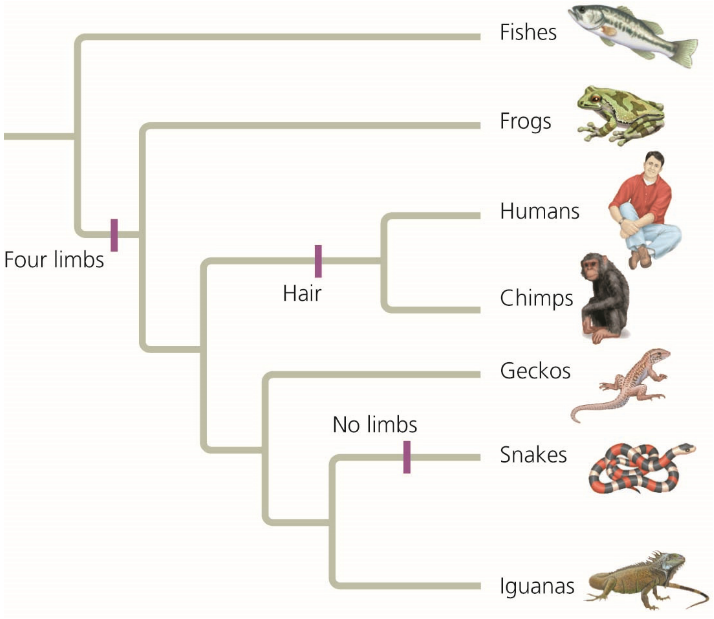
Chapter 26: Phylogeny and the Tree of Life

26.1 Define phylogeny and explain how phylogenies are used.
26.2 Explain how phylogenetic trees are inferred from data.
26.3 Differentiate between derived and ancestral characters and explain how they are used to construct phylogenetic trees.
26.4 Describe what evidence a genome provides about evolutionary history.
26.5 Explain what molecular clocks are and how they are used.
26.6 Describe the possible structure of the tree of all life.

Every topic you study ties in with evolution, but this chapter specifically deals with the evidence that can be used to build cladograms, and how these phylogenetic trees are interpreted. Throughout your study of biology, you will use this skill over and over.

Study Tip: The underlying concept in preparing phylogenetic trees, like the one in Figure 26.1 in your text, is to use traits shared due to *common ancestry* to classify organisms into groups that reflect their *evolutionary history*. Your first step in learning how to prepare and interpret phylogenetic trees is to label Figure 26. 1 below. Working from what you have labeled, explain the significance of *common ancestor*, *sister taxa*, and what a *character* represents.



Concept 26.1 Phylogenies show evolutionary relationships

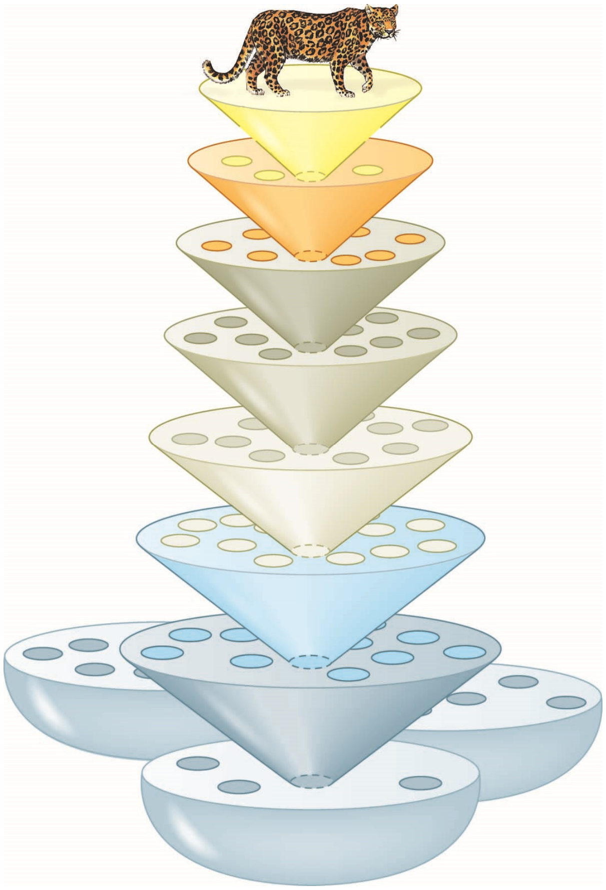
LO 26.1: Define phylogeny and explain how phylogenies are used.

