

7

The Phylogeny of Vertebrates

INVESTIGATION • 1–2 CLASS SESSIONS

OVERVIEW

Students study a data matrix of shared derived characters to create a tree for a group of vertebrates. Given additional morphological evidence, they decide which of three tree hypotheses is consistent with the evidence provided.

KEY CONTENT

1. The millions of species of plants, animals, and microorganisms that live on earth today are related by descent from common ancestors.
2. Modern biological classifications show how taxa are related based on similarities that reflect their genealogical relationships.
3. Shared derived characters as evidence of common ancestry determine where to place taxa on a tree.
4. Scientific hypotheses are tentative-and-testable statements that are either supported or not supported by observational evidence.
5. Morphological evidence, such as forelimb structure and function, combined with other evidence leads scientists to hypothesize the evolutionary relationships of taxa on a tree.
6. Scientific explanations must adhere to criteria such as the application of appropriate evidence, consistently logical reasoning, and basis in accepted historical and current scientific knowledge.

KEY PROCESS SKILLS

1. Students interpret data.
2. Students construct explanations based on knowledge and reasoning.

MATERIALS AND ADVANCE PREPARATION

For the teacher

- Transparency 7.1, “Taxonomy”
- Transparency 7.2, “Vertebrate Forelimbs”
- Transparency 7.3, “Homology and Analogy”
- Transparency 7.4, “Vertebrate Tree”
- Transparency 7.5, “Hypotheses for Vertebrate Phylogeny”

For each pair of students

- set of seven Vertebrate Cards
- set of seven Forelimb Skeleton Cards
- colored pencils*

For each student

- Student Sheet 7.1, “Evidence in Anklebones”
- Student Sheet 3.1, “Ideas about Evolution,” from Activity 3

TEACHING SUMMARY

Getting Started

- Review shared characters, and introduce a character matrix.

Doing the Activity

- Students observe vertebrate forelimbs as evidence for common ancestry.
- Students construct a tree from a character matrix and determine which of three tree hypotheses is most consistent with the evidence provided.
- Students revisit the statements on Student Sheet 3.1, “Ideas about Evolution.”

Follow-up

- ✓ The class discusses the three tree hypotheses for the evolutionary relationships of six vertebrates.

BACKGROUND INFORMATION

Classification

Swedish scientist Carolus Linnaeus (1707–1778) developed a binomial system of classification in which all living things were placed into a genus and species. As other scientists adopted and improved on Linnaeus's two-part taxonomy, an internationally accepted seven-level system developed, which is known today as the Linnaean system. The largest grouping was the kingdom, followed by a subgroup, the phylum, followed by the successively smaller subgroups of class, order, family, genus, and species. Another higher level of classification, the domain, was introduced in 1990. The chart below shows the classification for a sample set of taxa.

While a rose was still called a rose in common language, to the scientists studying plants, rose could refer to any one of 100–150 plants in the same genus. The Linnaean system allowed them to classify specific roses, such as *Rosa canina*, *Rosa stellata*, and *Rosa rugosa*. Linnaeus had combined two previous schools of thought about classification, which were classification by dividing into smaller groups and classification by observing similar characteristics and grouping by relationship. The seven-level system was, however, inherently flawed and arbitrary in that scientists accepted the existence of seven levels without investigation.

Recent Classification Strategies

Charles Darwin (1809–1882) took ideas about order in nature in a new direction. He developed a classification system based on phylogeny (common ancestry), rather than

morphology. His focus was on variation among individuals, natural selection, and descent with modification. Darwin recognized the heritability of characteristics and proposed that resemblances between species were due to characteristics inherited from common ancestral species. He looked at certain inherited characteristics—homologues—to identify common ancestry and to reconstruct evolutionary history. Unlike his predecessors, Darwin stated that classifications should be based on ancestry or genealogy alone.

Evolutionary Trees as Scientific Representations

German biologist Willi Hennig (1913–1976) proposed a way to classify living things genealogically in a method called either phylogenetic systematics or cladistics. Systematics is an analytical approach to understanding the diversity and relationships between living things based on shared derived characters rather than overall similarity. Systematists have in the past studied the fossils and the form and structure of an organism and its parts (morphology), and biochemical similarities or homologies as the bases for inferring relationships among taxa. The advent of molecular biology allowed systematists to add molecular data sets, including sequences of proteins and DNA and RNA, to compare taxa.

