

# 17 The Tree of Life

## KEY CONCEPTS

### 17.1 The Linnaean System of Classification

Organisms can be classified based on physical similarities.

### 17.2 Classification Based on Evolutionary Relationships

Modern classification is based on evolutionary relationships.

### 17.3 Molecular Clocks

Molecular clocks provide clues to evolutionary history.

### 17.4 Domains and Kingdoms

The current tree of life has three domains.

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## How would you classify this organism?

### Connecting CONCEPTS

**P**angolins, native to Africa and Asia, are not closely related to any other living mammals. Their backs and tails are covered with large scales similar in arrangement to dinosaur bone plates. Pangolins do not have teeth. Instead, they have an organ similar to a bird's gizzard. Due to these unique traits, pangolins are classified into their own group within class Mammalia.



**Evolution** The pangolin's long snout and tongue, sharp claws for digging, and the absence of teeth are all adaptations to an ant-eating lifestyle. Anteaters and armadillos have similar traits. However, these animals are not closely related. Instead, pangolins, anteaters, and armadillos display convergent evolution. Their similar characteristics arose independently as natural selection acted upon species with similar diets.



# 17.1

## The Linnaean System of Classification

**KEY CONCEPT** Organisms can be classified based on physical similarities.

### ▶ MAIN IDEAS

- Linnaeus developed the scientific naming system still used today.
- Linnaeus' classification system has seven levels.
- The Linnaean classification system has limitations.

### VOCABULARY

**taxonomy**, p. 518  
**taxon**, p. 518  
**binomial nomenclature**, p. 519  
**genus**, p. 519

**Review**  
species



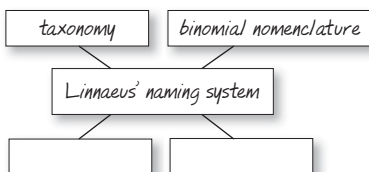
**Connect** The pangolin shown on the previous page may not look like any other animal that you are familiar with. However, scientists classify pangolins as mammals—the same group of animals that includes dogs, cats, mice, and humans. All female mammals have the ability to produce milk. Unlike pangolins, most mammals have hair. Scientists use key characteristics such as these to classify all living things.

### ▶ MAIN IDEA

**Linnaeus developed the scientific naming system still used today.**

### TAKING NOTES

Use a main idea web to take notes about the Linnaean system of classification.



### VOCABULARY

*Taxonomy* comes from the Greek *taxis*, which means “arrangement,” and *nomie*, which means “method.”

Before Swedish botanist Carolus Linnaeus introduced his scientific naming system, naturalists named newly discovered organisms however they wanted. In fact, they often named organisms after themselves. Because they had no agreed-upon way to name living things, it was difficult for naturalists to talk about their findings with one another. This all changed in the 1750s, when Linnaeus devised a system that standardized the way organisms are classified and named.

### Taxonomy

**Taxonomy** is the science of naming and classifying organisms. Taxonomy gives scientists a standard way to refer to species and organize the diversity of living things. Linnaean taxonomy classifies organisms based on their physical and structural similarities. Organisms are placed into different levels in a hierarchy—a multilevel scale in which each level is “nested” in the next-higher level. In other words, each level is included in a larger, more general level, which in turn is included in an even larger, more general level.

A group of organisms in a classification system is called a **taxon** (plural, *taxa*). The basic taxon in the Linnaean system is the species. In this system, species are most commonly defined as a group of organisms that can breed and produce offspring that can reproduce. Linnaeus' system gives each species a scientific name. With few changes, this method of naming is still used today.

## Scientific Names

**Binomial nomenclature** (by-NOH-mee-uhl NOH-muhn-KLAY-chuhr) is a system that gives each species a two-part scientific name using Latin words.

The first part of the name is the genus.

A **genus** (plural, *genera*) includes one or more physically similar species that are thought to be closely related. For example, the genus *Quercus* includes more than 500 species of oak trees. Genus names are always capitalized. They are written in italics or underlined.

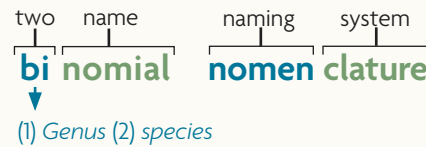
The second part of the name is the species descriptor. It can refer to a trait of the species, the scientist who first described it, or its native location. Like the genus, the species descriptor is written in italics or underlined. However, it is always lowercase. The species descriptor is never written alone because, as **FIGURE 17.1** shows, the same word may be used in different genera. *Quercus alba* is the scientific name for white oak trees (*alba* means “white”), but *Tyto alba* is the scientific name for barn owls.

You may wonder why biologists use scientific names. It may seem easier to use terms such as *white oak* instead of remembering two-part Latin names. However, scientific names are helpful in a number of ways. First, genera such as *Quercus* contain hundreds of species. Many of these species have very similar common names. Scientific names allow scientists to talk about particular species without confusion. Also, remember that biology is studied all over the world. One species may have many different common names. In fact, a species may have several different common names within a single country. *Armadillidium vulgare* is the scientific name for pill bugs. However, this species is also called roly-poly, sow bug, and potato bug. Scientific names allow scientists around the world to communicate clearly about living things.

**Contrast** Describe the difference between a genus and a species.

### VISUAL VOCAB

**Binomial nomenclature** is a standard naming system that gives each species a two-part name using Latin words.



**FIGURE 17.1** The white oak (*Quercus alba*) and the barn owl (*Tyto alba*) belong to different genera. The species parts of their scientific names are both *alba*, meaning “white.”



**FIGURE 17.2** SCIENTIFIC AND COMMON NAMES

COMMON NAMES	SCIENTIFIC NAME	
	Genus	species
Roly-poly, pill bug, sow bug, potato bug	<i>Armadillidium</i>	<i>vulgare</i>
Dandelion, Irish daisy, lion's tooth	<i>Taraxacum</i>	<i>officinale</i>
House sparrow, English sparrow	<i>Passer</i>	<i>domesticus</i>
Mountain lion, cougar, puma	<i>Puma</i>	<i>concolor</i>
Red maple, scarlet maple, swamp maple	<i>Acer</i>	<i>rubrum</i>

