

Chapter 14

Classification

14.1 Lesson 14.1: Form and Function

Lesson Objectives

- Define taxonomy, and understand why scientists classify organisms.
- Describe Linnaean taxonomy and binomial nomenclature.

Introduction

Billions of years of evolution on Earth have resulted in a huge variety of different types of organisms. For more than two thousand years, humans have been trying to organize this great diversity of life. The classification system introduced by the Swedish botanist Carolus Linnaeus in the early 1700s has been the most widely used classification for almost 300 years.

Taxonomy

Scientific classification is a method by which biologists organize living things into groups. It is also called **taxonomy**. Groups of organisms in taxonomy are called **taxa** (singular, taxon). You may already be familiar with commonly used taxa, such as the kingdom and species. A **kingdom** is a major grouping of organisms, such as plants or animals. A species includes only organisms of the same type, such as humans (*Homo sapiens*) or lions (*Panthera leo*). The modern biological definition of a **species** is a group of organisms that are similar enough to mate and produce fertile offspring together. In a classification system, kingdoms, species, and other taxa are typically arranged in a hierarchy of higher and lower levels. Higher levels include taxa such as kingdoms, which are more inclusive. Lower levels include taxa such as species, which are less inclusive.

This type of hierarchical classification can be demonstrated by classifying familiar objects. For example, a classification of cars is shown in **Figure 14.1**. The highest level of the classification system includes all cars. The next highest level groups cars on the basis of size. Then, within each of the size categories, cars are grouped according to first one and then another trait. Higher taxa (for example, compact cars) include many different cars. Lower taxa (for example, compact cars that are blue and have two doors and cloth seats) contain far fewer cars. The cars in lower taxa are also much more similar to one another.

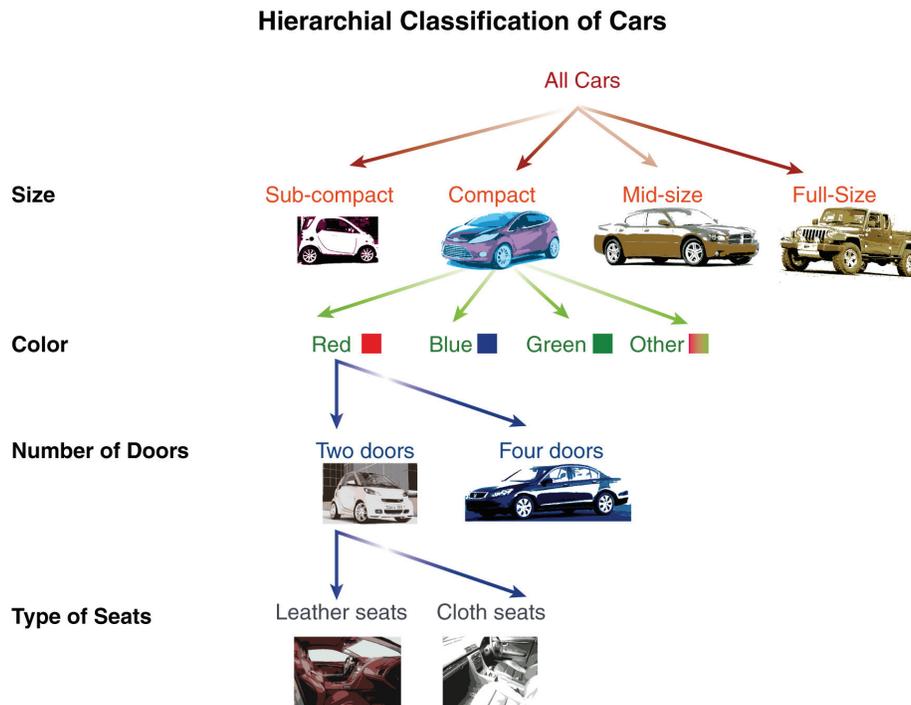


Figure 14.1: Cars can be classified, or grouped, on the basis of various traits. In this classification, the most inclusive groups are the size categories, such as all compact cars or all mid-size cars. The most exclusive groups in this classification share several additional traits, including color, number of doors, and type of seats. Note that just one group for each trait is further divided as an example. (19)

Why do biologists classify organisms? The major reason is to make sense of the incredible diversity of life on Earth. Scientists have identified millions of different species of organisms. Among animals, the most diverse group of organisms is the insects. More than one million different species of insects have already been described. An estimated nine million insect

species have yet to be identified. A tiny fraction of insect species is shown in the beetle collection in **Figure 14.2**.



Figure 14.2: Only a few of the more than one million known species of insects are represented in this beetle collection. Beetles are a major subgroup of insects. They make up about 40 percent of all insect species and about 25 percent of all known species of organisms. (4)

As diverse as insects are, there may be even more species of bacteria, another major group of organisms. Clearly, there is a need to organize the tremendous diversity of life. Classification allows scientists to organize and better understand the basic similarities and differences among organisms. This knowledge is necessary to understand the present diversity and the past evolutionary history of life on Earth.

Early Classification Systems

One of the first known systems for classifying organisms was developed by Aristotle. Aristotle was a Greek philosopher who lived more than 2,000 years ago. He created a classification system called the “Great Chain of Being” (See **Figure 14.3**). Aristotle arranged organisms in levels based on how complex, or “advanced,” he believed them to be. There were a total of eleven different levels in his system. At the lower levels, he placed organisms that he believed were less complex, such as plants. At higher levels, he placed organisms that he believed were more complex. Aristotle considered humans to be the most complex organisms in the natural world. Therefore, he placed them near the top of his great chain, just below angels and other supernatural beings.

Aristotle also introduced two very important concepts that are still used in taxonomy today:

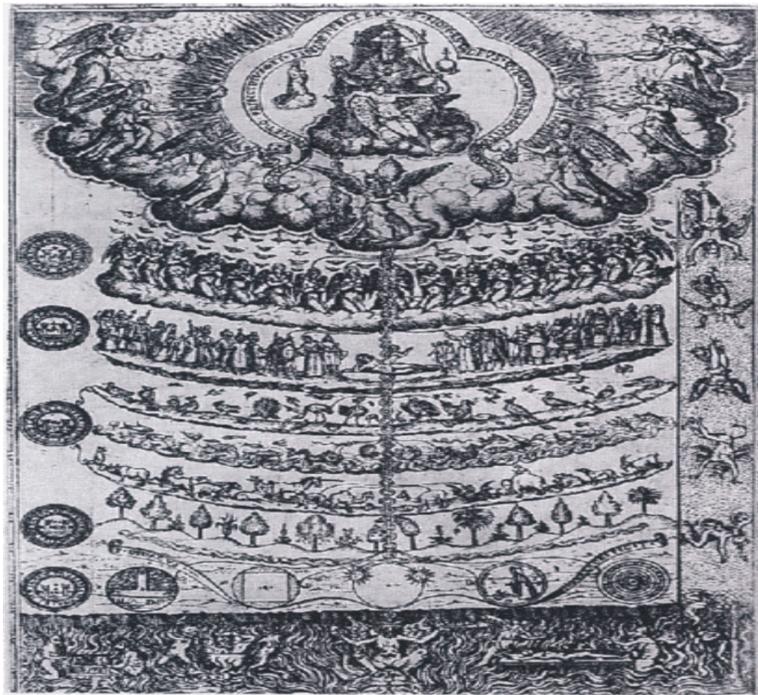


Figure 14.3: The Great Chain of Being was Aristotle's way of classifying organisms. The basis of Aristotle's classification was the presumed complexity of organisms. On that basis, Aristotle placed plants near the bottom of the classification and humans near the top. (16)

genus and species. Aristotle used these two concepts in ways that are similar to, but not as precise as, their current meanings. He used the term *species* to refer to a particular type of organism. He thought each species was unique and unchanging. He used the term **genus** (plural, genera) to refer to a more general grouping of organisms that share certain traits. For example, he grouped together in the same genera animal species with similar reproductive structures.