As new information becomes known and considered with all other available evidence, scientists might move taxa from one group to another on the evolutionary tree. Although scientists sometimes use the Linnaean system of classification for convenience, evolutionary biologists avoid it because the rankings are arbitrary and not based on evolutionary relationships.

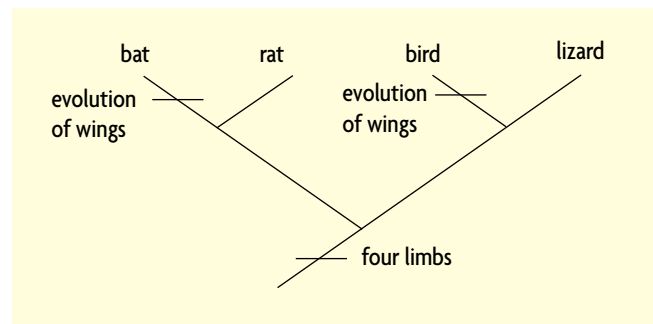
Biological Classification						
LEVEL	NORTHERN RED OAK TREE	MOUSE	E. COLI	HOUSE CAT	HUMAN	CHIMPANZEE
Domain	Eukarya	Eukarya	Bacteria	Eukarya	Eukarya	Eukarya
Kingdom	Plantae	Animalia	Eubacteria	Animalia	Animalia	Animalia
Phylum	Magnoliophyta	Chordata	Proteobacteria	Chordata	Chordata	Chordata
Class	Magnoliopsida	Mammalia	Gamma Proteobacteria	Mammalia	Mammalia	Mammalia
Order	Fagales	Rodentia	Enterobacteriales	Carnivora	Primates	Primates
Family	Fagaceae	Muridae (superfamily, Muroidea; subfamily, Murinae)	Enterobacteriaceae	Felidae	Hominidae	Hominidae
Genus	<i>Quercus</i>	<i>Mus</i>	<i>Escherichia</i>	<i>Felis</i>	<i>Homo</i>	<i>Pan</i>
Species	<i>Quercus rubra</i>	<i>Mus musculus</i>	<i>Escherichia coli</i>	<i>Felis domesticus</i>	<i>Homo sapiens</i>	<i>Pan troglodytes</i>

Homologies and Analogies

Because evolutionary trees are hypotheses about the evolutionary relationships of taxa, the characters that scientists identify to construct a tree must be reliable indicators of common ancestry. Shared characters are divided into two categories: homologous and analogous. Homologous characters are defined by evolutionary biologists as those that are shared by a species or a group of species and their common ancestor.

Homologous characters are further subdivided into shared derived and shared ancestral characters. Shared derived characters are unique to a lineage and the common ancestor and therefore help to define evolutionary relationships. Forelimbs are an example of a shared derived character. Shared ancestral characters are found in the common ancestor, but only in some of its descendants, making them less reliable than shared derived characters for showing common ancestry. For example, giraffes, hippopotamuses, and whales share a common ancestor that had legs and a neck, but only giraffes and hippos have legs and a neck; whales do not.

Analogous characters are shared by species, but are not present in their common ancestor. Analogous characters result from convergent evolution, which means that they evolved by natural selection independently but with similar selection pressures. Bird and bat wings are homologous as forelimbs, but analogous as wings. The wings are analogous because fossil evidence suggests that bird and bat wings were not inherited from a common winged ancestor. You can tell the wings are analogous by looking at the major differences in their structures. For example, bat wings have flaps of skin stretched between the bones, while birds' wings extend along the limb and are covered with feathers. A close look at the relationships between birds, bats, and other tetrapods show that wings evolved independently, as shown below.



GETTING STARTED

1 Write the words strawberry, apple, and orange on the board. Add the word “fruit” next to each. Ask students by what specific physical characteristic in these fruits we could classify them into two groups. One characteristic is that strawberries have external seeds, and oranges and apples have internal seeds. Write “external seeds” next to “fruit” for the strawberry, and “internal seeds” next to “fruit” for the apple and orange. Next ask students what physical characteristic distinguishes an orange from an apple.

Students might say that oranges have a peel or are segmented. Record the distinguishing characteristic next to internal seeds for the orange.

Tell students that physical characteristics such as these used to classify the fruits serve as data for one method of classifying objects or organisms. In this activity they will apply physical data based on common ancestry to make hypotheses—in the form of evolutionary trees—about the classification of taxa. The trees are branched diagrams that show the evolutionary relationships of taxa.

