

# Phylogeny and Modern Taxonomy

## 1.3

In 1859, Charles Darwin published *On The Origin of Species*, in which he described his theory of evolution. The theory of **evolution** states that all living things are descended from a common ancestor in the same way that family members are related to each other through a common ancestor. The theory describes how this principle applies to different species. When we say that two people are closely related to each other, we are usually thinking in terms of just one or two generations. When biologists say that two species are closely related to each other, they are often thinking in terms of many thousands of generations. Just as some people are much more closely related than others, some species are much more closely related than others.

Taxonomy—the classification, identification, and naming of organisms—aims to group organisms according to a set of criteria. One criterion is how closely related they are to each other.

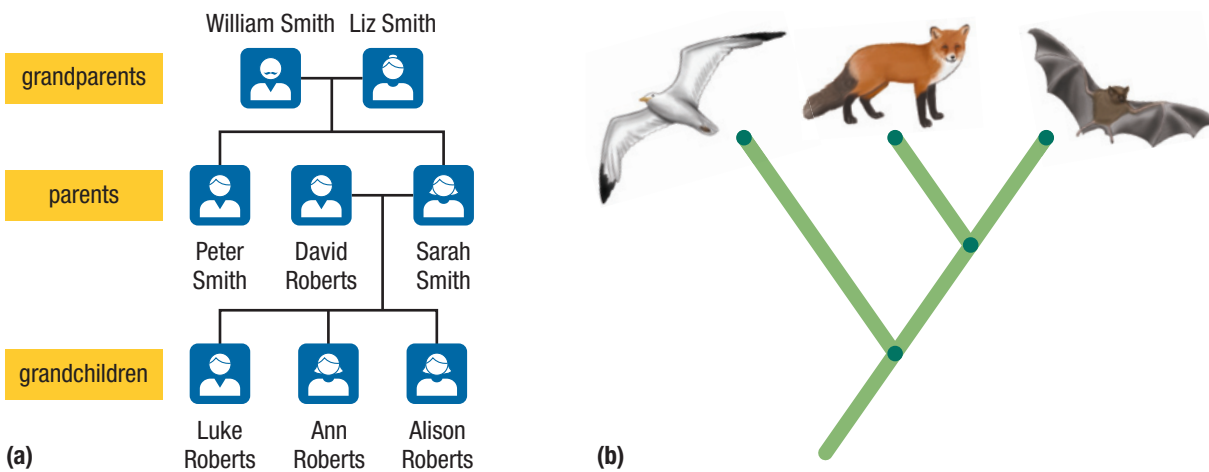
## Phylogeny

**Phylogeny** is the science that deals with evolutionary relationships between and among species—entire populations of individuals. In many ways, these relationships, or kinships, are similar to a large family tree (**Figure 1(a)**). Only instead of tracing the relationships between individual family members, phylogeny tracks relationships between entire species. These relationships can be presented in a **phylogenetic tree**, a branching diagram used to show the evolutionary relationships between and among species (**Figure 1(b)**).

**evolution** the scientific theory that describes changes in species over time and their shared ancestry

**phylogeny** the study of the evolutionary relatedness between, and among, species

**phylogenetic tree** a diagram depicting the evolutionary relationships between different species or groups



**Figure 1** (a) A family tree shows biological relationships between people. Kinships are represented by connecting lines. (b) Phylogenetic trees show the evolutionary relationships among species.