As early naturalists learned more about the diversity of organisms, they developed different systems for classifying them. All these early classification systems, like Aristotle's, were based on obvious physical traits of form or function. For example, in one classification system, animals were grouped together on the basis of similarities in movement. In this system, bats and birds were grouped together as flying animals, and fishes and whales were grouped together as swimming animals.

Linnaean System of Classification

The most influential early classification system was developed by Carolus Linnaeus. In fact, all modern classification systems have their roots in Linnaeus' system. **Linnaeus** was a Swedish botanist who lived during the 1700s. He is known as the "father of taxonomy." Linnaeus tried to describe and classify the entire known natural world. In 1735, he published his classification system in a work called *Systema Naturae* ("System of Nature").

Linnaean taxonomy divides all of nature into three kingdoms: animal, vegetable (or plant), and mineral. (The mineral kingdom does not include living organisms, so it is not discussed further here.) Both plant and animal kingdoms are subdivided into smaller and smaller categories of organisms. An updated version of Linnaean taxonomy is shown in **Figure 14.4**.

Linnaean Classification System (Revised)

The classification in **Figure 14.4** includes a few more taxa than Linnaeus identified. However, it follows the same general plan as Linnaeus' original taxonomy. The taxa are below:

- **Kingdom**—This is the highest taxon in Linnaean taxonomy, representing major divisions of organisms. Kingdoms of organisms include the plant and animal kingdoms.
- **Phylum** (plural, phyla)—This taxon is a division of a kingdom. Phyla in the animal kingdom include chordates (animals with an internal skeleton) and arthropods (animals with an external skeleton).
- **Class**—This taxon is a division of a phylum. Classes in the chordate phylum include mammals and birds.
- **Order**—This taxon is a division of a class. Orders in the mammal class include rodents and primates.
- **Family**—This taxon is a division of an order. Families in the primate order include hominids (apes and humans) and hylobatids (gibbons).

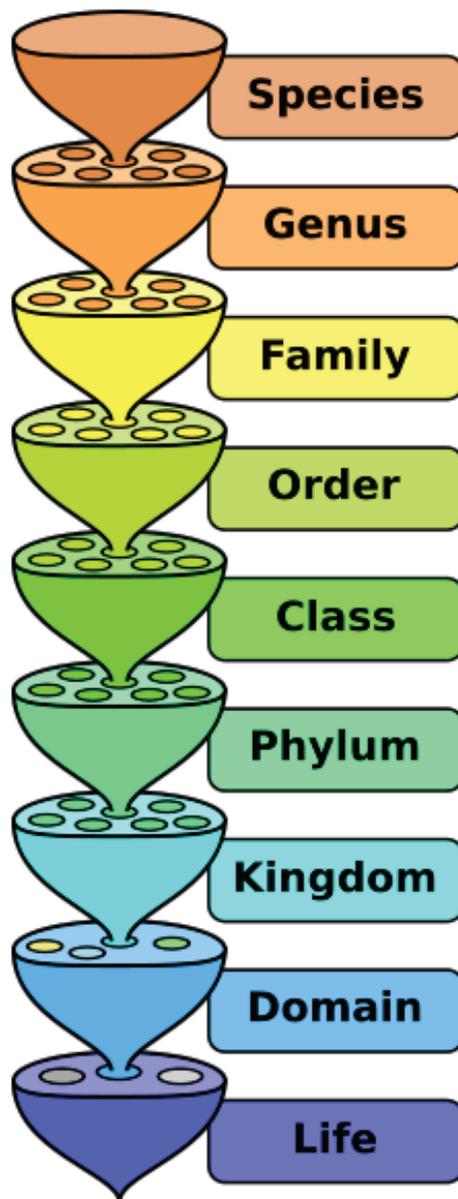


Figure 14.4: This is an updated version of Linnaeus' original classification system. In this classification system, organisms are classified into a hierarchy of taxa. First, all organisms are divided into kingdoms. Further subdivisions place organisms in smaller, more exclusive taxa, all the way down to the level of the species. (7)

- **Genus**—This taxon is a division of a family. Genera in the hominid family include *Homo* (humans) and *Pan* (chimpanzees).
- **Species**—This taxon is below the genus and the lowest taxon in Linnaeus' system. Species in the *Pan* genus include *Pan troglodytes* (common chimpanzees) and *Pan paniscus* (pygmy chimpanzees).

To remember the order of the taxa in Linnaean taxonomy, it may help to learn a mnemonic, a sentence to help remember a list, in which the words begin with the same letters as the taxa: k, p, c, o, f, g, and s. One sentence you could use is: **King Philip came over for green sugar**. Can you think of others?

Table 14.1 shows the classification of the human species. The table also lists some of the physical traits that are the basis of the classification. For example, humans are members of the animal kingdom. Animals are organisms capable of independent movement. Within the animal kingdom, humans belong to the mammal class. Mammals are animals that have fur or hair and milk glands. At each lower taxon, additional physical traits further narrow the group to which humans belong. The final grouping, the species *sapiens* (as in *Homo sapiens*), includes only organisms that have all of the traits listed in the table.

Table 14.1:

Taxon	Name	Traits ¹
Kingdom	Animal	Organisms capable of moving on their own.
Phylum	Chordate	Animals with a notochord (flexible rod that supports the body).
Class	Mammal	Chordates with fur or hair and milk glands.
Order	Primate	Mammals with collar bones, grasping hands with fingers.
Family	Hominid	Primates with three-dimensional vision, relatively flat face.
Genus	<i>Homo</i>	Hominids with upright posture, large brain.
Species	<i>sapiens</i>	Members of the genus <i>Homo</i> with a high forehead, thin skull bones.

¹ Only one or two traits per taxon are listed in the table as examples. Additional traits

may be needed to properly classify species. (Source : http://en.wikipedia.org/wiki/Linnaean_taxonomy)

Although Linnaeus grouped organisms according to their physical similarities, he made no claims about relationships between similar species. Linnaeus lived a century before Charles Darwin, so the theory of evolution had not yet been developed. Darwin explained how evolution, or changes in species over time, can explain the diversity of organisms (see the *Evolutionary Theory* chapter). In contrast, Linnaeus (like Aristotle before him) thought of each species as an unchanging "ideal type." Individual organisms that differed from the species' ideal type were considered deviant and imperfect.

Binomial Nomenclature

The single greatest contribution that Linnaeus made to science is his method of naming species. This method, called **binomial nomenclature**, gives each species a unique, two-word name (also called a scientific or Latin name). Just like we have a first and last name, organisms have a distinguishable two word name as well. The two words in the name are the genus name and the species name. For example, the human species is uniquely identified by its genus and species names as *Homo sapiens*. No other species has this name.

Both words in a scientific name are Latin words or words that have been given Latin endings. The genus name is always written first and starts with an upper-case letter. The species name is always written second and starts with a lower-case letter. Both names are written in italics.

As another example, consider the group of organisms called *Panthera*. This is a genus in the cat family. It consists of all large cats that are able to roar. Within the genus *Panthera*, there are four different species that differ from one another in several ways. One obvious way they differ is in the markings on their fur as shown in **Figure 14.5**, *Panthera leo* (lion species) has solid-colored fur, *Panthera tigris* (tiger species) has striped fur, and the other two *Panthera* species have fur with different types of spots. As this example shows, the genus name *Panthera* narrows a given cat's classification to big cats that roar. Adding the species name limits it to a single species of cat within this genus.

Why is Linnaeus' method of naming organisms so important? Before Linnaeus introduced his method, naming practices were not standardized. Some names were used to refer to more than one species. Conversely, the same species often had more than one name. In addition, a name could be very long, consisting of a string of descriptive words. For example, at one time, common wild roses were named *Rosa sylvestris alba cum rubore folio glabro*. Names such as this were obviously cumbersome to use and hard to remember.

