



18.2 Modern Evolutionary Classification

Key Questions

- What is the goal of evolutionary classification?
- What is a cladogram?
- How are DNA sequences used in classification?

Vocabulary

phylogeny
clade
monophyletic group
cladogram
derived character

Taking Notes

Outline Make an outline of this lesson using the green headings as the main topics and the blue headings as subtopics. As you read, fill in details under each heading.

BUILD Vocabulary

WORD ORIGINS The word **cladogram** comes from two Greek words: *klados*, meaning "branch," and *gramma*, meaning "something that is written or drawn." A cladogram is an evolutionary diagram with a branching pattern.

THINK ABOUT IT Darwin's ideas about a "tree of life" suggests a new way to classify organisms—not just based on similarities and differences, but instead based on evolutionary relationships. Under this system, taxa are arranged according to how closely related they are. When organisms are rearranged in this way, some of the old Linnaean ranks fall apart. For example, the Linnaean class reptilia isn't valid unless birds are included—which means birds are reptiles! And not only are birds reptiles, they're also dinosaurs! Wondering why? To understand, we need to look at the way evolutionary classification works.

Evolutionary Classification

What is the goal of evolutionary classification?

The concept of descent with modification led to the study of **phylogeny** (fy LAHJ uh nee)—the evolutionary history of lineages. Advances in phylogeny, in turn, led to phylogenetic systematics.

The goal of phylogenetic systematics, or evolutionary classification, is to group species into larger categories that reflect lines of evolutionary descent, rather than overall similarities and differences.

Common Ancestors Phylogenetic systematics places organisms into higher taxa whose members are more closely related to one another than they are to members of any other group. The larger a taxon is, the farther back in time all of its members shared a common ancestor. This is true all the way up to the largest taxa.

Clades Classifying organisms according to these rules places them into groups called clades. A **clade** is a group of species that includes a single common ancestor and all descendants of that ancestor—living and extinct. How are clades different from Linnaean taxa? A clade must be a monophyletic (mahn oh fy LET ik) group. A **monophyletic group** includes a single common ancestor and *all* of its descendants.

Some groups of organisms defined before the advent of evolutionary classification are monophyletic. Some, however, are paraphyletic, meaning that the group includes a common ancestor but excludes one or more groups of descendants. These groups are invalid under evolutionary classification.

In Your Notebook In your own words, explain what makes a clade monophyletic or paraphyletic.

Cladograms

What is a cladogram?

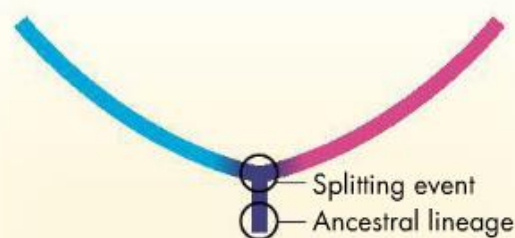
Modern evolutionary classification uses a method called cladistic analysis. Cladistic analysis compares carefully selected traits to determine the order in which groups of organisms branched off from their common ancestors. This information is then used to link clades together into a diagram called a **cladogram**.

A cladogram links groups of organisms by showing how evolutionary lines, or lineages, branched off from common ancestors.

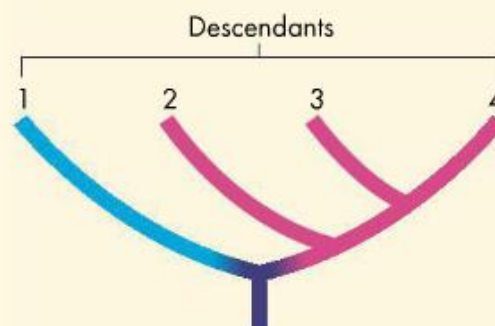
Building Cladograms To understand how cladograms are constructed, think back to the process of speciation. A speciation event, in which one ancestral species splits into two new ones, is the basis of each branch point, or node, in a cladogram. That node represents the last point at which the two new lineages shared a common ancestor. As shown in part 1 of **Figure 18-7**, a node splits a lineage into two separate lines of evolutionary ancestry.