If students are not familiar with biological taxonomy based on the system of seven levels of classification, you may wish to show Transparency 7.1, “Taxonomy,” to introduce the word and the Linnaean system. Taxonomy is the science of identifying characteristics that may be used to classify groups of organisms. Remind students that the term taxon describes any level of classification in the hierarchy from domain to kingdom, phylum, class, order, family, genus, and species. While some everyday names of organisms—such as ginkgo, human, and sugar maple—refer to species, others refer to higher taxa, such as oak trees (the genus *Quercus*), birds (the class *Aves*), or bacteria (the domain *Prokarya*).

This is also a good time to introduce or review the binomial system of nomenclature, by which the genus and species name describe a particular species. For example, the chim-

panzee’s scientific name is *Pan troglodytes*. Point out that the genus name is capitalized and both are italicized in this system. For a shorthand version of a name, scientists denote the genus with a capital first letter with a period followed by the full species name. For example, the chimpanzee is *P. troglodytes*.

Explain that in the past, taxonomy focused on observable characteristics of organisms, such as their structure or morphology, method of reproduction, and embryological development. Modern taxonomy is based on evidence about the evolutionary relationships between types of organisms. As scientists learn more about living organisms, additional evidence, including extensive molecular evidence, is moving taxonomy away from the seven-level classification system.

7 The Phylogeny of Vertebrates

1 **K**NOWLEDGE OF THE evolutionary history and relationships of groups of species helps scientists and conservationists understand the biodiversity of an area. Such information helps conservationists decide where and how to focus their efforts.

To understand the relationships of groups of species, scientists have devised various systems for classifying species. Some classification systems compare the observable characteristics of organisms, such as their physical structures, reproduction capabilities, and embryological development, and then assign the organism to a taxon. The higher-level taxa are those above the species level. Above species, starting at the highest, taxon classifications descend in this order: kingdom, phylum, class, order, family, and genus.

There are limitations, however, to classifying taxa based on their physical characteristics alone. That system raises several questions. For example, which similarities and differences are the most important to consider? Should whales be classified as fishes because they have flippers and live in the water? Or are whales mammals because they maintain a constant body temperature and produce milk?

Modern classification, therefore, is based on phylogenetics, which is the study of the evolutionary relationships among taxa. In a phylogenetic study, scientists work with specific characteristics, often called characters. A **character** is a recognizable structure, function, or behavior of an organism. A **homologous character**, or **homology**, is shared by taxa and their common ancestor. For example, all vertebrates and their common ancestor have a vertebral column. Homologous characters provide information about common ancestry, which is more reliable evidence for classifying organisms than their physical similarities and differences or ecological roles.



In the taxon classification system, the domestic cat’s classification levels are:

Kingdom: *Animalia*
Phylum: *Chordata*
Class: *Mammalia*
Order: *Carnivora*
Family: *Felidae*
Genus: *Felis*
Species: *F. domesticus*

DOING THE ACTIVITY

2 Distribute the cards, and monitor students' work as they complete Part A. The chart below shows sample student answers for Procedure Steps 1 and 2.

When students have completed Part A, project Transparency 7.2, "Vertebrate Forelimbs," and explain that the forelimbs they observed are an example of a shared derived character, which means they are unique to all the members of a clade and their common ancestor.

Sample Student Response to Procedure Steps 1 and 2

	Similarities	Differences
Vertebrate Cards	All forelimbs are used for movement. All have joints.	Some forelimbs are used for swimming. Some are used for walking on land. The shapes and lengths are different.
Forelimb Skeleton Cards	All have a humerus, radius, ulna, and carpals. All have similar positions and structures.	Sizes and shapes of bones differ. Numbers of carpels differ.

3 The evidence to support this is that the positions and structures of the parts of the forelimb skeletons are similar in all of the species. The statement in Procedure Step 3 is accurate because forelimbs are shared derived characters between the species, and, therefore, must have been present in their common ancestor. Explain that the forelimbs all have the same basic structures and bone parts, but have been modified through natural selection for different functions.

