

3. ***It is not that advantageous genes are selected for, so much as that disadvantageous genes are selected against***. For example, if you have a mutation that prevents adequate function of cellular respiration, you die. Keep in mind however, that what is a disadvantageous gene in one environment might be advantageous in another.

4. Note that these activities can be used to probe student understanding. They require students to recognize that they may need to modify their ideas and hypotheses based on differences in the evidence that is available at any one time.

Answers

Activity 22.1 How did Darwin view evolution via natural selection?

Darwin is remembered not because he was the first to propose that evolution occurs. Many others had presented this idea before. Instead, he is remembered for defining the mechanism behind evolution—that is, the theory of natural selection. To do this, Darwin integrated, or put together, information from a wide range of sources. Some of this information was provided by others; some he observed on his own.

Working alone or in groups of three or four, construct a concept map of Darwin's view of evolution via natural selection. Be sure to include definitions or descriptions of all the terms in the list below. Keep in mind that there are many ways to construct a concept map.

- Begin by writing each term on a separate sticky note or piece of paper.
- Then organize the terms into a map that indicates how the terms are associated or related.
- Draw lines between terms and add action phrases to the lines that indicate how the terms are related.
- When you finish your map, explain it to another group of students.

Here is an example:

Terms

fact	Darwin	fit individuals
biogeography	vertebrate limb structure	fossil record
gradualism	species population	embryology
uniformitarianism	individual	taxonomy
theory	variability	selective (domestic) breeding
Galápagos Islands	paleontology	
evolution	Malthus	limited resources
homology	population size	struggle for existence
natural selection	environment or resources	reproduction
analogy		extinction

Use the understanding you gained from creating the concept map to answer the questions.

1. In the 1860s, what types of evidence were available to indicate that evolution had occurred on Earth?

   Evidence was available from studies of taxonomy (classification of organisms based on similarities in morphology, for example), paleontology (fossil evidence that demonstrated how organisms had changed over geologic time), and biogeography (the study of the distribution of organisms in the present and the past).

2. How did knowledge of mechanisms of artificial selection (used in developing various strains of domesticated animals and plants) help Darwin understand how evolution could occur?

   Darwin knew that artificial selection could lead to dramatic changes in the phenotypes of individuals in a species population. As a result, he thought that natural selection could similarly lead to changes in populations. These changes would tend to occur more gradually, however. Similar to artificial selection, natural selection would eliminate or reduce the numbers of some variants in the population because these variants either didn't survive or did not reproduce as well as others.

3. Based on his studies, Darwin made a number of observations; they are listed in the chart. Complete the chart by answering how Darwin made the observations.

Observation	How did Darwin make this observation? That is, what did he read or observe that gave him this understanding?
a. All species populations have the reproduction potential to increase exponentially over time.	Darwin read Malthus's essay on the potential for human populations to grow at a rate far beyond the capacity of their food supply and other resources. He applied this concept to other populations and concluded that all natural populations have this potential.
b. The number of individuals in natural populations tends to remain stable over time.	Although this may not be true for the human population, it is true for most natural populations of organisms. Darwin observed that in nature, the number of organisms per species in a given area tends to remain relatively constant over time.
c. Environmental resources are limited.	This was made obvious in Mathus's essay. It was also obvious to Darwin as he observed natural populations. A given area has only so much food, only so many nesting sites, and so on.
d. Individuals in a population vary in their characteristics.	Darwin was an amateur naturalist even before his voyage on the *Beagle*. He was also a pigeon breeder. Both of these experiences led him to understand that there is considerable variation in populations of organisms.
e. Much of this variation is heritable.	As a pigeon breeder, Darwin could demonstrate this to himself. He also had a good understanding of the mechanism of artificial selection as it applied to animal husbandry and agriculture.

4. Based on these observations, Darwin made a number of inferences. Which of the observation(s) in question 3 allowed Darwin to make each inference?

Inference	Observations that led to the inference
a. Production of more individuals than the environment can support leads to a struggle for existence such that only a fraction of the offspring survive each generation.	Darwin combined his understanding of the first three observations just noted to make this inference.
b. Survival for existence is not random. Those individuals whose inherited traits best fit them to the environment are likely to leave more offspring than less fit individuals.	Using the first inference and the observations that variation exists and some of it is heritable, Darwin made the logical assumption or inference that the less fit variants would not survive as well. As a result, they would be removed or reduced in the population.
c. The unequal ability of individuals to survive and reproduce leads to a gradual change in the population, with favorable characteristics accumulating over the generations.	This is a logical extension of the previous two inferences. Removal of unfit individuals (or their reduction relative to others) would obviously lead to gradual change in the population over time.

5. Based on these observations and inferences, how did Darwin define fitness?

   Campbell Biology, 9th edition, defines fitness as "the relative contribution an individual makes to the gene pool of the next generation." Organisms less able to survive and reproduce are less fit. In contrast, the remaining organisms are considered more fit.

6. How did Darwin define evolution?

   Darwin preferred to talk about descent with modification, or the idea that all organisms are related through descent from some unknown ancestor. Evolution was, as a result, defined as a gradual change in species over time.

7. What is the unit of natural selection—that is, what is selected? What is the unit of evolution—that is, what evolves?

   The individual organism is the unit that is selected because it is the individual organism that either dies or survives, reproduces or does not reproduce. The unit of evolution is the species population.

8. In a population of mice, some individuals have brown fur and some have black fur. At present, both phenotypes are equally fit. What could happen to change the relative fitness of the two phenotypes in the population? For example, what could cause individuals with brown fur to show reduced fitness relative to individuals with black fur?

   There are different possible ways of answering this question. Here is one: If both populations are equally fit at present, we can assume that neither is more or less threatened by predation as a result of their color. In other words, both colors are equally visible (or invisible) to predators in the current environmental circumstances. Perhaps the ground and ground cover are a mix of both black and brown patches. If something occurs to change the background color of the environment, the colors of the mice may become more or less apparent. For example, assume a small colony of the mice is transported to another area where the ground and ground cover are a mix of black and green. In this environment, the brown mice would be more visible to predators than the black mice. As a result, the brown mice would become less fit.

9. Assume you discover a new world on another planet that is full of organisms.

   a. What characteristics would you look for to determine that these organisms arose as a result of evolutionary processes?

      Again, this question has many possible answers. One approach is to look for the same types of evidence that Darwin used. For example, if you look at taxonomy, can you develop groupings of organisms based on similarities in morphology? Is there a fossil record on the planet? Does the fossil record show a gradual change in species over time? Do any of the fossil organisms look similar to existing organisms? Is there any evidence that species in close proximity to each other appear more closely related than species at great distances from each other? (You could also go beyond what Darwin knew and use more modern techniques of

DNA analysis, assuming they have DNA or some similar hereditary material, and look for similarities among species.)

b. What characteristics would you look for to determine that these organisms did *not* arise as the result of evolutionary processes?

You would look for evidence that indicated there was no genetic relationship among different species. If the organisms did not arise as a result of evolutionary processes, there would be no reason for them to share any similarities in morphology, development, physiology, or molecular biology.

10. Why is it incorrect to say: Vertebrates evolved eyes in order to see?

Natural selection occurs in the present. Organisms that survive must have traits that allow them to survive under existing conditions. As a result, each mutation required to produce the eye must have made those individuals (relative to others without the mutations) more fit. Relative to the less fit individuals, they survived better and produced more offspring.

Activity 22.2 How do Darwin's and Lamarck's ideas about evolution differ?

Early in the 1800s Lamarck proposed a theory of evolution. He suggested that traits acquired during an organism's life—for example, larger muscles—could be passed on to its offspring. The idea of inheritance of acquired characteristics was popular for many years. No such mechanism is implied in Darwin's theory of evolution via natural selection, however. After Darwin published his work, scientists conducted many experiments to disprove the inheritance of acquired traits. By the middle of the 20th century, enough data had accumulated to make even its most adamant supporters give up the idea of inheritance of acquired characteristics.

Given your understanding of both Lamarck's and Darwin's ideas about evolution, determine whether the statements on the next page are more Lamarckian or more Darwinian. If the statement is Lamarckian, change it to make it Darwinian. Here are two example statements and answers.

Examples

A. The widespread use of DDT in the mid-1900s put pressure on insect populations to evolve resistance to DDT. As a result, large populations of insects today are resistant to DDT.

Answer: This is a Lamarckian statement. DDT worked only against insects that had no DDT-resistance genes. The genes for DDT resistance had to be present for insects to survive DDT use in the first place.

Suggested change: Wide-scale use of DDT in the mid-1900s selected against insects that had no resistance to DDT. Only the insects that were resistant to DDT survived. These insects mated and passed their resistance genes on to their offspring. As a result, large populations of insects today are resistant to DDT.

B. According to one theory, the dinosaurs became extinct because they couldn't evolve fast enough to deal with climatic changes that affected their food and water supplies.

Answer: This is a quasi-Lamarckian statement. Organisms do not purposefully evolve. (Genetic recombination experiments are perhaps an exception.) Once you are conceived, your genes are not going to change; that is, you are not going to evolve. The genetic composition of a species population can change over time as certain genotypes are selected against. Genes determine phenotypes. The environmental conditions may favor the phenotype produced by one genotype more than that produced by another.

Suggested change: According to one theory, the dinosaurs became extinct because their physiological and behavioral characteristics were too specialized to allow them to survive the rapid changes in climate that occurred. The climatic changes caused changes in the dinosaurs' food and water supplies. Because none of the dinosaurs survived, the genes and associated phenotypes that would have led to their survival must not have been present in the populations.

Statements

1. Many of the bacterial strains that infect humans today are resistant to a wide range of antibiotics. These resistant strains were not so numerous or common prior to the use of antibiotics. These strains must have appeared or evolved in response to the use of the antibiotics.

   Answer: This is a quasi-Lamarckian statement. Although the strains evolved in response to the use of antibiotics (the antibiotics killed off the strains that did not have genes for resistance), the strains did not appear in response to the antibiotics. If no resistance genes were present when antibiotics were applied, all would have died off.

   Suggested change: Many of the bacterial strains that infect humans today are resistant to a wide range of antibiotics. These resistant strains were not as numerous or common prior to the use of antibiotics. Antibiotic use must have selected against those bacterial strains that did not have resistance genes, leaving only those with resistance to survive.

