CHAPTERCLASSIFICATION OF17CLASSIFICATION OFORGANISMS

The ground pangolin, *Manis temminckii*, inhabits the forests, grasslands, and savannas of Africa. When threatened, it rolls into a tight ball, which exposes its razor-sharp scales. Its common name is *scaly anteater* because of its feeding habits, but it is not classified with other kinds of anteaters.

SECTION 1 Biodiversity SECTION 2 Systematics SECTION 3 Modern Classification

BIODIVERSITY

Biologists have named and classified almost 2 million species. However, they estimate that the total number of species on Earth is much greater. Over time, scientists have created various systems of classification to organize their knowledge of the tremendous number of species. Each system places species into categories based on particular characteristics.

CLASSIFYING ORGANISMS

One important branch of biology investigates **biodiversity**, the variety of organisms considered at all levels from populations to ecosystems. In general, the scientific catalogue of all biodiversity on Earth has increased over time. The number of identified species has grown from hundreds to millions. And scientists are certain that many more remain unidentified.

Since the 1980s, ecologist Terry Erwin and others have been working to catalog insect species in plots of tropical rain forest. To do this, researchers may fog the treetops with insecticide and then catch the falling insects in a net, as shown in Figure 17-1. Then, the scientists will count and classify the insects. Using such methods, Erwin collected over 1,000 species of beetles from just 19 trees of the same species in a limited area of rain forest. Furthermore, Erwin used his data to estimate the total possible number of insect species worldwide. He proposed that there could be more than 30 million species of insects on Earth!

Every year, biologists discover thousands of new species and seek to classify them in a meaningful way. Over the centuries, classification systems for organisms have been proposed and modified to include an increasing understanding of how organisms are structured and how they evolved. Biologists are challenged to organize their knowledge of such diversity in a way that makes sense.

For example, consider the pangolin, a species that is covered with scales and catches ants on its sticky tongue. Should pangolins be grouped in a category with other scaly animals, such as lizards and crocodiles? Biologists have decided against such a classification, because pangolins share many more similarities with mammals such as dogs and cats than with lizards or crocodiles. Should pangolins be grouped in a category with other mammals that use sticky tongues to eat ants? Again, biologists have decided against this grouping, because pangolins share more similarities with dogs and cats than with the other ant-eating mammal species.

SECTION 1

OBJECTIVES

- **Relate** biodiversity to biological classification.
- Explain why naturalists replaced Aristotle's classification system.
- Identify the main criterion that Linnaeus used to classify organisms.
- List the common levels of modern classification from general to specific.

VOCABULARY

biodiversity taxonomy taxon kingdom domain phylum division class order family genus species binomial nomenclature subspecies

FIGURE 17-1

These researchers are fogging a tree with insecticide to collect the insects that live on its leaves and branches.





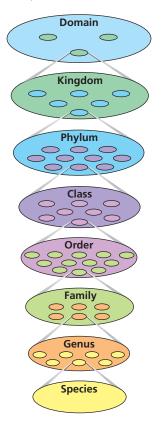
Word Roots and Origins

taxonomy

from the Greek words *taxis,* meaning "to put in order," and *nomia,* meaning "law"

FIGURE 17-2

Under the modern Linnaean system, the classification of an organism places the organism within a nested hierarchy of taxa. The hierarchy ranges from the most general category (domain) to the most specific (species).



TAXONOMY

The science of describing, naming, and classifying organisms is called **taxonomy** (taks-AHN-uh-mee). Any particular group within a taxonomic system is called a **taxon** (plural, *taxa*). Over time, scientists have created taxonomic systems that have different numbers and levels of taxa as well as different names for each taxon.

About 2,400 years ago, the Greek philosopher Aristotle classified organisms into only two taxa—either plants or animals. He grouped animals according to whether they lived on land, in water, or in air and grouped plants based on differences in their stems. As naturalists described more organisms, they realized that Aristotle's classification system was inadequate.

Early naturalists also found that common names, such as *robin* or *fir tree*, were not useful to identify organisms because common names vary from place to place and many don't accurately define a species. For example, the common name *jellyfish* is misleading. Although it has a jellylike body, a jellyfish is not a fish. Some naturalists named species by using long descriptions in Latin, but these names were difficult to remember and did not describe relationships among organisms.

The Linnaean System

Swedish naturalist Carolus Linnaeus (1707–1778) devised a system of grouping organisms into hierarchical categories according to their form and structure. Each category represents a level of grouping from larger, more general categories to smaller, more specific categories. Linnaeus's original system had seven levels. Figure 17-2 and Table 17-1 show a modern classification of different organisms in a hierarchical system similar to that used by Linnaeus.

TABLE 17-1	Classification Hierarc	rchy of Organisms		
	Pangolin	Dandelion		
Domain	Eukarya	Eukarya		
Kingdom	Animalia	Plantae		
Phylum/division	Chordata	Magnoliophyta		
Class	Mammalia	Magnoliopsida		
Order	Pholidota	Asterales		
Family	Manidae	Asteraceae		
Genus	Manis	Taraxacum		
Species	Manis temminckii	Taraxacum officinale		
	SS Come			

LEVELS OF CLASSIFICATION

The modern version of Linnaeus's nested hierarchy of organization is shown in Figure 17-2. His largest category was the **kingdom**, which was made up of only two kingdoms—animals and plants. Modern biologists adopted this system but added several other kingdoms as well as **domains**, which are categories above the kingdom level. Subsets below the kingdom level are called **phyla** (FIE-luh) (singular, *phylum*). Each phylum consists of **classes**, and each class contains **orders**. Still smaller groupings are the **family** and the **genus** (JEE-nuhs). The smallest grouping, which contains only a single kind of organism, is the **species** (SPEE-sheez).

Binomial Nomenclature

Linnaeus gave an organism a species name, or scientific name, with two parts: the genus name followed by the *species identifier*. This system of two-part names is known as **binomial nomenclature** (bie-NOH-mee-uhl NOH-muhn-KLAY-chuhr). The species name for humans is *Homo sapiens*. The species name is written in italics with the genus name capitalized. Species names generally come from Latin roots and are intended to be the same for all countries and in every language.

