

Chapter Outline

- 16.1 – All of Life Is Connected through Its Evolutionary History
- 16.2 – Phylogeny Can Be Reconstructed from Traits of Organisms
- 16.3 – Phylogeny Makes Biology Comparative and Predictive
- 16.4 – Phylogeny Is the Basis of Biological Classification

It is challenging to tell the full story of the amazing diversity of life; many attributes of living organisms are so different that the task seems hopelessly complex. Complications include an incredibly long passage of time, far removed from our daily experience of seconds, minutes, and hours, and we have only an incomplete record of all changes. Nonetheless, there are many, many similarities between organisms, both living and dead, and these provide clues used by biologists to follow the many branches in the vast tree of life.

Much as a family tree traces a family's generations over time, phylogenetic trees trace evolutionary history. A family tree includes the names of family members, whereas a phylogenetic tree is built with the units of taxonomic categories, such as orders and species. Phylogenetic trees reveal evolutionary history, and they permit us to make predictions about

what might be possible as life responds to the never-ending changes in environmental and other selection pressures.

The specific parts of the AP Biology curriculum in Chapter 16 addressing **Big Idea 1**: The process of evolution drives the diversity and unity of life, include:

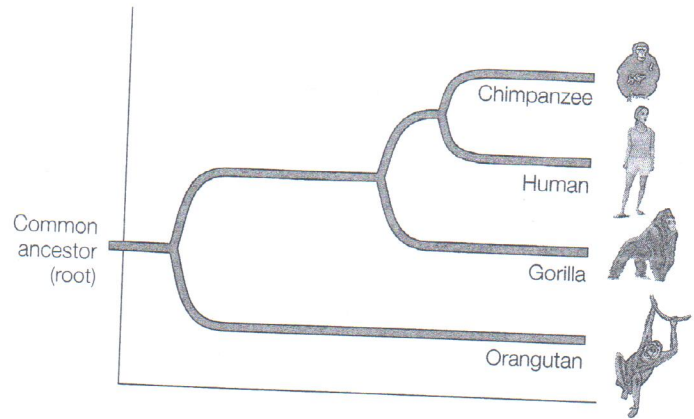
- **1.A.4:** Biological evolution is supported by scientific evidence from many disciplines, including mathematics.
- **1.B.1:** Organisms share many conserved core processes and features that evolved and are widely distributed among organisms today.
- **1.B.2:** Phylogenetic trees and cladograms are graphical representations (models) of evolutionary history that can be tested.

Chapter Review

Concept 16.1 examines how all of life is connected through its evolutionary history. Try to imagine the long personal history that led you to what you're doing right now. If you were to create your family tree, the logic and simplicity of your family pedigree would become clear. The same approach works with the history of relationships that preceded today's diverse plants and animals.

Evidence of species interconnectedness is particularly compelling when it comes to examining genomes, which are a kind of "molecular registry" of evolution. Relationships within a particular level of taxonomic organization are depicted using simple phylogenetic trees. Typically, these "trees" are presented sideways, with most branching on the right side of the tree, and time (usually in unspecified and varying intervals) along the horizontal axis. The branch-points in phylogenetic trees indicate occasions where one group developed a substantial difference from its ancestral group, justifying its placement away from a straight linear sequence of genetic inheritance.

1. Refer to the phylogenetic tree at the right.



a. What clades are indicated in the tree? _____

b. Choose the taxonomic branching that occurred most recently, and justify your selection. _____

c. Discuss the reasons why one of the organisms depicted would be interested in its evolutionary relationships to the other three organisms. _____

2. Homologous structures are of great use in determining evolutionary relationships. Explain the homology that is present in each pair of items below.