Each node represents the last point at which species in lineages above the node shared a common ancestor. The bottom, or “root” of a cladogram, represents the common ancestor shared by all of the organisms in the cladogram. A cladogram’s branching patterns indicate degrees of relatedness among organisms. Look at part 2 of **Figure 18-7**. Because lineages 3 and 4 share a common ancestor more recently with each other than they do with lineage 2, you know that lineages 3 and 4 are more closely related to each other than either is to lineage 2. The same is true for lineages 2, 3, and 4. In terms of ancestry, they are more closely related to each other than any of them is to lineage 1. Look at the cladogram shown in part 3 of **Figure 18-7**. Does it surprise you that amphibians are more closely related to mammals than they are to ray-finned fish? In terms of ancestry, it’s true!

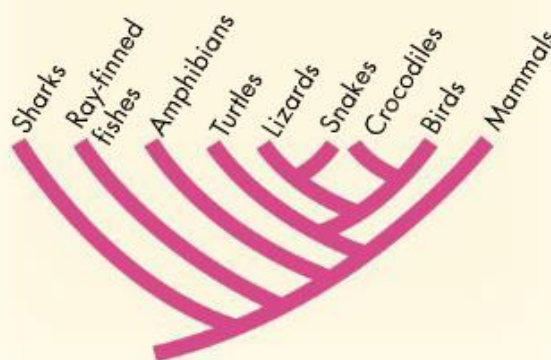
FIGURE 18-7 Building a Cladogram A cladogram shows relative degrees of relatedness among lineages.



1 Cladograms are diagrams showing how evolutionary lines, or lineages, split from each other over time. This diagram shows a single ancestral lineage splitting into two. The point of splitting is called a “node” in the cladogram.



2 How recently lineages share a common ancestor reflect how closely the lineages are related to one another. Here, lineages 3 and 4 are each more closely related to each other than any of them is to any other lineage.



3 This cladogram shows the evolutionary relationships among vertebrates, animals with backbones.

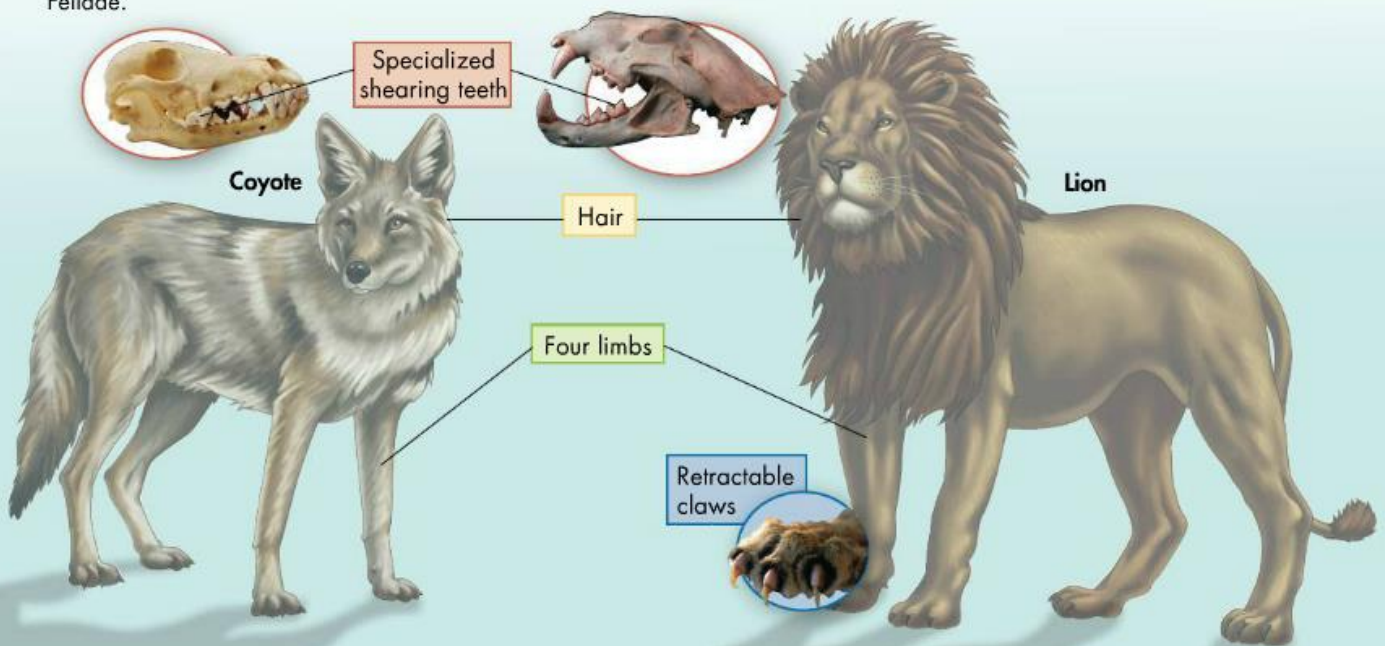
Derived Characters In contrast to Linnaean taxonomy, cladistic analysis focuses on certain kinds of characters, called derived characters, when assigning organisms into clades. A **derived character** is a trait that arose in the most recent common ancestor of a particular lineage and was passed along to its descendants.