For all these reasons, there was seldom a simple, fixed name by which a species could always be identified. This led to a great deal of confusion and misunderstanding, especially as more and more species were discovered. Linnaeus changed all that by giving each species a unique

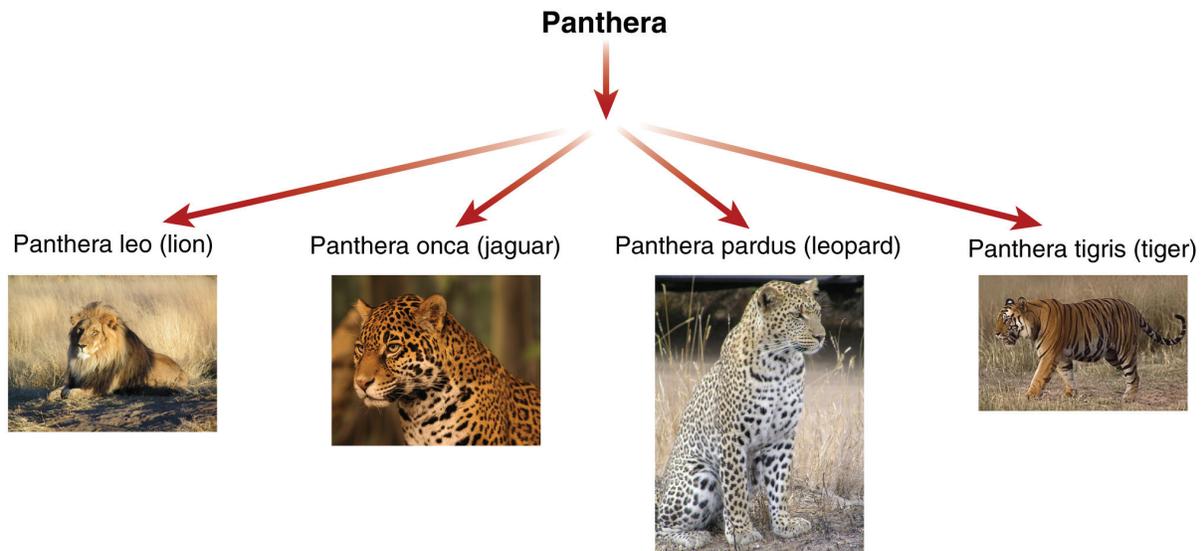


Figure 14.5: **Species in the Genus Panthera.** All four species in the Panthera genus are similar, but each is a unique type of organism, clearly identified by its combined genus and species name. (6)

and unchanging two-word name. Linnaeus’s method of naming organisms was soon widely accepted and is still used today.

Changes in the Linnaean System

Linnaean taxonomy has been revised considerably since it was introduced in 1735. One reason revisions have been needed is that many new organisms have been discovered since Linnaeus’ time. Another reason is that scientists started classifying organisms on the basis of evolutionary relationships rather than solely on the basis of similarities in physical traits.

Scientists have had to add several new taxa to the original Linnaean taxonomy in order to accommodate new knowledge of organisms and their evolutionary relationships. Examples of added taxa include the **subphylum**, **superfamily**, and **domain**.

- A subphylum is a division of a phylum that is higher than the class. An example of a subphylum is Vertebrates (animals with a backbone). It is a subphylum of the Chordate phylum (animals with a notochord).
- A superfamily is a taxon that groups together related families but is lower than the order. An example of a superfamily is Hominoids (apes). This superfamily consists of the Hominid family (gorillas, chimps, and humans) and the Hylobatid family (gibbons). **Figure 14.6** shows species from both of these families of the Hominoid superfamily.

- A domain is a taxon higher than the kingdom. An example of a domain is Eukarya, which includes both plant and animal kingdoms. You can read more about domains in Lesson 14.3.



Figure 14.6: The Hominoid superfamily includes the Hominid and Hylobatid families. Members of the Hominid family are chimpanzees (*Pan troglodytes*, left), gorillas, orangutans, and humans. Members of the Hylobatid are all gibbons (*Nomascus concolor*, right). (5)

Lesson Summary

- Taxonomy is the scientific classification of organisms. Scientists classify organisms in order to make sense of the tremendous diversity of life on Earth.
- Linnaean taxonomy groups organisms in a hierarchy of taxa, based on similarities in physical traits. Linnaeus' binomial nomenclature gives each species a unique two-word name.

Review Questions

1. Define taxonomy.
2. What contributions did Carolus Linnaeus make to taxonomy?
3. List the order of taxa in Linnaean taxonomy, from most to least inclusive.
4. What is binomial nomenclature?
5. Create a hierarchical taxonomy to classify writing implements, such as pens and pencils. Use a diagram to show your taxonomy.
6. Assume that a new organism has been discovered. It has a notochord, fur, forward-facing eyes, and grasping hands with fingers. In which taxa should the new organism be placed? Justify your answer.

7. Explain why biologists need to classify organisms.
8. Why was Linnaeus' naming system such an important contribution to biology?

Further Reading / Supplemental Links

- Wilfrid Blunt, *Linnaeus: The Compleat Naturalist*. Princeton University Press, 2002.
- Paul Lawrence Farber, *Finding Order in Nature*. Johns Hopkins University Press, 2000.
- Judith Winston, *Describing Species*. Columbia University Press, 1999.

Vocabulary

binomial nomenclature Linnaeus' method of naming species using a unique two-word name made up of the genus and species names.

class Taxon that is a division of a phylum.

family Taxon that is a division of an order.

genus Taxon that is a division of a family.

kingdom Major grouping of organisms, such as plants or animals.

Linnaeus Swedish botanist who lived during the 1700s and is known as the "father of taxonomy."

order Taxon that is a division of a class.

phylum Taxon that is a division of a kingdom.

species Group of organisms that are similar enough to mate and produce offspring together.

taxa Categories of organisms in a taxonomy.

taxonomy Method of organizing living things into groups.

Points to Consider

Linnaeus grouped together organisms on the basis of similarities in physical traits.

- Can you think of other similarities that could be used to group organisms?
- What other types of traits might related organisms share?
- What about similarities in molecules, such as DNA, among related organisms?

14.2 Lesson 14.2: Phylogenetic Classification

Lesson Objectives

- Understand the concept of phylogenetic classification.
- Outline how cladistics generates cladograms and identifies clades.
- Compare phylogenetic and Linnaean classification systems.
- Explain how nucleic acid base sequences are used in phylogenetic classification.

Introduction

In the century after Linnaeus published his system of classification, ideas about classifying organisms began to change. In 1859, Darwin published his major work on evolution, *On the Origin of Species by Natural Selection*. After that, there was more and more interest in classifying organisms, incorporating the evolutionary history, including the genetic relationships, of the organisms.

Phylogeny

The evolutionary history of a group of genetically related organisms is called a **phylogeny**. It includes ancestor species and descendant species. A phylogeny is usually represented by a tree diagram called a **phylogenetic tree**. An early example of a phylogenetic tree is Darwin's "Tree of Life" (see **Figure 14.7**). In this diagram, Darwin was trying to show how he thought evolution had occurred. The tree shows how species evolved through time, from the bottom of the tree to the top. As species evolved, they formed new branches on the tree of life. Some of these species eventually branched into additional descendant species. Others died out, or went extinct, without leaving any descendants.

Modern biologists still use phylogenetic trees to represent evolutionary histories. A simple phylogenetic tree is shown in **Figure 14.8**. The tips of the branches represent genetically related species. The branching points represent common ancestors. A **common ancestor** is the last ancestor species that two descendant species shared before they took different

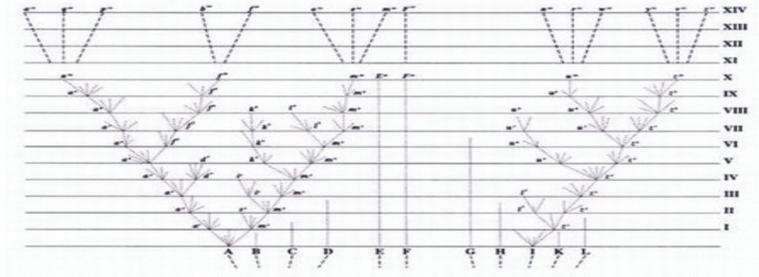


Figure 14.7: **Darwin's Tree of Life.** This branching diagram represents the evolutionary histories of different species. It is the only diagram that originally appeared in Darwin's famous 1859 book, *On the Origin of Species by Natural Selection.* (2)

evolutionary paths. In the tree in **Figure 14.8**, species 1 and 2 shared a more recent common ancestor with each other than with species 3. Therefore, species 1 and 2 are more closely related to one another than to species 3.