1. Let's get started by explaining two terms: *phylogeny* and *systematics*.

2. Every organism on Earth may be referred to by a unique *binomial*, or a two-part name. These are in Latin, or latinized. What is your binomial? What does it mean?

3. What are the two components of every binomial?

4. Taxonomy uses hierarchical categories that nest within each other, like Russian dolls. The following figure shows the categories, each called a *taxon*. Label each taxonomic category and then give the one that applies exclusively to this panther to the side of each level.



You will notice that the most general category, *domain*, the one that encompasses the most organisms, is shown at the bottom of the figure. As you move up in the figure, the organisms show greater and greater degrees of relatedness. In order to discuss groups of organisms, try to memorize these taxonomic categories in order. Most students use a mnemonic device linked to the first letter of each taxon to remember them. Make up your own, or try ours:

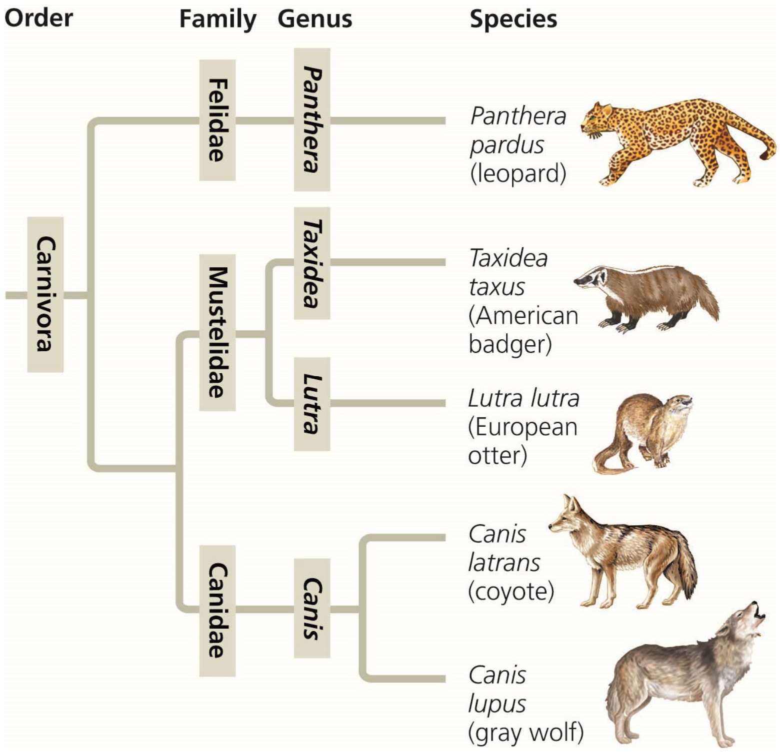
D K P C O F G S or *__D__ear __K__ing __P__hillip __C__omes __O__ver __F__or __G__ood __S__paghetti*

(You may choose to have Dear King Philip come over for something else—whatever you can remember best!)

5. So, which are more closely related: organisms in the same phylum or those in the same order?

6. How are the concepts of phylogeny and systematics used to develop *phylogenetic trees*?

7. In a *phylogenetic tree*, recall that branch points represent common ancestors of the two lineages beyond the branch or *node*. Circle the common ancestor of badgers and otters, and label it as A. Circle the common ancestor of cats and dogs, and label it as B. Explain the relationship between leopard, badger, and wolf.



8. Figure 26.5 in your text is critical to understanding phylogenetic trees and the relationships they display. Carefully read the top section of **Parts of a Phylogenetic Tree.**

   What does a *branch point* represent?

   What are *sister taxa*?