a. The spinal cord of a shark and that of a chimpanzee: _____

b. The wing of a bird and that of a bat: _____

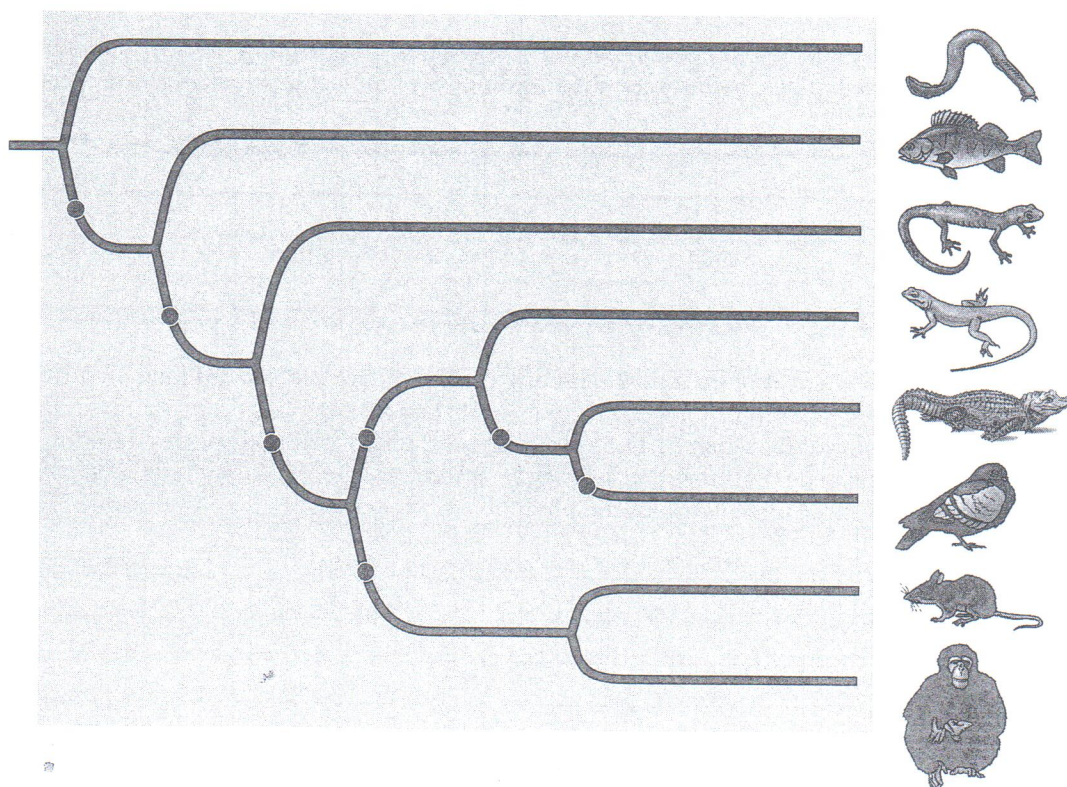
c. A vision-related gene in fruit flies that is identical to that in mice: _____

Concept 16.2 examines how phylogeny can be reconstructed by examining the traits of organisms. The physical and other traits of organisms help us organize groups to reveal evolutionary relationships. Such analyses are built on two assumptions: 1) There hasn't been any convergent evolution (i.e., a "new" trait arose only once in the set of organisms selected for analysis), and 2) Traits of interest were not lost over the evolutionary interval under consideration.

Information that is used to construct phylogenetic trees and cladograms includes morphology (physical features of traits, such as flowers), patterns seen during development (such as Hox genes in vertebrate and invertebrate development), behaviors (such as similar mating calls in varied frog populations), and molecular sequences in genes of interest, especially mitochondrial and chloroplast genes.

3. Use data from the table below to label the small dots in the phylogenetic tree with the appropriate derived traits.

EIGHT VERTEBRATES AND THE PRESENCE OR ABSENCE OF SOME SHARED DERIVED TRAITS								
Taxon	Derived trait							
	Jaws	Lungs	Claws or nails	Gizzard	Feathers	Fur	Mammary glands	Keratinous scales
Lamprey (outgroup)	–	–	–	–	–	–	–	–
Perch	+	–	–	–	–	–	–	–
Salamander	+	+	–	–	–	–	–	–
Lizard	+	+	+	–	–	–	–	+
Crocodile	+	+	+	+	–	–	–	+
Pigeon	+	+	+	+	+	–	–	+
Mouse	+	+	+	–	–	+	+	–
Chimpanzee	+	+	+	–	–	+	+	–



4. *Parsimony* refers to the way a particular analysis, among many analyses, generates the simplest possible solution to a problem. Describe what parsimony means in the context of Question 3.