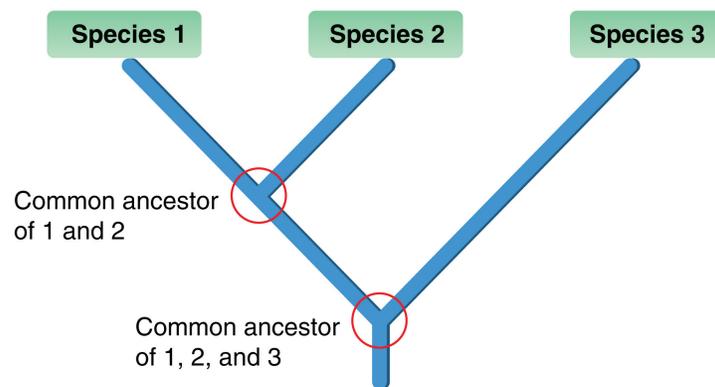


Figure 14.8: **Phylogenetic Tree.** This phylogenetic tree shows how hypothetical species 1, 2, and 3 are related to one another through common ancestors. (17)

Ancestor species are like your own ancestors. Your most recent common ancestor with any siblings you may have is a shared parent. Your most recent common ancestor with a first cousin is a shared grandparent. Your most recent common ancestor with a second cousin is a shared great-grandparent. In general, the more distant the relationship between you and relatives in your own generation, the farther in the past you shared a common ancestor. The same holds true for related species. The more distant the relationship between two related species, the farther back in time they shared a common ancestor.

The most common method of incorporating information into phylogenetic trees is called **cladistics**. Cladistics depicts hypotheses about how organisms are related, based on traits of ancestor and descendent species. Cladistics was developed in the 1950s by a scientist

named Willi Hennig. Over the next several decades, it became very popular, and is still widely used today.

The term *cladistics* comes from the word *clade*. A **clade** is a group of organisms that includes an ancestor species and all of its descendants. A diagram showing evolutionary relationships within one or more clades is called a **cladogram**. A clade is a relative concept. How you define a clade depends on which species you are interested in classifying. Small clades can include as few as two species and their common ancestor. The larger clades can include many more species and their common ancestors.

As another example, consider the cladogram of insect phylogeny shown in **Figure 14.9**. According to this cladogram, beetles first branched off from their common ancestor with other insects. Then, the group that includes wasps, bees, and ants branched off. Finally, flies branched off from their common ancestor with butterflies and moths. All insects can be considered a clade because they have a common ancestor. Butterflies, moths, and flies can also be considered a clade for the same reason. Can you identify other clades in **Figure 14.9**? For example, can you find the clade of all nonbeetle insects?

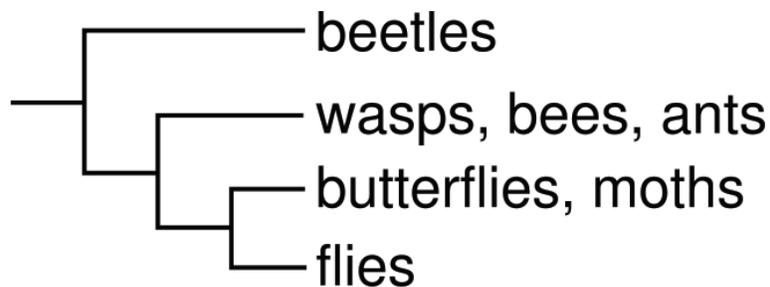


Figure 14.9: Cladogram of Insect Phylogeny. Based on this cladogram, flies shared a more recent common ancestor with butterflies and moths than either group shared with other insects. What other evolutionary relationships does the cladogram reveal? (18)

Generating Cladograms

How do scientists construct cladograms like the one in **Figure 14.10**? The starting point is a set of data on traits of a group of related species. The traits could be physical traits, genetic traits, or both (see **Evidence for Evolutionary Relationships** below). The next step is deciding which traits were inherited from the common ancestor and which traits evolved only in a descendant species after splitting off from the common ancestor. Traits inherited from a common ancestor are called **ancestral traits**. Traits that evolved since two groups shared a common ancestor are called **derived traits** and both types of traits are illustrated in **Figure 14.10**.

Ancestral and Derived Traits in Cladistic Analysis

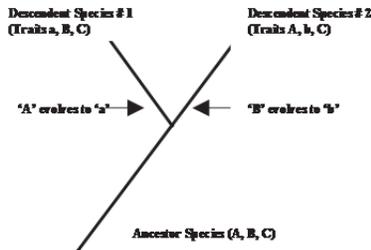


Figure 14.10: In this cladogram, the ancestor species has traits A, B, and C, so these are ancestral traits. During the process of evolution, trait A evolves to trait a and trait B evolves to trait b. These new traits (a and b) are derived traits. Organisms can be classified into separate groups (species #1 or species #2) on the basis of these derived traits. (8)

Consider birds as an example. A derived trait in birds is feathers. The trait is present only in birds and was not inherited from a common ancestor of birds and other organisms. An example of an ancestral trait in birds is the presence of eyes. Eyes are present not only in birds but also in many other groups of animals that share a common ancestor with birds. Therefore, the presence of feathers can identify an organism as a bird, but the presence of eyes cannot. In cladistics, the sharing of derived traits is the most important evidence for evolutionary relationships. Organisms with the same derived traits (such as feathers) are grouped in the same clade.

A derived trait is not necessarily an entirely new trait. More often it is a modified form of an ancestral trait. For example, birds evolved feathers from the scales that were already present in their reptile ancestor. Similarly, mammals evolved fur from the scales of their reptile ancestor.

More than one possible cladogram usually can be created from the same set of data. In fact, the number of possible cladograms increases exponentially with the number of species included in the analysis. Only one cladogram is possible with two species. More than 100 cladograms are possible with five species. With nine species, more than two million cladograms are possible! **Figure 14.11** shows just six of the many possible cladograms that can be generated for five species.

Six Possible Cladograms for Five Hypothetical Species

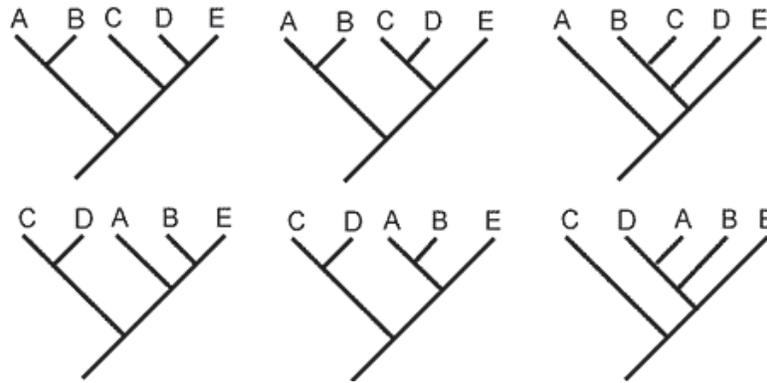


Figure 14.11: The same set of data on five related species may generate over 100 possible cladograms. Just six are shown here. In cladogram 1 (top, left), D and E share a more recent common ancestor than either shares with C. In cladogram 2 (top, middle), C and D share a more recent common ancestor than either shares with E. Compare how each of the remaining cladograms differs from the others. (9)

How do scientists know which of many possible cladograms is the “right” one? There is no right or wrong cladogram. However, some cladograms fit the facts better than others. Statistical methods can be used to determine which cladogram best fits a particular data set. An important deciding factor is parsimony. **Parsimony** means choosing the simplest explanation from among all possible explanations. In cladistics, parsimony usually means choosing the cladogram with the fewest branching points.