Next, point out to students that while they might have noticed similarities in the functions and shapes of the forelimbs in the Vertebrate Cards, function and overall shape alone do not mean the organisms have shared derived characters. Use the example of bird and bat wings. Project Transparency 7.3, "Homology and Analogy." It might seem like the wings of birds and bats are homologous because they

Homologies are shared by the common ancestor and some or all of its descendants. Those homologies shared by all populations of a single species or group of species descended from a common ancestor are called **shared derived characters**. Therefore, they are very important in determining relationships. To find shared derived characters, scientists examine large amounts of evidence, such as fossil, physical, and molecular (proteins, chromosomes, DNA) data. Scientists then construct an **evolutionary tree**, or tree, which is a branched diagram for classifying taxa. A tree represents a hypothesis about the evolutionary relationships of taxa.

In this activity you will examine the forelimbs of some vertebrates. You will then look at additional shared derived characters to determine which tree hypothesis best supports the evolution of vertebrates.

Challenge

► How do you test a tree hypothesis for a group of taxa?

MATERIALS

FOR EACH PAIR OF STUDENTS

set of seven Vertebrate Cards
set of seven Forelimb Skeleton Cards
colored pencils

FOR EACH STUDENT

Student Sheet 7.1, "Evidence in Anklebones"
Student Sheet 3.1, "Ideas about Evolution," from Activity 3

Procedure

Part A: Comparing Vertebrate Forelimbs

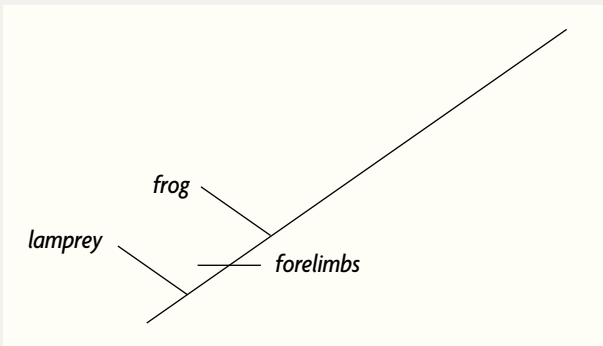
It is often difficult to determine if shared characters are also derived characters. One way scientists approach this is to compare the position and structures of the characters.

- 2**
1. With your partner, observe the forelimbs of the animals shown on the Vertebrate Cards. A forelimb is a front limb of an organism, such as the front leg of a horse, the arm of a human, or the wing of a bird. In your science notebook, record the similarities and differences you observe in the forelimbs of the seven organisms. For example, observe the function, such as walking or flying, the shape, and the number of digits (toes, fingers), if any.

serve the same function. However, the wings of birds and bats are not homologous because they were not present in the most recent common ancestor of birds and bats. If you examine fossils and the physical characteristics of the wings themselves, there are clues that the wings did not arise from a common ancestor that had wings. For example, a bird's wings are covered with feathers, while a bat's wings are made up of flaps of skin that are stretched between the bones. The wings evolved independently to serve the same function. Explain that bird and bat *forelimbs* are homologous as defined by evolutionary biologists, but bird and bat forelimbs as *wings* are analogous. An analogous character is one that is shared but was not present in the most recent common ancestor. Instead, an analogous character for two species evolved independently in similar environments.

4 Direct students’ attention to the character matrix in the Student Book. Explain that a character matrix helps to construct an evolutionary tree, which is a system for classifying taxa. Start at the bottom of the matrix with the vertebral column. Explain that all of the taxa shown at the top of the chart are vertebrates and, as their name reflects, have the shared derived character of a column of vertebrae. Therefore, the number one is noted in the bottom row for the vertebral column for each organism to show that it has that character. Explain that as you move up the rows of the matrix, organisms are separated from one another sequentially, based on whether or not they share specific derived characters. And, as you move up the rows of the matrix from the bottom, you see that fewer and fewer organisms have the character. Often, the character in the topmost row of the matrix is unique to one taxon.

Ask students which organisms have forelimbs or modified forelimbs. All but the lamprey have forelimbs or modified forelimbs as noted by the “0” in the row labeled “forelimbs” for “lamprey.” Next, project Transparency 7.4, “Vertebrate Tree.” Explain to students that they will use the character matrix to begin constructing a tree for the organisms. With a marker add forelimbs to the tree above the lamprey, and add the frog to the first branch just above it. A sample drawing is shown below.



2. With your partner, look at the Forelimb Skeleton Cards, showing all of the bones in the forelimbs of the organisms. In your science notebook, record the similarities and differences you observe between the skeletal structures of the forelimbs of the organisms. For example, note the types, positions, and structures of the bones and joints.

3 In your group, discuss and explain how the forelimb evidence supports the following statement:

All of the taxa share a common ancestor that had forelimbs with similar structures. The taxa gradually evolved as certain features enabled them to take advantage of opportunities in their environment.

Part B: Creating Trees with Evidence

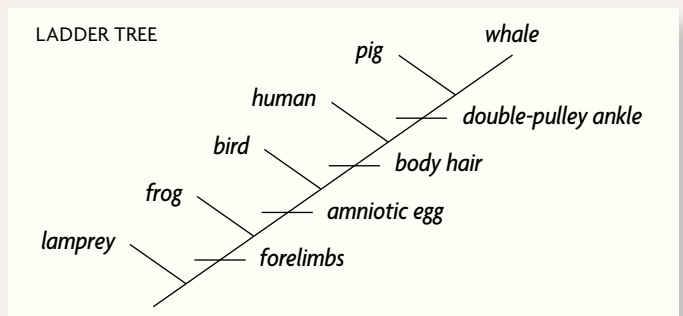
4 With your partner, examine the table below, which shows a matrix of characters for a set of species, including the forelimbs for some of the vertebrates you investigated in Part A (0 = absent, 1 = present). Follow your teacher’s instructions to construct an evolutionary tree in your science notebook for the six taxa in the matrix. Be sure to label the characters from the matrix and the names of the organisms on your tree.

Character Matrix for Six Vertebrates						
CHARACTER	LAMPREY	FROG	BIRD	WHALE	PIG	HUMAN
Pelvic remnants (small portion of what was once a whole pelvis)	0	0	0	1	0	0
Body hair	0	0	0	1	1	1
Amniotic egg	0	0	1	1	1	1
Forelimbs	0	1	1	1	1	1
Vertebral column (backbone)	1	1	1	1	1	1

5 Were any of the taxa difficult to place on the tree? List them, and explain why they were difficult to place.

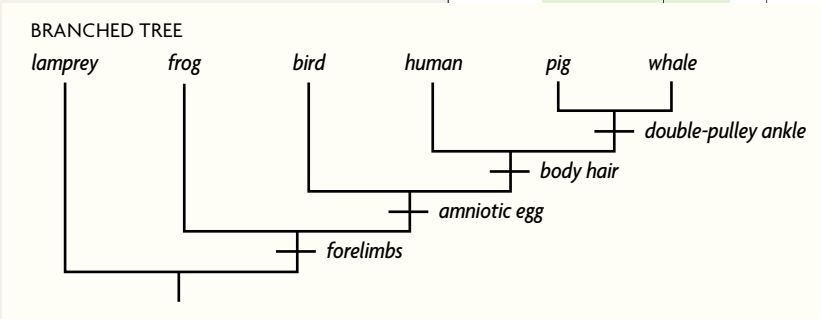
6 When scientists construct evolutionary trees, they sometimes need to gather more evidence to determine the most likely placement of each organism they are studying. Obtain Student Sheet 7.1, “Evidence in Anklebones.” This is one of many examples of evidence used to determine the evolutionary relationships of mammals. Record your observations of the positions, shapes, and parts of the bones.

A sample completed ladder for Procedure Step 4 is shown below.



Discuss with students that evolutionary trees can be drawn in two formats: tree and ladder. The tree format is preferred because it more accurately reflects the branching of descendants from common ancestors. The ladder format

can be misleading because it suggests progress up a ladder, that the taxon at the end is more complex, or that one taxa “evolves into” or “comes from” another. However, when first learning to draw trees, some people find it easier to draw a ladder first and convert the ladder to a tree as shown below.



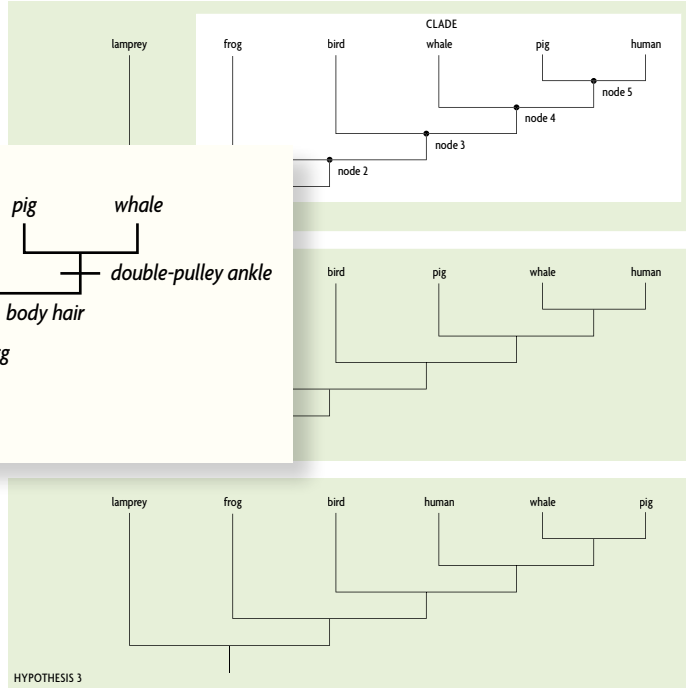
5 With the information provided on the matrix for this activity, students will not be able to distinguish the whale, pig, and human.

6 Before students complete Procedure Step 6, discuss which part of the tree was difficult to determine. Explain that when scientists are uncertain of where to place taxa on a tree, they examine additional characters. Tell students that they will have additional character evidence to determine the hypothesis that best supports the evidence.

Project Transparency 7.5, “Hypotheses for Vertebrate Phylogeny.” Explain that evolutionary trees are considered hypotheses because they are tentative-and-testable explanations for evolutionary relationships and common ancestry based on the available evidence in the form of characters. Students will determine which of the three tree hypotheses is best supported by the available evidence. Explain that, like any hypothesis, a tree hypothesis may change if additional evidence or other logical reasoning emerges to explain the relationships of the species.

While pointing out tree features on the transparency, explain to students how to read an evolutionary tree. The root of the tree represents the ancestor and the tips represent the descendants of the ancestor. A node is a place on the

7 Work by yourself to examine the three evolutionary tree hypotheses shown below. Decide which tree is consistent with the characters in the matrix and the anklebone evidence. In your science notebook, copy the tree you decided on. Then, write a four-to-six sentence explanation for which tree hypothesis you chose.



8 Go back to the statements on Student Sheet 3.1, “Ideas about Evolution,” from Activity 3. Record information from this activity to support whether any of the statements is correct or incorrect.


tree where a single lineage branches into two or more lineages. The node represents the characteristics of a common ancestor. The nodes lead to tips that represent descendent groups. A group that includes a common ancestor (node) and all of its descendants is called a clade. Two groups on a tree that share a more recent common ancestor represented by a node are more closely related to one another than they are to groups that share a more distant common ancestor. For example, in Hypothesis 1, the frog and bird are more closely related to one another than they are to the lamprey because the frog and bird share a more recent common ancestor, represented by node 2. Frogs, birds, and lampreys share a more distant ancestor farther back in time, represented by node 1.

The relationships shown on trees provide information about the biodiversity of the groups in the tree. A cluster of more closely related groups is most likely less biodiverse than a set of taxa that are spread out across the tree. For example, a group made up of the whale, pig, and human taxa is less diverse than a group made up of the lamprey, bird, and human taxa. Distribute copies of Student Sheet 7.1, “Evidence in Anklebones,” to each student for Procedure Step 6.

7 The following is a sample response for Procedure Step 7:

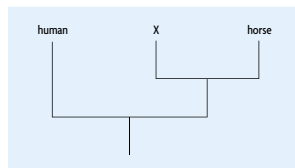
From the evidence in the character matrix and the ankle evidence, I think Hypothesis 3 is the most consistent with all of the evidence. The shared derived characters show evidence for the separation and grouping of the lamprey, frog, and bird. The data matrix did not give enough information to separate out the grouping of the whale, pig, and human. Based on the ankle evidence, the whale and pig share a more recent ancestor than either does with human. The evidence for this is the double-pulley ankle that whales and pigs share, with two trochleas. Humans have a single-pulley ankle with just one trochlea.

If students are confused about whether or not whales have ankles, explain that the ankle evidence came from a whale ancestor that had hind limbs with ankles and a pelvis. Modern whales evolved to no longer have hind limbs with ankles or a pelvis. Stress that these are examples of the many shared derived characters scientists observe in constructing tree hypotheses. Stress that some tree hypotheses are so strongly supported by the evidence that they are generally accepted by the scientific community. Other tree hypotheses are more tentative.