2. Life arose in the aquatic environment and later invaded land. Once animals came onto land, they had to evolve effective methods of support against gravity and locomotion in order to survive.

Answer: This is a Lamarckian statement. If the animals were not already able to support themselves and move in gravity, they would not have survived on land.

Suggested change: Life arose in the aquatic environment and later invaded land. The animals that came onto land had to have previously evolved effective methods of support against gravity and locomotion in order to survive.

3. A given phenotypic trait—for example, height, speed, tooth structure—(and therefore the genes that determine it) may have positive survival or selective value, negative survival or selective value, or neutral (neither positive nor negative) survival or selective value. Which of these it has depends on the environmental conditions the organism encounters.

   Answer: This statement is Darwinian. Each of the variants we see in phenotype has a specific fitness and, as a result, a selective value under the existing environmental conditions.

4. The children of bodybuilders tend to be much more athletic, on average, than other children because the characteristics and abilities gained by their parents have been passed on to the children.

   Answer: This is a Lamarckian statement. The parents cannot pass on traits they acquired during their lifetimes. They can pass on only the genes that they have.

   Suggested change: The children of bodybuilders tend to be more athletic, on average, than other children. Bodybuilders may tend to have specific genes for these traits, or they may train their children to become athletic more than other people do.

Activity 22.3 How would you evaluate these explanations of Darwin's ideas?

Unfortunately, even today some people get or give the impression that acquired characteristics can be inherited. As a result, we need to be very careful about how we state our understanding of evolution and evolutionary theory.

To test understanding of Darwin's ideas, this question was included on an exam.

4-point question: *In two or three sentences describe Darwin's theory of descent with modification and the mechanism, natural selection, that he proposed to explain how this comes about.*

Four student answers to the question are given. Based on what you know about Darwinian evolution and natural selection, evaluate and grade how well each answer represents Darwin's ideas. For any answer that does not receive full credit (4 points) be sure to indicate why points were lost.

Student 1. Darwin saw that populations increased faster than the ability of the land to support them could increase, so that individuals must struggle for limited resources. He proposed that individuals with some inborn advantage over others would have a better chance of surviving and reproducing offspring and so be naturally selected. As time passes, these advantageous characteristics accumulate and change the species into a new species.

(*Note:* The following are the grades the author of the workbook would have given for these answers.)

***Grade:* 4** This student demonstrates a good understanding of how fitness, resource limitation, population growth, and natural selection can cause changes in a species population over time. In addition, s/he is able to put the ideas into his/her own words.

(*Note:* Darwin's *Origin of Species* didn't deal directly with the production of new species. However, Darwin did indicate that all species could be arranged on a tree of life. This can be explained only if new species arise over time.)

Student 2. Darwin's theory of evolution explains how new species arise from already existing ones. In his mechanism of natural selection, organisms with favorable traits tend to survive and reproduce more successfully, while those that lack the traits do not. Beneficial traits are passed on to future generations in this manner, and a new species will be created in the end!

***Grade:* 3** As noted above, Darwin did not explain how new species arise from already existing ones. The rest of the answer indicates an understanding of the definition of natural selection. However, not enough information is provided to know whether the student understands the factors associated with natural selection—for example, overproduction of offspring, limited resources, heritability of traits.

Student 3. Descent with modification using natural selection was Darwin's attempt at explaining evolution. An organism is modified by its surroundings, activities, and lifestyle. These modifications, by natural selection, make the organism better suited to its life.

***Grade:* 0** In the first sentence, the student restates the information available in the question without providing any more information or clarification. The second sentence indicates that the student has a Lamarckian view of how organisms are changed over time. S/he mentions natural selection in the last sentence but does not define it or indicate how it will make the species "better suited to its life."

Student 4. Darwin's theory states that organisms can become modified by environmental conditions or use or disuse features and that the modifications can be passed down to succeeding generations. He proposes that nature selects for a characteristic trait that is beneficial to the survival of the organisms and that organisms would pass on this trait.

***Grade:* 0** The first sentence of this answer indicates that this student has a Lamarckian view of evolution. In contrast, the second sentence provides a fairly good description of natural selection. No credit is given, however, because this student obviously cannot distinguish between the Darwinian and Lamarckian views of evolution.

Notes to Instructors

Chapter 23 The Evolution of Populations

What is the focus of these activities?

Both genetics and ecology (more specifically, natural selection) play roles at many levels in the continued evolution of life. Chapter 23 presents these ideas:

1. ***Genetic mutation in nature occurs randomly***. Mutations in genes can produce changes in

    - the form, function, or both of individual organisms;
    - an organism's environmental requirements; and
    - the ways different types or species of organisms interact with one another.

2. ***Change in environmental conditions can affect an organism's ability to survive and reproduce; that is, it can affect natural selection.***

    - Organisms with mutations that decrease their ability to survive and/or reproduce will produce fewer offspring. As a result, the relative frequencies of these genes decrease in the next generation of the population.
    - Organisms with mutations that either have no effect on or improve their ability to survive and/or reproduce will produce more offspring than organisms without those mutations. As a result, the relative frequencies of these mutated genes increase in the next generation of the population.

Students need to understand, however, that the environment does not directly select for and increase the number of advantageous phenotypes or organisms (and their genes).

It is more appropriate to think of alterations in gene frequency occurring because of the loss of specific phenotypes (and the genes that cause them).

The activities can be used to generate discussion about all these ideas.

What are the particular activities designed to do?

Activity 23.1 A Quick Review of Hardy-Weinberg Population Genetics
This activity is designed to help students understand the logic behind the Hardy-Weinberg theorem. It also gives them practice using the theorem to determine whether a population is evolving.

Activity 23.2 What effects can selection have on populations?
This activity is designed to help students understand how natural selection can lead to the evolution of a population. They will learn why and how certain assumptions can be made in studying the evolution of populations.

What misconceptions or difficulties can these activities reveal?

Activity 23.1
Most of the difficulties students have solving Hardy-Weinberg problems result from a lack of understanding of basic probability.

Question 4, Part A: Some students are concerned about which allele is given the frequency p and which is given the frequency q. It helps to tell them that p is usually the frequency of the dominant allele and q is the frequency of the recessive allele. Be sure to note, however, that there is no hard-and-fast rule. For example, if two alleles are codominant, one is still assigned the frequency p and the other is given the frequency q.

For question 4e, many students know what the binomial expansion is. They may even recognize that ($p^2 + 2pq + q^2 = 1$) is the binomial expansion of ($p + q = 1$). However, many will not understand what this mathematical reality has to do with random mating. For this reason, it helps to set up a Punnett square with the frequencies for female gametes on one side and the frequencies for male gametes on the other. Combining the gametes gives all possible genotypes of offspring for the subsequent generation. The probability of a specific type of female gamete pairing with a specific type of male gamete is then the product of the individual probabilities. When the probabilities of the possible genotypes are added together, we get $p^2 + 2pq + q^2 = 1$.

Using the Punnett square raises another difficulty: how to determine what p and q are for the males alone and the females alone in a population. Pose the following problem in class: "Assume the frequency of the *b* allele in the population is 10% and the frequency of the *B* allele is 90%. If females make up half of the population, what is the frequency of the *b* allele in the female population alone?" A large percentage of the class will answer 5%. Push the issue further: "OK, here's another example. Let's assume that I have a cheesecake that contains 50% fat. If I cut it in half, what percent fat does each half contain? And if I cut it into quarters, what percent fat does each piece contain?" Eventually students will begin to realize that the percent of fat (or the frequency of alleles) doesn't change when the population is divided in two. In other words, if there is 50% fat in the whole cheesecake, then there is 50% fat in each piece (no matter how small). And if 10% of the alleles in the population are *b* alleles, then the female half of the population should contain 10% *b* and 90% *B* alleles.

Question 6, Part B: Many students don't understand why one can randomly assign only two alleles to each diploid organism in a population. For example, assume we want to know the allele frequency in an isolated subpopulation of birds. The population contains only six individuals: one of genotype *TT*, two of genotype *Tt*, and three of genotype *tt*.

To determine the allele frequencies of *T* and *t*, we randomly assign two alleles to each individual. We then calculate the frequencies of the alleles:

Number of individuals who are:	Number of *T* alleles	Number of *t* alleles
1 = *TT*	2	0
2 = *Tt*	2	2
3 = *tt*	0	6
Allele frequency:	4/12 = 1/3 = 33.3%	8/12 = 2/3 = 66.7%

It is helpful to explain that the assumption here is that each male and each female in the population, on average, produces the same number of gametes. Given that assumption, it doesn't matter how many each produces. All of the gametes from *TT* individuals will contain *T*s. Half of the gametes from *Tt* individuals will contain *T* and the other half will contain *t*. All of the gametes from *tt* individuals will contain *t*. Therefore, for ease of calculation, we assign the smallest possible number of gametes or alleles to each individual, and that number is two.

Activity 23.2

To answer any of these questions, students have to make some assumptions. In particular, they have to ask themselves whether or not the characteristic under selection could be heritable. If the characteristic is heritable and selection removes some types more often than others, then the population is likely to change over time.

Scenarios I, IIa and b, and IIIa and b are designed to require students to rethink the assumptions they made in light of additional information. Changing assumptions in response to the addition of new information seems logical to instructors, but the same is not true for many students. Some students balk at making any assumptions and make statements like: "How am I supposed to know whether this characteristic is heritable?" Other students get upset if the additional information seems to contradict an earlier assumption they made: "You can just change your assumptions whenever you want?" As a result, it is useful to have the students do this activity in small groups in class. Then collect their ideas and discuss them in large group.

Note: For scenario I, some students may answer that no selection is going on in this situation. When asked to explain, they may say, "There is no evidence of selection against any of the mice." Given the information provided, this is true. However, these students need a nudge to recognize that all living organisms, plants included, can be affected by selection.

After working through several of the scenarios, some students may get the idea that answering these types of questions can be done by formula: First assume that the characteristic being affected is heritable, and then ask what would happen to the population over time if many organisms with a particular characteristic were removed. This strategy works well only if the characteristics could be heritable. In some cases (for example, scenario IV), however, it is not reasonable to assume the characteristic is heritable. That it is not heritable usually becomes obvious when you take the example to extremes. For example, if you take scenario IV to the extremes, then over time, the population would contain fewer and fewer very young and very old individuals and more and more middle-aged individuals. If you explain this to the class, some will recognize that there's something wrong with this idea. Others may have to be nudged further. Ask: "Which individuals in the population are most likely to breed? Given this, how would the number of newborns in the population be likely to change over time?"