**▶ MAIN IDEA**

## Linnaeus' classification system has seven levels.

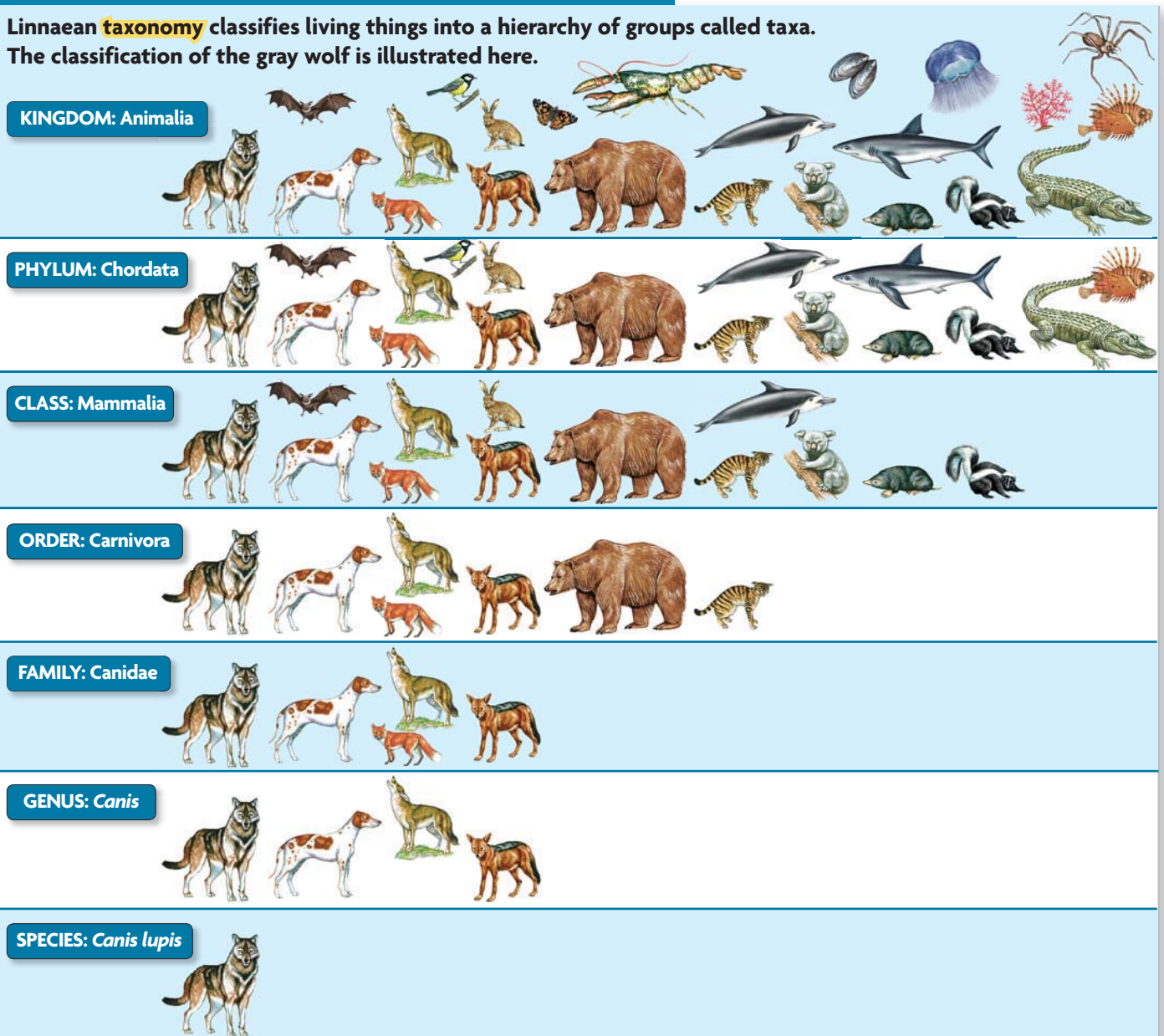
### Connecting CONCEPTS

**Domains** The tree of life has been updated since Linnaeus' time. Scientists now classify organisms into an even broader category, called the domain, above the kingdom level. You will learn more about domains and kingdoms in Section 17.4.

The Linnaean system of classification has seven levels, or taxa. From the most general to the most specific, these levels are kingdom, phylum (the term *division* is often used instead of *phylum* for plants and fungi), class, order, family, genus, and species. Each level in Linnaeus' system is nested, or included, in the level above it. A kingdom contains one or more phyla, a phylum contains one or more classes, and so forth. The classification of the gray wolf, *Canis lupus*, is shown in FIGURE 17.3. Moving down, the levels represent taxa that become more and more specific, until you reach the species level at the bottom.

**FIGURE 17.3** The Linnaean Classification System

Linnaean **taxonomy** classifies living things into a hierarchy of groups called taxa. The classification of the gray wolf is illustrated here.



**Analyze** Based on the taxonomy shown here, are bats or cats more closely related to gray wolves?



The top level represents all of the species in kingdom Animalia. As you move down, the levels show examples of species from phylum Chordata, class Mammalia, order Carnivora, family Canidae, genus *Canis*, and the species *Canis lupis*. Each level is included in all of the more general levels above it.

Notice that gray wolves are in the same genus, *Canis*, as dogs and coyotes. Because the Linnaean system is a nested hierarchy, wolves, dogs, and coyotes also belong to the same family, order, class, phylum, and kingdom. Foxes do not belong to the *Canis* genus, but they do belong to Canidae—the same family as wolves, dogs, and coyotes. Therefore, foxes also belong to the same order, class, phylum, and kingdom as wolves, dogs, and coyotes.

**Apply** If two species belong to the same order, what other levels in the Linnaean system must they have in common?

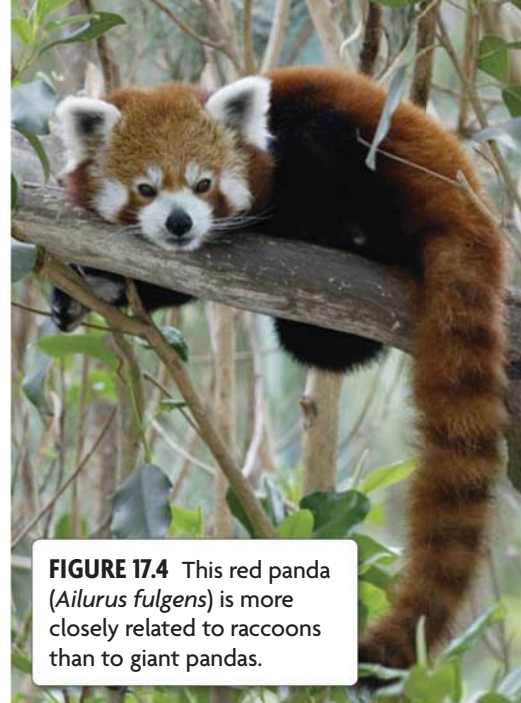
### ▶ MAIN IDEA

## The Linnaean classification system has limitations.

Linnaeus created his classification system before technology allowed us to study organisms at the molecular level. His system focuses on physical similarities alone. Remember that physical similarities between two species are not always a result of the species' being closely related. Unrelated species can evolve similar traits through convergent evolution. Linnaeus' system does not account for similarities that evolved this way. So today, scientists use genetic research to help classify living things. Genetic similarities between two species are more likely than physical similarities to be due to a common ancestor.

For example, the giant panda and the raccoon have similar ears and snouts. Because of these similarities, they have been placed in the same family in the Linnaean system. However, molecular biologists have found that the giant panda is more closely related to members of the bear family than it is to raccoons. Furthermore, the red panda, shown in **FIGURE 17.4**, is more closely related to the raccoon than to the giant panda.

**Infer** Why is the common name *red panda* misleading in terms of classification based on relatedness?



**FIGURE 17.4** This red panda (*Ailurus fulgens*) is more closely related to raccoons than to giant pandas.

### Connecting CONCEPTS

**Classification** Refer to the Appendix for a complete list of the kingdoms and their phyla.



To learn more about taxonomy, go to [scilinks.org](http://scilinks.org).  
Keycode: MLB017

## 17.1 ASSESSMENT



### REVIEWING ▶ MAIN IDEAS

1. What is **binomial nomenclature**?
2. Name each **taxon** in the Linnaean system of classification, from most general to most specific.
3. What are some limitations of the Linnaean classification system?

### CRITICAL THINKING

4. **Compare** How is a scientific name similar to an address that includes city and state?
5. **Apply** Which two species are more closely related: *Ursus maritimus*, *Ursus americanus*, or *Bufo americanus*? Explain your answer.

### Connecting CONCEPTS

6. **History of Science** During his voyages, Darwin collected thousands of organisms, which he classified using the Linnaean classification system. How did this system help him share his findings with other naturalists?

**MATERIAL**

set of or photographs  
of limpet shells

**PROCESS SKILLS**

- Observing
- Identifying
- Classifying

## Creating a Dichotomous Key for Limpet Shells

Limpets are marine invertebrates found along rocky shorelines around the world. The flattened shape of a limpet's shell allows it to withstand the impact of waves, and its muscular foot allows it to cling tightly to rocks. Although biologists today classify limpets by using traits of the entire organism, for this activity you will construct a dichotomous key based on shell characteristics.

Dichotomous keys are used to identify objects or organisms that have already been described by another scientist. As its name implies (*di-* means “two”), a dichotomous key is made up of paired statements. Each pair of statements divides the objects to be classified into two categories. This means that each object must fit into one category or the other, but not both. At the right is a simple example of a dichotomous key that identifies five common beans. As you proceed from step to step, the classification is narrowed down until all five beans are identified.

### SAMPLE DICHOTOMOUS KEY FOR BEANS

- 1.a. If the bean is round ..... it is a garbanzo bean.
  - 1.b. If the bean is oblong ..... go to step 2.
- 
- 2.a. If the bean is white ..... it is a white northern bean.
  - 2.b. If the bean is dark-colored ..... go to step 3.
- 
- 3.a. If the bean is a solid color ..... go to step 4.
  - 3.b. If the bean is speckled ..... it is a pinto bean.
- 
- 4.a. If the bean is black ..... it is a black bean.
  - 4.b. If the bean is reddish-brown .... it is a kidney bean.

**PROBLEM** What characteristics can you use to make a dichotomous key for limpet shells?

**PROCEDURE**

1. Identify some characteristics of each limpet shell. Characteristics may include margin (edge) variation, shape, color, and features on the shell.
2. Construct a dichotomous key, using the above sample for beans as a guide. Start with a general characteristic that separates your limpets into two groups. (**Example:** Keyhole limpets have a hole at the highest point of their shell; true limpets do not.)
3. Continue making paired statements that become more detailed.
  - Each pair of statements must contain only two choices, and these choices must refer to the same characteristic. (**Example:** Do not compare size and color in the same pair of statements.) Every limpet that has not yet been identified must fit one of the two choices.
  - Do not use vague terms such as *big* and *little*. Be as specific as possible.
  - Each statement must either identify a limpet or lead to another step in the key.
4. Trade dichotomous keys with another student or group in your class. Check to make sure you can identify each limpet using your classmates' key.