9. *Phylogenetic trees* can be presented in alternative forms, horizontal, vertical or diagonal, as illustrated in Figure 26.5 in your text. Note that *all* the trees on this page display the same information. Identify the sister taxa shown in the trees.

10. The final part of Figure 26.5, **Rotating Around Branch Points**, can be a point of confusion. When you are interpreting a tree, what matters is the branching pattern, not the order of the organisms. Both trees show the same evolutionary relationships. Note that rotating around branch points can change the way the tree looks but does not change the evolutionary relationships. In the phylogenetic tree on the right, are humans shown to be more closely related to frogs or to lizards? Explain.

11. In the space below, redraw the tree as directed in question 5 of this figure, rotating it around the green branch point. Does your new tree show any new evolutionary relationships?

12. What does it mean for a phylogenetic tree to be *rooted*?

    Look back at Figure 26.5 in your text. The horizontal tree is rooted to the left. Where is the vertical tree rooted?

13. Why are fishes considered the *basal taxon*?

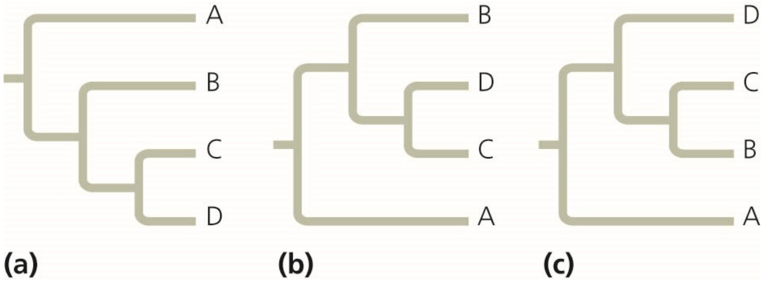
14. What three key points about phylogenetic relationships cannot be determined from phylogenetic trees?

    a.

    b.

    c.

15. Which of the trees shown here depicts an evolutionary history different from the other two? Explain.



Concept 26.2 ***Phylogenies are inferred from morphological and molecular data***

LO 26.2: Explain how phylogenetic trees are inferred from data.

Look back at the *Study Tip* from Chapter 22. This idea is repeated in the current chapter.

Study Tip

Homologous structures show evidence of relatedness (whale fin, bat wing).

Analogous structures are similar solutions to similar problems but do *not* indicate close relatedness (bird wing, butterfly wing).

16. How could convergent evolution be a confusing factor in developing phylogenetic trees?

17. Why is it important to sort homologous from analogous structures? Which are appropriately used in creating phylogenetic trees?

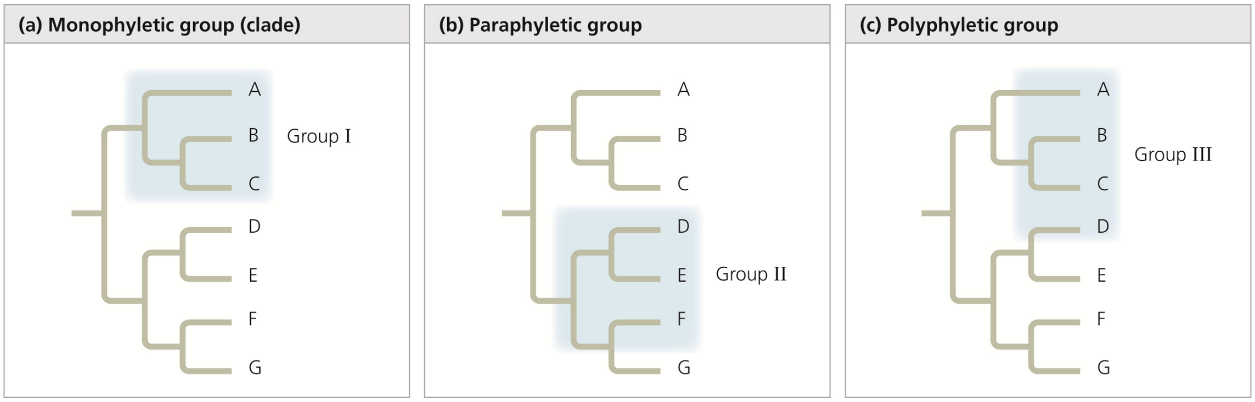
18. Study Figure 26.8 in your text. Mutations accumulate in similar gene sequences in different species over time. How can DNA homologies be determined after these genetic changes?

