

## Concept 15.4

### Modern Taxonomy reflects evolutionary history.

What is Taxonomy: identification, naming, and classification of species.

Common Names: can cause confusion

- May refer to several species (ex. pine, monkey)
- May refer to different organisms. (ex. gopher)
- Don't accurately reflect the organism.  
(ex. catfish, crayfish, silverfish)

### The Linnaean System of Classification

The system of classification most widely used in biology dates back to Swedish botanist Carolus Linnaeus (1707–1778).

This hierarchical system has two main characteristics—a two-part Latin name for each species and a hierarchy, or ordering, of species into broader and broader groups.

### Binomial nomenclature:

binomial (by NOH mee ul):

The first part of a binomial is the genus (plural, genera) to which the species belongs. (Capitalized)

The second part of a binomial refers to one species within the genus. (Not capitalized)

Ex. Wolf: *Canis lupus*

Domestic Dog: *Canis familiaris*

## Classification and Phylogeny of Animals

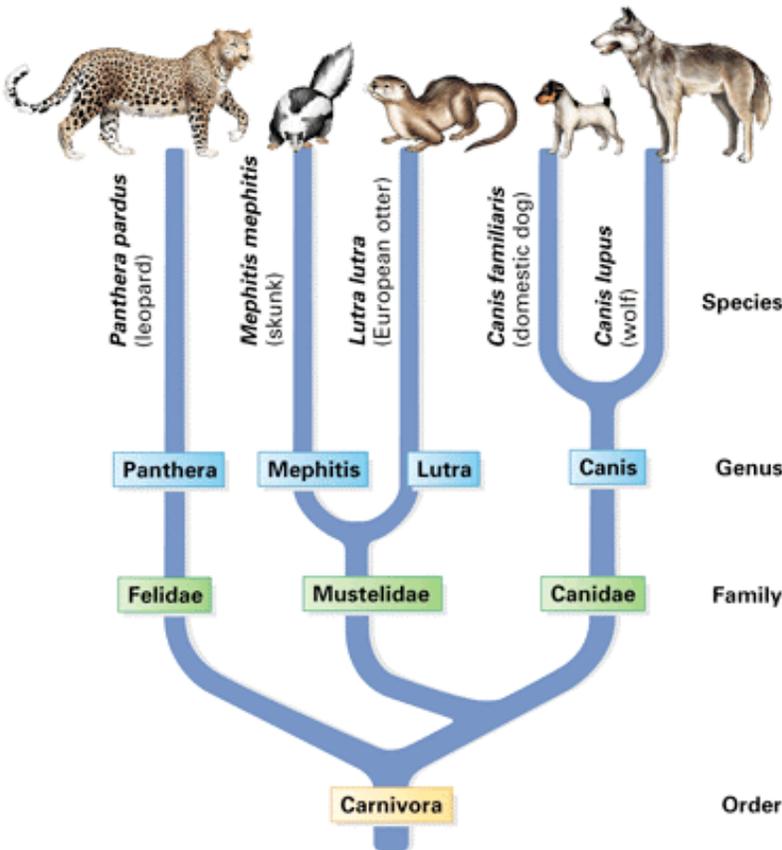
	<u>Humans</u>	<u>Gorilla</u>	<u>Katydid</u>
Kingdom	Animalia	Animal	Animalia
Phylum	Chordata	Chordata	Arthropoda
Class	Mammalia	Mammalia	Insecta
Order	Primates	Primates	Orthoptera
Family	Hominidae	Pongidae	Tettigoniidae
Genus	<i>Homo</i>	<i>Gorilla</i>	<i>Scudderia</i>
Species	<i>Homo sapiens</i>	<i>Gorilla gorilla</i>	<i>Scudderia furcata</i>

Pneumonic: **King Philip Came Over For Good Spaghetti**

### **Classification and Evolution**

phylogenetic tree: branching diagram, suggesting evolutionary relationships, that classifies species into groups within groups

( phylogeny, meaning "evolutionary history.")



**Homologous structures** are one of the best clues to assess how closely organisms are related.

Not all similar structures are inherited from a common ancestor

**convergent evolution:** process in which unrelated species from similar environments have adaptations that seem very similar.

**analogous structures:** similarities among unrelated species that result from convergent evolution

For example, the wings of insects and those of birds are analogous, not homologous, flight equipment—they evolved independently. And, they are built from entirely different structures. There is no evidence that insects and birds shared a common winged ancestor.