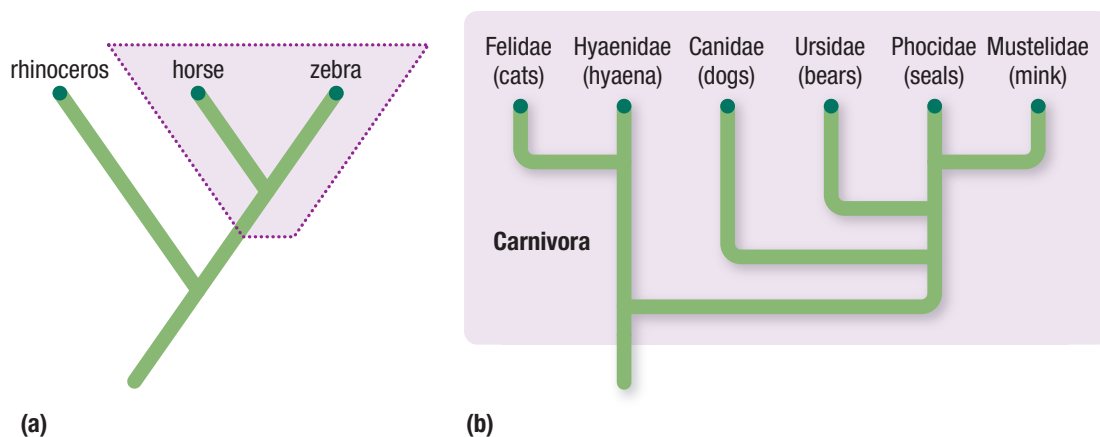
Just as individuals in a family tree are descendants from common ancestors, the groups of organisms in a phylogenetic tree are descendants of common ancestors, too. Most of the evidence for these relationships is based on similarities and differences in physical and genetic characteristics.

## Clades

In a phylogenetic tree, species are grouped into clades. A **clade** is a taxonomic group that includes a single ancestor species and all its descendants. Each clade on a phylogenetic tree can be thought of as a branch on the “tree of life.” The tips of a branch on a phylogenetic tree can represent a particular species or an entire group of species. Moving back along a branch is like moving back through time.

**clade** a taxonomic group that includes a single common ancestor and all its descendants

Clades can be small—including only a small number of species that share a very recent common ancestor. For example, the members of the horse family form a particularly small clade (**Figure 2(a)**). Clades can also be large—including all those species that share a more distant common ancestor—such as the order Carnivora of mammals (**Figure 2(b)**). Regardless of their size, clades are based on the most fundamental connection between species: their evolutionary relatedness.



**Figure 2** (a) The horse family is a small clade that includes the modern horse and zebra but not the rhinoceros. (b) The order Carnivora is a larger clade that includes many different families and is within the class Mammalia. Note that not all members of each clade are shown.

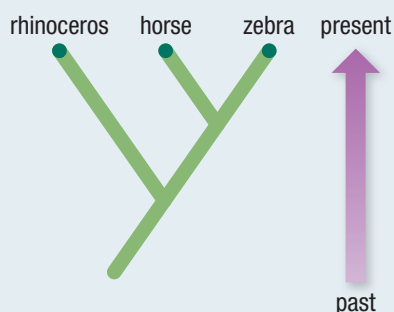
## Tutorial 1 Using Phylogenetic Trees

Phylogenetic trees can be used to infer evolutionary relationships between species, as illustrated by Sample Problem 1. Phylogenetic trees can also be used to identify clades, as you will see in Sample Problem 2.

### CASE 1: USING A PHYLOGENETIC TREE TO INFER EVOLUTIONARY RELATIONSHIPS

#### Sample Problem 1: Interpreting Phylogenetic Trees

**Figure 3** shows a simple phylogenetic tree. How closely are the rhinoceros, horse, and zebra related?



**Figure 3** A simple phylogenetic tree

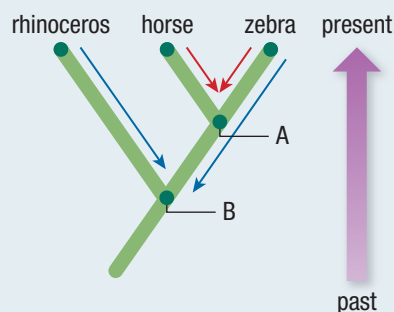
#### Solution:

**Step 1.** Carefully examine the phylogenetic tree in Figure 3. The species are placed at the tips of the branches across the top of the diagram. The lines, or branches, represent each species' ancestors going back in time.

**Step 2.** Look at the arrow to the right of the tree. The top of the tree represents the present day. As you follow the branches downward, you are going back in time.

**Step 3.** To interpret the kinship, or relatedness, of any two species, follow their branches backwards (downward) in time until you reach the place where they meet.