Answers

Activity 23.1 A Quick Review of Hardy-Weinberg Population Genetics

Part A. Review Chapter 23 of *Campbell Biology*, 9th edition. Then complete the discussion by filling in the missing information.

If evolution can be defined as a change in gene (or more appropriately, allele) frequencies, is it conversely true that a population not undergoing evolution should maintain a stable gene frequency from generation to generation? This was the question that Hardy and Weinberg answered independently.

1. **Definitions.** Complete these definitions or ideas that are central to understanding the Hardy-Weinberg theorem.

   a. Population: An interbreeding group of individuals of the same species.
   b. Gene pool: All the alleles contained in the gametes of all the individuals in the population.
   c. Genetic drift: Evolution (defined as a change in allele frequencies) that occurs in small populations as a result of chance events.

2. **The Hardy-Weinberg theorem.** The Hardy-Weinberg theorem states that in a population that is not (**is/is not**) evolving, the allele frequencies and genotype frequencies remain constant from one generation to another.

3. **Assumptions.** The assumptions required for the theorem to be true are listed on page 472 of *Campbell Biology*, 9th edition, and are presented here in shortened form.

   a. The population is very large.
   b. There is no net migration of individuals into or out of the population.
   c. There is no net mutation; that is, the forward and backward mutation rates for alleles are the same. For example, *A* goes to *a* as often as *a* goes to *A*.

d. Mating is at random for the trait/gene(s) in question.
e. There is no selection. Offspring from all possible matings for the trait/gene are equally likely to survive.

4. **The Hardy-Weinberg proof.** Consider a gene that has only two alleles, *R* (dominant) and *r* (recessive). The sum total of all *R* plus all *r* alleles equals all the alleles at this gene locus or 100% of all the alleles for that gene.

   Let p = the percentage or probability of all the *R* alleles in the population

   Let q = the percentage or probability of all the *r* alleles in the population

   If all *R* + all *r* alleles = 100% of all the alleles, then

   $$p + q = 1 \text{ (or } p = 1 - q \text{ or } q = 1 - p\text{)}$$

   (*Note:* Frequencies are stated as percentages [e.g., 50%] and their associated probabilities are stated as decimal fractions [e.g., 0.5].)

   Assume that 50% of the alleles for fur color in a population of mice are *B* (black) and 50% are *b* (brown). The fur color gene is autosomal.

   a. What percentage of the gametes in the females (alone) carry the *B* allele? 50%
   b. What percentage of the gametes in the females (alone) carry the *b* allele? 50%
   c. What percentage of the gametes in the males carry the *B* allele? 50%
   d. What percentage of the gametes in the males carry the *b* allele? 50%
   e. Given the preceding case and all the Hardy-Weinberg assumptions, calculate the probabilities of the three possible genotypes (*RR*, *Rr*, and *rr*) occurring in all possible combinations of eggs and sperm for the population.

		Female gametes and probabilities	
		R (p)	*r* (q)
Male gametes and probabilities	*R* (p)	RR (p^2)	Rr (pq)
	r (q)	Rr (pq)	rr (q^2)

   Because the offspring types represent all possible genotypes for this gene, it follows that

   $$p^2 + 2pq + q^2 = 1 \text{ or } 100\% \text{ of all genotypes for this gene}$$

Part B. Use your understanding of the Hardy-Weinberg proof and theorem to answer the questions.

1. According to the Hardy-Weinberg theorem, $p + q = 1$ and $p^2 + 2pq + q^2 = 1$. What does each of these formulas mean, and how are the formulas derived?

   $p + q = 1$: If you add all the dominant alleles for a gene to all the recessive alleles for the gene, you get all of the alleles for that gene, or 100% of the alleles for the gene. (*Note*: This assumes the gene has only two alleles.)

   $p^2 + 2pq + q^2 = 1$: If you combine all the individuals that are homozygous dominant for a gene with all the heterozygotes and homozygous recessive individuals for that gene, you have counted or combined all the individuals in the population that carry that gene.

2. Assume a population is in Hardy-Weinberg equilibrium for a given genetic autosomal trait. What proportion of individuals in the population are heterozygous for the gene if the frequency of the recessive allele is 1%?

   Assume that *D* is the dominant allele and *d* is the recessive allele. Because all the alleles are either *d* or *D*, if the frequency of the *d* alleles is 1% or 1/100 (= q), then the frequency of the *D* alleles must be 99% or 99/100 (= p). The frequency of heterozygous individuals in the population is $2pq$ or 2(99/100)(1/100) = 198/10,000.

3. About one child in 2,500 is born with phenylketonuria (an inability to metabolize the amino acid phenylalanine). This is known to be a recessive autosomal trait.

   a. If the population is in Hardy-Weinberg equilibrium for this trait, what is the frequency of the phenylketonuria allele?

      Assume *P* is the normal allele and *p* is the phenylketonuria allele. The frequency of homozygous *pp* individuals in the population is then equal to q^2, which is 1/2,500. The frequency of the *p* allele is the square root of 1/2,500 = 1/50 or 2%.

   b. What proportion of the population are carriers of the phenylketonuria allele (that is. what proportion are heterozygous)?

      Heterozygotes should occur in the frequency $2pq$: $2pq$ = 2(1/50)(49/50) = 98/2,500.

4. In purebred Holstein cattle, about 1 calf in 100 is spotted red rather than black. The trait is autosomal and red is a recessive to black.

   a. What is the frequency of the red alleles in the population?

      If 1 calf out of 100 is spotted red, then the frequency of the recessive red genotype is $1/100 = q^2$. Therefore, q (the frequency of the red allele) = 1/10 or 10%.

   b. What is the frequency of black homozygous cattle in the population?

      $p^2 = (1 - q)^2 = (9/10)^2 = 81/100$

c. What is the frequency of black heterozygous cattle in the population?

$2pq = 2(1/10)\ (9/10) = 18/100$

5. Assume that the probability of a sex-linked gene for color blindness is $0.09 = q$ and the probability of the normal allele is $0.91 = p$. This means that the probability of X chromosomes carrying the color blindness allele is 0.09 and the probability of X chromosomes carrying the normal allele is 0.91.

a. What is the probability of having a color-blind male in the population?

Remember, males have only one X chromosome. Color blindness is a sex-linked gene and is found on the X chromosome and not on the Y. As a result, a male has a 0.09 probability of having the X with the color blindness allele and a 0.91 probability of having an X with the normal allele. For sex-linked genes, males display the allele frequency.

b. What is the probability of a color-blind female?

Unlike males, females have two copies of the X chromosome. As a result, they display the genotype frequency for genes on the X. A color-blind female is homozygous recessive for the color blindness allele. The frequency of the homozygous recessive genotype is q^2, or $(0.09)^2 = 0.0081$.

6. The ear tuft allele in chickens is autosomal and produces feathered skin projections near the ear on each side of the head. This gene is dominant and is lethal in the homozygous state. In other words, homozygous dominant embryos do not hatch from the egg. Assume that in a population of 6,000 chickens, 2,000 have no ear tufts and 4,000 have ear tufts. What are the frequencies of the normal versus ear tuft alleles in this population?

This gene is lethal in the homozygous condition. Therefore, homozygotes that are produced do not hatch and do not appear in the population. The population contains 4,000 heterozygous tufted chickens and 2,000 homozygous normal chickens. Because we don't know how many eggs did not hatch (or how many of these contained homozygous tufted chickens), we need to calculate the allele frequencies by assigning alleles to the existing population.

	Number of *T* (tufted) alleles	Number of *t* (normal) alleles
4,000 tufted chickens	4,000 *T*	4,000 *t*
2,000 normal chickens	______	4,000 *t*
Total alleles	4,000 *T*	8,000 *t*
Allele frequencies	4,000/12,000	8,000/12,000
	0.33	0.66

If these are in Hardy-Weinberg equilibrium, we would expect the following offspring in the next generation:

Frequency of alleles in eggs → Frequency of alleles in sperm ↓	*T* ($p = 1/3$)	*t* ($q = 2/3$)
T ($p = 1/3$)	*TT* (1/9)	*Tt* (2/9)
t ($q = 2/3$)	*Tt* (2/9)	*Tt* (4/9)

In the next generation, when you remove the homozygous lethals, the frequency of *Tt* and *tt* genotypes would be equal. This indicates that the assumption is incorrect. In other words, the population is not in Hardy-Weinberg equilibrium.

7. How can one determine whether or not a population is in Hardy-Weinberg equilibrium? What factors need to be considered?

   To determine whether a population is in Hardy-Weinberg equilibrium, you need to be able to calculate the numbers of individuals in the population that are homozygous versus heterozygous for the alleles. If you know the frequencies of each genotype, you can calculate the allele frequencies (as in question 6). Given the allele frequencies, you can calculate the genotype frequencies that would be expected if the population were in Hardy-Weinberg equilibrium. Then compare these values to the known values for the population. In reality, this is difficult to do because if alleles show dominance, it is hard to distinguish the homozygous dominants from the heterozygotes. As a result, we tend to look at the frequency of the homozygous recessive phenotype in a population. If this remains relatively constant from one generation to the next, we use it as evidence to assume that the population is in Hardy-Weinberg equilibrium.

8. Is it possible for a population's genotype frequencies to change from one generation to the next but for its gene (allele) frequencies to remain constant? Explain by providing an example.

   There are a number of ways that this is possible. Here is one example of how it could occur: Assume inbreeding has occurred in two populations of mice. In one population, the mice have become homozygous *AA* at a particular gene locus. In the other population, the mice have become homozygous *aa* at that gene locus. Equal numbers of *aa* and *AA* mice happen to migrate to a new habitat. The frequency of the *A* allele is 0.5 and the frequency of the *a* allele is 0.5 in this new population. All possible combinations of matings of these mice are listed in the following table.

	AA males	aa males
AA females	$AA \times AA \rightarrow$ all AA offspring	$AA \times aa \rightarrow$ all Aa offspring
aa females	$AA \times aa \rightarrow$ all Aa offspring	$aa \times aa \rightarrow$ all aa offspring

Each of these matings should occur with equal probability. Therefore, each of the offspring types should occur with equal probability. As a result, $\frac{1}{4}$ of the offspring will be *AA*, $\frac{1}{2}$ will be *Aa*, and $\frac{1}{4}$ will be *aa*. In this case, within one generation the population has gone to Hardy-Weinberg equilibrium for genotypes; however, the allele frequency has remained the same.