Whether or not a character is derived depends on the level at which you're grouping organisms. Here's what we mean. **Figure 18–8** shows several traits that are shared by coyotes and lions, both members of the clade Carnivora. Four limbs is a derived character for the entire clade Tetrapoda because the common ancestor of all tetrapods had four limbs, and this trait was passed to its descendants. Hair is a derived character for the clade Mammalia. But for mammals, four limbs is *not* a derived character—if it were, only mammals would have that trait. Nor is four limbs or hair a derived character for clade Carnivora. Specialized shearing teeth, however, is. What about retractable claws? This trait is found in lions but not in coyotes. Thus, retractable claws is a derived character for the clade Felidae—also known as cats.

Losing Traits Notice above that four limbs is a derived character for clade Tetrapoda. But what about snakes? Snakes are definitely reptiles, which are tetrapods. But snakes certainly don't have four limbs! The *ancestors* of snakes, however, did have four limbs. Somewhere in the lineage leading to modern snakes, that trait was lost. Because distantly related groups of organisms can sometimes lose the same character, systematists are cautious about using the *absence* of a trait as a character in their analyses. After all, whales don't have four limbs either, but snakes are certainly more closely related to other reptiles than they are to whales.

FIGURE 18–8 Derived Characters

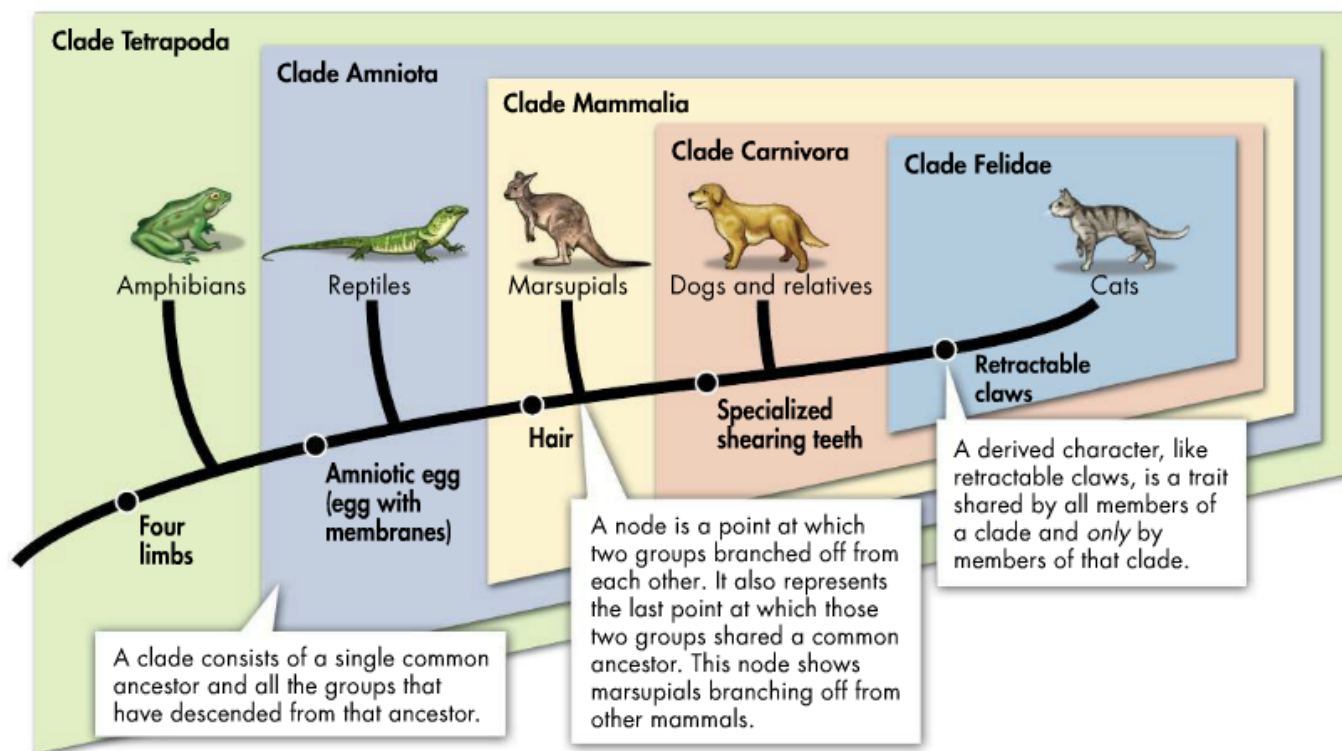