The name of a species is often quite descriptive. One kind of amoeba, which changes its shape seemingly randomly as it crawls in a pond, is *Chaos chaos*. The ground pangolin's species identifier is *temminckii*, which commemorates C. J. Temminck, a 19th-century Dutch naturalist who first collected a specimen of this species.

Biologists refer to variations of a species that live in different geographic areas as **subspecies.** A subspecies name follows the species identifier. For example, *Terrapene carolina triunui* is a subspecies of the common eastern box turtle, *Terrapene carolina*.

Quick Lab

Practicing Classification

Materials paper, pencil Procedure Using Table 17-1 as a model, classify a fruit or vegetable that you would find in a grocery store. Use all eight levels of classification.

Analysis At which level did you assign the least specific name? At which level did you assign the most specific name? Would Aristotle have classified your item differently? Explain your answer.

SECTION 1 REVIEW

- **1.** Explain how Earth's biodiversity relates to classification.
- 2. In what ways was Aristotle's classification system inadequate?
- **3.** What criteria did Linnaeus use to classify organisms?
- 4. What are the eight levels of the modern classification system?
- 5. What are two reasons that species names are more precise than common names?
- 6. How is a subspecies given a scientific name?

CRITICAL THINKING

- 7. Analyzing Models Explain why many of Linnaeus's categories are still used.
- 8. Calculating Information Suppose that there are 67 butterfly species for every 22,000 insect species and there are 15,000 to 22,000 species of butterflies worldwide. How many insect species are there?
- **9. Applying information** Organize ten produce items from the grocery store into a hierarchy, and make up a species name for each one based on Linnaean principles.



IN Classification of Organisms

Timeline



340

For uncounted millennia, humans have been observing Earth's organisms and trying to make sense of their diversity. Over time, a naming system that lumped all life-forms into "plants" or "animals" gave way to more sophisticated and accurate approaches to classification based on shared traits and ancestry. The modern approach can logically organize millions of species, including those yet to be discovered.

Prehistoric humans survived by hunting animals and gathering plants. Their lives depended on recognizing the edible and the harmful. Indeed, native cultures have passed along a deep store of knowledge about thousands of plant and animal species organized by utility, such as edibility, toxicity, and medicinal value.

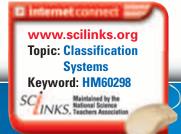
The Greek philosopher Aristotle observed and recorded nature in a scholarly way. His student Theophrastus, who lived from 370 BCE to 285 BCE, recorded 500 plant types, classified into herbs, shrubs, "pre-shrubs," and trees.

Advances in transportation, navigation, and exploration in the Middle Ages greatly expanded people's lists of observed organisms. In 1555, Swiss naturalist Conrad Gessner published Historia Animalium, categorizing thousands of animals into quadrupeds, birds, fish, and snakes. One hundred years later in his Historia Plantarum, English naturalist John Ray organized thousands of plants based on visual similarities and differences. In 1735. Swedish naturalist Carolus Linnaeus produced Systema Naturae, which categorized thousands of organisms into a hierarchy starting with genus and species and building to higher taxa including two kingdoms.

Several refinements have come to these higher taxa. German biologist Ernst Haeckel organized a "Tree of Life" in 1866. In 1894, he redrew its branches into three kingdoms. In 1959, American ecologist R. H. Whittaker established a five-kingdom taxonomy. In 1966, German biologist Willi Hennig invented cladistics, which classifies organisms based on their shared, derived traits in order to reflect their evolutionary history. Molecular data obtained by using ribosomal RNA sequences as an evolutionary measure allowed American molecular biologist Carl Woese to propose in 1977 a six-kingdom system that divided the then-existing kingdom Monera into two new kingdoms: Archaebacteria and Eubacteria. In 1990, Woese introduced the three-domain system that is used today.

Review

- 1. Describe how prehistoric humans "classified" species.
- 2. Why has the need for a system of classification grown over the centuries?
- **3.** How do modern classification systems differ from the system of classification used by John Ray?
- Describe a scientific advancement that enabled Woese to introduce the sixkingdom system.



SYSTEMATICS

More than 200 years ago, Linnaeus grouped organisms according to similarities that he could readily see. Modern biologists consider not only visible similarities but also similarities in embryos, chromosomes, proteins, and DNA. In **systematics**, the goal is to classify organisms in terms of their natural relationships. This section will discuss some modern methods of systematics.

PHYLOGENETICS

Biologists today may choose among and sometimes combine several systems of classification. Increasingly, systematic taxonomists agree that an organism's classification should reflect phylogeny. Recall that *phylogeny* is the evolutionary history of a species or a taxon. Thus, modern taxonomists are often involved in **phylogenetics**, the analysis of the evolutionary or ancestral relationships among taxa.

Systematists usually use several types of evidence to hypothesize about phylogenetics. Often, they compare the visible similarities among currently living species or fossils from extinct organisms. Biologists may also compare patterns of embryonic development and the ways in which the embryos of different species express similar genes. Furthermore, they may compare similar chromosomes and macromolecules, such as DNA or RNA, from different species to deduce phylogenetic relationships.

Systematists often represent their hypotheses in the form of a **phylogenetic diagram**, also called a *phylogenetic tree*. This type of diagram looks like a family tree and has a branching pattern that indicates how closely related a subset of taxa are thought to be. As with all hypotheses, phylogenetic diagrams may change whenever new discoveries and investigations cause scientists to revise their hypotheses.

Evidence of Shared Ancestry

Biologists use fossils as important clues for the timing of evolutionary changes and divergence. The use of fossils in the study of evolutionary relationships is critical, but the fossil record may lack evidence about many kinds of organisms, especially small and softbodied organisms, such as worms, fungi, or bacteria. The fossil record can help provide the framework of a phylogenetic diagram, but a systematist would test inferred relationships with additional evidence.

SECTION 2

OBJECTIVES

- Identify the kinds of evidence that modern biologists use in classifying organisms.
- Explain what information a phylogenetic diagram displays.
- State the criteria used in cladistic analysis.
- **Describe** how a cladogram is made.
- Discuss how proteins and chromosomes are used to classify organisms.
- Explain cladistic taxonomy, and identify one conclusion that is in conflict with classical taxonomy.