A cladogram shows just one of many possible phylogenies for a group of organisms. It can provide insights about how evolution occurred. However, a cladogram should not be considered a model of actual evolutionary events. It does not necessarily show what really happened. It just shows what could have happened.

Phylogenetic Classification

A cladogram shows how species may be related by descent from a common ancestor. A classification of organisms on the basis of such relationships is called a **phylogenetic classification**. A phylogenetic classification involves placing organisms in a clade with their common ancestor. Consider the cladogram in **Figure 14.12**. It groups birds in the same clade as reptiles, because a variety of evidence suggests that birds evolved from a reptile ancestor. The cladogram places mammals in a separate clade, because evidence suggests that mammals evolved from a different ancestor.

Figure 14.13 shows the phylogenetic classification of reptiles, birds, and mammals based on the cladogram in **Figure 14.12**. Birds are grouped with reptiles in one clade, called the

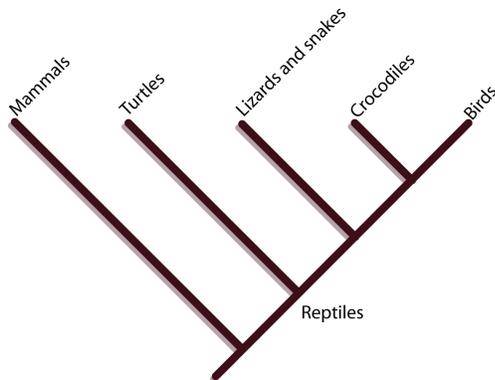


Figure 14.12: **Cladogram of Reptiles, Birds, and Mammals.** This cladogram represents the evolutionary history of reptiles, birds, and mammals. The reptile clade includes birds. Mammals are in a separate clade. (11)

Sauropsids. Mammals and their reptile-like ancestor are grouped in a separate clade, called the Synapsids. Compare this phylogenetic classification with the Linnaean classification, also shown in **Figure 14.13**. In the Linnaean classification, reptiles, birds, and mammals are all placed in separate classes based on differences in physical traits. This classification artificially separates both birds and mammals from their reptilian ancestors. It also illustrates the difficulty of showing evolutionary relationships with Linnaean taxonomy.

Phylogenetic and Linnaean Classifications of Reptiles, Birds, and Mammals

Both phylogenetic and Linnaean classification systems have advantages and drawbacks (see the point by point comparison in the two lists, below). As an overall approach, most biologists think that phylogenetic classification is preferable to Linnaean classification. This is because it is based on evolutionary relationships and not just similarities in physical traits that may or may not have evolutionary significance. However, both approaches have a place in the classification of organisms. Linnaean binomial names are still needed to identify species, because phylogenetics does not include a method for naming species. In addition, many higher taxa in the Linnaean system, such as birds and mammals, remain useful in phylogenetic classifications. This is because they are also clades.

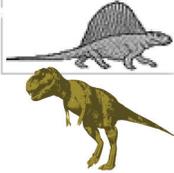
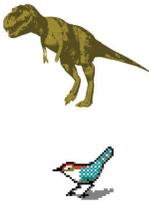
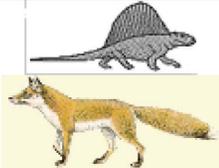
Linnaean Classification - based on shared traits		Phylogenetic Classification - based on common ancestor	
<p>Class: Reptiles (cold-blooded, scaly, lay eggs)</p> 		<p>Clade: Sauropsids</p> 	
<p>Class: Birds (warm-blooded, feathered, lay eggs)</p> 			
<p>Class: Mammals (warm-blooded, furry, live young)</p> 		<p>Clade: Synapsids</p> 	

Figure 14.13: The cladistic classification on the right assumes that mammals and birds evolved from different reptile ancestors. Mammals are placed in one clade, and birds are placed in another clade (with modern reptiles). Compare this classification with the Linnaean classification on the left. Why are birds and reptiles placed in separate classes in the Linnaean taxonomy (14)

Phylogenetic Classification

1. Treats all levels of a cladogram as equivalent.
2. Places no limit on the number of levels in a cladogram.
3. Primary goal is to show the process of evolution.
4. It is limited to organisms that are related by ancestry.
5. Does not include a method for naming species.

Linnaean Classification

1. Treats each taxa uniquely and has a special name for each (e.g., genus, species).
2. Has fixed numbers and types of taxa.
3. Primary goal is to group species based on similarities in physical traits.
4. Can include any organisms without regard to ancestry.
5. Has a method for giving unique names to species.

Phenetics is an older method to classify organisms. Phenetics is based on overall similarity, usually in morphology or other observable traits, regardless of their evolutionary relation. Phenetics has largely been replaced by cladistics for research into evolutionary relationships among

species. Phenetic techniques include various forms of clustering and ordination of traits. These are sophisticated ways of reducing the variation displayed by organisms to a manageable level. Phenetic analyses do not distinguish between traits that are inherited from an ancestor and traits that evolved anew in one or several lineages. Consequently, phenetic analyses can be misled by convergent evolution and adaptive radiation.

Evidence for Evolutionary Relationships

Traditionally, evidence for evolutionary relationships included similarities in physical traits of form or function. For example, in Linnaean taxonomy, homeothermy (warm-bloodedness) is one of the traits used to separate both birds and mammals from other animals (see **Figure 14.13**). However, this trait is not suitable for showing evolutionary relationships between birds and mammals. This is because birds and mammals did not inherit the trait of homeothermy from a common ancestor. Both groups independently evolved the trait. The presence of homeothermy in both birds and mammals is an example of convergent evolution (see the *History of Life* chapter). In general, convergent evolution may make two groups seem to be more closely related than they really are. Using such traits for phylogenetic analysis can lead to misleading phylogenetic classifications.

Similarities among nucleic acid base sequences provide some of the most direct evidence of evolutionary relationships (see the *Evolutionary Theory* chapter). Nucleic acids directly control genetic traits and copies of nucleic acids are actually passed from parents to offspring. Therefore, similarities in these traits are likely to reflect shared ancestry. By the 1960s, scientists had found ways to sequence the bases in nucleic acids. This coincided with the growing popularity of cladistics. In cladistic analysis, similar nucleic acid base sequences are assumed to indicate descent from a common ancestor. The more similar the sequences, the more recently two groups are assumed to have shared a common ancestor.

Many base sequence comparisons have confirmed genetic relationships that were assumed on the basis of similarities in physical traits. For example, 96 percent of the DNA in humans and chimpanzees is the same. This agrees, in general, with the Linnaean classification of chimpanzees as close human relatives (see Lesson 14.1).

Most biologists interested in taxonomy now use nucleic acid sequences or other related molecular data to classify organisms. However, using nucleic acid base sequences for phylogenetic analysis is not without its drawbacks. Two of the drawbacks are:

- Data on nucleic acids can rarely be obtained for extinct species. This is true even for species represented by fossils. Fossil DNA and RNA generally are not sufficient in quantity or quality to be useful for such analyses.
- Base sequence data may be influenced by horizontal gene transfer. This occurs when an organism passes DNA to an unrelated organism. First discovered in bacteria in 1959,

it is now known to be common in bacteria and some other microorganisms. Horizontal gene transfer can make species seem more closely related than they really are.

Because of horizontal gene transfer, some biologists have started to question whether phylogenetic trees are the best way to show evolutionary relationships. This is especially true for those biologists that are interested in classifying bacteria. An entirely new process of determining evolutionary relationships may be needed in order to include horizontal gene transfer.