23.1 Test Your Understanding

In each of the following scenarios, choose which assumption of the Hardy-Weinberg Law is being violated.

1. In a particular region of the coast, limpets (a type of mollusc) live on near shore habitats that are uniformly made up of brown sandstone rock. The principle predators of these limpets are shorebirds. The limpets occur in two morphs, one with a light-colored shell and one with a dark-colored shell. The shorebirds hunt by sight and are able to see the light ones on the dark sandstone easier than the dark ones.

   No selection—The shorebirds are selectively taking the most visible (light) limpets.

2. In *Chen caerulescens* (a species of goose), the white body form, the snow goose and the blue body form, the blue goose, occasionally coexist. In these areas of contact, white-by-white and blue-by-blue matings are much more common than white-by-blue matings.

   Random mating—Selective mating is occurring when white by white and blue by blue mating are more common than white by blue.

3. Prior to the Mongolian invasions which occurred between the 6th and 16th centuries, the frequency of blood type B across Europe was close to zero. The frequency of blood type B among the Mongols was relatively high. Today, it is possible to see fairly high frequencies of blood type B in the Eastern European countries and a gradual decrease in the frequency of blood type B as one moves from the Eastern European countries to the Western European countries, such as France and England.

   No migration—Mongolian invasions were more common in Eastern European countries than Western European countries. Offspring of Eastern Europeans and Mongols with blood type B led to the variability in distribution of the blood type in Europe.

Activity 23.2 What effects can selection have on populations?

1. What effects can natural selection have on populations? For example, what types of selection can occur in a population, and how does each affect a population?

   Selection can be directional, stabilizing, or disruptive. If selection removes individuals at one of the extremes of a phenotypic characteristic, then the mean for the characteristic can appear to move in a more positive (or more negative) direction—directional selection. Alternatively, selection can act against both extremes at the same time, and the characteristic will appear to stabilize around the mean—stabilizing selection. If selection acts against the mean or average phenotype, it can lead to the production of a polymorphic population—disruptive selection.

2. Examine the scenarios on the following pages. For each scenario:

   a. Decide whether or not natural selection is operating. In doing this, indicate whether there is variability in the population(s).

      If *no*, what does this imply about evolution?
      If *yes*, what is the nature of the variation? For example, what characteristics must the variation have for selection to operate on it?

   b. Is there any indication that members of the population(s) differ in fitness?

      If *no*, what does this imply about the operation of natural selection?
      If *yes*, describe the difference in fitness.

   c. Given your answers to parts a and b, what trend should characterize the future behavior or composition of the population(s)?

   Be sure to indicate any assumptions you make in answering the questions.

   The key to analyzing these scenarios is to ask first what is being selected against and then whether or not this phenotype or trait could have a genetic basis; that is, could the trait be inherited genetically? If the answer is yes, you are likely to see selection. Then you need to determine what type of selection.

Scenario I. A particular species of mouse feeds on the seeds of a single species of cherry tree. When the mice eat a seed, they digest it completely. The mice choose seeds of intermediate and large sizes, leaving the very small seeds of the cherry tree uneaten.

a. Selection is occurring. The variation is in cherry seed size. For selection to be operating, the assumption is that seed size is a heritable trait.
b. Individual seeds do differ in fitness. The mice are selecting against the very large and intermediate-sized seeds. Only the very small seeds are not eaten. Therefore, many more small seeds will be left (relative to other sizes) to produce the next generation of cherry trees.
c. If this selection occurs long term, future generations of cherry trees will produce more small-sized seeds.

Scenario IIa. Small island A contains three separate populations of a single species of cherry tree. The seed size varies between trees. That is, some trees produce seeds that are all in the small size ranges, others produce seeds all in the middle size ranges, and others produce seeds in the large size ranges. A small population of mice is introduced to the island. The mice eat cherries and are the only predators on the cherry trees. When the mice eat a cherry, they completely digest it and the pit or seed inside it. The mice choose medium and large seeds and leave the smallest seeds uneaten.

a. Selection is occurring. The variation is in cherry seed size. For selection to be operating, the assumption is that seed size is a heritable trait.
b. Individual seeds do differ in fitness. The mice are selecting against the very large and medium seeds. Only the small seeds are not eaten. Therefore, many more small seeds will be left (relative to other sizes) to produce the next generation of cherry trees.
c. If this selection occurs long term, future generations of cherry trees will produce more small seeds. Furthermore, since the three populations are each made up of trees with different sized seeds, the population with small seeds will become much larger over time compared to the other two populations.

Scenario IIb. Would your answer for Scenario IIa change given the following information? Explain. As you continue to study the populations of trees, you note that the viability of the seeds varies with size such that the viability of the small seeds is less than that of the middle-sized seeds, which is less than that of the largest seeds.

a. Again, selection is occurring. The variation is in cherry seed size. For selection to be operating, the assumption is that seed size is a heritable trait.
b. Individual seeds differ in fitness. The mice are selecting against the very large and middle-sized seeds. Only the small seeds are not eaten. Therefore, many more small-sized seeds will be left (relative to the other sizes). In addition, there is a difference in fitness related to seed size. The larger the seed, the more likely it is to survive and produce a new tree.
c. In this scenario, you need to consider both the effects of selection by mice and the difference in relative fitness of the seeds associated with size. If the mice are not eating all of the large and middle-sized seeds, some will remain to produce

individuals in the next generation. In the future populations, the proportion of trees producing each seed type depends on both the numbers of large, middle-sized, and small seeds that are uneaten and the relative viability of each of these.

Scenario IIIa. Small island B contains three separate populations of a single species of cherry tree. Unlike the species on island A, in this species seed size varies within trees. That is, each tree produces seeds that range in size from large to small. A small population of mice is introduced to the island. These are the only predators on the cherry trees. When the mice eat a cherry, they digest it and the pit or seed completely. The mice choose medium and large seeds and leave the smallest seeds uneaten.

a. Again, selection could be occurring if you assume that seed size is a heritable trait. If each flower on a tree is independently pollinated to produce its seeds, then the individual seeds on a tree can have different combinations of genes. However, if you noticed that the most shaded parts of the tree produced cherries with small seeds and the sunniest parts of the tree produced the cherries with the largest seeds, you might reconsider your assumption. In that case, seed size may be the result of available nutrients or growth conditions and not the result of genetic differences.
b. If seed size varies with nutrition (as opposed to genetics), the selection against large and small seeds is not necessarily selection against any particular genotype. Then there is no genetic difference in fitness.
c. If there are no selection and no difference in fitness among the surviving seeds, then the population should remain relatively stable in genetic composition over time.

Scenario IIIb. Would your answer for Scenario IIIa change given the following information? Explain. As you continue to study these populations, you note that the viability of the seeds does not vary with size. Over time, however, you find that the trees that grow from the smallest seeds produce fewer large seeds.

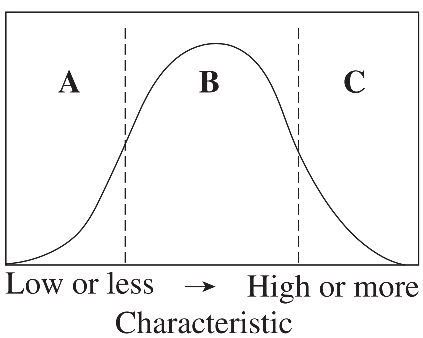
a. This information provides additional evidence that seed size is heritable and not the result of growth conditions. As a result, selection is occurring.
b. Small seeds or individuals would survive more frequently (compared to medium and large seeds, which would be preferentially eaten and therefore removed from the population).
c. Over time, you would expect to see more offspring from small-sized seeds and, as a result, more production of small-sized seeds.

Scenario IV. After a severe spring ice storm, about half of the finches (small birds) in a population are found dead. Examination of the dead birds indicates that they vary in age from young to old. About 60% of the dead are new fledglings (just left the nest); about 20% are over 3 years of age (old for this species).

a. I'd argue that this is not selection. The vast majority of the dead birds are the very young (just fledged and without parental support) and the very old. Individuals in these age categories are less able to survive based on their level of experience and general health. These characteristics are not necessarily based on genetic differences in these individuals compared to the rest of the population that survived.
b. If this were selection, it would be against young and old ages. If we took this to extremes, we would have to argue that over time each subsequent generation would have more middle-aged individuals (compared to the numbers of young and old individuals). Because middle-aged individuals must have at one time been young, this doesn't make logical sense.
c. Without any further information to indicate that only specific types of young and old birds died, we cannot say that genetic selection occurred. Therefore, we would expect to see no significant changes in the genetics of this population over time.

23.2 Test Your Understanding

The figure below shows the distribution of a phenotypic characteristic in a population of organisms. Also shown are three portions (A, B, and C) of that distribution.



For the situations described in questions 1 to 3 below, which portion(s) of the population will be *selected against* and *least likely* to have their genes represented in the next generation? Explain your answers.

Use the following set of answers

A. Portion A only
B. Portion B only
C. Portion C only
D. Portions A and C simultaneously
E. Portions B and C simultaneously

1. Male sticklebacks with bright red coloring are favored by female stickleback as mates. However, the bright red color makes the males more likely to be seen by predators.

   D. In this example, the bright red color is both selected against (by predators) and for (by females during mating). As a result, there will be a relative equilibrium set up between these two forces, which will tend to stabilize the color at some intermediate level.

2. On Island Z in the Galápagos the plant population contains only two species. One of the two plant species produces very large seeds and the other produces small seeds. A species of seed-eating finch has lived on the island for many years. This established species has large beaks and prefers large seeds. A small population of a different species of seed eating finch has migrated to the island. The beak size in the new species varies over a continuum from relatively small to large. *How will evolution of the new finch species be affected?*

   C. The established species with large beaks are likely to be better competitors for the large seeds. As a result, the members of the new species, that can only eat large seeds are likely to be at a disadvantage relative to those members of the new species that can eat smaller seeds. As a result, selection in the new species will be against larger-beaked birds.

3. In a species of plant-eating land snail, the shell color is variable and ranges from very light to intermediate to very dark in color. The snails are preyed upon by birds that use sight to find their prey. A small population of these snails is moved to an island where the food plants in their preferred habitat are either very light in color or very dark.