*Cellana testudinaria*  
Common turtle limpet



*Collisella striata*  
Striate limpet



*Patelloida saccharina*  
Sugar limpet



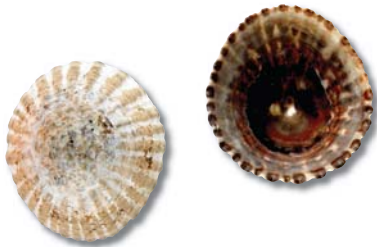
*Fissurella nodosa*  
Knobbed keyhole limpet



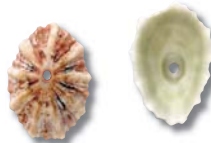
*Fissurella maxima*  
Giant keyhole limpet



*Cellana radiata*  
Rayed limpet



*Nacella deaurata*  
Patagonian copper limpet



*Fissurella barbadensis*  
Barbados keyhole limpet



*Megathura crenulata*  
Great keyhole limpet

## ANALYZE AND CONCLUDE

- 1. Summarize** How did you organize the limpet shells?
- 2. Analyze** What different categories did other groups use to organize the shells?
- 3. Identify Problems** What problems arose as you constructed your key?
- 4. Infer** If you were given the actual shells, what additional characteristics could you have used to make your key?
- 5. Apply** Two outcomes are said to be mutually exclusive if they cannot both occur at the same time. For example, heads and tails are mutually exclusive outcomes of flipping a coin. Why is it important that the paired statements in a dichotomous key describe mutually exclusive characteristics?



# 17.2

## Classification Based on Evolutionary Relationships

**KEY CONCEPT** Modern classification is based on evolutionary relationships.

### ▶ MAIN IDEAS

- Cladistics is classification based on common ancestry.
- Molecular evidence reveals species' relatedness.

### VOCABULARY

**phylogeny**, p. 524  
**cladistics**, p. 525  
**cladogram**, p. 525

**derived character**, p. 525

**Review**  
taxon



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**Connect** If you've ever observed bats in a zoo or in the night sky, you've likely noticed that they have several features in common with birds, such as wings. However, bats are actually more closely related to rodents and primates than they are to birds. Today, scientists agree that species should be classified based on evolutionary relationships rather than just physical similarities.

### ▶ MAIN IDEA

## Cladistics is classification based on common ancestry.

Similar traits between species are often the result of sharing a common ancestor, such as the ancestor shared by dogs and wolves. However, scientists now know that similar traits, such as the wings of bats and birds, can also evolve in species that are adapting to similar environmental conditions. As you read in Chapter 11, this process is called convergent evolution.

To classify species according to how they are related, scientists must look at more than just physical traits. Modern classification is based on figuring out evolutionary relationships using evidence from living species, the fossil record, and molecular data. The evolutionary history for a group of species is called a **phylogeny** (fy-LAHJ-uh-nee).

Phylogenies can be shown as branching tree diagrams. In a way, these diagrams are like family trees. The branches of a family tree show how family members are related to each other. The branches of an evolutionary tree show how different groups of species are related to each other.

**FIGURE 17.5** The glyptodon (*Glyptotherium arizonae*), illustrated here, was the size of a small car and lived more than 10,000 years ago. It is the common ancestor to about 20 modern armadillo species, including the nine-banded armadillo (*Dasypus novemcinctus*).

Glyptodon



Armadillo



## Cladistics

The most common method used to make evolutionary trees is called cladistics. **Cladistics** (kluh-DIHS-tihks) is classification based on common ancestry. The goal of cladistics is to place species in the order in which they descended from a common ancestor. A **cladogram** is an evolutionary tree that proposes how species may be related to each other through common ancestors.

At the root of the words *cladistics* and *cladogram* is the word *clade*. A clade is a group of species that shares a common ancestor. For example, the glyptodon in **FIGURE 17.5** is the common ancestor of about 20 modern species of armadillos. Together, the glyptodon and all of its descendants form a clade.

Through the course of evolution, certain traits change in some species of a clade but stay the same in other species. Therefore, each species in a clade has some traits that have not changed from its ancestors, such as the similar shells of glyptodons and modern armadillos. However, each species also has traits that have changed over evolutionary time.

The traits that can be used to figure out evolutionary relationships among a group of species are those that are shared by some species but are not present in others. These traits are called **derived characters**. As you will soon see, cladograms are made by figuring out which derived characters are shared by which species. The more closely related species are, the more derived characters they will share. A group of species that shares no derived characters with the other groups being studied is called an outgroup.

### VOCABULARY

The word *derived* comes from the Latin *de-*, meaning “from,” and *rivus*, meaning “stream.” Therefore, *derived* refers to something that has “flowed” from a source. The term *derived characters* refers to characters that have evolved in a species since sharing a common ancestor.

## QUICK LAB CLASSIFYING

### Construct a Cladogram

You can think of a cladogram as an evolutionary family tree in which things that are more closely related share more characteristics. As an analogy, processes that have evolved due to new technologies can be organized using cladistics. In this lab, you will fill in a cladogram for methods of transportation.

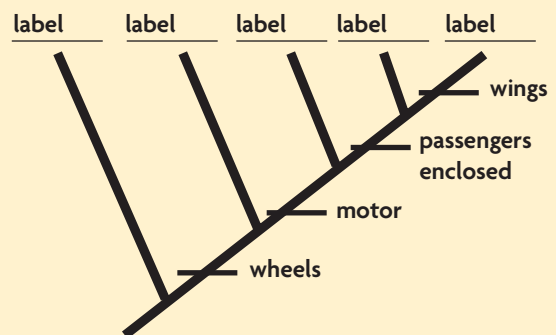
**PROBLEM** How can methods of transportation be organized using a cladogram?

#### PROCEDURE

1. Copy the cladogram axes on the right into your notebook.
2. Think about the characteristics of the following methods of transportation: bicycle, car, motorcycle, airplane, and on foot.
3. Complete your cladogram by filling in each method of transportation listed in step 2 on the appropriate line at the top.

#### ANALYZE AND CONCLUDE

1. **Identify** What “derived characters” are used in this cladogram?
2. **Analyze** Which mode of transportation may be considered an “outgroup”—a group that has none of the characteristics labeled on the cladogram?
3. **Connect** A species that has evolved a new trait is not better than a species without that trait. Each species is just adapted to a certain way of life. When might riding a bike have an advantage over flying in an airplane?





## Interpreting a Cladogram

The main features of a cladogram are shown in **FIGURE 17.6**. Tetrapods are vertebrates that have four limbs—amphibians, reptiles, birds, and mammals. Some tetrapods, such as snakes and marine mammals, no longer have the four limbs that their known ancestors had. However, they are still members of the tetrapoda clade because they share a common ancestor.

**Derived characters** In a cladogram, groups of species are placed in order by the derived characters that have added up in their lineage over time. This order is hypothesized to be the order in which they descended from their common ancestor. Derived characters are shown as hash marks between the branches of the cladogram. All species above a hash mark share the derived character it represents.

**Nodes** Each place where a branch splits is called a node. There are five nodes on the tetrapod cladogram. The first node is where the amphibian branch splits off from the rest of the cladogram. Nodes represent the most recent common ancestor shared by a clade. Therefore, the first node of the tetrapod cladogram represents a common ancestor for the whole tetrapod clade.

**Identifying clades** You can identify clades by using the “snip rule.” Whenever you “snip” a branch under a node, a clade falls off. In this cladogram, if you were to “snip” below the node where turtles and tortoises branch off, you would be left with the reptilia clade. This clade includes turtles and tortoises, lizards and snakes, crocodiles and alligators, and birds. As you can see, each clade is nested within the clade that forms just before it. There are five clades in the tetrapod cladogram. Crocodiles, alligators, and birds belong to all five clades.

### Connecting CONCEPTS

**Animals** The amniotic sac is a key characteristic of amniotes, animals that are fully adapted for life on land. The amniotic sac allows amniotes to reproduce on land; non-amniotes must return to the water to reproduce. You will learn much more about amniotes in **Chapter 26**.

- 1 All of the organisms in this cladogram belong to the tetrapoda clade (brown). They all share the derived character of four limbs.
- 2 An embryo protected by a fluid filled sac is a derived character for all organisms in the amniota clade (blue). Because amphibians do not produce an amniotic sac, the amphibian branch splits off from rest of the branches before the mark that represents this trait.
- 3 Organisms in the reptilia clade (yellow) have a common ancestor that had four legs, produced protected eggs, and had a skull with openings behind the eyes. The third node in the cladogram represents this common ancestor. Because mammal skulls do not have these openings, they are not part of the reptilia clade.
- 4 Organisms in the diapsida clade (green) have openings in the side of the skull. The skulls of turtles and tortoises do not have these openings, so they are not part of the diapsida clade.
- 5 Lizards and snakes branch off of the cladogram next. Their skulls do not have certain openings in the jaw that are found in crocodiles, alligators, and birds. This is the derived character shared by all organisms in the archosauria clade (pink). Feathers and toothless beaks separate crocodiles and alligators from birds within the archosauria clade.

