



Name

Period

Date

SECTION
17.2

CLASSIFICATION BASED ON EVOLUTIONARY
RELATIONSHIPS

Reinforcement

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?