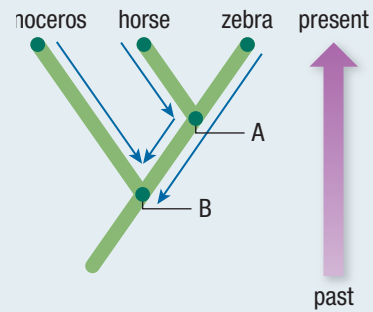
**Step 4.** Look at the branches for the zebra and the horse. Species A represents their *most recent common ancestor* (**Figure 4**.)



**Figure 4** The red arrows trace the ancestors of the horse and zebra until they meet at species A. The blue arrows trace the ancestors of the zebra and rhinoceros until they meet at species B.

**Step 5.** Look at the branches for the zebra and the rhinoceros. Their most recent common ancestor is species B in Figure 4. Species B is located “further back in time” than species A. This means that the rhinoceros and zebra are more distantly related than the horse and zebra.

**Step 6.** Note that the horse has the same relationship to the rhinoceros as the zebra does (Figure 5). The rhinoceros is just as closely related to the horse as it is to the zebra. Species B is the most recent common ancestor of all three species.



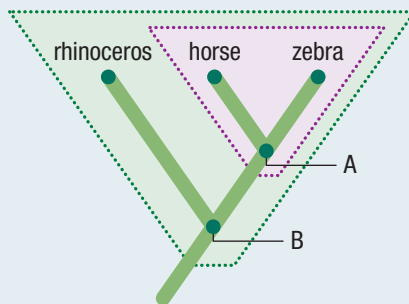
**Figure 5** The horse and the zebra have the same relationship to the rhinoceros.

## CASE 2: IDENTIFYING CLADES USING PHYLOGENETIC TREES

### Sample Problem 2: Identifying Clades Using Phylogenetic Trees

How can phylogenetic trees be used to identify clades? The steps outlined below explain the process.

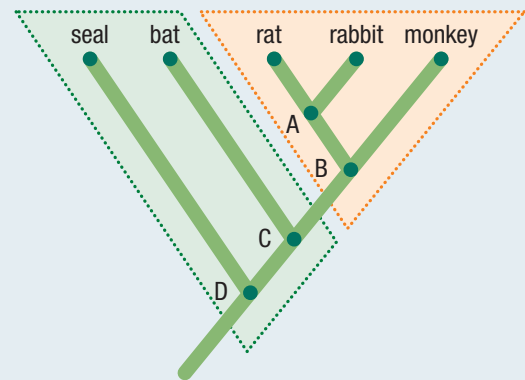
**Step 1.** Figure 6 shows two clades. The horse family clade (outlined in purple) includes species A and all its descendants. The rhinoceros is not a member of this clade because it is not a descendant of species A.



**Figure 6** Clades can be part of larger clades.

**Step 2.** Look at the green outline in Figure 6. All three species are in this larger clade, which includes all the descendants of species B.

**Step 3.** Look at Figure 7. Phylogenetic trees can portray any number of different groups. This tree shows the evolutionary relationships of a few familiar mammals. Note that the species outlined in orange form a clade. The species outlined in green do *not* form a clade. The most recent common ancestor of the bat and seal is species D. However, the rat, rabbit, and monkey are also descendants of species D, so they must be included in any clade that includes species D.