Lesson Summary

- Phylogeny is the evolutionary history of a group of genetically related organisms. It is usually represented by a diagram called a phylogenetic tree.
- Cladistics is the most widely used method of generating phylogenetic trees. It is based on evolutionary ancestry and generates trees called cladograms. Cladistics also identifies clades, which are groups of organisms that include an ancestor species and its descendants.
- Classifying organisms on the basis of descent from a common ancestor is called phylogenetic classification. Phylogenetic classification may or may not agree with Linnaean taxonomy, which is based on similarities in physical traits regardless of ancestry.
- The most direct evidence for evolutionary relationships is similarity in base sequences of the nucleic acids DNA and RNA. The more similar the base sequences of two species, the more closely related the species are assumed to be.

Review Questions

1. What is a phylogeny?
2. Define cladistics.
3. What does phylogenetic classification involve?
4. Why are nucleic acid base sequences directly related to evolution?
5. In cladogram 6 of **Figure 14.11**, explain how the five species are related to one.
6. Identify an ancestral trait and a derived trait in mammals. Explain your answer.
7. Explain why a cladogram represents only one hypothesis about how evolution occurred.
8. Compare the advantages of Linnaean and phylogenetic classification systems.

Further Reading / Supplemental Links

- http://evolution.berkeley.edu/evolibrary/article/0_0_0/phylogenetics_01
- D.Graham Burnett, *Trying Leviathan: The Nineteenth-Century Court Case that Put the Whale on Trial and Challenged the Order of Nature*. Princeton University Press, 2007.

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- Transformed Cladistics, Taxonomy, and Evolution. Cambridge University Press, 2009.
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- <http://mansfield.osu.edu/~sabedon/biol3005.htm>
- http://news.nationalgeographic.com/news/2005/08/0831_050831_chimp_genes.html
- <http://users.rcn.com/jkimball.ma.ultranet/BiologyPages/T/Taxonomy.html>
- <http://www.genome.gov/12514316>
- <http://www.palaeos.com/Systematics/Cladistics/incomptable.html>

Vocabulary

ancestral traits Traits inherited from a common ancestor.

clade Group of organisms that includes an ancestor species and all of its descendants.

cladistics Method of making evolutionary trees based on comparisons of traits of ancestor and descendant species.

cladogram Diagram showing evolutionary relationships within one or more clades.

common ancestor Last ancestral species that two descendant species shared before they took different evolutionary paths.

derived traits Traits that evolved since two groups shared a common ancestor.

parsimony Choosing the simplest explanation from among all possible explanations.

phylogenetic classification Classification of organisms on the basis of evolutionary relationships.

phylogenetic tree Diagram representing a phylogeny.

phylogeny Evolutionary history of a group of genetically related organisms.

Points to Consider

When Linnaeus developed his classification system in the early 1700s, he knew almost nothing about microorganisms (microscopic organisms). Therefore, he did not include microorganisms in his taxonomy.

- How do you think microorganisms should be classified?
- Where do you think microorganisms should be placed in Linnaean taxonomy?
- Do you think a new taxon might be needed for microorganisms?

14.3 Lesson 14.3: Modern Classification Systems

Lesson Objectives

- Identify the four new kingdoms that were added to the original Linnaean taxonomy.
- Describe the three domains of the three-domain system of classification.
- Explain why the three-domain system may need revision in the future.

Introduction

Linnaeus established two kingdoms of organisms in his classification system: Plantae (the plant kingdom) and Animalia (the animal kingdom). Since then, scientists have repeatedly revised the Linnaean system. They have added several new kingdoms and other taxa. These changes were necessary as scientists learned more about life on Earth.

New Kingdoms

Between 1866 and 1977, a total of four new kingdoms were added to the original plant and animal kingdoms identified by Linnaeus. The new kingdoms include Protista (protists), Fungi, Monera (eubacteria), and Archaea (archaeobacteria). **Table 14.2** identifies the scientists who introduced the kingdoms and the dates the kingdoms were introduced. The table starts with the two-kingdom system introduced by Linnaeus in 1735.

Table 14.2: **Kingdoms in the Classification of Organisms**

Number of Kingdoms	Two	Three	Four	Five	Six
Scientist	Linnaeus	Haeckel	Copeland	Whittaker	Woese
Date	1735	1866	1956	1969	1977

Table 14.2: (continued)

Number of Kingdoms	Two	Three	Four	Five	Six
Names of Kingdoms	Plantae Animalia	Plantae Animalia Protista	Plantae Animalia Protista Monera	Plantae Animalia Protista Fungi Monera	Plantae Animalia Protista Fungi Monera Archaea

(Source: http://en.wikipedia.org/wiki/Kingdom_%28biology%29, License: GNU Free Documentation)

The Protist Kingdom

When Linnaeus created his taxonomy, microorganisms were almost unknown. As scientists began studying single-celled organisms under the microscope, they generally classified them as either plants and or animals. For example, bacteria are single-celled organisms, some of which make their own food. They were classified as plants, which also make their own food. Protozoa are single-celled organisms that can move on their own. They were classified as animals, which are organisms that have independent movement.

As more single-celled organisms were identified, many didn't seem to fit in either the plant or the animal kingdom. As a result, scientists could not agree on how to classify them. To address this problem, in 1866, biologist Ernst Haeckel created a third kingdom for all single-celled organisms. He called this kingdom Protista. **Figure 14.14** shows drawings that Haeckel made of several different types of **protists** as they looked under a microscope. The drawings show some of the diversity of microorganisms.

The Bacteria Kingdom

Haeckel's protist kingdom represented all known single-celled organisms, including both bacteria and protozoa. In the early 1900s, scientists discovered that bacterial cells are very different not only from plant and animal cells but also from the cells of protists, such as protozoa. **Figure 14.15** shows a bacterial cell, a protozoan cell, and an animal cell. When you compare the three cells, what differences do you see? The major difference is that, unlike the protozoan and animal cells, the bacterial cell does not contain a nucleus surrounded by

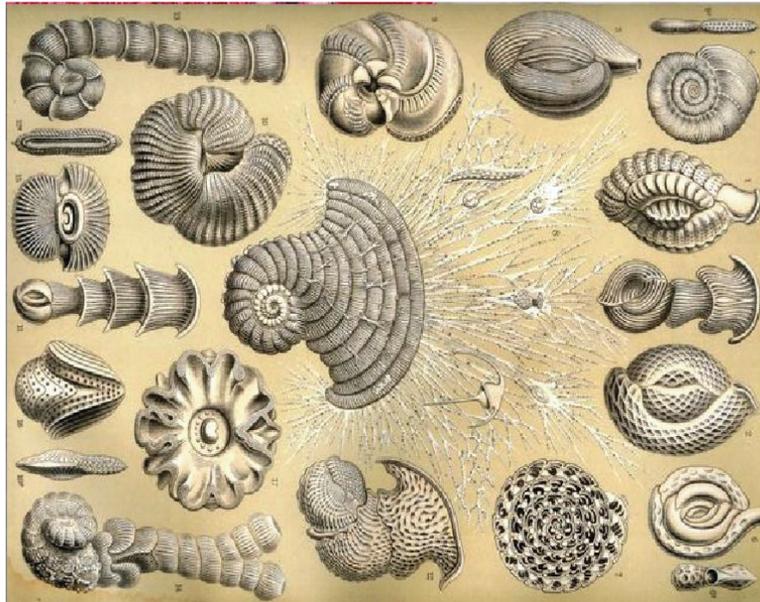


Figure 14.14: **Diversity of Protists.** Biologist Ernst Haeckel made these drawings of various types of single-celled organisms as viewed under a microscope. Based on his extensive knowledge of the diversity of microorganisms, Haeckel introduced a new kingdom just for single-celled life forms, called the protist kingdom. This was the first major change in the original Linnaean taxonomy. (12)

a nuclear membrane. Instead, its DNA is found in the cytoplasm of the cell. Organelles in the bacterial cell also lack surrounding membranes.

In the 1920s, microbiologist Edouard Chatton gave bacteria the name prokaryotes. He defined **prokaryote** as an organism whose cells lack nuclei. He gave the name eukaryotes to all other organisms. He defined **eukaryote** as an organism whose cells have nuclei (see the *Cell Structure and Function* chapter). Chatton proposed placing prokaryotes and eukaryotes in a new taxon above the kingdom, called the superkingdom. However, this idea did not catch on, and most biologists continued to place bacteria in the protist kingdom.