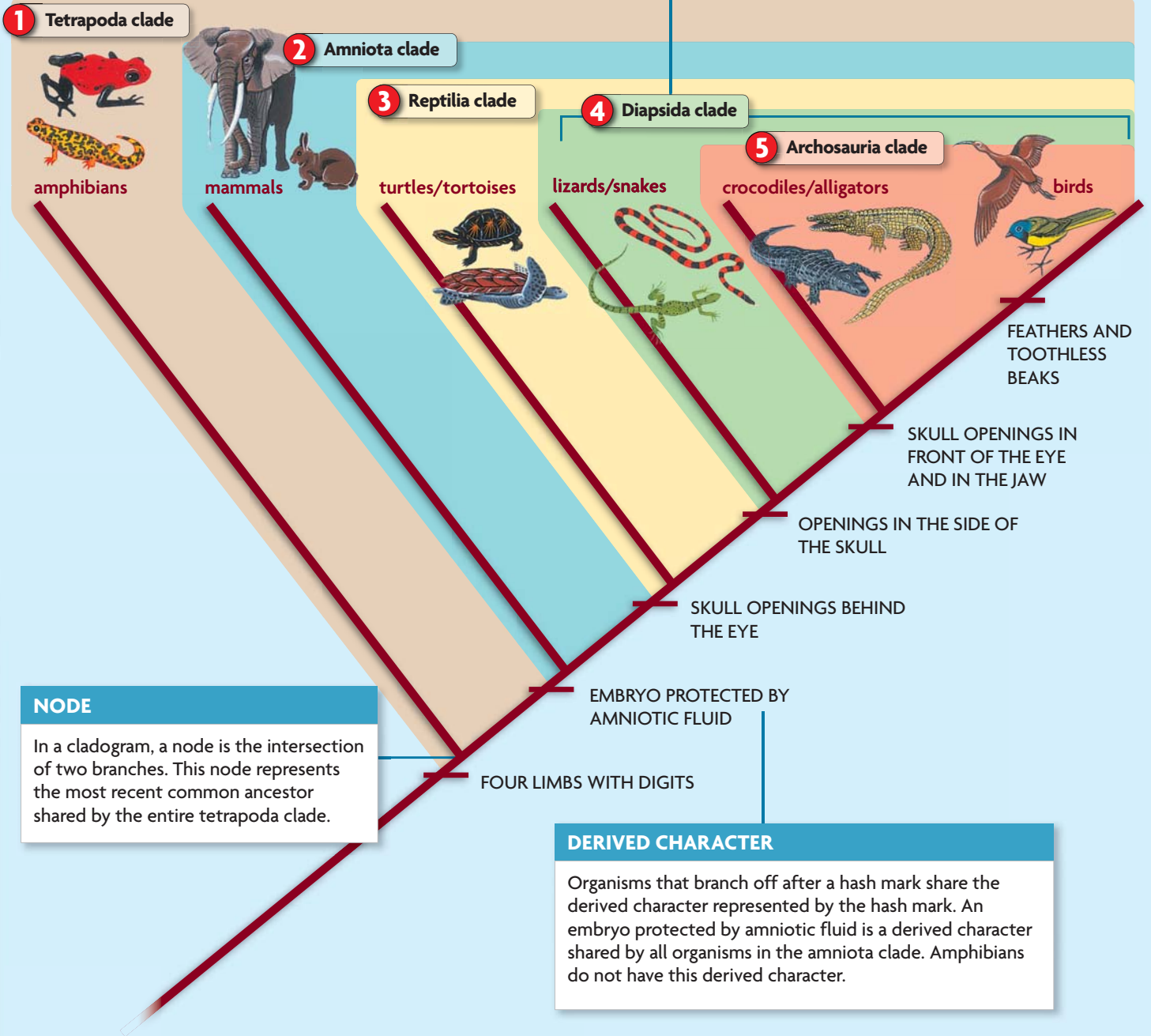
**Contrast** What is the difference between a clade and a taxon?

## FIGURE 17.6 Cladogram for Tetrapods

A **cladogram** presents hypothesized evolutionary relationships among a group of species based on common ancestry and derived characters.

### CLADE

A clade is a group of organisms that share certain traits derived from a common ancestor. In this cladogram, a clade looks like the letter V, including all the branches that extend from the right end of the V. The diapsida clade includes lizards and snakes, crocodiles and alligators, and birds.



### CRITICAL VIEWING

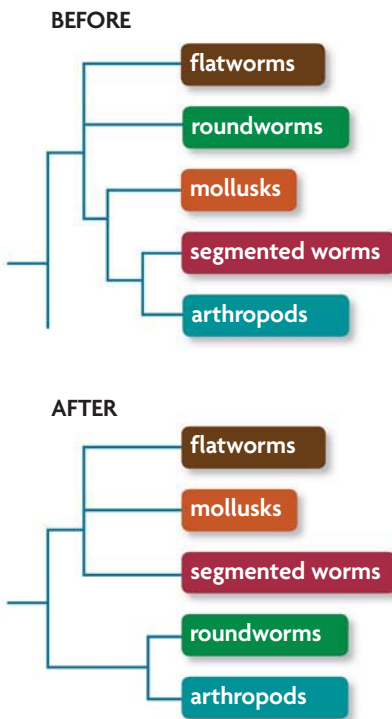
Which groups of animals belong to the amniota clade? Which belong to the archosauria clade?



## ▶ MAIN IDEA

# Molecular evidence reveals species' relatedness.

**FIGURE 17.7** Based on structural similarities, scientists previously classified segmented worms and arthropods as sister taxa. The discovery of a hormone found only in roundworms and arthropods has led scientists to propose a new phylogeny for these taxa.



You have learned how physical characteristics, such as protected eggs, can be used to build evolutionary trees. In this example, a protected egg is a derived character shared by all species in the amniota clade. Today, new technology allows biologists to compare groups of species at the molecular level. Molecular evidence, such as a certain DNA sequence, can be used as a derived character if it is shared among certain groups of species.

In many cases, molecular data agree with classification based on physical similarities. In other cases, this type of data leads scientists to classify species in a different way. An evolutionary tree is always a work in progress. With new evidence, trees can be changed to show how species are likely related.

For example, based on physical traits, most biologists considered segmented worms and arthropods (crabs, lobsters, insects, and their relatives) to be more closely related to each other than to any other group of species. However, the discovery of a certain hormone has provided new information. This hormone affects molting, and it is found only in arthropods and roundworms. Biologists have now proposed a new evolutionary tree, shown in **FIGURE 17.7**. In this tree, roundworms and arthropods are grouped closer together. This tree is based on the idea that the hormone evolved only once, in an ancestor shared by arthropods and roundworms.

Proteins and genes are also used to help learn about evolutionary relationships. In fact, DNA is considered by many scientists to have the “last word” when figuring out how related two species are to each other. After all, any traits that can get passed on to offspring must have a genetic basis. The more similar to each other the genes of two species are, the more closely related the species are likely to be. In the next section, you will see how DNA and protein sequences can be used to measure evolutionary time itself.

**Analyze** Why does DNA often have the “last word” when scientists are constructing evolutionary relationships?

## 17.2 ASSESSMENT



### REVIEWING ▶ MAIN IDEAS

1. What is the goal of **cladistics**?
2. What role does molecular evidence play in determining how closely two species are related to each other?

### CRITICAL THINKING

3. **Compare and Contrast** Discuss some similarities and differences between the Linnaean system of classification and cladistics.
4. **Analyze** Describe the relationship between clades and shared **derived characters**.

### Connecting CONCEPTS

5. **Scientific Method** Recall that a hypothesis is a possible explanation for a set of observations. Why are **cladograms** considered to be hypotheses?

## Amino Acid Differences Among Species

Researchers rarely publish raw data by itself. Instead, data are usually analyzed in some way. This is because certain types of observations and patterns can be made clearer when data are presented in different ways. For example, data that show change or difference may be best represented as percentage difference.

### EXAMPLE

Cytochrome C is a protein that functions in cellular respiration. A sequence of 104 amino acids make up the cytochrome C protein. Scientists have compared this sequence of amino acids in humans with the sequence in a variety of other species. The number of amino acid differences between cytochrome C in humans and in other species has been used to help determine species' relatedness.

Look at the data table at the right. Notice that the cytochrome C of chimpanzees most closely resembles that of humans, while the cytochrome C of lampreys, a type of jawless fish, has more differences. To more clearly represent how different they are, these data can be transformed into percentage differences. To calculate the percentage difference of cytochrome C between humans and lampreys, follow this procedure.