19. The WHAT IF? question on p. 559 of your textbook is a good check to see if you understand the point about molecular homologies. Suppose that two species, A and B, have similar appearances but very divergent gene sequences, whereas species B and C have very different appearances but similar gene sequences. Which pair of species is more likely to be closely related: A and B or B and C? Explain.

Concept 26.3 Shared characters are used to construct phylogenetic trees

LO 26.3: Differentiate between derived and ancestral characters and explain how they are used to construct phylogenetic trees.

20. The following figure shows three *cladograms*. What is a *clade*? Circle a clade that is not highlighted below.



21. Why is Group I *monophyletic*?

22. Explain why Group II is *paraphyletic*.

23. Why is Group III *polyphyletic*?

24. Clades are developed by using *shared derived characters*. What are these?

25. Explain why, for mammals, hair is a *shared derived character*, but a backbone is a *shared ancestral character.*

26. Study the relationship between the character table and the phylogenetic tree in Figure 26.12 in your text. Why is the lancelet considered the outgroup?

    How many characters does the lancelet share with the other taxa in the figure?

    What animals would be included in a clade that started with four limbs?

27. Earlier, we emphasized that the sequence of branching in a tree does not necessarily indicate the actual ages of the species or the amount of genetic change. However, phylogenetic trees can be created that show these features. Study the phylogenetic trees in Figures 26.13 and 26.14 in your text. Explain what is different about them in comparison to the other trees you have examined so far.

28. Explain how evolutionary biologists use *maximum parsimony* and “Occam’s razor” to help determine the most likely phylogenetic tree.

29. Phylogenetic trees represent a ______________ about how the organisms in the tree are related to one another.

30. Parsimony and phylogenetic trees were used to create this hypothesis: the closest living relatives of birds are crocodiles. What evidence supports this hypothesis?

Study Tip

If you are still struggling with this concept, go to Figure 26.12 in your text, cover the phylogenetic tree portion, then create your own tree from the character table. The exercise will be worth your time!

Concept 26.4 An organism's evolutionary history is documented in its genome

LO 26.4: Describe what evidence a genome provides about evolutionary history.

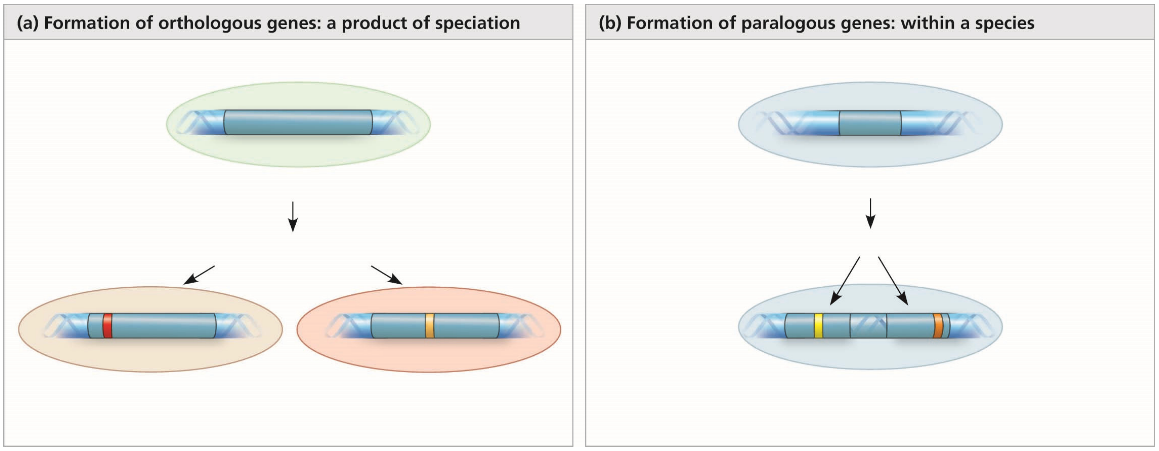
Let's summarize some important information from this section. The rate of evolution of DNA sequences varies from one part of the genome to another; therefore, comparing different sequences helps us to investigate relationships between groups of organisms that diverged a long time ago. For example, DNA that codes for *ribosomal RNA (rRNA*) changes relatively slowly and is useful for investigating relationships between taxa that diverged hundreds of millions of years ago. DNA that codes for *mitochondrial DNA (mtDNA)* evolves rapidly and can be used to explore recent evolutionary events.

31. Which method reveals that fungi are more closely related to animals than to plants?

32. Which method reveals that the Pima of Arizona and Yanomami of Venezuela are descendants of the same Native Americans who crossed the Bering Land Bridge 15,000 years ago?

33. How do *orthologous genes* indicate descent from a common ancestor? You might use humans and mice and humans and yeast as examples.

34. Gene duplication leads us to distinguish two types of homologous genes. Label the figure, and then below the figure explain the difference between *orthologous* and *paralogous genes.*



35. Explain why mice are often excellent model organisms that can be used in the study of human diseases.

36. A phrase that you will encounter in other contexts is that the genes for these shared biochemical and developmental pathways are *conserved.* How does this indicate descent from a common ancestor?

Concept 26.5 Molecular clocks help track evolutionary time

LO 26.5: Explain what molecular clocks are and how they are used.

37. What are *molecular clocks*?

38. What are the basic assumptions in using molecular clocks with orthologous and paralogous genes?

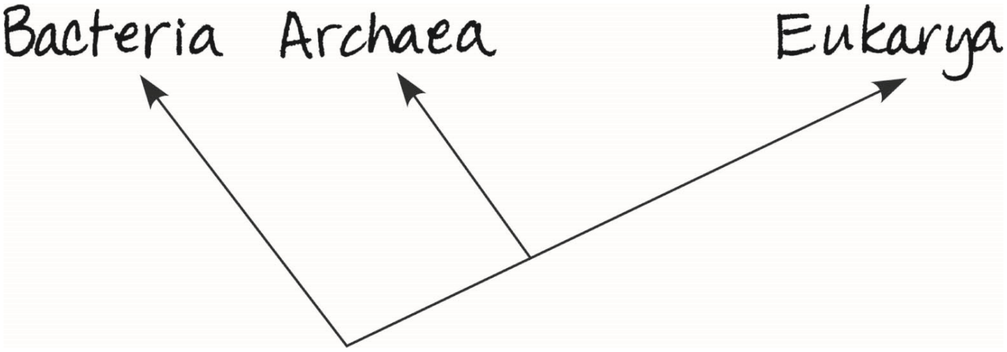
39. If we use a *molecular clock*, approximately when did HIV emerge?

40. What are two problems with molecular clocks?

Concept 26.6 Our understanding of the tree of life continues to change based on new data

LO 26.6: Describe the possible structure of the tree of all life.

Taxonomy is in flux! When your authors were in high school, we were taught there were two kingdoms: Plants and Animals. Then in our college courses, we were introduced to five kingdoms: Monera, Protista, Plantae, Fungi, and Animalia. Now biologists have adopted a *three-domain system*, which consists of the domains Bacteria, Archaea, and Eukarya, shown here. This system arose from the finding that there are two distinct lineages of prokaryotes.



41. What two domains include all prokaryotes? ______________________________

42. Which two domains are most closely related? Explain your reasoning.

43. Which kingdom is made obsolete by the three-domain system? Why?

44. Which kingdom crumbled because it is polyphyletic?

45. *Horizontal gene transfer* has played a key role throughout the evolutionary history of life. What is it?

46. Explain the role of horizontal gene transfer in the tree of life by giving three examples.

Test Your Understanding, p. 572

Now you should be ready to test your knowledge. Place your answers here:

1. _________ 2. _________ 3. _________ 4. _________ 5. _________

6. _________ 7. _________