   B. In this scenario the landscape is either light or dark. As a result, light snails would be less visible on light landscape and dark snails would be less visible on dark landscapes. However, intermediate shades of snails would be visible on all landscapes and therefore selected against (seen and eaten) more often than either light or dark snails.

Notes to Instructors

Chapter 24 The Origin of Species

What is the focus of this activity?

As noted earlier, certain key words used in discussions of evolution may have very different meanings to students. For example, *adaptation, fitness, primitive*, and *advanced* have very different meanings in common use compared to their meanings in the study of evolution. Many other words used in discussing evolution and speciation may be new to students—for example, *anagenesis, cladogeneis, allopatric*, and *sympatric*. In this activity, students learn the meanings of these words in context as they examine how speciation occurs.

What is the particular activity designed to do?

Activity 24.1 What factors affect speciation?
This activity is designed to help students understand how evolutionary changes in a population can lead to speciation. As they examine how speciation can occur, students also learn key terms used to describe processes associated with speciation.

Activity 24.2 How does hybridization affect speciation?
This activity is designed to help students understand how environmental differences and interactions between species in zones of hybridization function either to reinforce species differences or to fuse species.

Answers

Activity 24.1 What factors affect speciation?

1. The Galápagos Archipelago consists of a dozen islands all within 64 km of their nearest neighbor. From 1 to 11 of the 13 species of Darwin's finches live on each island. Many evolutionary biologists believe that if there had been only one island, there would be only one species of finch. This view is supported by the fact that Cocos Island is isolated (by several hundred kilometers of open ocean) from the other islands in the archipelago and only one species of finch is found there.

    a. How does the existence of an archipelago promote speciation? Explain and provide an example.

The distance between islands makes it very difficult for organisms on one island to migrate to another island. For example, it is likely that only a few birds made it to one of the Galápagos Islands from the mainland (Ecuador). Birds without phenotypes that allowed them to survive on the island were eliminated. Phenotypes that survived increased in number. Because conditions on the island differed from those on the mainland, this population diverged from the population on the mainland. As genetic changes accumulated in this island population, the population may have become reproductively isolated from the mainland species and could then be considered a new species.

As the population on the first island became more numerous, a few birds from the island may have successfully migrated to the next island in the archipelago. (Many may have tried, but only a few succeeded.) The few that migrated would establish a new colony of birds. If the environmental conditions on the new island differed from those on the old island, the phenotypes that survived could also differ. Over time, the colony on the second island could diverge enough genetically to become reproductively isolated from the first island population. At this point, it would be considered another new species. This type of progressive migration to the various islands could result in the formation of a new species on each of the islands. Additional migration events between islands could account for the presence of more than one species per island. For more than one species to exist on an island, however, each species must have adopted a separate niche.

b. Is the mode of speciation that occurred on these islands more likely to have been allopatric or sympatric? Explain.

This mode of speciation is more likely allopatric. For genetic changes to accumulate differentially in two populations, gene flow must be limited between the populations. For these species, allopatric isolation of species populations is the most likely mechanism for limiting gene flow.

c. Is the type of speciation seen on the Galápagos Archipelago more likely to be the result of anagenesis or cladogenesis? Explain.

It is more likely the result of cladogenesis. Anagenesis is the gradual change of one species into another over time. The species may change over time; however, at any point in time, only one species is present. Cladogenesis is the divergence of a species into two or more species.

2. Hybrids formed by mating two different species are often incapable of reproducing successfully with each other or with the members of their parent populations. Explain why this is the case. (*Hint:* Consider what you know about chromosome numbers and meiosis.)

In diploid animals, meiosis produces gametes that each contain half of the chromosomes of the parent cell. Each gamete receives a very specific half of the chromosomes, however. Each gamete receives one member of each homologous pair. As a result, when the zygote forms, it contains a complete set of chromosomes (two members of each pair). The partitioning of one member of each homologous pair to each gamete occurs as a result of synapsis and separation of the members of each pair to opposite poles at anaphase I of meiosis.

Hybrid organisms have one member of each homologous pair of chromosomes from the male parent and one member of each homologous pair from the female parent. The haploid number of chromosomes may differ for the two species. In addition, during meiosis, synapsis of chromosomes from different species may not occur. As a result, the division of chromosomes to opposite poles at anaphase I of meiosis occurs randomly. There is no control over which chromosomes will appear in the gametes. Combinations of gametes from hybrids most often result in zygotes that are aneuploid for a number of the chromosomes and therefore nonviable. Combinations of gametes from hybrids with gametes from either of the parental types also result in the production of nonviable aneuploids.

3. Because most hybrids can't reproduce, their genes (and the genes of their parents) are removed from the population. Only the genes of individuals who breed with members of their own species remain in the population. This implies that there is a strong selective advantage for genes that enable individual organisms to recognize members of their own species. Today a wide range of reproductive isolating mechanisms has been identified.

   Each of the following scenarios describes a reproductive isolating mechanism. Indicate whether each is a prezygotic or postzygotic isolating mechanism. Explain your answers.

   (*Note:* A prezygotic isolating mechanism by definition prevents the formation of the zygote. A postzygotic isolating mechanism affects the viability or reproduction of zygotes that are produced.)

   a. Crickets use species-specific chirp patterns to identify a mate of their own species.
      This is a prezygotic mechanism because it prevents matings between different species.

   b. Two species of butterfly mate where their ranges overlap and produce fertile offspring, but the hybrids are less viable than the parental forms.
      Hybrids are produced; however, the hybrids are less viable than either parent species. As a result, this is a postzygotic isolating mechanism.

   c. Two species of a plant cannot interbreed because their flowers differ in size and shape and require pollination by different species of bee.
      This is a prezygotic mechanism because it prevents pollen from one plant from fertilizing the other species of plant. As a result, it blocks zygote formation.

d. Two species of firefly occupy the same prairie and have similar flash patterns, but one is active for a half-hour around sunset while the other doesn't become active until an hour after sunset.

This is another prezygotic isolating mechanism. The behavior of the two species prevents them from interacting and, as a result, prevents the production of hybrid zygotes.

4. Many of our most successful grain crops arose as hybrids; most are also allopolyploids. These crops can successfully reproduce. Explain.

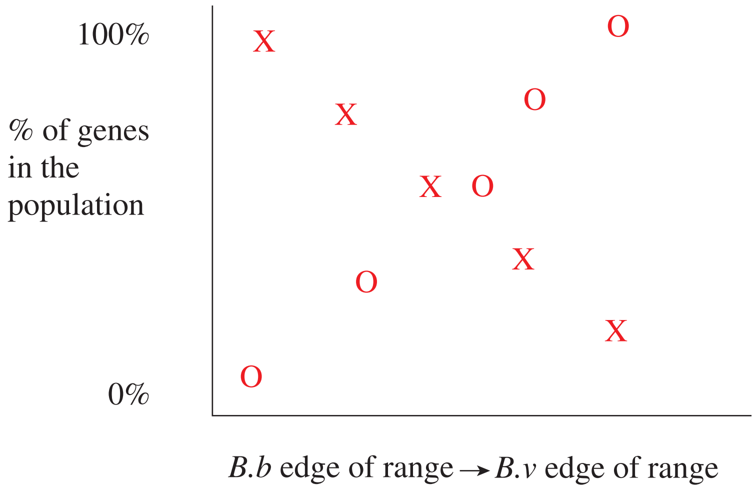
An allopolyploid can be produced by hybridization between two species to form a zygote. If the chromosomes of the zygote duplicate for the first mitotic division but that division fails, the zygote becomes an allopolyploid. In other words, the zygote contains two copies of each of the chromosomes donated by each of the parents. These copies can synapse in meiosis I and separate to opposite poles at anaphase I. As a result, meiosis produces gametes, each with one member of each pair of chromosomes.

If this type of allopolyploidy occurred in a sexually reproducing animal, the story would stop there. The likelihood that a sexually reproducing allopolyploid animal would find another similar allopolyploid of the opposite sex to mate with is about zero. On the other hand, many plants produce both pollen (containing male gametes) and eggs. If such a plant becomes allopolyploid and is capable of self-fertilization, it automatically becomes a new species.

Activity 24.2 How does hybridization affect speciation?

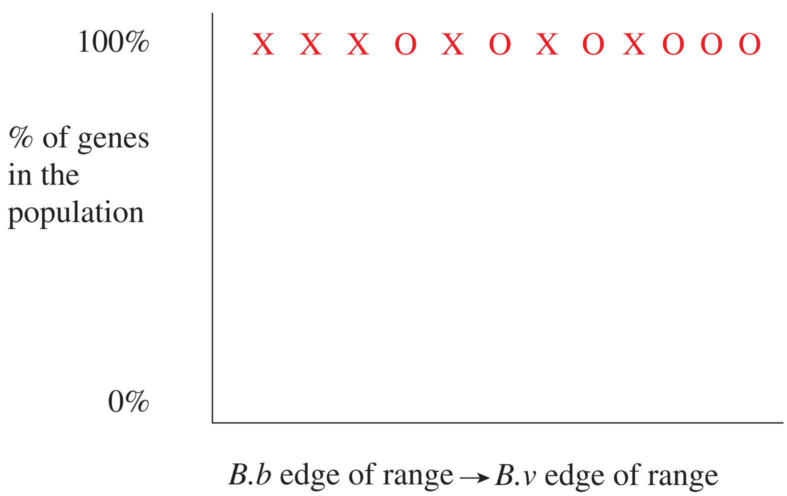
As noted in the text, two species of toads, *Bombina bombina* and *Bombina variegata*, share a hybrid zone that is 4,000 km in length and only 10 km wide. The frequency of alleles specific to *B. bombina* decreases from close to 100% on one edge of the hybrid zone to 0% on the opposite edge. Similarly, the frequency of *B. variegata*–specific alleles decreases across the hybrid zone (beginning at the opposite edge) from close to 100% to 0%.

1. On the following graph, map the general percentage of each type of species-specific genes across the hybrid zone. Use an X to indicate the frequency of *B. bombina*–specific genes and an O to indicate the frequency of *B. variegata*–specific genes.