1. First, transform the number of amino acid differences into a fraction of the total number of amino acids that make up the cytochrome C protein (104).

$$\frac{20 \text{ differences}}{104 \text{ total amino acids}}$$

2. Next, perform the division.

$$20 \div 104 = 0.1923$$

3. Transform this number into a percentage by multiplying by 100.

$$0.1923 \times 100 = 19.23\% \text{ difference}$$



Lampreys such as this one are jawless fish with a round sucking mouth.

**TABLE 1. AMINO ACID DIFFERENCES COMPARED WITH HUMAN CYTOCHROME C**

Organism	Number of Differences
Chimpanzee	0
Rhesus monkey	1
Whale	10
Turtle	15
Bullfrog	18
Lamprey	20
Tuna	21

Source: M. Dayhoff, *Atlas of Protein Sequence and Structure*.

### TRANSFORM DATA

1. **Calculate** Use the procedure outlined above to find percentage differences in cytochrome C between humans and the following animals: tunas, bullfrogs, turtles, whales, rhesus monkeys, and chimpanzees.
2. **Apply** What do the transformed data suggest about how related each type of animal is to humans?
3. **Infer** What percentage of the human cytochrome C protein is the same as that of whales?  
 Hint: 100 percent – percentage difference = percentage similarity.



# 17.3

## Molecular Clocks

**KEY CONCEPT** Molecular clocks provide clues to evolutionary history.

### ▶ MAIN IDEAS

- Molecular clocks use mutations to estimate evolutionary time.
- Mitochondrial DNA and ribosomal RNA provide two types of molecular clocks.

### VOCABULARY

**molecular clock**, p. 530  
**mitochondrial DNA**, p. 532  
**ribosomal RNA**, p. 532

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**CLASSZONE.COM**

**Connect** Have you ever played the game telephone? One person whispers a message to another person, who repeats it to yet another person, and so on. By the time it reaches the final person, the message has changed. In a similar way, DNA changes slightly each time it is passed from generation to generation.

### ▶ MAIN IDEA

## Molecular clocks use mutations to estimate evolutionary time.

In the early 1960s, biochemists Linus Pauling and Emile Zuckerkandl proposed a new way to measure evolutionary time. They compared the amino acid sequences of hemoglobin from a wide range of species. Their findings show that the more distantly related two species are, the more amino acid differences there are in their hemoglobin. Using this data, they were able to calculate a mutation rate for part of the hemoglobin protein.

### Connecting CONCEPTS

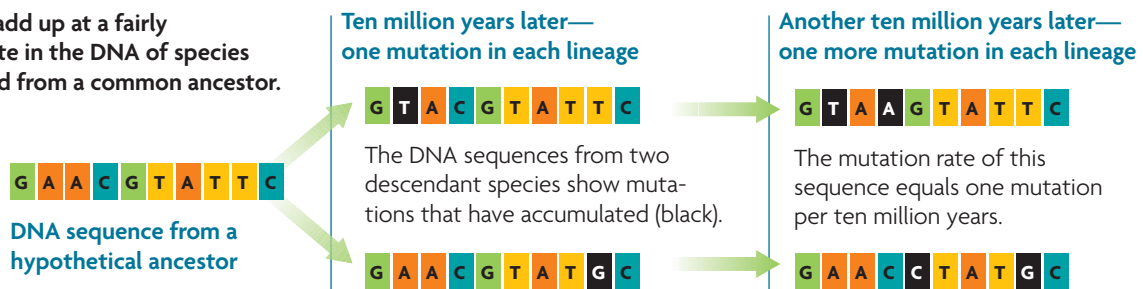
**Human Biology** Hemoglobin is an oxygen-carrying protein that is found in the blood cells of all vertebrates, including humans. You will learn more about hemoglobin in Chapter 30.

### Molecular Evolution

**Molecular clocks** are models that use mutation rates to measure evolutionary time. Recall that mutations are nucleotide substitutions in DNA, some of which cause amino acid substitutions in proteins. Pauling and Zuckerkandl found that mutations tend to add up at a constant rate for a group of related species. As shown in **FIGURE 17.8**, the rate of mutations is the “ticking” that powers a molecular clock. The more time that has passed since two species have diverged from a common ancestor, the more mutations will have built up in each lineage, and the more different the two species will be at the molecular level.

**FIGURE 17.8 MOLECULAR EVOLUTION**

Mutations add up at a fairly constant rate in the DNA of species that evolved from a common ancestor.



## Linking Molecular Data with Real Time

To estimate mutation rates, scientists must find links between molecular data and real time. Often this link comes from the timing of a geologic event that is known to have separated the species they are studying. If scientists know when the species began to diverge from a common ancestor, they can find the mutation rate for the molecule they are studying. For example, scientists know that marsupials of Australia and those of South America diverged about 200 million years ago, when these two continents split.

A link can also come from fossil evidence. Pauling and Zuckerkandl compared their molecular data with the first appearance of each type of organism in the fossil record. Using these dates, they confirmed that the number of amino acid differences increases with the evolutionary time between each group of species. The number of amino acid differences between human hemoglobin and the hemoglobin of several other types of organisms is shown in **FIGURE 17.9**. Human hemoglobin is most different from species that diverged earliest in evolutionary time.

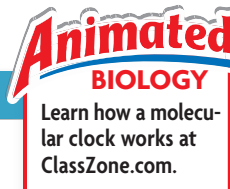
**Infer** Why is the hemoglobin of humans more different from that of sharks than that of birds?

**FIGURE 17.9 LINKING MOLECULAR AND FOSSIL DATA**

Animal species that evolved longer ago compared with humans have more amino acid differences in the beta chain of their hemoglobin.

ANIMAL	AMINO ACID DIFFERENCES COMPARED WITH HUMANS	APPEARANCE IN FOSSIL RECORD (millions of years ago)
Mouse	16	70
Horse	18	70
Bird	35	270
Frog	62	350
Shark	79	450

**Analyze** Which two animals in this table are least related to humans?



Frogs and humans have 62 differences in the beta chain of hemoglobin.

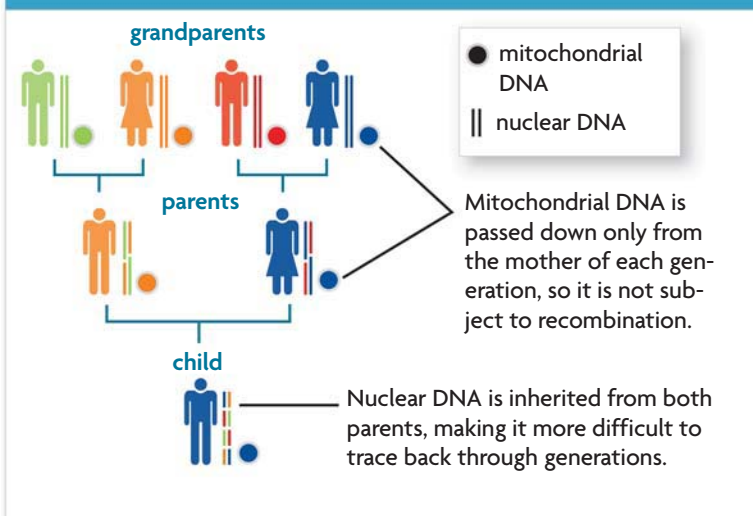
### MAIN IDEA

## Mitochondrial DNA and ribosomal RNA provide two types of molecular clocks.

Different molecules have different mutation rates. For example, some sequences of DNA accumulate mutations relatively quickly in a lineage, while others have very low mutation rates. Depending on how closely two species are related, scientists choose a molecule with an appropriate mutation rate to use as a molecular clock.



FIGURE 17.10 INHERITANCE OF MITOCHONDRIAL DNA



## Mitochondrial DNA

**Mitochondrial DNA** (mtDNA) is DNA found only in mitochondria, the energy factories of cells. The mutation rate of mtDNA is about ten times faster than that of nuclear DNA, which makes mtDNA a good molecular clock for closely related species. Furthermore, as shown in **FIGURE 17.10**, mtDNA is always inherited from the mother because the mitochondria in a sperm cell are lost after fertilization. This type of inheritance is different from that of nuclear DNA, which is a combination of DNA from both parents. Scientists use the fact that mtDNA is passed down unshuffled to trace mutations back through many generations in a single species. In fact, mutations in mtDNA have been used to study the migration routes of humans over the past 200,000 years.

### VOCABULARY

In this context, the word *conservative* means “resistant to change.” Because ribosomes play such a crucial role in cell function, even small changes can be very disruptive and damaging to the cell. Therefore, most mutations in rRNA do not accumulate within the genome.