**Figure 7** The species that are outlined in green do not form a clade.

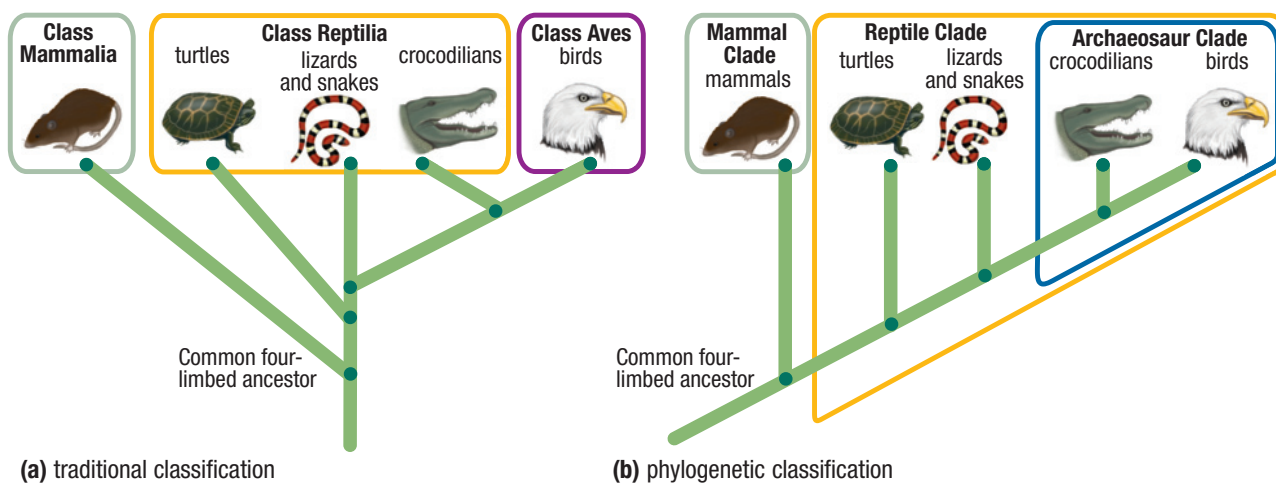
### Practice

- Sketch Figure 1(b) (page 21) in your notebook and answer the following questions. [K/U](#) [T/I](#) [C](#) [A](#)
  - Indicate the location of the species that is
    - the most recent common ancestor of foxes and bats
    - the most common recent ancestor of all three species
  - Based on this tree, is a bird more closely related to a fox or to a bat? Explain your reasoning.
- In your notebook, sketch the phylogenetic tree in Figure 7, above. Do not include the coloured outlines. Use different colours to show the following clades: [K/U](#) [T/I](#) [C](#) [A](#)
    - the smallest clade that contains the bat and rabbit
    - the smallest clade that contains the seal and the rat
  - What is the maximum number of unique clades (of any size) that can be found in this tree?

## Taxonomy Today

One of the major strengths and weaknesses of the traditional classification system is that it groups species primarily by observed morphological characteristics. These groups are then arranged into a set number of taxonomic ranks. Grouping species this way is simple and convenient but may overlook less obvious characteristics that often provide strong evidence about relatedness.

In contrast, phylogenetic analysis can uncover the evolutionary relatedness of organisms (**Figure 8**). The organisms are grouped into different-sized clades that are not limited to a set number of taxonomic ranks. One challenge of using this system is uncovering evolutionary relatedness that may go back millions of years—a task that may require detailed analysis of both fossil and genetic evidence.



**Figure 8** In the (a) traditional classification system, crocodiles are grouped with turtles, snakes, and lizards because of their shared physical features. In (b) modern taxonomy, crocodilians are grouped with birds because they share a more recent common ancestor. Both birds and crocodilians are included in the larger reptile clade.

## The International Barcode of Life Project

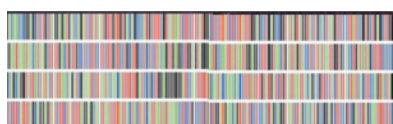
Modern genetics is providing taxonomists with a powerful new tool for identifying species. DNA barcoding was first proposed by Paul Herbert, a researcher at the University of Guelph. The idea is to use DNA technology to create a DNA profile of every species in the form of a barcode. Ultimately researchers in the field will be able to use a handheld device to immediately identify any species from a tiny sample of DNA (**Figure 9**). This will have tremendous benefits. Because DNA is found in all cells the identification system can be used on organisms at any stage of their life, from egg to adult, and can even be used to identify tissue samples such as hair, feathers, or meat. This can be a very useful tool for controlling the trafficking in products made from endangered species.

The International Barcode of Life Project (iBOL) was launched in 2010. It is supported by 25 countries and involves hundreds of leading research scientists. The project's hub will be at the Biodiversity Institute of Ontario at the University of Guelph.

Dr. Herbert's lab has already used DNA barcoding technology to reveal widespread false labelling of fish products sold in Canada and the U.S. Investigative journalists bought 153 samples of fish from grocery stores across Canada. DNA testing revealed that 34 of the samples were mislabelled. For example, fish labelled as wild-caught coho salmon was actually farm-raised Atlantic salmon, and fish labelled as cod was actually haddock.