The coyote and lion share several characters—hair, four limbs, and specialized shearing teeth. These shared characters put them in the clades Tetrapoda, Mammalia, and Carnivora. The lion, however, has retractable claws. Retractable claws is the derived character for the clade Felidae.



VISUAL SUMMARY

INTERPRETING A CLADOGRAM

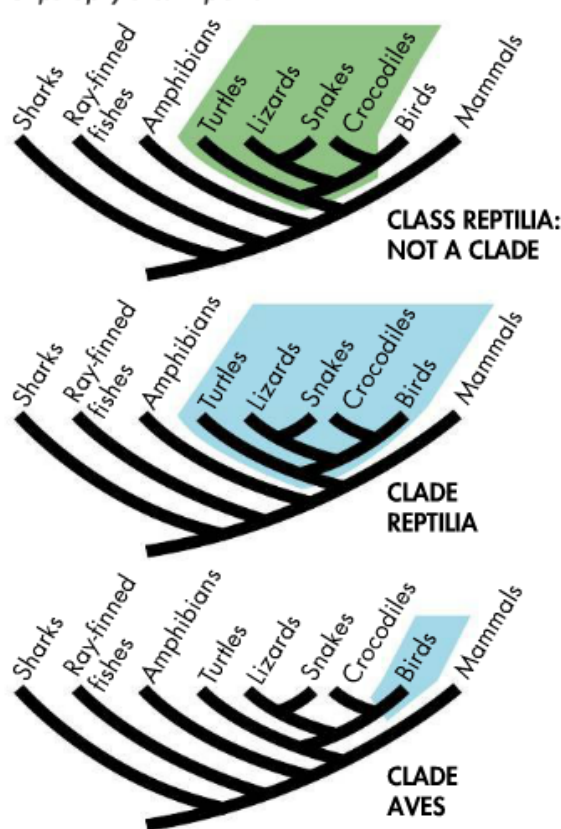
FIGURE 18-9 This cladogram shows the evolutionary history of cats. In a cladogram, all organisms in a clade share a set of derived characters. Notice that smaller clades are nested within larger clades. **Interpret Visuals** For which clade in this cladogram is an amniotic egg a derived character?



Interpreting Cladograms We can now put this information together to “read” a cladogram. **Figure 18-9** shows a simplified phylogeny of the cat family. The lowest node represents the last common ancestor of all four-limbed animals—members of the clade Tetrapoda. The forks in this cladogram show the order in which various groups branched off from the tetrapod lineage over the course of evolution. The positions of various characters in the cladogram reflect the order in which those characteristics arose in this lineage. In the lineage leading to cats, for example, specialized shearing teeth evolved before retractable claws. Furthermore, each derived character listed along the main trunk of the cladogram defines a clade. Hair, for example, is a defining character for the clade Mammalia. Retractable claws is a derived character shared only by the clade Felidae. Derived characters that occur “lower” on the cladogram than the branch point for a clade are not derived for that particular clade. Hair, for example, is not a derived character for the clade Carnivora.