## Ribosomal RNA

Ribosomes, the organelles that manufacture proteins in cells, contain **ribosomal RNA** (rRNA). Ribosomal RNA is useful for studying distantly related species, such as species that are in different kingdoms or phyla. When studying the relationships among species over longer time scales, it is best to use a molecule that has a lower mutation rate. Ribosomal RNA has conservative regions that accumulate mutations at a low rate relative to most DNA. Over long periods of geologic time, mutations that do build up in the rRNA of different lineages are relatively clear and can be compared. American microbiologist Carl Woese first used rRNA to establish that archaea diverged from the common ancestor they share with bacteria almost 4 billion years ago. As you will learn in the next section, these findings supported a restructuring of the tree of life at its highest level.

**Summarize** Why is rRNA useful for studying more distantly related species?

## 17.3 ASSESSMENT



### REVIEWING MAIN IDEAS

1. How are **molecular clocks** used to measure evolutionary time?
2. What are the benefits of **mitochondrial DNA** and **ribosomal RNA** as molecular clocks?

### CRITICAL THINKING

3. **Explain** How do rates of mutation “power” molecular clocks?
4. **Apply** What molecular clock might be useful to examine the evolutionary relationship between several phyla in the kingdom Plantae? Explain your answer.

### Connecting CONCEPTS

5. **History of Life** The theory of endosymbiosis explains how eukaryotic cells may have evolved from prokaryotic cells. According to this theory, explain why mitochondria have their own DNA, separate from nuclear DNA.

# 17.4

## Domains and Kingdoms

**KEY CONCEPT** The current tree of life has three domains.

### ▶ MAIN IDEAS

- Classification is always a work in progress.
- The three domains in the tree of life are Bacteria, Archaea, and Eukarya.

### VOCABULARY

- Bacteria**, p. 534
- Archaea**, p. 534
- Eukarya**, p. 534

### Review

prokaryote, eukaryote



REVIEW AT  
CLASSZONE.COM

**Connect** Have you ever swum in a pond? Every drop of pond water is teeming with single-celled organisms. At one time, scientists classified these organisms as either plants or animals. However, classification schemes change. Single-celled eukaryotes such as these pond dwellers now have a kingdom of their own.

### ▶ MAIN IDEA

## Classification is always a work in progress.

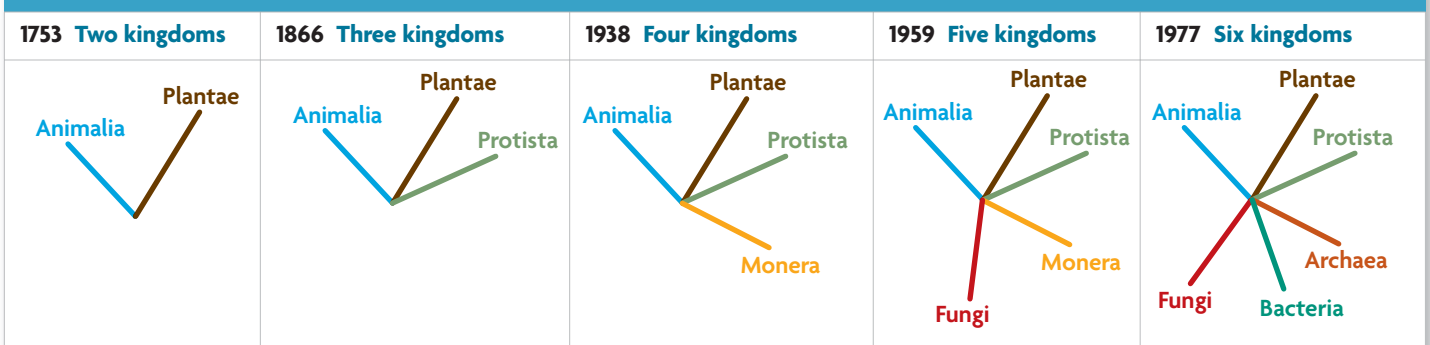
The tree of life is a model that shows the most current understanding of how living things are related. Some new discoveries confirm parts of the tree that were once based on similarities in form alone. But as **FIGURE 17.11** shows, new findings can also lead scientists to change how they classify certain organisms.

- The two-kingdom system was accepted by biologists until 1866, when German biologist Ernst Haeckel proposed moving all single-celled organisms to the kingdom Protista.
- In 1938, American biologist Herbert Copeland argued that the prokaryotes deserved their own kingdom, called Monera. Prokaryotes are single-celled organisms that do not have membrane-bound nuclei or organelles.
- In 1959, American ecologist Robert Whittaker proposed that because of how they feed, fungi should be placed into their own kingdom apart from plants. The kingdom Fungi includes molds and mushrooms.
- In 1977, rRNA research by Carl Woese revealed two genetically different groups of prokaryotes. His findings led scientists to split the kingdom Monera into two kingdoms, called Bacteria and Archaea.

### Connecting CONCEPTS

**Fungi** Fungi are heterotrophs that feed by absorbing dead organic materials from the environment. This is one characteristic that distinguishes fungi from plants, which are autotrophs, or organisms that make their own food. You will learn more about fungi in **Chapter 19**.

**FIGURE 17.11 HISTORY OF THE KINGDOM SYSTEM**



Woese's discovery did more than split the kingdom Monera. The two groups of prokaryotes that he studied have very different cell wall chemistry. In terms of genes, these two groups are more different from each other than animals are from plants, fungi, and protists. Based on these differences, Woese proposed that all life be divided into three domains. These domains are above the kingdom level.

**Analyze** Why did Woese propose classifying bacteria and archaea into separate domains, rather than just separate kingdoms?

**▶ MAIN IDEA**

## The three domains in the tree of life are Bacteria, Archaea, and Eukarya.

Most biologists now accept Woese's domain system. This system more clearly shows the great diversity of prokaryotes in the tree of life by dividing them into two domains. These domains are called Bacteria and Archaea. All eukaryotes are placed into a third domain, called Eukarya.

**TAKING NOTES**

Use a three-column chart to take notes about the three domains and six kingdoms in the modern classification of life.

Domain Name	Characteristics	Kingdoms Included

### Bacteria

The domain **Bacteria** includes single-celled prokaryotes in the kingdom Bacteria. The domain Bacteria is one of the largest groups of organisms on Earth. In fact, there are more bacteria in your mouth than there are people that have ever lived! Bacteria can be classified by many traits, such as their shape, their need for oxygen, and whether they cause disease.

### Archaea

Like bacteria, organisms in the domain **Archaea** (ahr-KEE-uh) are single-celled prokaryotes. However, the cell walls of archaea and bacteria are chemically different. Archaea, like those in **FIGURE 17.12**, are known for their ability to live in extreme environments, such as deep sea vents, hot geysers, Antarctic waters, and salt lakes. All archaea are classified in the kingdom Archaea.

### Eukarya

The domain **Eukarya** (yoo-KAR-ee-uh) is made up of all organisms with eukaryotic cells. Eukaryotic cells have a distinct nucleus and membrane-bound organelles. Eukarya may be single-celled, such as most protists. They can also be colonial, such as some algae, or multicellular, like you. The domain Eukarya includes the kingdoms Protista, Plantae, Fungi, and Animalia.

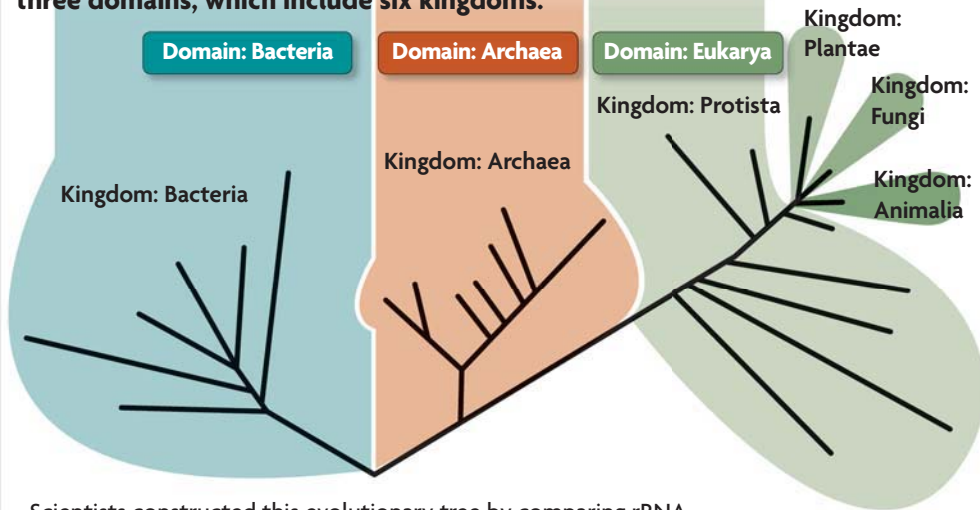


**FIGURE 17.12** This archaean species, *Pyrococcus furiosus*, can be found in undersea hot vents and in the sand surrounding sulfurous volcanoes. These organisms live without oxygen and can grow in temperatures higher than the boiling point of water. (colored SEM; magnification 6500×)



## FIGURE 17.13 Tree of Life

The most recent classification system divides life into three domains, which include six kingdoms.