Over the next several decades, scientists learned more about the tremendous number and diversity of bacteria. They started to see a need for a separate bacteria kingdom. By 1956, biologist Herbert Copeland proposed placing bacteria in a new kingdom called Monera. With the addition of the **Monera** kingdom, Linnaean taxonomy became a four-kingdom system (See **Table 14.2**).

Bacteria are the most numerous organisms on Earth. In a single gram of soil, there are typically 40 million bacterial cells. The human body also contains 10 times as many bacterial cells as human cells. Most of these bacteria are on the skin or in the digestive tract.

The Fungi Kingdom

In the late 1960s, ecologist Robert Whittaker proposed adding a fifth kingdom to Linnaean taxonomy to represent fungi. **Fungi** are eukaryote organisms such as mushrooms and molds. Up until then, fungi had been classified in the plant kingdom. Whittaker separated fungi from plants on the basis of differences in metabolism. Plants make their own food in the process of photosynthesis, whereas fungi obtain nutrients by breaking down dead organisms (see the *Fungi* chapter). Separating fungi from plants resulted in five kingdoms, which are illustrated in **Figure 14.16**. The five-kingdom system soon became widely accepted.

Two Bacterial Kingdoms

By the 1970s, scientists had started to classify organisms in ways that reflected evolutionary relationships. They had also started using nucleic acid base sequences to identify these relationships (see Lesson 14.2). Nucleic acid sequence data are especially useful for studying bacteria. These organisms are so small that they have few physical traits.

Studies have bacterial nucleic acid sequences have yielded some surprising results. For example, in their research on ribosomal RNA base sequences, microbiologist Carl Woese and his colleagues discovered that bacteria actually include two very different groups of organisms. They called the two groups Eubacteria and Archaeobacteria. Examples of organisms from each group are shown in **Figure 14.17**. Although the two types of organisms are similar

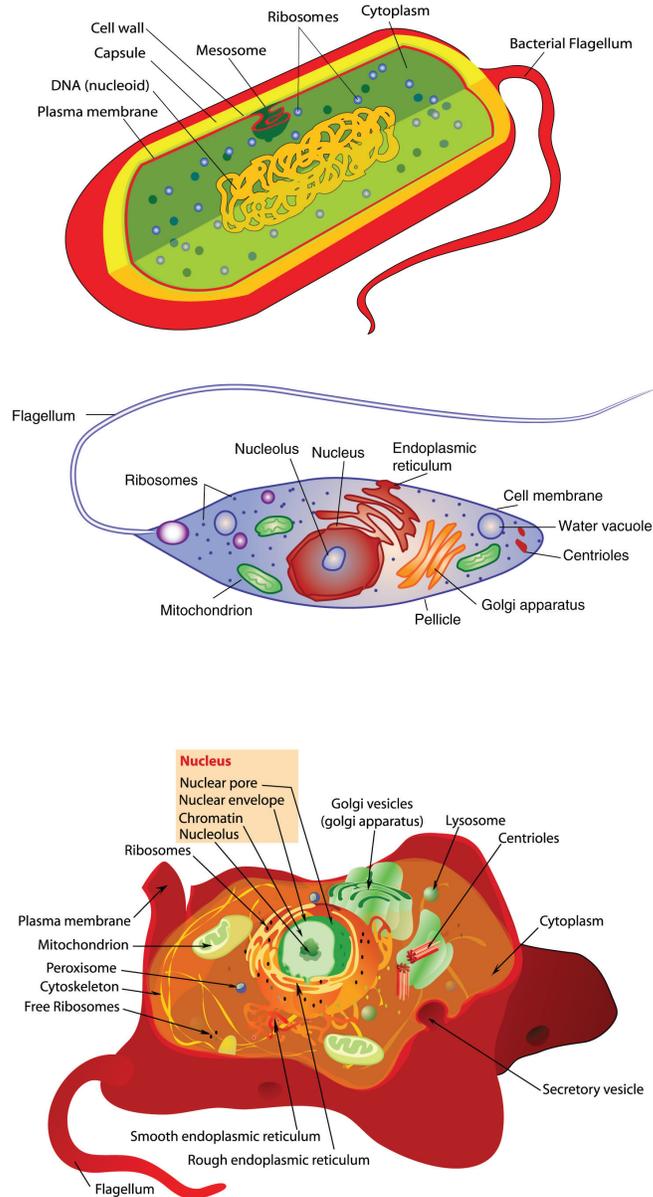


Figure 14.15: **Prokaryote and Eukaryote Cells.** Prokaryote and eukaryote cells differ significantly in their structure. Unlike prokaryote cells (upper figure), eukaryote cells (middle figure, protist cell; lower figure, animal cell) have a nucleus, which is separated by membranes from the cytoplasm of the cell. Their organelles also have membranes. Herbert Copeland thought that these and other differences were significant enough to place prokaryote and eukaryote organisms in different superkingdoms. (15)

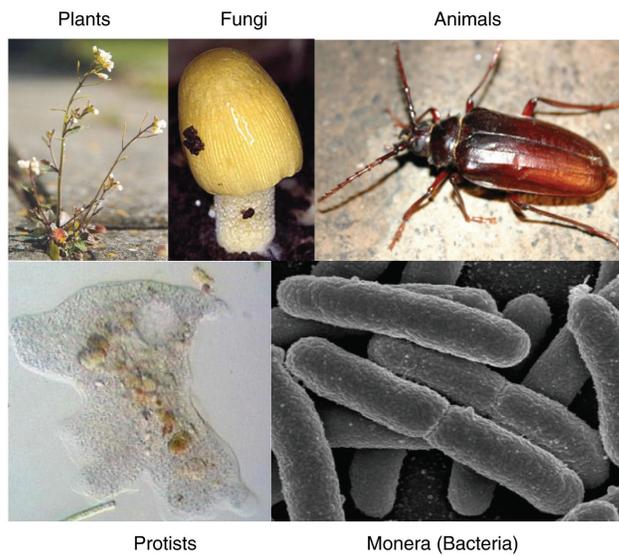


Figure 14.16: This five-kingdom system of classification was proposed by ecologist Robert Whittaker in the late 1960s. Whittaker added the Fungi kingdom to the earlier four-kingdom classification system. (3)

in appearance, their ribosomal RNA sequences are very different. In 1977, Woese and his colleagues suggested that the original bacteria kingdom should be divided into two new kingdoms, called Eubacteria and Archaeobacteria. This resulted in a six-kingdom taxonomy that has been widely accepted for many years.

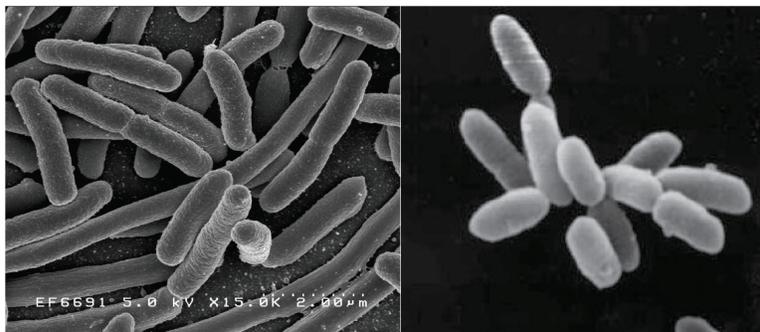


Figure 14.17: Left, Eubacteria (now called Bacteria), Right, Archaeobacteria (now called Archaea). Appearances can be deceiving! These two microorganisms are very different from one another, despite their outward similarities. Both organisms used to be classified in the bacteria kingdom. Woese suggested placing them in different kingdoms, called the eubacteria and archaeobacteria kingdoms. (10)

Domains

Woese wasn't completely happy with the six-kingdom system. It didn't show that all four eukaryote kingdoms are more closely related to each other than to the two bacteria kingdoms. It also didn't show that the two bacteria kingdoms are as different from each other as they are from the eukaryote kingdoms. To show these similarities and differences, Woese introduced a new taxon called the **domain**. He defined domain as a taxon higher than the kingdom.