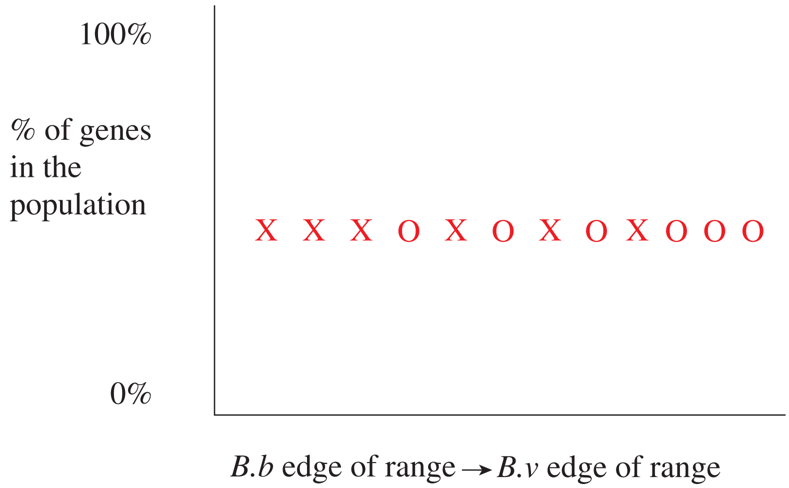
2. How would you predict this gene distribution would change over time if:

   a. reinforcement occurs?



Note: In the graph above, each X or O represents the percentage of *B.b* or *B.v* alleles in a sampled individual. If reinforcement occurs and is extreme, each toad would contain either entirely *B.b*-specific genes or entirely *B.v*-specific genes—that is, there would be no hybridization or mixing of genes.

b. fusion occurs?



Note: In the graph above, each X or O represents the percentage of *B.b* or *B.v* alleles in a sampled individual. If fusion or weakening of reproductive barriers occurs, so much gene flow may occur that the gene pools of the two species will become alike. In the extreme, a new hybrid species would replace the separate species.

c. Hypothetically, which (a or b) is more likely to occur if all environmental conditions across the two species ranges are similar? Explain.

Similar environmental conditions across the range imply no selective advantage for one set of genes over the other. As a result, fusion would be more likely. This assumes hybrids are viable and not at a selective disadvantage for survival compared to the parent types.

d. Hypothetically, which (a or b) is more likely to occur if the environmental conditions vary gradually across the species ranges such that one end of the range was much colder than the other for example? Explain.

Very different environmental conditions at the ends of the hybrid range imply that the two species are differently adapted. As a result, reinforcement would be favored over fusion. This assumes that even if hybrids are viable, they are at a selective disadvantage for survival at the edges of the hybrid range compared to the parent types.

e. As noted in the text, what changes in allele frequencies have been recorded over this hybrid range in the last 20 years? What does this indicate?

In reality, there has been little change observed in the hybrid ratio for these two species over the past 20 years. The authors propose that this may be the result of extensive gene flow from outside the zone.

24.2 Test Your Understanding

Read the following statement. Then, based on your knowledge of cell biology, genetics and evolution, decide to agree or disagree with the statement. Whichever you decide, write a short paragraph that provides solid evidence defending your choice.

"When you think about sexual reproduction, it makes no sense. After all, evolution selects for organisms that are best fit. In a population of sexually reproducing organisms, a mutant that reproduced asexually would increase its representation more quickly than the wild type, that is, it would have a higher fitness. So we should expect asexual reproduction to be much more widespread among eukaryotic species than it is."

While there are many ways of addressing this, a reasonable student answer may be similar to the following:

Because all members of an asexually reproducing species can produce offspring, one could argue that asexual reproduction results in a more rapid population expansion than sexual reproduction (where only the females produce the offspring). However, this does not necessarily mean that it is more beneficial for the population to only reproduce asexually. The recombination of genes that occurs in meiosis and fertilization in sexual reproduction generates much of the genetic variation on which natural selection acts. Asexual reproduction is limited in the sense that many fewer new genetic material/combinations are introduced into the offspring. Offspring are for the most part clones of their parents. It is genetic variation that provides new combinations of genes that may allow for future adaptation and evolution in changing environments.

Notes to Instructors

Chapter 25 The History of Life on Earth

What is the focus of these activities?

All the evidence we have been able to gather indicates that life on Earth began about 3.5 billion years ago. For the first 1.5 billion years, life-forms on Earth were similar to today's prokaryotes.

What are the particular activities designed to do?

Activity 25.1 What do we know about the origin of life on Earth?
Students can use this activity to review the types of evidence that exist for the origin of life on Earth as well as current ideas about the characteristics of early life-forms.

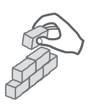
Activity 25.2 How can we determine the age of fossils and rocks?
This activity is designed to help students understand some of the methods used to age the Earth.

What misconceptions or difficulties can these activities reveal?

Activity 25.1
Students often have difficulty "putting all the pieces together." This type of activity will help them integrate the various ideas and theories about the evolution of life on the early Earth.

Activity 25.2
While the math involved here is fairly simple, many students still have difficulty with it. Actually doing a few problems will help them understand not only how to do the calculations, but the theoretical reasoning behind them.

Answers



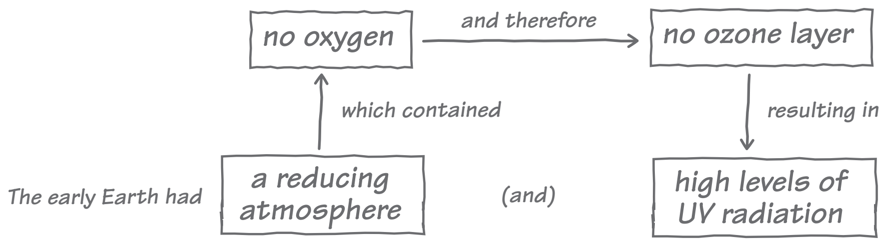
Activity 25.1 What do we know about the origin of life on Earth?

Construct a concept map of conditions on the early Earth and the origin of life-forms. Be sure to include definitions or descriptions of all the terms in the list below. Keep in mind that there are many ways to construct a concept map.

- Begin by writing each term on a separate sticky note or piece of paper.
- Then organize the terms into a map that indicates how the terms are associated or related.

- Draw lines between terms and add action phrases to the lines that indicate how the terms are related.
- If you are doing this activity in small groups in class, explain your map to another group of students when you are done.

Here is an example:



Terms

no oxygen
reducing atmosphere
high-oxygen atmosphere
sunlight
electrical discharge (for example, lightning)
amino acids
ozone layer
sugars
nucleic acids
DNA
inorganic compounds
organic compounds
carbon dioxide

protobiont
micelle
phospholipid bilayer
ammonia
phospholipids
water
Stanley Miller
methane
molecular clocks
heat
heterotrophs
autotrophs
high levels of UV radiation

low levels of UV radiation
prokaryotes
RNA world
Eukarya
energy source
carbon source
mode of nutrition
anaerobic bacteria
cyanobacteria (blue-green algae)
Gram stain
antibiotics
penicillin

Use the understanding you gained from creating the concept map to answer the questions.

1. Modern theory suggests that the early (pre-life) atmosphere on Earth was a reducing one. Why (for what reasons) is it believed that oxygen was not present when life formed on Earth?

   One key piece of evidence is the lack of oxidized iron in rocks that are more than 2.7 billion years old. Therefore, oxygenic photosynthesis is thought to have evolved about 2.7 billion years ago. As oxygen accumulated in the oceans, iron oxides were formed and precipitated out. Eventually enough oxygen was formed not only to saturate the ocean water but also to outgas or move from the ocean into the atmosphere. As oxygen levels rose in the atmosphere, iron compounds on land also oxidized. (*Note*: Rust is a form of oxidized iron.)

2. What proposed energy sources existed on this early (pre-life) Earth?

   Energy sources on the early Earth included geothermal energy, volcanic energy, and lightning.

3. In the 1950s, Stanley Miller performed a set of experiments to determine whether life could have evolved given the conditions stated in the answers to questions 1 and 2.

   a. How was the experiment designed?

      Miller created a sealed system. The only compounds in the system were water and a number of the different atmospheric gases thought to have been present on the early Earth—for example, methane, ammonia, and hydrogen. Miller used heat to vaporize the water. The steam passed through the chamber that contained the atmospheric gases. The vapor cooled, and the water was collected and recirculated to be heated again to produce steam.

   b. What were the necessary controls?

      The system had to be meticulously cleaned and sterilized to be sure it contained no organic molecules. This included evacuating all the air out of the system and replacing it with the ammonia, methane, and hydrogen.

      Another control was an identical system that was provided with no energy source. This would allow Miller to determine whether the macromolecules produced were contaminants or direct results of the experiment.

      In subsequent experiments, Miller also varied the concentrations and presence or absence of various compounds to determine which were required to produce specific types of macromolecules.

   c. What was produced in the experiment?

      In the first experiment, organic molecules, including some amino acids, were found in the system after only about 10 days of operation. In subsequent experiments, Miller was able to produce additional amino acids, carbohydrates, nucleotide bases, and other macromolecules by adjusting the gas composition of the atmosphere in the system.

   d. What did the results imply about the possible origin of life on Earth?

      Miller's experiments showed that organic compounds could be produced in an anaerobic, reducing atmosphere. The results implied that life could have evolved under these conditions as well.

e. There is general agreement that life must have evolved in the oceans originally and only much later invaded land. What factors of the physical environment on the early and evolving earth support these ideas? Changes in which of these were essential to allow life to survive on land?

The early Earth's atmosphere contained little or no oxygen. No ozone layer existed in the upper atmosphere. Though many of the early organisms on Earth did not require oxygen, with no ozone layer, the Earth was bombarded by high levels of UV light, which can easily mutate DNA and therefore kill organisms. Some scientists estimate that life on land was not possible until the atmosphere reached a minimum of about 10% oxygen and the ozone layer was formed.

f. Most of us can't imagine a world without oxygen. However, as you learned earlier, chemically oxygen is a powerful oxidizing compound. What effect(s) would the increase in oxygen levels of the atmosphere have on the organisms that existed at that time?

Most anaerobic organisms (e.g., prokaryotes) alive at the time would be unlikely to have mechanisms to counteract the oxidizing effects of oxygen. As a result, most of them would have died off. Only those that lived in anaerobic environments that were not exposed to oxygen and those that had random mutations that equipped them with antioxidant capabilities (e.g., peroxidases) would have survived.

Activity 25.2 How can we determine the age of fossils and rocks?