Scientists constructed this evolutionary tree by comparing rRNA sequences from species in each of the six recognized kingdoms. The distances between branches are proportional to the number of differences in rRNA sequences among these species.

Source: C. Woese, *PNAS* 97:15.

### Connecting CONCEPTS

**Kingdoms and Phyla** See the Appendix for a detailed description of each kingdom and its phyla.

### Classifying Bacteria and Archaea

Some scientists think that bacteria and archaea have no true species. This is because many of these organisms transfer genes among themselves outside of typical reproduction. This sharing of genes blurs the lines between “species” as we define them in the Linnaean system. One study found that almost a quarter of the genes in the bacterium *Thermotoga maritima* are similar to archaean genes. Our understanding of how to classify prokaryotes is just beginning. You will learn more about these organisms in Chapter 18.

**Analyze** Why are protists, plants, fungi, and animals classified into the same domain but into different kingdoms?

## 17.4 ASSESSMENT



### REVIEWING MAIN IDEAS

1. Why is the classification of life considered a work in progress?
2. What kingdoms are included in each of the three domains in the modern tree of life?

### CRITICAL THINKING

3. **Apply** If you come across an unusual single-celled organism, what parts of the cell would you study in order to classify it into one of the three domains?
4. **Analyze** Explain, using the traditional definition of species, why it is difficult to classify some **bacteria** and **archaea** at the species level.

### Connecting CONCEPTS

5. **History of Life** The Archaea lineage may include the first life on Earth, which began under much different environmental conditions from those present today. What characteristics of archaea help to support this statement?

Use these inquiry-based labs and online activities to deepen your understanding of classification.

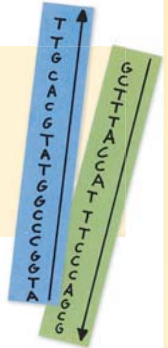
**INVESTIGATION**

## Modeling DNA Hybridization

Remember that two strands of DNA are held together by hydrogen bonds to form a double helix. Double-stranded DNA can be separated with heat. Separated DNA strands from two different species can then be combined to form hybrid double-stranded DNA.

**MATERIALS**

- DNA Hybridization Sequences
- 5 different colored pencils



Scientists can use the “melting” point of hybrid DNA to estimate how closely related two different species are to each other. The more mismatched bases there are, the fewer hydrogen bonds there will be, and the more easily the strands from the different species will separate when heated. In this lab, you will use DNA fragments from five hypothetical species to estimate how related the species are.

**SKILL Modeling**

**PROBLEM** How is DNA hybridization used to study species relatedness?

**PROCEDURE**

1. Copy the grid shown here into your notebook.
2. Recall the base-pairing rules for DNA:
  - A pairs with T, forming two hydrogen bonds.
  - C pairs with G, forming three hydrogen bonds.

If adjoining bases do not form one of these pairs, no hydrogen bonds form.

3. Using the DNA sequence fragments, put the strands from the original species (same color) together. Count the number of hydrogen bonds that would form for each species’ DNA fragment. Record this number in your grid. Notice that these counts will go in the gray diagonal boxes of the grid.
4. Form hybrid DNA fragments for each possible combination of species by matching the strands up with the arrows pointing in opposite directions. Count and record the number of hydrogen bonds holding each hybrid together. Notice that each of these counts will be recorded in one of the white boxes of the grid.

	Species				
	1	2	3	4	5
1					
2					
3					
4					
5					

**ANALYZE AND CONCLUDE**

1. **Analyze** Which DNA hybrid had the most hydrogen bonds? Which had the fewest?
2. **Analyze** Which species is the least related to the other four species?
3. **Synthesize** How has DNA technology changed the way scientists classify some organisms?

## INVESTIGATION

### Defining Species

The biological species concept is often used to define species. According to this definition, a species is a group of individuals that can mate and produce offspring that are able to reproduce. However, this definition has limitations. For example, a tiger is the offspring of a male lion and a female tiger. Some female tigers have been able to reproduce. This ability blurs the line between lions and tigers as species, as defined by the biological species concept.

### SKILL Evaluating

**PROBLEM** What are some different ways to define species?

### PROCEDURE

1. Research the definition of one of the species concepts listed below.
  - morphological species concept
  - paleontological species concept
  - ecological species concept
  - phylogenetic species concept
2. Write two paragraphs evaluating the species concept you have chosen. Be sure to include answers to the following questions:
  - How are species defined by this concept?
  - What are the advantages and limitations of the concept?
  - In what types of scientific research might this concept be the most useful?
  - Would this concept be more appropriate than the biological species concept in classifying bacteria and archaea?

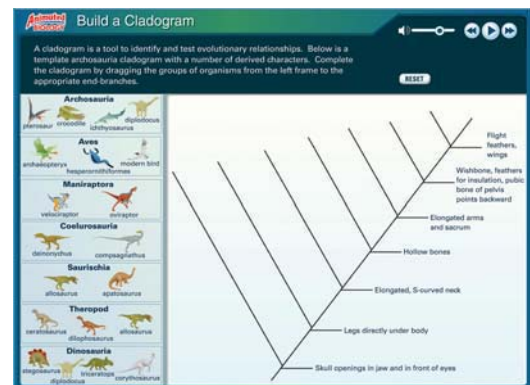


The tiger shown here, named Patrick, lives in the Shambala Preserve in California. He has a mane like a lion and stripes like a tiger.

## ANIMATED BIOLOGY

### Build a Cladogram

How are crocodiles related to birds? Use derived characters to build a cladogram of taxa within the archosauria clade.



## WEBQUEST

How do you classify a sea cucumber, an animal that looks like a water balloon? Complete this WebQuest to find out. Discover the evolutionary history of these animals and examine the traits that define them. Explore how sea cucumbers fit in the tree of life.



## BIOZINE

Stories about the diversity of life—such as “New Species Found in New York’s Central Park” and “Parasitic Fungus Drives Ant to Self-Destruction”—are often in the headlines. Read the latest news about the diversity of life in the BioZine.



KEY CONCEPTS

Vocabulary Games

Concept Maps

Animated Biology

Online Quiz

17.1 The Linnaean System of Classification

Organisms can be classified based on physical similarities. The Linnaean system of classification groups organisms based on shared physical or structural characteristics. This system is a nested hierarchy with seven taxa, or levels. The most specific level in this system is a species. Species are named according to binomial nomenclature, which gives each species a two-part scientific name using Latin words.

GENUS: *Canis*  
SPECIES: *Canis lupis*



Common name:  
gray wolf

17.2 Classification Based on Evolutionary Relationships

Modern classification is based on evolutionary relationships. Cladistics is a common method used to group species based on the order in which they diverged from a common ancestor. These evolutionary relationships can be presented in a branching diagram called a cladogram. Cladograms are constructed by identifying which derived characters are shared by which species in the group being analyzed.



Glyptodon



Armadillo

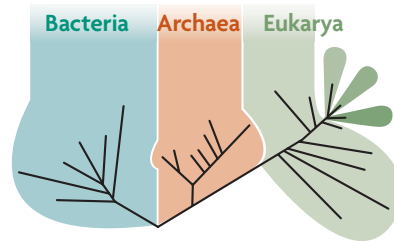
17.3 Molecular Clocks

Molecular clocks provide clues to evolutionary history. Mutations tend to accumulate at a constant rate for a group of related species. The longer that two species are separated after diverging from a common ancestor, the more different the two species will be at the molecular level. Biologists use molecular clocks by linking molecular data to real time. They can then measure the rate of evolution for these species. Ribosomal RNA and mitochondrial DNA provide two types of molecular clocks, used to measure evolution at different time scales.

17.4 Domains and Kingdoms

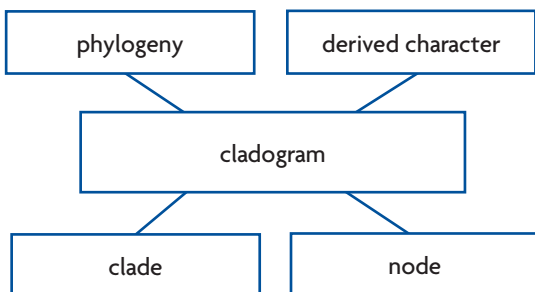
The current tree of life has three domains. The domains are based on fundamental differences at the cellular level. Within these domains are a total of six kingdoms. The Bacteria and Archaea domains include all organisms in the Bacteria and Archaea kingdoms, respectively. Bacteria and archaea are unicellular prokaryotes, but the genetic and cellular differences between these groups are greater than the differences between any other two kingdoms. The domain Eukarya includes all organisms with eukaryotic cells—kingdoms Protista, Fungi, Plantae, and Animalia.