Eventually DNA barcoding technology may allow for very low cost routine sampling and monitoring of species diversity in entire ecosystems. As of November 2010 a barcode database had already been created for about 90 000 species.

Today, taxonomists choose different methods for classifying organisms. Some are “purists,” basing classifications strictly on phylogenetic relationships. Others still prefer to group species by more easily recognizable features. Throughout the rest of this



**Figure 9** The barcode for the frog-eating bat *Trachops cirrhosus*.

### WEB LINK

To learn more about the International Barcode of Life Project,



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unit, you will have opportunities to use your understanding of both traditional and modern classification systems to examine the major groups of Earth's organisms. For convenience, we may use the names of the traditional ranks to describe groups. You will also explore some surprising evolutionary relationships between some of the most well known groups of organisms. 🌐

### CAREER LINK

#### Taxonomist

Taxonomists are scientists who specialize in the identification and classification of species. To learn more about a career as a taxonomist,



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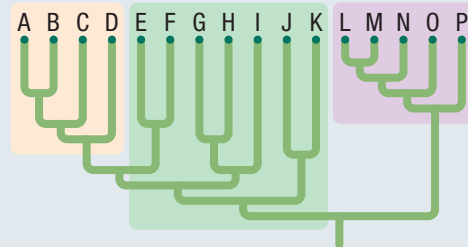
## 1.3 Summary

- Modern biological classification is based on phylogeny—the evolutionary relatedness of species.
- A clade is a taxonomic group that includes all the descendants of a common ancestor.
- Phylogenetic trees are used to show evolutionary relationships among species and groups.
- Both traditional and phylogenetic classification systems have advantages and disadvantages.

## 1.3 Questions

1. Why is a classification system based on relatedness more objective than a classification system based on the comparison of observed characteristics? **K/U**
2. Clades can be described as “natural groups.” Why do you think this is so? **T/I**
3. What do the “tips” and “branches” of a phylogenetic tree represent? **K/U**
4. Describe how you “trace ancestors back through time” on a phylogenetic tree. **K/U**
5. Compare and contrast traditional and phylogenetic classification systems. **K/U T/I**
  - (a) What are the advantages and disadvantages of each?
  - (b) Think of an example of when it would be useful to use a traditional classification. Why would this system be the best choice in this case?
  - (c) Think of a situation where it would be useful to use a phylogenetic classification system. Why would this system be the best choice in this case?
6. Traditional and phylogenetic classification systems *usually* place species in the same groups. For example, both systems place lions and tigers together, and horses and zebras together. Why is this not surprising? **K/U T/I**
7. Sketch a simplified version of the phylogenetic tree from Figure 8(b) (page 24) in your notebook: **T/I C A**
  - (a) Place the letter “A” at the location that represents the most recent common ancestor of mammals and lizards.
  - (b) Are mammals more closely related to one taxonomic group than any other? Explain.
  - (c) The closest relatives of crocodiles are birds. Why do you think traditional taxonomists place crocodiles in the same class as turtles, lizards, and snakes?
8. Brainstorm why an understanding of phylogenetic analysis might be useful to scientists working to preserve biodiversity. **T/I A**

9. Sketch the phylogenetic tree in **Figure 10** in your notebook. **T/I C**



**Figure 10** A phylogenetic tree

- (a) Which coloured groups represent a clade? Explain.
  - (b) Are the orange groups more or less closely related to the green groups than they are to the pink groups? Explain.
  - (c) Place a letter “X” on the tree to represent the most recent common ancestor to all the orange and green groups.
  - (d) Circle three true clades that occur *within* the green box.
10. Examine Figure 2(b) on page 22 and answer the following questions. **K/U T/I**
    - (a) The Mustelidae family includes both mink and otters. Both of these species spend most of their time in the water. Using evidence from the phylogenetic tree, explain why this makes sense.
    - (b) In your opinion, does a bear seem more similar to a dog or to a seal? Consider its physical appearance, ecological niche, and behaviour.
    - (c) Is a bear more closely related to a seal or to a dog? How do you know?
    - (d) Evolutionary changes do not occur at the same rate in different groups. How might this help explain your answer to (c)?