To determine the age of fossils and rocks, scientists determine the amounts of radioactive compounds and their stable daughter products present in the sample. Radioactive elements are known to decay into stable daughter compounds at specific rates. A number of radioactive compounds, their stable daughter compounds and their half lifes are shown in the table below.

Radioactive Compound	Stable daughter compound	Half life
Carbon 14	Nitrogen 14	5370 years
Potassium 40	Argon 40	1.25 billion years
Rubidium 87	Strontium 87	48.8 billion years
Thorium 232	Lead 208	14 billion years
Uranium 235	Lead 207	704 million years
Uranium 238	Lead 206	4.47 billion years

For dating rocks, the potassium-argon method is often used because:

- Argon is a gas. When rock is molten, any existing argon gas will escape. As a result, newly formed rocks contain no argon.
- As the ^{40}potassium naturally occurring in the rock decays to ^{40}argon, the ^{40}argon is trapped in pocket in the rock. The ratio of ^{40}potassium to ^{40}argon can be measured to determine the rock's age.

For dating organic material, carbon-nitrogen dating is often used because:

- The ratio of radioactive to nonradioactive carbon dioxide in the atmosphere is fairly constant over time. As a result, the levels of these elements in organic tissue remain relatively constant as long as the organism is alive.
- Once the organism is dead, no new inputs of carbon occur and the existing radioactive-carbon-to-nonradioactive-carbon ratio will decrease over time as the radioactive carbon decays.

1. In one half life, half of the original radioactive compound will decay into its stable daughter compound.

   a. If a newly formed rock contains 100 units of ^{40}potassium (^{40}K), how many units of ^{40}pottassium would it contain after 1.25 billion years?

   It would contain 50 units.

   b. How many units of ^{40}argon (^{40}Ar) would the rock contain when newly formed vs. after 1.25 billion years?

   The rock would contain 0 units of ^{40}argon when newly formed and 50 units after 1.25 billion years.

   c. After the 1.25 billion years, what would be the ratio of ^{40}K to ^{40}Ar in the rock?

   Half of the ^{40}K would be gone. The ratio would be 50 units of ^{40}K to 50 units of ^{40}Ar, or 50:50 or 1:1.

   d. After 2.5 billion years, what would be the ratio of ^{40}K to ^{40}Ar?

   After the next 1.25 billion years, 25 of the 50 remaining ^{40}K molecules would decay to ^{40}Ar. In other words, only 1/4; of the original ^{40}K would be present and the ratio would now be 25 units of ^{40}K to 75 units of ^{40}Ar or 1:3.

2. You are fossil hunting and find a trilobite fossil in an old riverbed. You have it radiometrically dated and are told it is 275 million years old.

   a. In this amount of time, how many half lifes of ^{40}K have elapsed?

   275 million divided by 1.25 billion = $2.75 \times 10^8 / 1.25 \times 10^9$ = about 2×10^{-1} or 0.2 half-lives.

b. Given your answer in a, what would be the ratio of ^{40}K to ^{40}Ar found in the fossil remains?

In 0.2 half-lives, 0.2 of a half-life has elapsed. Therefore, 0.2 of half of the ^{40}K would have decayed to ^{40}Ar, or 0.1 or 1/10 would have decayed to ^{40}Ar. As a result, the ratio of ^{40}K to ^{40}Ar would be 9 to 1.

3. You want to date some fabric that you have discovered at an archeologic dig.

a. What method of dating would be best for this? Describe the general procedure for dating the cloth.

Since human civilizations arose fairly recently in geologic time, it would be best to use carbon dating for the cloth sample. The lab would need to test the relative proportions of carbon 14 to carbon 12 in the sample. Carbon 14: carbon 12 ratios in organic material will decrease over time proportional to the half-life of carbon 14.

b. Assume the cloth is 2,000 years old. How would the level of radioisotope used change in this period of time?

Two thousand years is 2000/5730 or about 0.35 of the half-life for carbon 14. As a result, 0.35×0.5, or about 0.18 or 18%, of the normal level of carbon 14 would have been removed, leaving the carbon 14 level at about 82% of normal.

Notes to Instructors

Chapter 26 Phylogeny and the Tree of Life

What is the focus of these activities?

One of the most valuable lessons we can teach students is that their minds should always be open to new ideas and evidence. Scientific study is based on the accumulation of evidence and information in order to understand how organisms work, evolve, and function. As a result, scientific understanding is not static. New discoveries continually lead to new ideas and new ways of looking at existing evidence. This is true for all areas of science. In recent years, it has been especially true for the field of systematics.

What are the particular activities designed to do?

Activity 26.1 How are phylogenies constructed?
This activity is designed to help students get a better understanding of how taxonomy and phylogeny differ. They will learn how phylogenies (as cladograms) are developed and what we can do when new discoveries change our ideas about phylogenies.

Activity 26.2 What is parsimony analysis?
In this activity, students apply parsimony analysis to three bird species using morphological characters and compare their analysis to the analysis in the text that is based on a sequence of DNA. This is designed to help them address the question of which phylogeny is more correct. The answer is that each is correct for the data used.

Activity 26.3 Put yourself in the professor's shoes: What questions would you ask?
This activity asks students to put themselves in the instructor's shoes to see how exam questions are developed to test understanding. Students will learn to sort out the major ideas and concepts in this section and then use these concepts and ideas to develop exam questions that test understanding.

What misconceptions or difficulties can these activities reveal?

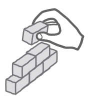
Activity 26.1
Activity 23.2 pointed out that many students are unfamiliar with, and therefore uncomfortable with, making assumptions about the possible heritability of phenotypic characteristics. In Activity 26.1, many students will be similarly uncomfortable with the idea that "what we know" in science can change in light of new evidence or information.

These same students will be uncomfortable trying to answer question 4b: "The phylogenies developed using DNA sequence analysis may differ from those constructed using morphology and physiology. How do scientists know which way is more correct?"

This is a good place to reintroduce the idea that not only are organisms evolving but also that our understanding of them and all of life evolves as we gather new evidence. In other words, what we know or teach as fact today may be modified in the future.

Activity 26.2
This activity reinforces the idea that our present understandings may be modified in the future. To help students understand that this is what science is all about, present this example: Today it is a fact that there is no cure for AIDS. In the future, I don't think any of us would be upset if new evidence proves this fact false.

Answers



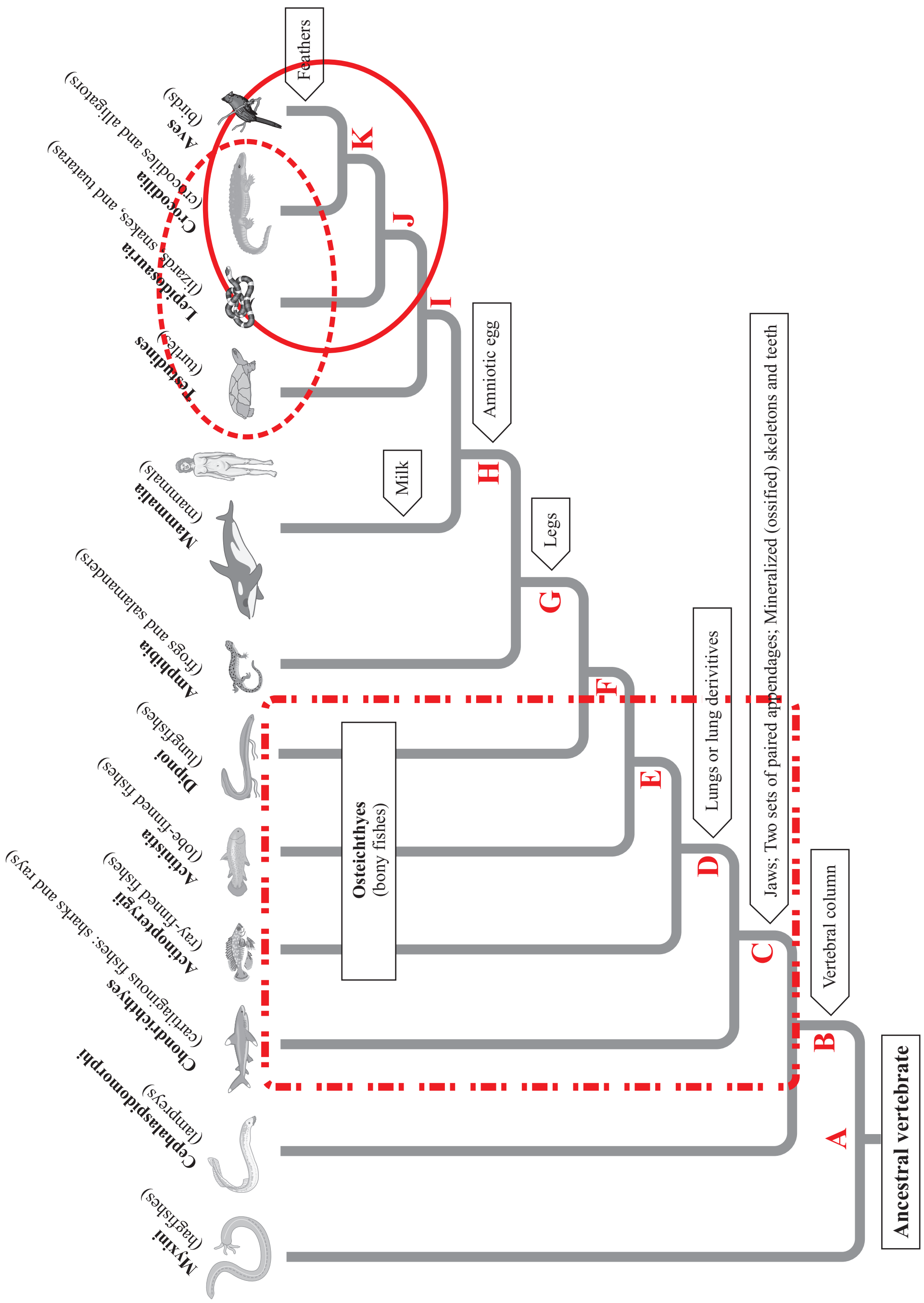
Activity 26.1 How are phylogenies constructed?

Construct a modified concept map to relate the ideas of phylogeny and systematics listed below to the phylogenetic tree on the next page.