Tree of life

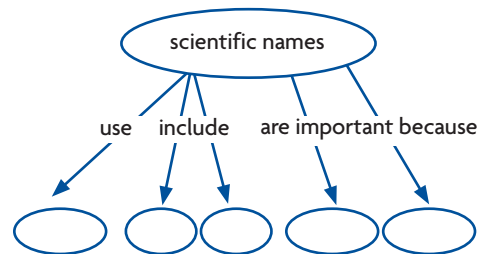


Synthesize Your Notes

**Main Idea Web** Use a main idea web to take notes about cladograms.



**Concept Map** Summarize what you know about taxonomy using a concept map.



# Chapter Assessment

## Chapter Vocabulary

**17.1** taxonomy, p. 518  
taxon, p. 518  
binomial nomenclature, p. 519  
genus, p. 519

**17.2** phylogeny, p. 524  
cladistics, p. 525  
cladogram, p. 525  
derived character, p. 525

**17.3** molecular clock, p. 530  
mitochondrial DNA, p. 532  
ribosomal RNA, p. 532

**17.4** Bacteria, p. 534  
Archaea, p. 534  
Eukarya, p. 534

## Reviewing Vocabulary

### Vocabulary Connections

For each group of words below, write a sentence or two to clearly explain how the terms are connected. For example, for the terms *taxonomy* and *taxon*, you could write “In Linnaean taxonomy, each level of classification is called a taxon.”

1. binomial nomenclature, genus, species
2. Bacteria, Archaea, Eukarya
3. molecular clock, mitochondrial DNA, ribosomal RNA

### Write Your Own Questions

Think about the relationship between each pair of terms below. Then write a question about the first term that uses the second term as the answer. For the pair *taxonomy*, *taxon*, the question could be “In Linnaean taxonomy, what is each level of classification called?” Answer: taxon

4. phylogeny, cladistics
5. cladogram, derived characters

### Greek and Latin Word Origins

6. *Klados* is Greek for “branch,” and *-gram* is a suffix meaning “something written or drawn.” Explain how this meaning relates to *cladogram*.
7. The prefix *archaeo-* comes from the Greek word *arkhaio*, which means “ancient” or “primitive.” Explain how this meaning relates to *Archaea*.

## Reviewing MAIN IDEAS

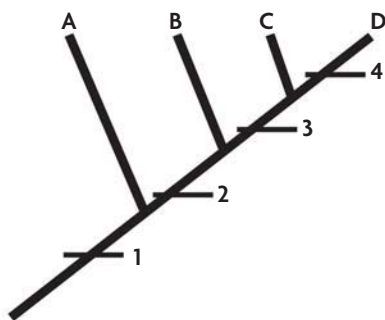
8. The scientific name for humans is *Homo sapiens*. What genus do humans belong to?
9. Why is it important for biologists to include scientific names when reporting their research to other biologists around the world?
10. Name the seven levels of organization in Linnaean taxonomy, from the most general to the most specific.
11. Current technology allows scientists to examine organisms at the molecular level. How has this technology exposed limitations in Linnaean taxonomy?
12. What basic idea does cladistics use to classify groups of organisms?
13. Two species with similar adaptations are found to have key differences at the molecular level. Scientists conclude that these species are not as closely related as previously thought. Why should the molecular evidence outweigh physical similarities that the species share?
14. A particular DNA sequence accumulated three mutations over 10,000 years. After how much time would you expect this sequence to have accumulated six more mutations? Explain.
15. Mutations accumulate more slowly in ribosomal RNA than in mitochondrial DNA. Which of these molecules would provide a better molecular clock for studying the evolution of species from different kingdoms?
16. The original Linnaean system of classification had two kingdoms. Biologists now use six kingdoms. What does this change suggest about the nature of classification?
17. What distinguishes the three domains in the tree of life from one another?

## Critical Thinking

18. **Apply** Are species in the same family more or less closely related than species in the same class? Explain your answer.
19. **Synthesize** Scientists have used mtDNA as a molecular clock to trace human evolution and early migration routes. Explain why mtDNA would be more useful in this research than rRNA.
20. **Apply** Refer to the cladogram on page 527. Are crocodiles and alligators more closely related to snakes or to birds? Explain your answer using the terms *common ancestor* and *derived characters*.
21. **Compare and Contrast** What types of evidence are used for classifying organisms in the Linnaean classification system? What types of evidence are used for classifying organisms based on evolutionary relationships?
22. **Evaluate** What is the significance of grouping the six kingdoms into three domains? How does the domain model more clearly represent the diversity of prokaryotes than a system with the six kingdoms as its broadest divisions?

## Interpreting Visuals

Use the cladogram, which classifies species A, B, C, and D, to answer the next three questions.



23. **Apply** What represents the derived characters that were used to construct this cladogram?
24. **Analyze** Where are the nodes in this cladogram, and what do they represent?
25. **Analyze** How many clades are represented in this cladogram?

## Analyzing DATA

The family Ursidae contains all bear species. The data below show the number of species in each of the five genera of this family. Use this data to answer the next three questions.

GENERA OF THE FAMILY URSIDAE	
Genus Names	Number of Species
<i>Ailuropoda</i>	1
<i>Helarctos</i>	1
<i>Melursus</i>	1
<i>Tremarctos</i>	1
<i>Ursus</i>	4

Source: University of Michigan Museum of Zoology

26. **Analyze** How many species belong to family Ursidae?
27. **Transform Data** Transform the number of species in each genus to a percent of the total number of bear species in family Ursidae.
28. **Analyze** What do the transformed data show that raw data do not show?

## Connecting CONCEPTS

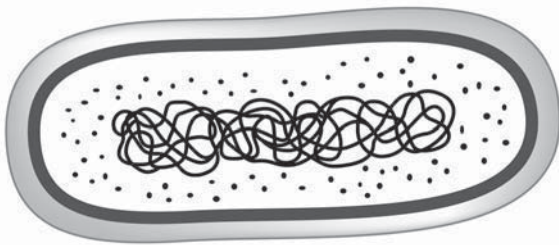
29. **Write a Letter** Imagine that you are a modern-day molecular biologist. Write a letter to Linnaeus explaining how advances in technology have affected the way that scientists classify living organisms. Describe the parts of his classification system that are still used in the same way today. Also describe the aspects of his system that have changed over the years.
30. **Compare and Contrast** The pangolin on page 517 shares many physical traits, such as a long snout, with anteaters and armadillos. However, these traits are known to have evolved separately in each of these groups of species. Write a paragraph that compares how Linnaeus and a modern taxonomist would likely classify pangolins. Include in your paragraph the kinds of additional information that a modern taxonomist might look for in order to classify the pangolin.





- In the past 150 years, the classification of life has changed through the addition and restructuring of kingdoms and domains. This system is always changing because
  - scientific study keeps producing more data.
  - evolution keeps producing unique organisms.
  - extinctions change evolutionary relationships.
  - humans increase the rate of speciation.
- Birds and snakes share a common ancestor from over 250 million years ago, but now they show many physical differences. These differences are *most* directly the result of
  - coevolution between species.
  - molecular clocks ticking at different rates.
  - the long-term accumulation of mutations.
  - differences in the alleles of the ancestor.

3.



Scientists isolate this organism from marsh water. Based on this illustration, the organism would *most* likely be classified as a

- protist.
- bacterium.
- plant.
- fungus.

- Mammals are multicellular organisms with about 3 billion base pairs in their genome. Yeasts are single-celled organisms with about 13 million base pairs in their genome. Both of these groups are classified as eukaryotes because they
  - have over one million base pairs.
  - can reproduce sexually.
  - utilize aerobic respiration.
  - have a similar basic cellular structure.

### THINK THROUGH THE QUESTION

Do not get confused by extra information provided in this question. Focus on the definition of eukaryotes. The number of base pairs is not relevant to this question.

- Scientists notice very few differences in the DNA sequences of individual cheetahs. This indicates that modern cheetahs likely descended from only a few individuals because
  - smaller populations have less genetic variation.
  - genetically different individuals are less fit.
  - the mutation rate depends on population size.
  - mutations do not affect small populations.

6.

ginger	a t g c g c c g a t c c t t a c g t c g a a t c g g a a c
corn	a c g c a c c g a t a c t t a c g t c g a t t c g g g a c
orchid	a c g c g c c g a t a c t t a c g t c g a a t c g g g a c
lily	a c g c g c c g a t a c t t c c g t c g a a t c t g g a c

The DNA sequences above show a conserved gene among four related plants. The highlighted differences are *most* directly the result of

- crossing over.
- adaptation.
- mutation.
- meiosis.