VOCABULARY

systematics phylogenetics phylogenetic diagram cladistics shared character derived character clade cladogram



Word Roots and Origins

clade

from the Greek *klados,* meaning "a branch" or "a shoot"

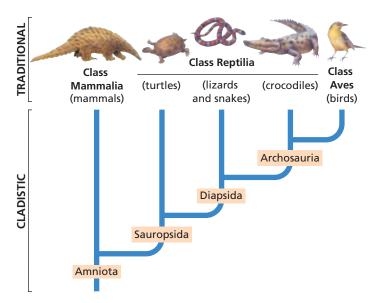
FIGURE 17-3

Traditional systematists placed crocodiles in the class Reptilia, but placed birds in the class Aves. In contrast, cladistic taxonomists have grouped crocodiles and birds together in a clade named *Archosauria*. Notice that clades do not have category names such as "class" or "phylum." Systematists also compare *homologous* features, items that share a common ancestry. For example, the jaws of pangolins and of dogs are homologous. It is essential to separate homologous features from *analogous* features (features that are similar because they have a similar function rather than a similar lineage). Scales are an example of analogous features. Both pangolins and snakes have scales, but the fossil record shows that scales evolved independently in the two taxa. The greater the number of homologous features shared by two organisms, the more closely related the organisms are.

Embryological evidence also helps establish phylogenetic relationships. For example, a fluid-filled sac called an *amnion* surrounds the embryos of reptiles, birds, and mammals. The embryos of other vertebrates lack an amnion. This shared and homologous embryological feature is used to define *amniotes*. All amniotes are combined into one taxon that includes all reptiles, birds, and mammals but excludes other vertebrates.

CLADISTICS

In 1966, German biologist Willi Hennig developed **cladistics** (kluh-DIS-tiks), a system of phylogenetic analysis that uses shared and derived characters as the only criteria for grouping taxa. A **shared character** is a feature that all members of a group have in common, such as hair in mammals or feathers in birds. A **derived character** is a feature that evolved only within the group under consideration. For example, feathers are thought to be a derived character for birds. Among living and fossil animals, the only animals that have feathers are birds and a few extinct reptiles that were very similar to birds in other ways. Therefore, it is reasonable to hypothesize that feathers evolved only within the bird lineage and were not inherited from the ancestors that birds share with reptiles.



Cladists assume that organisms that share one or more derived characters probably inherited those characters from a common ancestor. Cladists use the term **clade** for the group of organisms that includes an ancestor plus all of its descendants. Notice that clades do not have category names such as "class" or "phylum." Cladists create phylogenetic diagrams called **cladograms** (KLAD-uh-GRAMZ), such as the one in Figure 17-3.

Because cladists use strict criteria, their taxonomies may differ from those of traditional systematists. For example, traditional systematists grouped crocodiles with turtles, lizards, and snakes in the class Reptilia, but placed birds in their own class, Aves. In contrast, cladistic taxonomists have grouped crocodiles and birds together in a clade named *Archosauria*. This grouping reflects the hypothesis that crocodiles and birds share a more recent ancestor than either group shares with any other animals. Archosauria is then grouped with successively less-related clades of animals.

Constructing a Cladogram

Because cladistic analysis is comparative, the analysis deliberately includes an organism that is only distantly related to the other organisms. This organism is called an *out-group*. The out-group is a starting point for comparisons with the other organisms being evaluated.

To make a cladogram like Figure 17-4, start by making a data table like Table 17-2. Place organisms in a column at the left and their characteristics in a row at the top. Choose an out-group organism. In our example, moss has fewer traits in common with and seems most distantly related to the other groups in the table. So, moss is the choice for an out-group. Score the characters that are lacking in the out-group as a 0, and score the presence of a derived character as a 1. For example, mosses lack seeds, so they receive a 0 for the "seeds" character. Only pines and flowering plants have seeds, so they receive a 1 for that character.

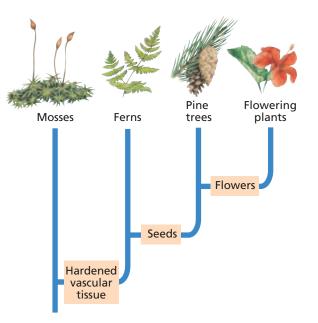
The table now reveals the derived character that is shared by most of the taxa. In this example, that character is vascular tissue vessels that transport water and sugars. This character is shown at the base of the first branch of the cladogram. The second most common character is seeds. Because ferns lack seeds, they are placed on the second branch of the cladogram. The least common character is flowers. Because pines lack flowers, they are placed on the third branch. Finally, flowering plants are placed on the last branch.

The resulting "tree" is a cladistic hypothesis for the evolutionary relationships among these plants. In addition to considering obvious physical characters, such as seeds and flowers, cladists may consider molecular characters, such as an individual nucleotide in a gene sequence or an amino acid sequence within a protein.

TABLE 17-2 Data Table for Cladogram Characters Vascular tissue Group of organisms Seeds Flowers Mosses (out-group) 0 0 0 1 0 0 Ferns Pine trees and 1 1 0 other conifers Flowering plants 1 1 1

FIGURE 17-4

This cladogram groups several major kinds of plants according to their shared, derived characters. The most common character (vascular tissue) is shared by all groups. The least common character (flowers) separates flowering plants from all the other plants.





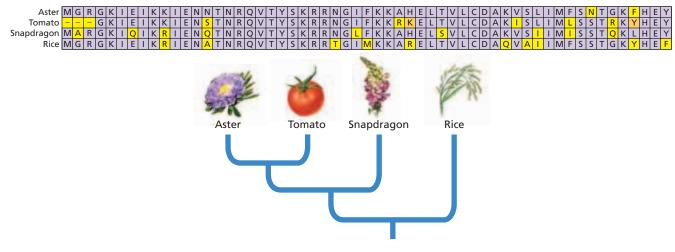
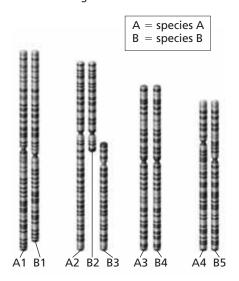


FIGURE 17-5

This cladogram is based on similar amino acid sequences in a specific protein produced by these plants. The initials M, G, and so on indicate different amino acids. The yellow squares indicate differences within the otherwise-identical sequences.

FIGURE 17-6

In this example, the karyotype of species A is very similar to that of species B. The diagram compares 4 of species A's chromosomes with 5 of species B's chromosomes. The banding pattern similarities suggest that chromosomes B2 and B3, combined, are homologous to chromosome A2.



Molecular Cladistics

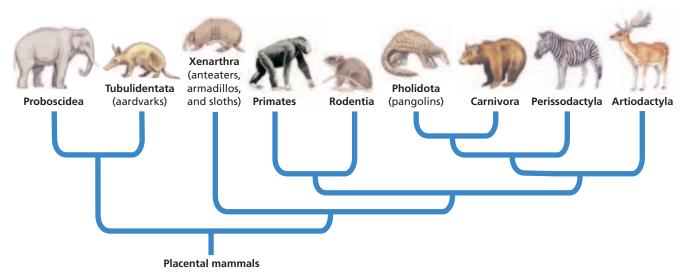
A biologist can count the shared, derived amino acids at each position in a protein and, from the analysis, construct a tree that hypothesizes relationships between various species. On a molecular cladogram, branch lengths are proportional to the number of amino acid changes. Such molecular data are independent of physical similarities or differences. The analysis shown in Figure 17-5 is of the amino acid sequence of a protein involved in flower development.

Biologists have used evolutionary changes in the sequence of macromolecules, such as DNA, RNA, and proteins, as a form of *molecular clock*, a tool for estimating the sequence of past evolutionary events. The molecular clock hypothesis suggests that the greater the differences between a pair of sequences, the longer ago those two sequences diverged from a common ancestor. A researcher who matches a molecular clock carefully with the fossil record can use it to hypothesize when various characteristics arose and when organisms diverged from ancestral groups.

Chromosomes

Analyzing karyotypes can provide still more information on evolutionary relationships. As Figure 17-6 shows, chromosomes can be stained to reveal a pattern of bands. If two species have the same banding pattern in regions of similar chromosomes, the regions are likely to have been inherited from a single chromosome in the last common ancestor of the two species. Karyotypic data are totally independent of both physical similarities and molecular data.

For example, the chromosomes of two species are shown in Figure 17-6. Several of the chromosomes have similar banding patterns, suggesting that the chromosomes are homologous. In addition, two of species B's chromosomes are similar to parts of one of species A's chromosomes. In such cases, biologists may still hypothesize that all of the chromosomes were inherited from the same ancestor. It is possible that in one of the descendants, one chromosome became two or two chromosomes became one.



PUTTING IT ALL TOGETHER

To classify an organism and represent its systematics in an evolutionary context, biologists use many types of information to build and revise phylogenetic models. Systematists will use data about physical features, embryos, genes in the nucleus, mitochondrial DNA, and ribosomal RNA.

Consider the classification of pangolins that is shown in Figure 17-7. African and Asian pangolins share several adaptations with other mammals that eat ants, including African aardvarks and South American anteaters. These adaptations include narrow snouts, strong digging claws, and long, sticky tongues. These shared characteristics, however, are analogous, not homologous. Deeper analysis of other characteristics, such as skeletal structures and nucleotide sequences in several genes, indicate that all three anteating taxa—pangolins, anteaters, and aardvarks—occupy quite different branches on the mammalian phylogenetic tree. Therefore, systematists place pangolins closer to the group that includes dogs and bears than to either aardvarks or anteaters.

FIGURE 17-7

This phylogenetic diagram is based on analyses of the DNA of many kinds of mammals. These analyses do not support a systematic grouping of pangolins with either African aardvarks or South American anteaters. Instead, pangolins seem to be most closely related to carnivores, such as bears and dogs. Biologists sometimes revise their classifications in light of such new evidence.

SECTION 2 REVIEW

- **1.** Identify two types of information that modern taxonomists use to classify organisms.
- 2. What is systematics, and what kinds of data are used by a systematist?
- **3.** Define the term *phylogenetic diagram*.
- 4. What is a shared, derived character?
- **5.** Compare cladistic taxonomy with more traditional taxonomy.
- **6.** How can a comparative analysis of the karyotypes of two species provide clues to the degree of relatedness between the species?

CRITICAL THINKING

- 7. Analyzing Models Examine the phylogenetic model shown in Figure 17-3, and explain why the Class Reptilia is not a clade.
- 8. Making Inferences Explain how a taxonomist might use embryological evidence in classifying an organism.
- **9. Evaluating Concepts** How could a biologist use cladistics to deduce whether the flippers of a sea lion and a whale are homologous or analogous characters?

SECTION 3

OBJECTIVES

- **Describe** the evidence that prompted the invention of the three-domain system of classification.
- List the characteristics that distinguish between the domains Bacteria, Archaea, and Eukarya.
- Describe the six-kingdom system of classification.
- Identify problematic taxa in the six-kingdom system.
- Explain why taxonomic systems continue to change.

VOCABULARY

Bacteria Archaea Eukarya Eubacteria Archaebacteria Protista Fungi Plantae Animalia

MODERN CLASSIFICATION

Biologists continue to develop taxonomies to organize life's enormous diversity. They regularly revise the many branches of the "tree of life" to reflect current hypotheses of the evolutionary relationships between groups. They have even revised the largest and most fundamental categories of the Linnean-inspired classification system—domains and kingdoms.

THE TREE OF LIFE

Looking at the cells of any organism under a microscope, biologists can easily identify one of two fundamental types of cells. On this basis, biologists may divide all life into two large groups. One of these groups consists of *eukaryotes*, or organisms whose cells possess a membrane-enclosed nucleus and many other cell organelles. Eukaryotes include organisms such as pangolins, people, and amoebas. The second group consists of *prokaryotes*. Prokaryotic cells are smaller than eukaryotic cells and have neither a nucleus nor membrane-enclosed organelles. Prokaryotes include bacteria.

Revising the Tree

Although the differences between eukaryotes and prokaryotes are obvious, systematists cannot assume that all organisms in one of these groups are equally related. A systematist can draw inferences about evolutionary relationships only by identifying homologous features. Because all members of one of these groups have few other physical traits in common, it is difficult to make comparisons between them. However, eukaryotes and prokaryotes do contain homologous macromolecules, such as proteins and RNAs used for storing and translating genetic information. When methods became available to compare such macromolecules, biologists began to use macromolecules in phylogenetic analyses.