- Begin by writing each term on a separate sticky note or piece of paper.
- Then indicate how the terms are associated or related to each other and to the phylogenetic tree on the next page.
- Be sure to include definitions or descriptions of all the terms as you use them to explain these relationships.

Terms

clade	monophyletic	shared derived character
cladistics	polyphyletic	outgroup
phylogenetic tree	paraphyletic	ingroup
homology	convergent evolution	taxonomy
analogy	shared primitive character	phylogeny



Myxini (hagfishes)
Cephalaspidomorphi (lampreys)
Chondrichthyes (cartilaginous fishes: sharks and rays)
Actinopterygii (ray-finned fishes)
Actinistia (lobe-finned fishes)
Dipnoi (lungfishes)
Amphibia (frogs and salamanders)
Mammalia (mammals)
Testudines (turtles)
Lepidosauria (lizards, snakes, and tuataras)
Crocodilia (crocodiles and alligators)
Aves (birds)
Feathers
Amniotic egg
Milk
Legs
Lungs or lung derivitives
Jaws; Two sets of paired appendages; Mineralized (ossified) skeletons and teeth
Vertebral column
Ancestral vertebrate
Osteichthyes (bony fishes)
A
B
C
D
E
F
G
H
I
J
K

Use the understanding you gained from creating the concept map to answer the questions.

1. Compare the taxonomy of a group with its phylogeny (in general terms).

	Taxonomy	Phylogeny
a. Definition or purpose of a:	A taxonomy is a system for naming and classifying organisms.	A phylogeny categorizes organisms based on their evolutionary relatedness.
b. Types of characters used to develop a:	Most taxonomies are based on visible characteristics of organisms—for example similarities in morphology.	Phylogenetic relationships are determined based on historical information—for example, the fossil record and, more recently, similarities in DNA sequence.
c. What similarities could there be between the taxonomy of a given group and its phylogeny?	Phylogenetically related organisms often share similarities in morphology. As a result, many taxonomies reflect phylogenetic relationships as well.	
d. What are the key differences between the taxonomy of a given group and its phylogeny?	By definition, taxonomies are developed to categorize and name organisms. There is no specific intent to determine phylogenetic relationships in the development of a taxonomy.	

2. On the phylogenetic tree shown earlier, are the groups that contain humans, whales, crocodiles, and birds monophyletic, polyphyletic, or paraphyletic? Explain.

   The group containing humans, whales, crocodiles, and birds would be considered polyphyletic because no common ancestor is included.

   An example of a monophyletic group: The group circled with the solid line includes a common ancestor, and all the other members in the group are descended from this common ancestor.

   Another example of a polyphyletic group: The group circled with the simple dashed line includes two sets of organisms, each descended from a separate common ancestor.

   An example of a paraphyletic group: The group circled with the heavy dashed and dotted line is a paraphyletic. If you did not know the other species in the complete cladogram existed, this group would appear to be a monophyletic group. However, because the other species do exist and are related to the common ancestor of this group, the group is paraphyletic.

3. Considering only the individual representative organisms in the phylogenetic tree (e.g., bird, whale, frog), which can be used as good examples of analogy or convergent evolution? As good examples of homology? Explain your reasoning.

   The fish and whale are a good example of convergent evolution. Fish evolved in aquatic habitats. The whale evolved from a mammalian terrestrial ancestor that took up an aquatic habitat. The ability of large animals to survive in an aquatic habitat is directly related to their abilities to move through that habitat efficiently to both gather food and avoid predators. As a result, over time, the body forms not suited to efficient movement in water were eliminated. Both the fish and whale have similar body forms. The body is torpedo-shaped, and the fins and tail are used as broad paddles for locomotion and orientation.

   The crocodile, bird, human, and whale are all homologous with regard to their pentadactyl limb structure. Although their specific structure is modified from species to species, each species has one upper limb bone, two lower limb bones, and five digits or phalanges (fingers or toes).

4. In recent years, DNA sequence analysis has been used in developing phylogenetic relationships among organisms.

   a. What type of DNA has been used most commonly in this analysis? Why was this type chosen over others?

      The genes for the small subunit ribosomal RNA molecule tend to change relatively slowly. As a result, they are used to determine relationships among groups of organisms that are not closely related. When scientists examine closely related groups, they tend to use mitochondrial DNA instead. Mitochondrial DNA mutates at a faster rate and is therefore more likely to provide evidence of more recent divergences or evolutionary changes that occur among closely related species.

   b. The phylogenies developed using DNA sequence analysis may differ from those constructed using morphology and physiology. How do scientists know which method is more correct?

      If the mechanisms used to develop competing phylogenies are both valid, there is no easy way to know which is correct. As a result, until more data become available, scientists may fuse the different results and produce a reconciled phylogeny.

5. Based on DNA sequence analysis three major domains of life have been proposed What are the three major domains of life? What sets of characteristics place organisms into one domain versus another?

Major domains of life	Key characteristics For a more complete list, see Table 27.2.
Bacteria	Bacteria display the prokaryote cell structure. Bacteria have a circular chromosome. Bacterial cell walls contain peptidoglycan. All bacterial species use the same type of RNA polymerase. Bacteria use formyl methionine as their initiator amino acid to start protein synthesis.
Archaea	Archaea display the prokaryote cell structure. Archaea have a circular chromosome. Archaeal cell walls do not contain peptidoglycan. Several types of RNA polymerase can be found among the different archaeal species. Archaea use methionine as the initiator amino acid in translation.
Eukarya	Eukaryotes have the eukaryotic cell structure, which includes a double-membrane-bound nucleus and membrane-bound organelles. Eukaryotes have linear chromosomes. Eukaryotic cell walls (for example, around plant cells) do not contain peptidoglycan. Methionine is the initiator amino acid in translation.

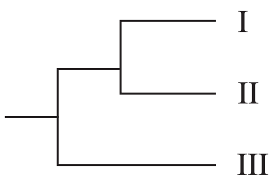
Activity 26.2 What is parsimony analysis?

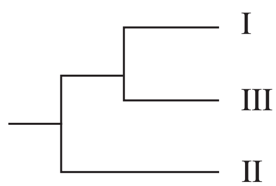
To determine relatedness among species, parsimony analysis is often used. In Figure 26.15 of *Campbell Biology*, 9th edition, parsimony analysis is applied to matched DNA sequences from three species of birds. The same type of analysis can be applied to morphological and developmental characteristics of species. Review Figure 26.15 and the parsimony method used. Then conduct your own parsimony analysis using the morphological characteristics of these birds in the table below.

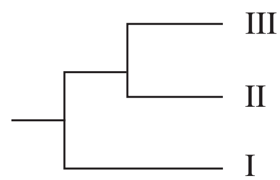
1. Begin by recording in the table below the morphological characteristics of the three bird species in Figure 26.15.

2. On the three possible phylogenies for these species (below the table) indicate the number of changes that must have occurred for each of the proposed phylogenies to be correct.

Traits	A	B	C	D	E
Species	Eye ring (light/dark)	Red bar on breast (yes/no)	Red wing bar (yes/no)	Light bar on tail tip (yes/no)	Beak shape (curved/point)
I	D	N	N	Y	P
II	L	N	Y	N	C
III	L	Y	N	N	P
Ancestral	D	N	Y	N	C







3. Based on your analysis, which of the phylogenies is most parsimonious? How does this result compare to the result given in Figure 26.15?

   Using the characteristics in the table, the second proposed phylogeny is most parsimonious. This required six changes in morphology where the first required eight and the third required seven.

   In Figure 26.15, the first proposed phylogeny was most parsimonious.

4. Which of the proposed phylogenies (the one you developed or the one in Figure 26.15) is more correct? Explain your answer.

   Each is equally correct for the data used. Keep in mind that any analysis is only as good as the data used. In both cases, only a few characteristics/bases were used. In reality, many more characteristics/bases are used to make inferences about phylogenetic relationships.

   While some phylogenies based on analyses of DNA sequence data agree with those based on morphological and behavioral characteristics, in others there is disagreement. Because such analyses are based on comparison of a limited number of genes, scientists are cautious in declaring one more correct than the other. Rather, they will state the differences and what these may imply about our previous ideas. Scientists will seldom make definitive statements about phylogenies based on DNA sequence analysis until a significant amount of research on additional gene sequences is shown to support the findings.

Activity 26.3 Put yourself in the professor's shoes: What questions would you ask?

One of the best ways to study for an exam is to put yourself in the professor's shoes. For example, ask yourself: What questions would I ask about the material if I were Professor __________. Asking and answering such questions are good practice for taking the actual exam. They also help you to better understand and organize the major ideas and concepts you have studied.

Write three exam questions designed to test how well a student understands the major concepts in Chapters 22–26. Indicate the correct answer to each question and also tell the reason why each alternative answer is incorrect. Your questions should be of the following types:

I. Problem solving or application of a concept or principle to a problem

For example: The little-known hypothetical organism *Skyscra parius* is a long-necked animal that feeds on the leaves of Australian trees that grow to heights of 30 feet. Being a hooved animal, *S. parius* cannot climb trees, so it feeds much like modern-day giraffes do. Fossil evidence indicates that the ancestors of *S. parius* had fairly short necks. Read the arguments presented below. For each, indicate whether or not the factors described could have affected neck length or tree height over the course of evolution of *S. parius*. [A = factors described could have affected neck length; B = factors described probably did not affect neck length]

A 1. *S. parius* ancestors likely demonstrated significant variation in neck length, with some having shorter necks and others having longer necks.

B 2. When first born, juveniles of *S. parius* were much shorter than adults, so they were not able to compete successfully with adults that had longer necks.

A 3. Female *S. parius* preferentially mate with longer-necked males.

II. Translation: the ability to recognize concepts restated in a different form or to restate concepts in a different form

For example: In what ways are the structure and function of the angiosperm seed and the amniotic egg (in this example, the chicken's egg) similar? In what ways are they different?

T/F 1. Both the angiosperm seed and the chicken's egg contain stored food for the early development of the embryo.

T/F 2. When released from the plant or laid by the chicken, both the angiosperm seed and the chicken's egg contain a partially developed diploid embryo/offspring generation.

T/F 3. The seed coat of the seed and the shell of the egg help prevent desiccation (water loss).

T/F 4. Seeds may remain dormant and viable for hundreds of years; the same is true of chicken eggs.

Write your exam questions in the spaces provided.

Exam Question 1:

Answer:

Exam Question 2:

Answer:

Exam Question 3:

Answer: