**SECTION 17.1**  
THE LINNAEAN SYSTEM OF CLASSIFICATION  
Study Guide

**KEY CONCEPT**
Organisms can be classified based on physical similarities.

**MAIN IDEA:** Linnaeus developed the scientific naming system still used today. Fill in the concept map with details about Linnaean taxonomy.

**VOCABULARY**
<table>
<thead>
<tr>
<th>taxonomy</th>
<th>binomial nomenclature</th>
</tr>
</thead>
<tbody>
<tr>
<td>taxon</td>
<td>genus</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Linnaean taxonomy</th>
</tr>
</thead>
<tbody>
<tr>
<td>classifies</td>
</tr>
<tr>
<td>names</td>
</tr>
</tbody>
</table>

1. based on  
2. into groups called  
3.  
4. using a system called  
5. which gives each species a  
6.  

**MAIN IDEA:** Linnaeus’ classification system has seven levels.

7. How are the seven levels of Linnaeus’ classification system organized?

8. Describe the trend in the levels, or taxa, as you move down from kingdom to species.
Fill in the seven taxa of the Linnaean classification system into the appropriate boxes below.

a.  

b.  

c.  

d.  

e.  

f.  

g.  

**MAIN IDEA:** The Linnaean classification system has limitations.

**9.** Why did Linnaeus base his system of classification on physical similarities alone, as opposed to including molecular and genetic similarities?

**10.** Why are physical similarities among species not always the result of being closely related?

**11.** Why do scientists today rely on molecular and genetic similarities to classify organisms?

**Vocabulary Check**

**12.** Taxonomy is the science of _______________ and _______________ organisms.

**13.** Words from the __________ language are used in binomial nomenclature.

**14.** In the binomial nomenclature naming system, each species is given a unique scientific name that includes a _______________ name and a _______________ descriptor.
SECTION 17.1

THE LINNAEAN SYSTEM OF CLASSIFICATION

Power Notes

Taxonomy:

Scientific names

Linnaean classification

Binomial nomenclature:

How it's organized:

Genus:

The seven taxa:

Species descriptor:

1. 

2. 

3. 

4. 

5. 

6. 

7. 

Advantages over common names:

Limitations:
KEY CONCEPT Organisms can be classified based on physical similarities.

Taxonomy is the science of naming and classifying organisms. Until the 1750s, scientists named organisms however they wanted. However, in 1753, Swedish botanist Carolus Linnaeus introduced a system of taxonomy that standardized the way that organisms are named and classified.

Linnaeus’ method of naming organisms, called binomial nomenclature, is still used today. In this system, each species is given a scientific name using Latin words. These names are always written in italics or underlined. A scientific name has two parts:

- The genus is the first part of the name. A genus includes one or more physically similar species that are thought to be closely related. The genus name is always capitalized.
- The species descriptor is the second part of the name. A species descriptor often refers to a certain trait of the species. A species descriptor is always written after the genus name, and it is always lowercase.

Linnaeus’ system of classification groups organisms into seven levels based on physical similarities. Each level is called a taxon (plural, taxa). The seven taxa form a multilevel scale in which each taxon is included in a larger, more general taxon. From the most general to the most specific, these taxa are kingdom, phylum, class, order, family, genus, and species.

Because Linnaeus created his classification system before organisms could be studied at the molecular level, it is based on physical similarities alone. However, physical similarities are not always the result of species being closely related. Unrelated species can also evolve similar traits through convergent evolution. Therefore, the Linnaean system of classification has limitations. Today, scientists also use molecular and genetic similarities to classify organisms.

1. How are organisms named in Linnaean taxonomy?

2. How are organisms classified in Linnaean taxonomy?

3. What is a major limitation of Linnaean taxonomy?
SECTION 17.2
CLASSIFICATION BASED ON EVOLUTIONARY RELATIONSHIPS

Study Guide

KEY CONCEPT
Modern classification is based on evolutionary relationships.

VOCABULARY
- phylogeny
- cladogram
- cladistics
- derived character

MAIN IDEA: Cladistics is classification based on common ancestry.

1. What is a phylogeny?

2. How can a phylogeny be shown?

3. Describe the main goal of cladistics.

Use the word box below to label the main features of a cladogram.

<table>
<thead>
<tr>
<th>clade</th>
<th>node</th>
<th>taxon being classified</th>
<th>derived character</th>
</tr>
</thead>
</table>

4. 
5. 
6. 
7. 
8. What is a clade?

9. How are derived characters used in making a cladogram?

10. On a cladogram, what is a node and what does it represent?

**MAIN IDEA:** Molecular evidence reveals species’ relatedness.

11. Give two examples of molecular evidence that can be used to help determine species’ relatedness.

12. Why are evolutionary trees often changed?

13. What can be concluded if the genes of two species are found to be nearly identical?

**Vocabulary Check**

14. *Phylo-* comes from the Greek word meaning “class,” and the suffix -*geny* means “origin.” How do these meanings apply to the term *phylogeny*?

15. How are the words *cladistics* and *cladogram* related?

16. Traits that are shared by some species of a group being studied, which other species in that group do not have, are called __________ characters.
SECTION 17.2 | CLASSIFICATION BASED ON EVOLUTIONARY RELATIONSHIPS

**Power Notes**

Phylogenies

- can be shown using diagrams called
- can be determined using evidence such as

1. which are defined as

2. which are constructed by identifying

3. 

4. 

Clade:

Species A

Species B

Species C

Species D

Derived character:

Node:
KEY CONCEPT  Modern classification is based on evolutionary relationships.

Today, scientists use evidence from living species, the fossil record, and molecular data to figure out evolutionary relationships among species. The evolutionary history for a group of species is called a **phylogeny**. Phylogenies can be shown as branching tree diagrams. The branches on these trees show how different groups of species are related to each other.

**Cladistics** is classification based on common ancestry. The goal of cladistics is to place species in the order in which they descended from a common ancestor. This order can be shown in a **cladogram**, which is an evolutionary tree that proposes how species may be related to each other through common ancestors. A clade is a group of species that shares a common ancestor.

Each species in a clade has some traits that have not changed from its ancestors and some traits that have changed over time. To make a cladogram, scientists must figure out which traits are shared by some of the species being studied but are not present in others. These traits are called **shared derived characters**. The more closely related two species are, the more derived characters they will share.

Physical characteristics are often used as derived characters when building a cladogram. However, today biologists can also compare species at the molecular level. Molecular evidence, such as proteins and genes, can also be used as derived characters. In fact, DNA is considered by many scientists to have the “last word” when figuring out how closely related two species are to each other. The more similar the genes of two species are, the more closely related the species are likely to be.

1. What is a phylogeny?

2. What does a cladogram show?

3. How can molecular evidence show how closely related species are to each other?
KEY CONCEPT
Molecular clocks provide clues to evolutionary history

VOCABULARY
- molecular clock
- ribosomal RNA
- mitochondrial DNA

MAIN IDEA: Molecular clocks use mutations to estimate evolutionary time.

1. What are molecular clocks?

2. Explain how species become more and more different at the molecular level, after they have diverged from a common ancestor.

3. Using Figure 17.8 as a reference, draw your own set of DNA sequences that illustrate molecular evolution.

4. How can scientists estimate mutation rates for use in developing a molecular clock?

MAIN IDEA: Mitochondrial DNA and ribosomal RNA provide two types of molecular clocks.

5. Depending on how closely related species are, scientists must choose a molecule with an appropriate ________________ rate to use as a molecular clock.
6. In the table below, take notes about two commonly used molecular clocks.

<table>
<thead>
<tr>
<th>Molecular Clock</th>
<th>Description of Molecule</th>
<th>Why It's Unique</th>
<th>How It's Useful as a Molecular Clock</th>
</tr>
</thead>
<tbody>
<tr>
<td>mtDNA</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>rRNA</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Vocabulary Check

<table>
<thead>
<tr>
<th></th>
<th>7. Useful for studying closely related species</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>8. Model that uses mutation rates to measure evolutionary time</td>
</tr>
<tr>
<td></td>
<td>9. Useful for studying species in different kingdoms or phyla</td>
</tr>
</tbody>
</table>
SECTION 17.3 | MOLECULAR CLOCKS

Power Notes

How they work:

Linking molecular data with real time:

Molecular Clocks:

Mitochondrial DNA (mtDNA):

Ribosomal RNA (rRNA):
KEY CONCEPT  Molecular clocks provide clues to evolutionary history.

Mutations are nucleotide substitutions in DNA, some of which cause amino acid substitutions in proteins. Mutations tend to add up at a fairly constant rate for a group of related species. The more time that has passed since two species diverged from a common ancestor, the more mutations will have built up in each species. Molecular clocks are models that use these mutation rates to measure evolutionary time.

To figure out mutation rates, scientists must count up the number of genetic differences between species and then figure out how long ago the species diverged from a common ancestor. Often this link between genetic data and real time comes from the timing of a geologic event that is known to have separated the species being studied. Scientists can also find out when each species first appeared in the fossil record.

Different molecules have different mutation rates. Depending on how closely two species are related, scientists choose a molecule with an appropriate mutation rate to use as a molecular clock. Two molecules commonly used as molecular clocks are mitochondrial DNA and ribosomal RNA.

- **Mitochondrial DNA** (mtDNA) is DNA found in mitochondria, the energy factories of cells. This molecule provides a good molecular clock for closely related species because the mutation rate is relatively high. Scientists also use the fact that mtDNA is passed down unshuffled from mother to offspring to trace mutations back through many generations.

- **Ribosomal RNA** (rRNA) is RNA found in ribosomes, the organelles that manufacture proteins in cells. This molecule provides a good molecular clock for studying distantly related species because the mutation rate is relatively low. Therefore, mutations that do build up in rRNA over long periods of time are clear and can be easily compared.

1. What are molecular clocks?

2. How can scientists figure out mutation rates?

3. Describe the use of mtDNA and rRNA as molecular clocks.
KEY CONCEPT
The current tree of life has three domains.

VOCABULARY
<table>
<thead>
<tr>
<th>Bacteria</th>
<th>Eukarya</th>
</tr>
</thead>
<tbody>
<tr>
<td>Archaea</td>
<td></td>
</tr>
</tbody>
</table>

MAIN IDEA: Classification is always a work in progress.

1. Why is classification considered a work in progress?

2. How has the kingdom system changed over the last three hundred years?

3. Describe Woese’s discovery and the impact it had on the tree of life.

On the timeline below, fill in the major changes to the kingdom system that have occurred over the past three hundred years.

1753:  
1700 1800 1900 2000  
1938:  
1977:  
1866:  
1959:  
MAIN IDEA: The three domains in the tree of life are Bacteria, Archaea, and Eukarya.
Fill in the table below with notes about the three-domain system.

<table>
<thead>
<tr>
<th>Domain</th>
<th>Characteristics</th>
<th>Kingdoms Included</th>
</tr>
</thead>
<tbody>
<tr>
<td>4. Bacteria</td>
<td></td>
<td></td>
</tr>
<tr>
<td>5. Archaea</td>
<td></td>
<td></td>
</tr>
<tr>
<td>6. Eukarya</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

7. Why is it difficult to classify bacteria and archaea down to the species level?

_____________________________________________________________________

_____________________________________________________________________

Vocabulary Check

<table>
<thead>
<tr>
<th>Bacteria</th>
<th>Archaea</th>
<th>Eukarya</th>
</tr>
</thead>
<tbody>
<tr>
<td>_____________</td>
<td>8. Have cells with distinct nucleus and membrane-bound organelles</td>
<td></td>
</tr>
<tr>
<td>_____________</td>
<td>9. Known for their ability to live in extreme environments</td>
<td></td>
</tr>
<tr>
<td>_____________</td>
<td>10. Classified by their shape, need for oxygen, and whether they cause disease</td>
<td></td>
</tr>
</tbody>
</table>
Woese’s discovery:

resulted in dividing all life into three

1. called

2. which includes kingdom

3. which includes kingdom

4. which includes kingdom

5. 

6. which includes kingdoms

7. 

1700 1800 1900 2000

2 kingdoms: 4 kingdoms: 6 kingdoms:

3 kingdoms: 5 kingdoms:

Power No
tes

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The tree of life is a model that shows the most current understanding of how living things are related. This model has changed from a two-kingdom system devised by Linnaeus in 1753, to the six-kingdom and three-domain system used today. It will continue to change as scientific research leads to new discoveries about evolutionary relationships.

The most recent change in the kingdom system involved prokaryotes, which at one time were grouped together in a kingdom called Monera. Research by biologist Carl Woese revealed that there are two genetically distinct groups of prokaryotes, which have very different cell wall chemistry. This discovery led to the splitting of kingdom Monera into two kingdoms: Bacteria and Archaea. Therefore, the most current tree of life includes six kingdoms: Bacteria, Archaea, Protista, Fungi, Plantae, and Animalia.

Woese’s research showed that in terms of genes, bacteria and archaea are actually more different from each other than animals, plants, fungi, and protists are from each other. Based on these differences, Woese proposed that all life be divided above the kingdom level into three domains. These domains are called Bacteria, Archaea, and Eukarya.

- The domain **Bacteria** is made up of single-celled prokaryotes in the kingdom Bacteria. Bacteria are classified by many traits, such as their shape, their need for oxygen, and whether they cause disease.
- The domain **Archaea** is made up of single-celled prokaryotes in the kingdom Archaea. Archaea are known for their ability to live in extreme environments.
- The domain **Eukarya** is made up of all organisms with eukaryotic cells. It includes the kingdoms Protista, Plantae, Fungi, and Animalia.

1. Why is the tree of life considered a work in progress?

2. What kind of research prompted living things to be classified into domains, a grouping above the kingdom level?

3. Name the three domains in the current tree of life, including what kingdoms they contain.
The same data can often be presented in more than one format. For example, some data can be shown in both a bar graph and a circle graph.

This table contains data on the number of species in each family of Order Rodentia in Yellowstone National Park.

**NUMBER OF SPECIES PER FAMILY**

<table>
<thead>
<tr>
<th>Family</th>
<th>Number of Species</th>
</tr>
</thead>
<tbody>
<tr>
<td>Castoridae</td>
<td>1</td>
</tr>
<tr>
<td>Sciuridae</td>
<td>8</td>
</tr>
<tr>
<td>Geomyidae</td>
<td>1</td>
</tr>
<tr>
<td>Cricetidae</td>
<td>10</td>
</tr>
<tr>
<td>Erethizontidae</td>
<td>1</td>
</tr>
</tbody>
</table>

1. **Graph Data**  In the space below, make a bar graph to represent the data in the table.

2. **Calculate**  Find the percent of each species per family in the park. Graph the results in a circle graph.
In Chapter 17, you have learned that Carolus Linnaeus developed a system of scientific nomenclature that standardized how all known organisms were classified and named. Linnaeus’s system provided a way for scientists to communicate about an organism in an unambiguous, precise way.

ARISTOTLE’S SYSTEM

The first known system of classifying organisms was developed more than 2000 years ago by Aristotle, a Greek philosopher. He divided all living organisms into plants and animals. He further divided animals according to whether they moved on land, in the air, or in water. Thus, bats and birds were classified together, as were whales and fish and mollusks. Plants were subdivided according to differences in their stems.

LINNAEUS’S SYSTEM DEVELOPED OVER TIME

When Linnaeus first began to devise his system in the 18th century, he used the polynomial system (*poly* = “many”; *nomial* = “name”) that was common at the time. For example, he named the red oak *Quercus foliis obtuse-sinuatis setaceo-mucronatis*, which meant “oak with leaves with deep blunt lobes bearing hairlike bristles.” He also gave each species a shorthand binomial name. For the red oak, the binomial name was *Quercus rubra*. It is Linnaeus’ shorthand binomial system that is still used today, although he considered the longer name to be the true name.

Linnaeus chose Latin for his system because it was the universal language of scientists. In fact, when he visited England in 1736, he had to speak Latin to the scientists he met because he knew no English.

THE SPECIES DESCRIPTOR

The first part of a species’ binomial classifies it according to its structures or similarities to other organisms. Thus, the genus name indicates relationships among a group of closely related organisms. The second part, however, is specific to the particular organism. This part is often called a specific epithet or species descriptor. It may refer to a trait or the native location of the species, or it could be named for a scientist who worked in the field. For example, the species descriptor in the tiger shark’s scientific name, *Galeocerdo cuvier*, is for Georges Cuvier, an important zoologist whose students first described this particular shark. Today, scientists use bodies of rules, called nomenclature codes, to name new species. The rules differ in plant codes and animal codes, but one rule is common to all codes: although many species can have the same specific epithet, no two different species can have the same combination of genus name and specific name.

Some scientists are realizing that they can help conserve wildlife by auctioning the naming rights of newly discovered species. In 2005, Robert Wallace, a scientist with the Wildlife Conservation Society, found a new species of monkey in Bolivia. To name the new monkey species, he set up an auction to raise money for protection of the monkey’s habitat. The online casino company GoldenPalace.com placed the $650,000 winning bid. They chose,
Callicebus aureipalatii, which means “golden palace.” This name will have to be approved by the International Commission on Zoological Nomenclature.

Match each description below with one of the Latin names by looking for familiar roots.

____ 1. big-horned sheep from Canada
____ 2. bird with blue-green wings
____ 3. house sparrow
____ 4. an extinct human that walked upright
____ 5. tree with large flowers

a. Passer domesticus  
b. Homo erectus  
c. Cyanopica cyana  
d. Magnolia grandiflora  
e. Ovis canadensis

What do you think these names might mean?

6. Velociraptor mongoliensis
7. Ludwigia hexapetala
8. Monotropa uniflora
9. Ninox novaeseelandiae

10. The nomenclature code for plants does not allow a scientific name in which the genus name and the species descriptor are the same. The nomenclature code for animals allows such names. For example, Gorilla gorilla is the scientific name for the Western gorilla. Suggest a new species descriptor for this animal if the animal nomenclature code is changed to agree with the plant code. Explain your choice.

11. Many people call Latin a “dead” language because so few people speak it or even have any knowledge of it. Explain why it makes sense to continue to name new species using Latin roots and words despite Latin’s declining popularity or utility in the world today. Why not use common names and forget about this “dead” language?

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You have learned about cladistics in Chapter 17, and more specifically, how cladograms are used to illustrate hypotheses of evolutionary relationships. What is challenging for systematists—scientists who use cladistics to find relationships among species and other taxa—is how to discern which characters are derived from those that are analogous.

**DERIVED CHARACTERS**

Many years ago, before the discoveries of the fossil record or DNA, a taxonomist might have deemed “wings” a derived character, and created a cladogram or phylogeny that grouped birds, bees, and bats into a “winged” clade, thereby separating these distantly related groups from their true relatives. Another example: If you were to catch a sixgill shark, a bull shark, and a Southern stingray and examine them, you might infer that the two sharks are more closely related to each other than either is to the ray; but in fact, the sixgill shark is more closely related to the stingray.

**CHARACTER MATRIX**

A good first step in building a cladogram is to organize your data to clarify which derived characters are shared by which species or taxa in question. For example, data gathered into a character matrix, such as the one below, can be reorganized so that the hypothetical evolutionary relationships are more obvious.

<table>
<thead>
<tr>
<th>Derived Character</th>
<th>Shark</th>
<th>Swordfish</th>
<th>Alligator</th>
<th>Gull</th>
<th>Lamprey</th>
<th>Frog</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vertebrae</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>Jaws</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>Bones</td>
<td></td>
<td>X</td>
<td>X</td>
<td>X</td>
<td></td>
<td>X</td>
</tr>
<tr>
<td>Four Limbs</td>
<td></td>
<td></td>
<td></td>
<td>X</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Amniotic Egg</td>
<td></td>
<td></td>
<td></td>
<td>X</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>Feathers</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>X</td>
</tr>
</tbody>
</table>

Reorganizing the table according to the number of derived characters yields the matrix on the following page.
From the second table, it is not difficult to draw a cladogram like the one shown here. Notice that the animal that had only one of the derived characters in the matrix is the first outgroup, the one with just two shared derived characters is next, and so on.

**BUILD YOUR OWN MATRIX AND CLADOGRAM**

Now, imagine that you are given a list of the following animals and their characters:

- **Mouse**: hair, claws or nails, lungs, backbone, distinct tail
- **Salamander**: backbone, lungs, distinct tail
- **Fish**: backbone, distinct tail
- **Ape**: opposable thumbs, backbone, hair, lungs, claws or nails
- **Lizard**: distinct tail, claws or nails, lungs, backbone
- **Human**: hair, backbone, lungs, claws or nails, opposable thumbs, fully bipedal

Use a separate piece of paper or a computer application to sort out these animals’ characters, determine which should be considered derived, construct a table to organize them, and draw a cladogram. If you find yourself having difficulty, consider the possibility that one of the listed characters may be analogous rather than homologous and derived.
CHAPTER 17 | THE TREE OF LIFE

Vocabulary Practice

1. taxonomy
2. taxon
3. binomial nomenclature
4. genus
5. phylogeny
6. cladistics
7. ribosomal RNA
8. Bacteria
9. Archaea
10. Eukarya

A. Categorize Words  Write N next to words that are involved with naming organisms. Write C next to words that are involved with classifying organisms. Write B next to words that can be involved with both.