5. Though their body shapes are similar, snakes and worms have substantially different evolutionary histories. Discuss how this convergence might have occurred, and suggest additional data that could be sought in determining the differences in their evolutionary lineages.

6. Explain why phylogenetic trees based on gene sequences are more accurate in showing evolutionary relationships than phylogenetic trees based on morphology.

Concept 16.3 explores how phylogeny makes biology both comparative and predictive. Phylogenetic analysis of organisms that appear to be similar has often shown that they arrived at such similarity via convergent evolution, rather than simply being closely related to one another.

Knowing phylogenetic pathways helps us see the broad scope of evolutionary change, but it also reveals some of its limitations. Such knowledge is used in choosing genes from wild plants to engineer into domestic plants and in analyzing patterns of pathogen diversification. Therefore, phylogeny is of considerable value in solving the problems faced by our species.

7. Explain how protein analyses can help meet the challenge of determining the approximate time that an evolutionary change took place, including a discussion of the "molecular clock of protein changes."

8. Female swordtail fish (*Xiphophorus*) show a mating preference for males with long swordtails, suggesting that sexual selection for longer tails over evolutionary time has occurred. Even though the males of a related species of platyfish do not have long tails, females of that species demonstrate a preference to mate with male platyfish that have been fitted with artificial long tails. Discuss what the females' mating preference suggests about the phylogenetic background of both groups of fish.

9. Discuss how studies of the "molecular clock of DNA changes" allowed an estimate of the specific year of origin for the human immunodeficiency virus.

Concept 16.4 explains how phylogeny has become the basis of biological classification. Making sense of the immense biological diversity requires us to examine the relationships of all organisms. Phylogenetic analysis is really evolutionary history, and with it, we know more about the possible directions that evolution may take in the future, with or without our help. The development of taxonomic rules will result in the most parsimonious and accurate description of evolutionary consequences: speciation.

10. Describe the Linnaean binomial nomenclature of your own species.

11. Place the taxonomic terms *order*, *genus*, *family*, *species*, *class*, *phylum*, *kingdom* in correct sequence, from most inclusive to most specific.

12. Explain why it is essential that each group of organisms included in genetic databases has an accurate and specific taxonomic identity.

13. An article in a recent newspaper placed humans in the genus *sapiens*. Explain why this is inaccurate and why *sapiens* cannot be used by itself.

Science Practices & Inquiry

In the AP Biology Curriculum Framework, there are seven **Science Practices**. In this chapter, we focus on **Science Practice 5**: The student can use mathematics appropriately. More specifically, we focus on **Science Practice 5.3**: The student can evaluate the evidence provided by data sets in relation to a particular scientific question.

Question 14 provides an opportunity to evaluate evidence and find patterns and relationships. We examine characteristics of animals that spend most of their time in water, and we attempt to determine their evolutionary relationships (**Learning Objective 1.9**).

14. Sharing aquatic habitats suggests a shared evolutionary heritage, but there are many other things to consider. Here we will survey traits of four animals with aquatic lifestyles: sponges, fish, newts, and whales. Sponges do not have circulatory systems, fish have two-chambered hearts, aquatic newts have three-chambered hearts, and whales have four-chambered hearts. Sponges, fish, and newts are poikilothermic (cold-blooded), whereas whales are homeothermic (warm-blooded). Sponges reproduce both asexually and sexually; when reproducing sexually, sponges shed gametes externally. The fish and newt shed their gametes externally; internal fertilization, internal development (gestation, or pregnancy), and nursing of offspring are reproductive characteristics of whales. Sponges do not have true tissues, while fish, newts, and whales do.

- a. Create a table to describe these animals and their characteristics.

- b. Draw a phylogenetic tree using this information.

- c. Indicate on your cladogram where each of the characteristics arose. Then provide an evolutionary justification for where you placed the characteristics.