In Your Notebook List the derived characters in **Figure 18-9** and explain which groups in the cladogram have those characters.

FIGURE 18–10 Clade or Not? A clade includes an ancestral species and all its descendants. Linnaean class Reptilia is not a clade because it does not include modern birds. Because it leaves this descendant group out, the class is paraphyletic. Clades Reptilia and Aves, however, are monophyletic and, therefore, valid clades. **Apply Concepts** Would a group that included all of clade Reptilia plus amphibians be monophyletic or paraphyletic? Explain.



Clades and Traditional Taxonomic Groups Which of the Linnaean groupings form clades, and which do not? Remember that a true clade must be monophyletic, which means that it contains an ancestral species and *all* of its descendants—it can't leave any out. It also cannot include any species which are not descendants of that original ancestor. Cladistic analysis shows that many traditional taxonomic groups do form valid clades. For example, Linnaean class Mammalia corresponds to clade Mammalia (shown in **Figure 18–9**). Members of this clade include all vertebrates with hair and several other important characteristics.

In other cases, however, traditional groups do not form valid clades. **Figure 18–10** shows why. Today's reptiles are all descended from a common ancestor. But birds, which have traditionally not been considered part of the Linnaean class Reptilia, are also descended from that same ancestor. So, class Reptilia, without birds, is not a clade. However, several valid clades *do* include birds: Aves (the birds themselves), Dinosauria, and the clade named Reptilia. So, is it correct to call birds reptiles? An evolutionary biologist would say yes!

You may be wondering: class Reptilia, clade Reptilia, who cares? But the resulting names aren't as important as the concepts behind the classification. Evolutionary biologists look for links between groups, figuring out how each is related to others. So the next time you see a bird, thinking of it as a member of a clade or class isn't as important as thinking about it not just as a bird, but also as a dinosaur, a reptile, a tetrapod, and a chordate.

Quick Lab

GUIDED INQUIRY

Constructing a Cladogram

- 1 Identify the organism in the table that is least closely related to the others.
- 2 Use the information in the table to construct a cladogram of these animals.

Analyze and Conclude

1. **Interpret Tables** What trait separates the least closely related animal from the other animals?
2. **Apply Concepts** Do you have enough information to determine where a frog should be placed on the cladogram? Explain your answer.

Derived Characters in Organisms


Organism	Derived Character		
	Backbone	Legs	Hair
Earthworm	Absent	Absent	Absent
Trout	Present	Absent	Absent
Lizard	Present	Present	Absent
Human	Present	Present	Present

3. **Draw Conclusions** Does your cladogram indicate that lizards and humans share a more recent common ancestor than either does with an earthworm? Explain your answer.

DNA in Classification

How are DNA sequences used in classification?

The examples of cladistic analysis we've discussed so far are based largely on physical characteristics like skeletons and teeth. But the goal of modern systematics is to understand the evolutionary relationships of all life on Earth—from bacteria to plants, snails, and apes. How can we devise hypotheses about the common ancestors of organisms that appear to have no physical similarities?

Genes as Derived Characters Remember that all organisms carry genetic information in their DNA passed on from earlier generations. A wide range of organisms share a number of genes and show important homologies that can be used to determine evolutionary relationships. For example, all eukaryotic cells have mitochondria, and all mitochondria have their own genes. Because all genes mutate over time, shared genes contain differences that can be treated as derived characters in cladistic analysis. For that reason, similarities and differences in DNA can be used to develop hypotheses about evolutionary relationships.  **In general, the more derived genetic characters two species share, the more recently they shared a common ancestor and the more closely they are related in evolutionary terms.**

New Techniques Suggest New Trees The use of DNA characters in cladistic analysis has helped to make evolutionary trees more accurate. Consider, for example, the birds in **Figure 18–11**. The hooded vulture from Africa in the top photograph looks a lot like the American vulture in the middle photograph. Both were traditionally classified in the falcon clade. But American vultures have a peculiar behavior: When they get overheated, they urinate on their legs, relying on evaporation to cool them down. Storks share this behavior, while hooded vultures and other vultures from Africa do not. Could the behavior be a clue to the real relationships between these birds?

Biologists solved the puzzle by analyzing DNA from all three species. Molecular analysis showed that the DNA from American vultures is more similar to the DNA of storks than to the DNA of African vultures. DNA evidence therefore suggests that American vultures and storks share a more recent common ancestor than the American and African vultures do. Molecular analysis is a powerful tool that is now routinely used by taxonomists to supplement data from anatomy and answer questions like these.



FIGURE 18–11 DNA and Classification Scientists use similarities in the genetic makeup of organisms to help determine classification. Traditionally African vultures and American vultures were classified together in the falcon family. But DNA analysis suggests that American vultures are actually more closely related to storks.

MYSTERY CLUE



DNA comparisons show that some populations of brown bears are more closely related to polar bears than they are to other brown bears. What do you think this means for the classification of polar bears?

Often, scientists use DNA evidence when anatomical traits alone can't provide clear answers. Giant pandas and red pandas, for example, have given taxonomists a lot of trouble. These two species share anatomical similarities with both bears and raccoons, and both of them have peculiar wrist bones that work like a human thumb. DNA analysis revealed that the giant panda shares a more recent common ancestor with bears than with raccoons. DNA places red pandas, however, outside the bear clade. So pandas have been reclassified, placed with other bears in the clade Ursidae, as shown in **Figure 18-12**. What happened to the red panda? It is now placed in a different clade that also includes raccoons and other organisms such as seals and weasels.

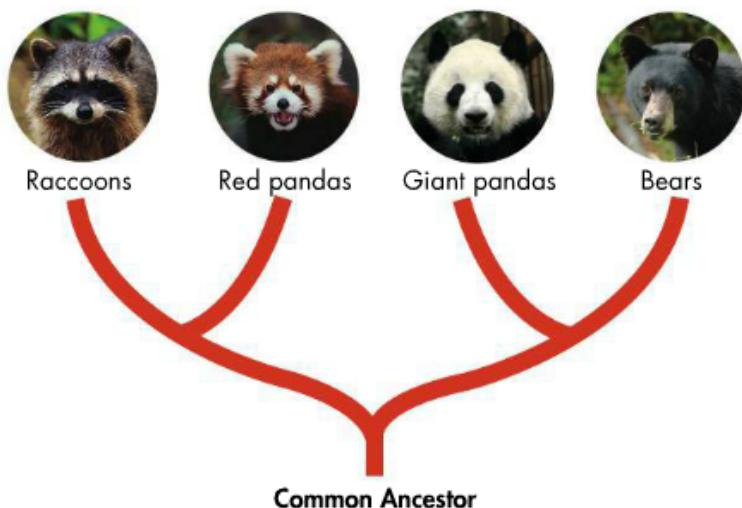


FIGURE 18-12 Classification of Pandas Biologists used to classify the red panda and the giant panda together. However, cladistic analysis using DNA suggests that the giant panda shares a more recent common ancestor with bears than with either red pandas or raccoons.

18.2 Assessment

Review Key Concepts

- Explain** How does evolutionary classification differ from traditional classification?
 - Apply Concepts** To an evolutionary taxonomist, what determines whether two species are in the same genus?
- Explain** What is a derived character?
 - Interpret Diagrams** Along any one lineage, what do the locations of derived characters on a cladogram show? In your answer, use examples from **Figure 18-9**.
- Review** How do taxonomists use the DNA sequences of species to determine how closely two species are related?
 - Relate Cause and Effect** Explain why the classification of American vultures has changed.

VISUAL THINKING

- Examine the cladogram.
 - Interpret Diagrams** Which groups—X and Y, or X, Y, and Z—have the most recent common ancestor?
 - Infer** Which species—X and Y, or X and Z—share more derived characters?