1. ___ derived character  6. ___ binomial nomenclature
2. ___ Archaea          7. ___ genus
3. ___ taxonomy          8. ___ Bacteria
4. ___ phylogeny          9. ___ cladistics
5. ___ Eukarya

B. Word Origins  Circle the Greek and Latin word parts in each vocabulary term. Then use the Greek and Latin meanings to construct a very basic definition of the vocabulary word.

<table>
<thead>
<tr>
<th>WORD</th>
<th>DEFINITION</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. taxonomy</td>
<td></td>
</tr>
<tr>
<td>2. taxon</td>
<td></td>
</tr>
<tr>
<td>3. binomial nomenclature</td>
<td></td>
</tr>
<tr>
<td>4. phylogeny</td>
<td></td>
</tr>
<tr>
<td>5. cladogram</td>
<td></td>
</tr>
<tr>
<td>6. Archaea</td>
<td></td>
</tr>
</tbody>
</table>
C. Stepped-Out Vocabulary  Define each word. Then write two additional facts that are related to the word.

<table>
<thead>
<tr>
<th>WORD</th>
<th>DEFINITION</th>
<th>MORE INFORMATION</th>
</tr>
</thead>
<tbody>
<tr>
<td>Example genus</td>
<td>taxon that includes one or more physically similar species</td>
<td>first name in a scientific name</td>
</tr>
<tr>
<td>1. taxon</td>
<td></td>
<td>2nd most specific taxon in Linnaean system</td>
</tr>
<tr>
<td>2. binomial nomenclature</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3. cladistics</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4. derived character</td>
<td></td>
<td></td>
</tr>
<tr>
<td>5. molecular clock</td>
<td></td>
<td></td>
</tr>
<tr>
<td>6. mitochondrial DNA</td>
<td></td>
<td></td>
</tr>
<tr>
<td>7. ribosomal RNA</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
**D. Analogy Vocabulary Set**  On one blank line next to each vocabulary word, write the letter and number of the definition that best matches. On the other blank line, write the letter and number of the analogy that best matches.

<table>
<thead>
<tr>
<th>DEFINITIONS</th>
<th>WORDS</th>
<th>ANALOGIES</th>
</tr>
</thead>
<tbody>
<tr>
<td>D1. taxon that includes one or more physically similar species</td>
<td>1. binomial nomenclature</td>
<td>A1. a family tree</td>
</tr>
<tr>
<td>D2. trait that is shared to different degrees among a group of species</td>
<td>2. genus</td>
<td>A2. how a group of neighboring countries was founded</td>
</tr>
<tr>
<td>D3. standard that gives each species a two-part name</td>
<td>3. molecular clock</td>
<td>A3. optional features available on cars</td>
</tr>
<tr>
<td>D4. evolutionary tree constructed using cladistics</td>
<td>4. phylogeny</td>
<td>A4. a sun dial</td>
</tr>
<tr>
<td>D5. evolutionary history of a group of species</td>
<td>5. cladogram</td>
<td>A5. street name and address</td>
</tr>
<tr>
<td>D6. theoretical clock used to measure evolutionary time</td>
<td>6. derived character</td>
<td>A6. all the shades of blue in a crayon box</td>
</tr>
</tbody>
</table>

**E. Cartoon Dialogue**  Read the dialogue below and then answer the questions.

Mother tree: “You failed your Latin test?”
Seedling: “Who cares, Mom. No one even speaks Latin anymore.”
Mother tree: “But honey, all of our names have Latin roots!”

1. How does this dialogue relate to *binomial nomenclature*?  

2. Which of the three domains would these trees be classified into: Bacteria, Archaea, or Eukarya? Explain your answer.
F. Tree of Life Crossword Puzzle  Use the clues below to fill in the crossword puzzle.

**Across**

3. Domain often classified by their shape
6. Used to study closely related species
8. Used to measure evolutionary time
10. Domain including all eukaryotes
11. Used to construct evolutionary trees
12. Domain often classified by their extreme environment
13. Used to study distantly related species

**Down**

1. Gives each species a two-part name
2. Science of naming and classifying organisms
4. Type of evolutionary tree
5. Trait used in constructing cladograms
7. Evolutionary history for a group of species
9. Level in the Linnaean classification system