Such analyses led molecular microbiologist Carl Woese of the University of Illinois to propose a major revision of the system that had classified Earth's diversity into six kingdoms. In 1977, Woese began comparing ribosomal RNA (rRNA) sequences from many different organisms and then grouping these organisms according to their similarities. All of today's living organisms, even prokaryotes, have ribosomes. Furthermore, the nucleotide sequences of the genes that encode rRNA seem to have changed little throughout most of evolutionary history. Thus, rRNA genes are uniquely useful for studying the most basic evolutionary relationships between Earth's diverse organisms.



THREE DOMAINS OF LIFE

Phylogenetic analyses of rRNA genes gave scientists new insights about the relationships between major groups and suggested a new "tree of life." Three of the most important insights were as follows:

- **1.** The data are consistent with the hypothesis that all living organisms inherited their rRNA genes from an ancient organism or form of life. Scientists refer to this unknown ancestor as the *last universal common ancestor*.
- **2.** At the broadest level, all living things seem to be related by ancestry to one of three major lineages, or *domains*. The three domains are named *Bacteria, Archaea*, and *Eukarya*. Most of the organisms that we are familiar with, such as plants and animals, belong to just one of the domains—Eukarya. Figure 17-8 shows a phylogenetic diagram for the three domains.
- **3.** The most surprising insights were those related to the domain Archaea. The species in this domain were identified and studied more recently than those in the other two domains. At first, the archaea were classified as bacteria. However, scientists have found that archaea differ greatly from bacteria in many important ways. More recently, scientists hypothesized that modern archaea descended from a unique kind of prokaryotes that existed early in Earth's history.

Domain Bacteria

The domain **Bacteria** is made up of small, single-celled prokaryotic organisms that usually have a cell wall and reproduce by cellular fission. Each bacterium has a cell wall, a plasma membrane, a cytoplasm that lacks complex organelles, and at least one circular chromosome. Bacteria do not have a membrane-bound DNA and thus lack a true nucleus. Most bacteria are small—many are just 2 μ m long. By comparison, human cells can be 6 μ m long or more. The oldest known fossils of cells appear to be bacterial cells.

Domain Archaea

The second domain also consists of prokaryotes and is named **Archaea**. The archaea have distinctive cell membranes and other unique biochemical and genetic properties. Some archaeal species are autotrophic and are able to produce food by chemosynthesis. Some species produce flammable gases, such as methane, as waste products. Many archaeal species inhabit harsh environments, such as sulfurous hot springs, deep-sea thermal vents, salty lakes, wastewater from mining, and the intestines of some animals.

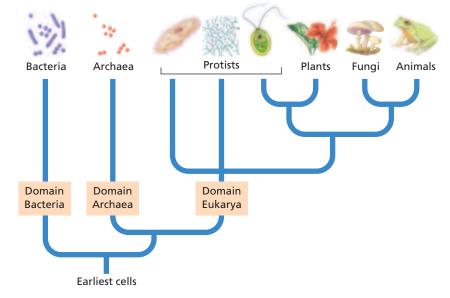
Word Roots and Origins

domain

from the Latin *dominium,* meaning "right of ownership"

FIGURE 17-8

This phylogenetic diagram represents hypotheses of the evolutionary relationships between the major recognized groups of organisms. Notice the alignment of the three domain names (*Bacteria, Archaea,* and *Eukarya*) with three major "branches" of the "tree" of all life. For updates on phylogenetic information, visit **go.hrw.com** and enter the keyword **HM6 Phylo**.



Because of the unique adaptations of the archaea, scientists think that archaea were among the earliest organisms on Earth. Furthermore, scientists think that archaea and bacteria have coevolved during Earth's history, meaning that the cells have interacted closely within environments and that the cells could have exchanged nutrients and genetic material. These possibilities, along with biochemical evidence, have led to the theory of endosymbiosis, which holds that eukaryotic cells arose when ancient prokaryotic cells began to live together as one cell.

Domain Eukarya

The most familiar groups of organisms are members of the domain Eukarya (yoo-KAR-ee-uh), which consists of eukaryotic organisms. The cells of these organisms are large and have a true nucleus and complex cellular organelles. The domain Eukarya includes plants, animals, fungi, and a variety of single-celled organisms.

SIX KINGDOMS

The system of three domains generally aligns with the more traditional system of six kingdoms, as represented in Figure 17-9 and summarized in Table 17-3. In the six-kingdom system, the first kingdom aligns with the domain Bacteria, the second kingdom aligns with the domain Archaea, and the remaining four kingdoms align with the domain Eukarya.

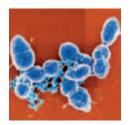
FIGURE 17-9

The six-kingdom system of classification can be aligned with the newer system of three domains. However, biologists have proposed adding, subdividing, or replacing some kingdoms. Biologists have also proposed other levels of taxa.

Kingdom Eubacteria

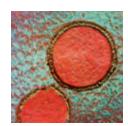
The kingdom Eubacteria (YOO-bak-TIR-ee-uh) aligns with the domain Bacteria. The name Eubacteria means "true bacteria," distinguishing this group from the archaea, which are no longer considered to be bacteria.

Domain Bacteria



Kingdom Eubacteria

Domain Archaea



Kingdom Archaebacteria

Domain Eukarya



Kingdom Protista



Kingdom Fungi





Kingdom Plantae



Kingdom Animalia

Kingdom Archaebacteria

The kingdom **Archaebacteria** (AHR-kee-bak-TIR-ee-uh) aligns with the domain Archaea. The name *Archaebacteria* means "ancient bacteria," but archaea are so different from bacteria that many biologists now prefer to use only the name *archaea* for this group.

Kingdom Protista

One of the four kingdoms of eukaryotes is **Protista** (proh-TIST-uh), whose members are called *protists*. This kingdom has been defined as those eukaryotes that are not plants, animals, or fungi. This definition is troublesome because it defines organisms based on what they are *not* rather than on what they *are*. Most protists are unicellular organisms, but it is difficult to make other generalizations about them. Molecular analyses indicate that many protists are less related to each other than plants are to animals. For all of these reasons, many biologists think that the taxon *Protista* is no longer useful, and several new taxa are being considered.

Common examples of unicellular protists are amoebas and paramecia. Examples of multicellular protists include some kinds of seaweeds and molds. Each of these protists is similar to animals, plants, or fungi in some ways yet different in other ways.

Taxon	Cell type	Cell surfaces	Body plan	Nutrition
Domain Bacteria (aligns with Kingdom Eubacteria)	prokaryotic; lack nucleus and other organelles	cell wall:contains peptidoglycans; cell membrane: contains fatty acids	unicellular	heterotrophic and autotrophic by chemosynthesis or photosynthesis
Domain Archaea (aligns with Kingdom Archaebacteria)	prokaryotic; lack nucleus and other organelles	cell wall: lacks unicellular peptidoglycan; cell membrane: contains hydrocarbons other than fatty acids		heterotrophic and autotrophic by chemosynthesis
Domain Eukarya Kingdom Protista	eukaryotic; have nucleus and complex organelles	cell wall: made of cellulose or other materials; cell membrane: contains fatty acids	mostly unicellular; multicellular forms: lack tissue organization	autotrophic by photosynthesis, some heterotrophic by phagocytosis, or both
Domain Eukarya Kingdom Fungi	eukaryotic; have nucleus and complex organelles	cell wall: made of chitin; cell membrane: contains fatty acids	unicellular and multicellular	heterotrophic by secreting digestive enzymes into environment
Domain Eukarya Kingdom Plantae	ngdom Plantae nucleus and of cellulose; dev		multicellular; develop from embryos	autotrophic by photosynthesis
Domain Eukarya Kingdom Animalia	eukaryotic; have nucleus and complex organelles	cell wall: none cell membrane: contains fatty acids	multicellular; develop from embryos	heterotrophic by phagocytosis

TABLE 17-3 Kingdom and Domain Characteristics

Kingdom Fungi

The second kingdom of eukaryotes is **Fungi** (FUHN-jie). The kingdom Fungi consists of eukaryotic, heterotrophic organisms that are unicellular or multicellular and that gain nutrients in a unique way. Unlike animal cells and some protists, fungi absorb rather than ingest nutrients. The about 70,000 species of fungi include mushrooms, puffballs, rusts, smuts, mildews, and molds.

Kingdom Plantae

The third kingdom of eukaryotes is **Plantae** (PLAN-tee), which consists of eukaryotic, multicellular plants. Except for a few parasitic species, most plants are autotrophic, use photosynthesis as a source of energy, and develop from embryos. Most plants live on land and include mosses, ferns, conifers, and flowering plants.

Kingdom Animalia

The fourth kingdom of eukaryotes is **Animalia** (AN-uh-MAH-lee-uh). Animals are eukaryotic, multicellular, and heterotrophic organisms that develop from embryos. Most animals have symmetrical body organization and move around their environment to find and capture food.

Future Taxonomic Systems

Because taxonomic systems are scientific models, they are subject to change. Since the time of Linnaeus, biologists have proposed, used, evaluated, and modified many classification systems. Modern biologists have proposed alternatives to the six-kingdom and three-domain systems. For example, some biologists have proposed three or more new kingdoms to replace Kingdom Protista. Some use taxonomic categories such as "subkingdom" and "superorder" to adapt the more traditional Linnaean categories to newer systematic models. Some favor pure cladistics over Linnaean categories. Surely, new systems will result from future investigations into the millions of known and unknown species on Earth.

SECTION 3 REVIEW

- **1.** What kind of evidence supports the classification of all organisms into the three-domain system?
- 2. Contrast bacteria with archaea.
- **3.** List and briefly describe the kingdoms in the sixkingdom system of classification.
- **4.** What is problematic about the kingdom name *Archaebacteria*?
- **5.** What is problematic about defining the kingdom Protista?
- **6.** Why do protists, fungi, plants, and animals share a single domain in the three-domain system?

CRITICAL THINKING

- **7. Evaluating Viewpoints** Biologists once classified all species of prokaryotes in a single kingdom called *Monera*. Justify their reasoning.
- **8.** Applying Information You have discovered a new organism. It is unicellular and has mitochondria, chloroplasts, and a nucleus. To what kingdom does this organism belong? Justify your answer.
- **9. Recognizing Differences** Describe the characteristics that differentiate plants from fungi. In what ways are plants and fungi similar?

SECTION 1 Biodiversity

- Naturalists have invented several systems for categorizing biodiversity, which is the variety of organisms considered at all levels from populations to ecosystems.
- Naturalists replaced Aristotle's classification system because it did not adequately cover all organisms and because his use of common names was problematic.
- Taxonomy is the science of describing, naming, and classifying organisms.
- Carolus Linnaeus devised a seven-level hierarchical system for classifying organisms according to their form and structure. From the most general to the most specific, the levels are kingdom, phylum, class, order, family, genus, and species. An adaptation of this system is still in use today.
- An important part of Linnaeus's system was assigning each species a two-part scientific name — a genus name, such as *Homo*, and a species identifier, such as *sapiens*.

Vocabulary

biodiversity (p. 337) taxonomy (p. 338)	domain (p. 339) phylum (p. 339)	order (p. 339) family (p. 339)	binomial nomenclature (p. 339)
taxon (p. 338)	division (p. 339)	genus (p. 339)	subspecies (p. 339)
kingdom (p. 339)	class (p. 339)	species (p. 339)	

SECTION 2

Systematics

- A modern approach to taxonomy is systematics, which analyzes the diversity of organisms in the context of their natural relationships.
- When classifying organisms, scientists consider fossils, homologous features, embryos, chromosomes, and the sequences of proteins and DNA.
- A phylogenetic diagram displays how closely related a subset of taxa are thought to be.
- Homologous features as well as similarities in patterns of embryological development provide information about common ancestry.
- Cladistics uses shared, derived characters as the only criterion for grouping taxa.
- Molecular similarities, such as similar amino acid or nucleotide sequences, as well as chromosome comparisons can help determine common ancestry.