8  Sample student responses to Procedure Step 8 are shown on the sample Student Sheet 3.1, “Ideas about Evolution,” at the end of this activity.

9 Analysis

- How would fossil evidence provide additional support for the statement in Step 3?
- A **clade** is a group on an evolutionary tree that includes a common ancestor and all of its descendants. Draw a box around one clade in the tree from Step 7.
- Based on the tree you chose:
 - Which are more closely related to humans: birds or frogs? Support your answer with evidence.
 - Which are more distantly related to birds: humans or lampreys? Support your answer with evidence.
 - Which group shares a more recent common ancestor with whales: pigs or humans? Support your answer with evidence.
- Based on the portion of a tree shown below, what can you say about the relationship of taxa X to horses and humans?




KEY VOCABULARY

character	hypothesis
clade	node
evidence	phylogenetics
evolutionary tree	shared derived character
homologous character	taxa
homology	taxon

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FOLLOW-UP

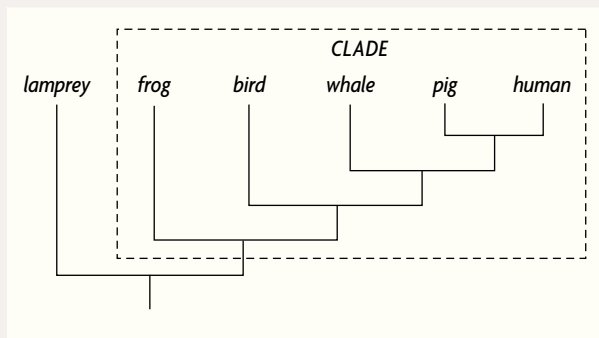
9  Project Transparency 7.5, “Hypotheses for Vertebrate Phylogeny.” Review with students that the tree that best represents the evidence in the character matrix and the anklebones is Hypothesis 3, which shows the whale and pig branching from a more recent common ancestor. Review with students that in Activity 5, “Using Fossil Evidence to Investigate Whale Evolution,” they worked in the same way that paleontologists do, analyzing fossil skeleton evidence to understand how whales evolved as mammals that live in water. In this activity, they observed additional skeleton evidence in the anklebones of pigs, humans, and a whale ancestor. This is one piece of evidence that supports the evolution of whales as mammals. Because pigs (mam-

mals) and the whale ancestor share a double-pulley ankle, and other derived characters are not shared with humans, this supports the hypothesis that they share a more recent common ancestor that also had the double-pulley ankle. If you wish, explain that a double-pulley ankle bone has two deep grooves, one on each end. Another bone fits into these grooves to form a sliding joint. A single-pulley ankle bone has only one groove.

Analysis Questions 3 and 4 are Quick Check assessments of students' understanding of how to read and interpret evolutionary trees.

SAMPLE RESPONSES

1. The fossils provide additional evidence of shared characters present in all the taxa with forelimbs, supporting the hypothesis that the forelimbs were inherited from a common ancestor.
2. One possible answer follows.



3. a. ✓ Birds are more closely related to humans because they share a more recent common ancestor with humans than humans do with frogs.
b. Lampreys are more distantly related to birds than humans because birds and lampreys share a more distant common ancestor than do birds and humans.

- c. Pigs share a more recent ancestor with whales because they have in common more shared derived characters such as the double-pulley ankle bone.
4. ✓ Taxa X is more closely related to horses than it is to humans because X shares a more recent common ancestor with horses that it does not share with humans.

REVISIT THE CHALLENGE

Review with students how evolutionary trees are constructed from evidence of shared derived characters. Remind them that in this activity they focused on shared derived characters that were or are physical characteristics of the organisms, but that shared derived characters are also based on DNA or other molecular evidence. Point out that physical and molecular evidence is also obtained from fossils. Scientists look at many shared derived characters when they are constructing evolutionary trees. Trees show the evolutionary relationships of groups of organisms, and are the current method for classifying them.

Emphasize that trees are considered hypotheses because they are tentative-and-testable explanations for evolutionary relationships and common ancestry based on the available evidence. Some tree hypotheses are so strongly supported by the evidence that scientists do not dispute them. An example is the tree that shows that dinosaurs are the evolutionary ancestors of birds. Other tree hypotheses may change if new evidence or logical reasoning explains the relationships of the species.