The Three-Domain System

In 1990, Woese and his colleagues proposed a new classification system containing three domains: Bacteria, Archaea, and Eukarya. As shown in **Figure 14.18**, the **Bacteria** domain was formerly the Eubacteria kingdom, and the **Archaea** domain was formerly the Archaeobacteria kingdom. The **Eukarya** domain includes all four eukaryote kingdoms: plants, animals, protists, and fungi. The three-domain system emphasizes the similarities among eukaryotes and the differences among eukaryotes, bacteria, and archaea. By using domains, Woese was able to show these relationships without replacing the popular six-kingdom system.

Archaea were first found in extreme environments. For example, they were found in the hot water geysers in Yellowstone National park. Archaea have since been found in all of

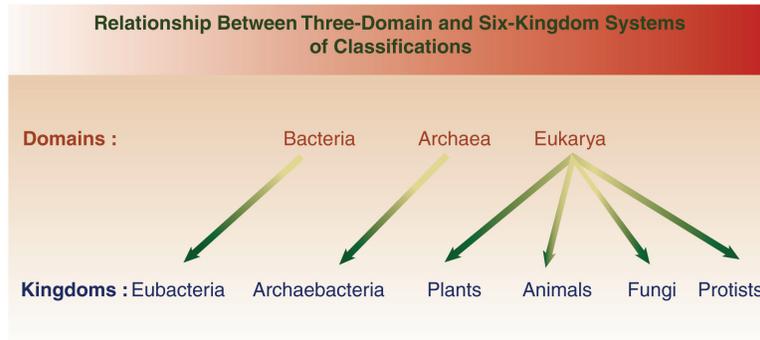


Figure 14.18: This diagram shows how the three-domain system of classification is related to the six-kingdom system. Both Eubacteria and Archaeobacteria kingdoms are raised to the level of domains (Bacteria and Archaea domains, respectively) in the three-domain system. The other four kingdoms make up the third domain (Eukarya domain). (1)

Earth's habitats. They are now known to be present everywhere in high numbers. They may contribute as much as 20 percent to Earth's total biomass.

Woese's three-domain system was quickly adopted by many other biologists. There were some critics, however, who argued that the system put too much emphasis on the uniqueness of Archaea. Later studies confirmed how different Archaea are from other organisms. For example, organisms belonging to Archaea were found to differ from both Eukarya and Bacteria in the composition of their cell membranes and the system they use for DNA replication. These differences convinced most critics that the three-domain system was justified. After its introduction in 1990, the three-domain system became increasingly popular. Within a decade of its introduction, it had largely replaced earlier classifications.

How Are the Three Domains Related?

Comparing ribosomal RNA base sequences, Woese and his colleagues also showed that organisms belonging to Eukarya are more similar to Archaea than they are to Bacteria. **Figure 14.19** is a phylogenetic tree based on their analysis. This tree places Archaea and Eukarya in the same clade (see Lesson 2). It represents the hypothesis that Archaea and Eukarya shared a more recent common ancestor with each other than with Bacteria.

The results of a study published in 2007 seem to conflict with this hypothesis. Comparing DNA base sequences, the 2007 study suggested that the domain Archaea may be older than either Bacteria or Eukarya. That would make Archaea the most ancient group of organisms on Earth. It is not yet known, which, if either, hypothesis is correct. Scientists need to learn more about Archaea and their relationships with other organisms to resolve these questions.

Phylogenetic Tree of Life

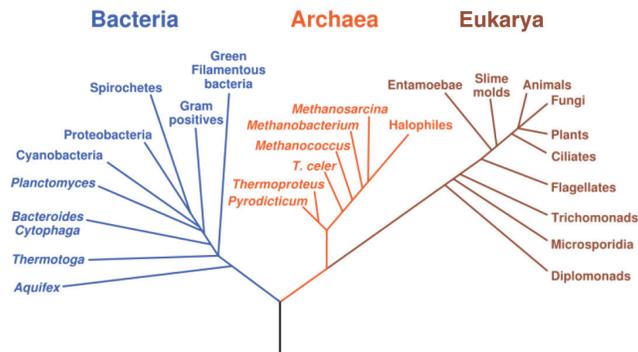


Figure 14.19: This phylogenetic tree is based on comparisons of ribosomal RNA base sequences among living organisms. The tree divides all organisms into three domains: Bacteria, Archaea, and Eukarya. Humans and other animals belong to the Eukarya domain. From this tree, organisms that make up the domain Eukarya appear to have shared a more recent common ancestor with Archaea than Bacteria. (13)

The Future of Classification

The three-domain system is unlikely to be the final word on classification. The system is based on the current state of knowledge. As knowledge increases, the three-domain system may need revision. For example, the number of domains may change as scientists learn more about those life forms we currently know least about.

A recent discovery illustrates this point. In 2003, scientists identified a new virus called mimivirus. It resembles bacteria in size and number of genes. However, the virus cannot respond to stimuli or grow by cell division, both of which are traits of bacteria and other living organisms. Mimivirus' unique combination of traits seems to place it at the boundary between living and nonliving things. Some scientists think mimivirus might represent a new domain of life.

Lesson Summary

- By 1977, four new kingdoms had been added to the plant and animal kingdoms of the original Linnaean taxonomy: Protista, Fungi, Eubacteria, and Archaeobacteria.
- In 1990, the three-domain system was introduced and is now the most widely used classification system. The three domains are Bacteria, Archaea, and Eukarya.
- As knowledge of organisms increases in the future, the three-domain system may need revision. For example, new domains may need to be added.

Review Questions

1. Name four new kingdoms that were added to the original Linnaean taxonomy.
2. How do prokaryotes and eukaryotes differ?
3. Why were fungi placed in a separate kingdom from plants?
4. What is a domain?
5. Describe the relationship between the original bacteria kingdom called monera and the domain called bacteria.
6. Explain in which domain you would classify an organism that consists of a single cell with a nucleus.
7. Compare and contrast bacteria, Archaea, and Eukarya.
8. What problem with the six-kingdom classification system was addressed by the three-domain classification system? How did it address the problem?

Further Reading / Supplemental Links

- Olaf Breidbach, *Visions of Nature: The Art and Science of Ernst Haeckel*. Prestel Publishing, 2006.
- John L. Howland, *The Surprising Archaea: Discovering Another Domain of Life*. Oxford University Press, 2000.
- Oladele Ogunseitan, *Microbial Diversity: Form and Function in Prokaryotes*. Wiley-Blackwell, 2004.

Vocabulary

archaea Domain that was formerly the Archaeobacteria kingdom.

bacteria Domain that was formerly the Eubacteria kingdom.

domain Taxon higher than the kingdom.

eukarya Domain that includes all four eukaryote kingdoms: plants, animals, protists, and fungi.

eukaryote Organisms whose cells have nuclei.

fungi Kingdom of eukaryote organisms such as mushrooms and molds.

monera Original name of the kingdom that included all bacteria.

prokaryote Organism whose cells lack nuclei.

protista Kingdom of single-celled, eukaryote organisms such as protozoa, often called “protists.”

Points to Consider

Robert Whittaker separated the fungi from the plant kingdom on the basis of their different ways of obtaining energy. You might expect Whittaker to focus on this type of difference because he was an ecologist.

- What do you think ecology is?
- What do you think ecologists study?
- In addition to ways of obtaining energy, what traits of organisms do you think ecologists are likely to be most interested in?

Image Sources

- (1) .
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- (3) <http://upload.wikimedia.org/wikipedia/en/a/a4/5kingdoms.png>. Commons.
- (4) http://en.wikipedia.org/wiki/Image:Beetle_collection.jpg. GNU-FDL.
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