Vocabulary

systematics (p. 341) phylogenetics (p. 341) phylogenetic diagram (p. 341) cladistics (p. 342) shared character (p. 342) derived character (p. 342) clade (p. 342) cladogram (p. 342)

SECTION 3 Modern Classification

- The phylogenetic analysis of rRNA nucleotide sequences led to a new "tree of life" consisting of three domains aligned with six kingdoms.
- The three domains are Bacteria, Archaea, and Eukarya.
- Domain Bacteria aligns with Kingdom Eubacteria, which consists of single-celled prokaryotes that are true bacteria.

Vocabulary

Bacteria (p. 347) Archaea (p. 347) Eukarya (p. 348) Eubacteria (p. 348) Archaebacteria (p. 349)

- Domain Archaea aligns with Kingdom Archaebacteria, which consists of single-celled prokaryotes that have distinctive cell membranes and cell walls.
- Domain Eukarya includes the kingdoms Protista, Fungi, Plantae, and Animalia. All members of this domain have eukaryotic cells.

Protista (p. 349) **Fungi** (p. 350) **Plantae** (p. 350) **Animalia** (p. 350)



USING VOCABULARY

- **1.** Use each of the following terms in a separate sentence: *biodiversity, binomial nomenclature, species identifier,* and *subspecies.*
- **2.** Explain the relationship between a phylum and a division.
- **3.** Choose the term that does not belong in the following group, and explain why the term does not belong: *homologous, derived character, shared character,* and *analogous.*
- **4. Word Roots and Origins** The word *taxonomy* is derived from the Greek words *taxis*, which means "to put in order," and *nomia*, which means "a set of rules or laws." Using this information, explain why the term *taxonomy* is a good name for the process that the term describes.

UNDERSTANDING KEY CONCEPTS

- **5. Explain** the primary difficulty of organizing Earth's biodiversity.
- **6. Describe** how Aristotle's and Linnaeus's classification systems for organisms were similar.
- **7. Explain** why a consistent naming system for species is important in scientific work.
- **8.** List the seven levels of Linnaeus's classification hierarchy from most general to most specific.
- **9. Name** the kinds of evidence that systematists use in constructing a phylogenetic tree.
- **10. Identify** the system of classification that is based on an analysis of shared, derived characters.
- **11. Describe** how amino acid and nucleotide sequences function as a molecular clock.
- **12. Summarize** one way that cladistic taxonomy differs from traditional taxonomy.
- **13. Name** the three domains and six kingdoms, and indicate the relationships of the two sets of taxa.
- **14. Describe** the molecular evidence that led to the three-domain system of classification.
- 15. Differentiate between bacteria and archaea.
- **16. Compare** plants and fungi, and describe what they have in common with animals.
- **17. CONCEPT MAPPING** Use the following terms to create a concept map that describes how biologists classify a new species: genus, species, binomial nomenclature, kingdom, homologous structures, taxonomy, derived characters, cladogram, and systematics.

CRITICAL THINKING

- **18. Evaluating Viewpoints** Scientists sometimes disagree about the phylogenetic histories of organisms. Cladistic taxonomists see reptiles in a different light than traditional taxonomists do. Why might scientists disagree with each other about the history of evolution?
- **19. Evaluating Models** The evolutionary history of reptiles can be studied by comparing their macromolecules. The degree of difference can be related to the time that has passed since any two species descended from a common ancestor. Would the phylogenetic tree derived from macromolecular comparisons more closely resemble the results of cladistic analysis or the traditional classification?
- **20. Evaluating Information** Biologists think that there may be millions of undescribed and unclassified species on Earth. Why might so many species still be undescribed or unclassified today?
- **21. Analyzing Concepts** Legs are an example of a shared, derived character in vertebrates. Arthropods, such as lobsters and crickets, also have legs, but their legs are not homologous to the legs of vertebrates. Explain this difference.
- **22.** Justifying Conclusions Several years ago, scientists found a living coelacanth, a fish that was thought to have become extinct 65 million years ago. The earliest fossils of coelacanths are about 350 million years old. The appearance of this species has changed little in 350 million years. If you could obtain macromolecules, such as proteins, from a 350 million–year-old fossil coelacanth and compare them with those of a freshly caught coelacanth, what would you expect to find and why?
- **23. Interpreting Graphics** A taxonomist has recorded the data below.

Derived Characters in Plants

Plants	Seeds	Vascular system	
Horsetails	no	yes	
Liverworts	no	no	
Pine trees	yes	yes	

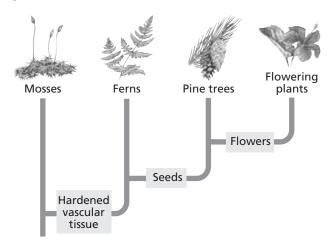
Identify the least common derived character. List the order that the plants in the table would be placed on a cladogram.

Standardized Test Preparation

DIRECTIONS: Choose the letter of the answer choice that best answers the question.

- 1. Which information is given in a species name?
 - A. genus and order
 - **B.** division and genus
 - **C.** genus and species identifier
 - **D.** species identifier and phylum
- **2.** To which level of classification does a group of closely related species of organisms belong?
 - F. class
 - G. order
 - H. genus
 - J. kingdom
- **3.** Eukaryotic organisms that have a nucleus and organelles, have a cell wall made of chitin, and secrete digestive enzymes belong to which kingdom?
 - **A.** Fungi
 - **B.** Plantae
 - C. Protista
 - **D.** Animalia

INTERPRETING GRAPHICS: The cladogram below shows the phylogenetic relationships among four kinds of plants. Use the cladogram to answer the question that follows.

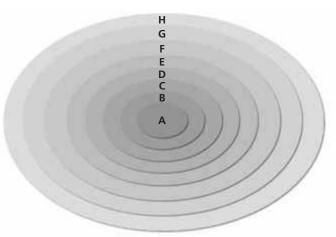


- 4. On the basis of this cladogram, which plants share the most recent common ancestor?F. mosses and ferns
 - **G.** mosses and pine trees
 - **H.** ferns and flowering plants
 - **J.** pine trees and flowering plants

DIRECTIONS: Complete the following analogy.

- 5. class : order :: kingdom :
 - A. genus
 - **B.** domain
 - **C**. species
 - **D.** phylum

INTERPRETING GRAPHICS: The diagram below represents the eight levels of classification. Use the diagram to answer the question that follows.



- **6.** Which level of classification represents a species? **F.** A
 - **G.** C
 - **H.** D
 - **J.** G

SHORT RESPONSE

Consider the characteristics of members of Kingdom Protista.

Explain why Kingdom Protista includes so many diverse organisms.

EXTENDED RESPONSE

To study the biodiversity of a rain forest, researchers sometimes collect species in vast numbers.

- Part A How would traditional taxonomy aid a researcher who found 955 beetle species in one kind of tropical tree?
- *Part B* How could molecular phylogenetics assist that same researcher?

Test TIP If time permits, take short mental breaks to improve your concentration during a test.



Using and Formulating Dichotomous Keys

OBJECTIVES

- Use a dichotomous key to identify leaves.
- Construct a dichotomous identification key.

PROCESS SKILLS

- identifying
- classifying
- designing
- interpreting
- organizing data
- comparing and contrasting

MATERIALS

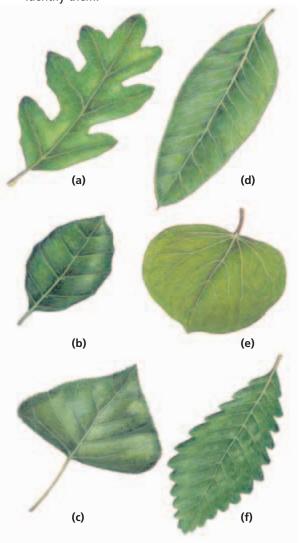
- pencil
- paper
- shoes
- masking tape
- marker

Background

- **1.** Taxonomy is the science of naming, describing, and classifying organisms.
- 2. Why is classification essential to biology?
- **3.** A dichotomous key uses pairs of contrasting, descriptive statements to lead to the identification of an organism (or other object).
- 4. The principle behind dichotomous keys—the forced choice—is used in many different situations to narrow the path toward an answer. If you have ever had your eyes examined for corrective lenses, you are familiar with the series of forced choices that end with the choice of the correct lenses for your eyes.
- **5.** Do not confuse a dichotomous key with a cladogram. A cladogram represents evolutionary relationships, whereas a dichotomous key does not.

PART A Using a Dichotomous Key

 Field guides often use dichotomous keys to help you identify organisms. Use the dichotomous key shown here to identify the tree leaves below. Begin with the paired descriptions 1a and 1b, and follow the directions. Proceed through the list of paired descriptions until you identify the leaf in question. In your lab report, write the names of the leaves as you identify them.



Dichotomous Key for Identifying Common Leaves

- **1a.** If the edge of the leaf has no teeth and has no lobes, go to 2 in the key.
- **1b.** If the edge of the leaf has teeth or lobes, go to 3 in the key.
- 2a. If the leaf has slightly wavy edges, the plant is a shingle oak.
- **2b.** If the leaf has smooth edges, go to 4 in the key.
- **3a.** If the leaf edge is toothed, the plant is a Lombardy poplar.
- **3b.** If the leaf edge has lobes, go to 5 in the key.
- 4a. If the leaf is heart-shaped with veins branching from the base, the plant is a redbud.
- **4b.** If the leaf is not heart-shaped, the plant is a live oak.
- 5a. If the leaf edge has a few large lobes, the plant is an English oak.
- 5b. If the leaf edge has many small lobes, the plant is a chestnut oak.

PART B Making a Dichotomous Key

- 2. Gather 10 different single shoes, and use masking tape and a marker to label the soles of the shoes with the owner's name. The labeled shoes should then be placed on a single table in the classroom.
- 3. Form small groups. Discuss the appearance of the shoes. In your lab report, make a table like the one below that lists some of the shoes' general characteristics, such as the type and size. Also list the names of the students who own the shoes. Complete the chart by describing the characteristics of each person's shoe.
- 4. Use the information in your table to make a dichotomous key that can be used to identify the owner of

each shoe. Remember that a dichotomous key includes pairs of opposing descriptions. At the end of each description, the key should either identify an object or give directions to go to another specific pair of descriptions. Write your dichotomous key in your lab report.

- 5. After all groups have completed their key, exchange keys with a member of another group. Use the key to identify the owner of each shoe, and then verify the accuracy of your identification by reading the label on the shoe. If the key has led you to an inaccurate identification, return the key so that corrections can be made.
- 🕦 Clean up your materials before leaving 6. the lab.

Analysis and Conclusions

- 1. What other characteristics might be used to identify leaves with a dichotomous key?
- 2. Were you able to identify the shoes using another group's key? If not, describe the problems you encountered.
- 3. How was it helpful to list the characteristics of the shoes before making the key?
- **4.** Does a dichotomous key begin with general descriptions and then proceed to more specific descriptions, or vice versa? Explain your answer, giving an example from the key you made.
- 5. Are dichotomous keys based on a phylogenetic or morphological approach to classification? Explain your answer.

Further Inquiry

List characteristics that might be used to identify birds or other animals using a dichotomous key. Compare your list of characteristics with those used in a dichotomous key in a field guide for identifying birds or other animals.

	DISTINGUISHING FEATURES OF A SAMPLE OF SHOES					
	Left/right	Men's/women's	Laced/slip-on	Color	Size	Owner
1						
2						
3						
4					_	
5						

CHAPTERS

- 18 Introduction to Ecology
- **19** Populations
- 20 Community Ecology
- 21 Ecosystems
- 22 Humans and the Environment

ECOLOGY

66 We and our fellow vertebrates are largely along for the ride on this planet. If we want to perpetuate the dream that we are in charge of our destiny and that of our planet, it can only be by maintaining biological diversity—not by destroying it. In the end, we impoverish ourselves if we impoverish the biota. ??

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References to *Scientific American* project ideas are located throughout this unit.

internet connect

National Science Teachers Association *sci* LINKS Internet resources are located throughout this unit.

> Maintained by the INKS. Teachers Association



Coral reef communities are second only to rain forests in diversity.



Bears are among the largest terrestrial predators.

The biosphere

Mimicry helps this mantid hide from both predators and potential prey.