## Molecular Data as a Taxonomic Tool

relatedness of species can be measured by comparing their genes and gene products (proteins). The more the sequences match up, the more closely the species are probably related.

Such molecular comparisons provide a new way to test hypotheses about evolutionary history. For instance, fossil data have indicated that whales are closely related to the group of mammals that includes hippos, cows, deer, and pigs. Molecular data have backed up this hypothesis.

## A Closer Look at Phylogenetic Trees

A key feature of a phylogenetic tree is the pattern of branches. The tree can be expanded to include additional species, as in the diagram on the right. The "deeper" branch point represents the evolutionary split from a common ancestor of the wolf and cat groups.

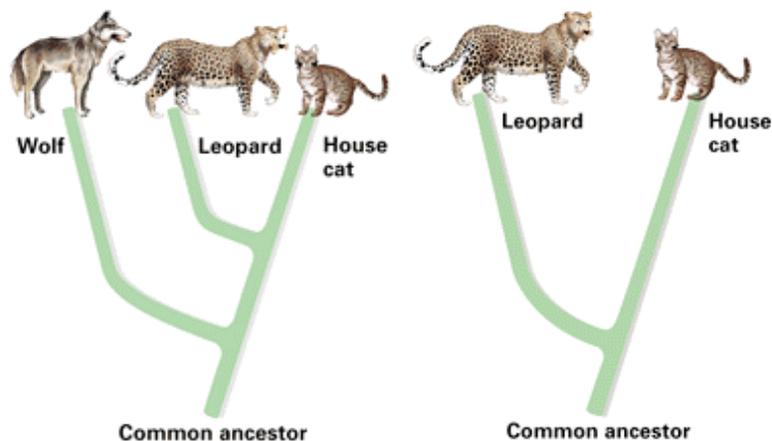


Figure 15-28

Leopards and house cats compose a branch of two species that share a common ancestor (far left). A larger branch that also includes wolves (near left) has a common ancestor that would have lived longer ago than the ancestor of leopards and house cats.

## Identifying Clades

Each evolutionary branch in a phylogenetic tree is called a **clade**.

Clades, like taxonomic levels in classification, can nest within larger clades.

Look at the phylogenetic tree in Figure 15-29. Species B through H are members of a clade (yellow). So are species I through K (orange). But these two groups only become part of a larger clade (blue) when you include species A. Species A is an ancestral species to all of the others in this larger clade. (See if you can identify all five clades in the figure.)

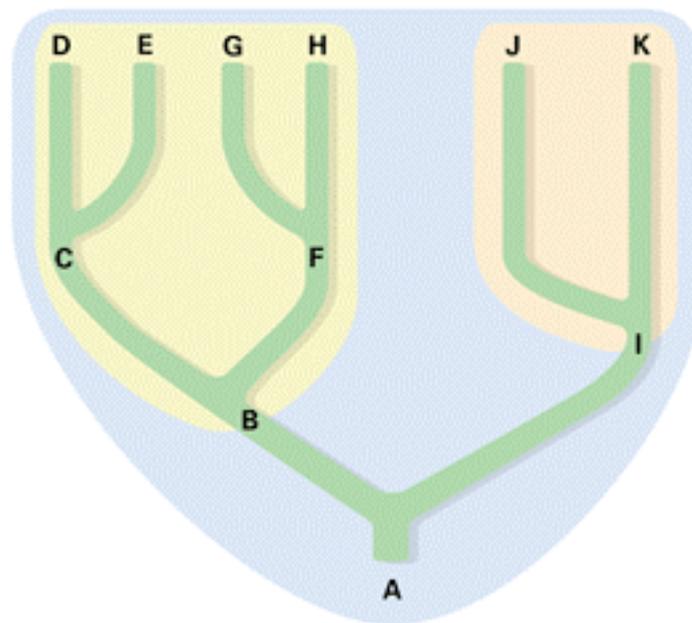


Figure 15-29

Each shaded area in the phylogenetic tree highlights one clade, such as the yellow area including species B through H.

**Cladistics:** How can a biologist determine the sequence of branching in a phylogenetic tree?

The most common method today is called **cladistics** (from the word clade, meaning branch).

The key rule in cladistics is that all of the organisms of a particular clade must share homologous structures that do not occur outside the clade.

These unique features that unite the organisms as a clade are called [derived characters](#).

**derived character:** homologous characteristic that unites organisms as a group

**cladogram:** phylogenetic tree constructed from a series of two-way branch points, suggesting ancestral relationships among species

A phylogenetic diagram that specifies the derived characters of clades is called a [cladogram](#).

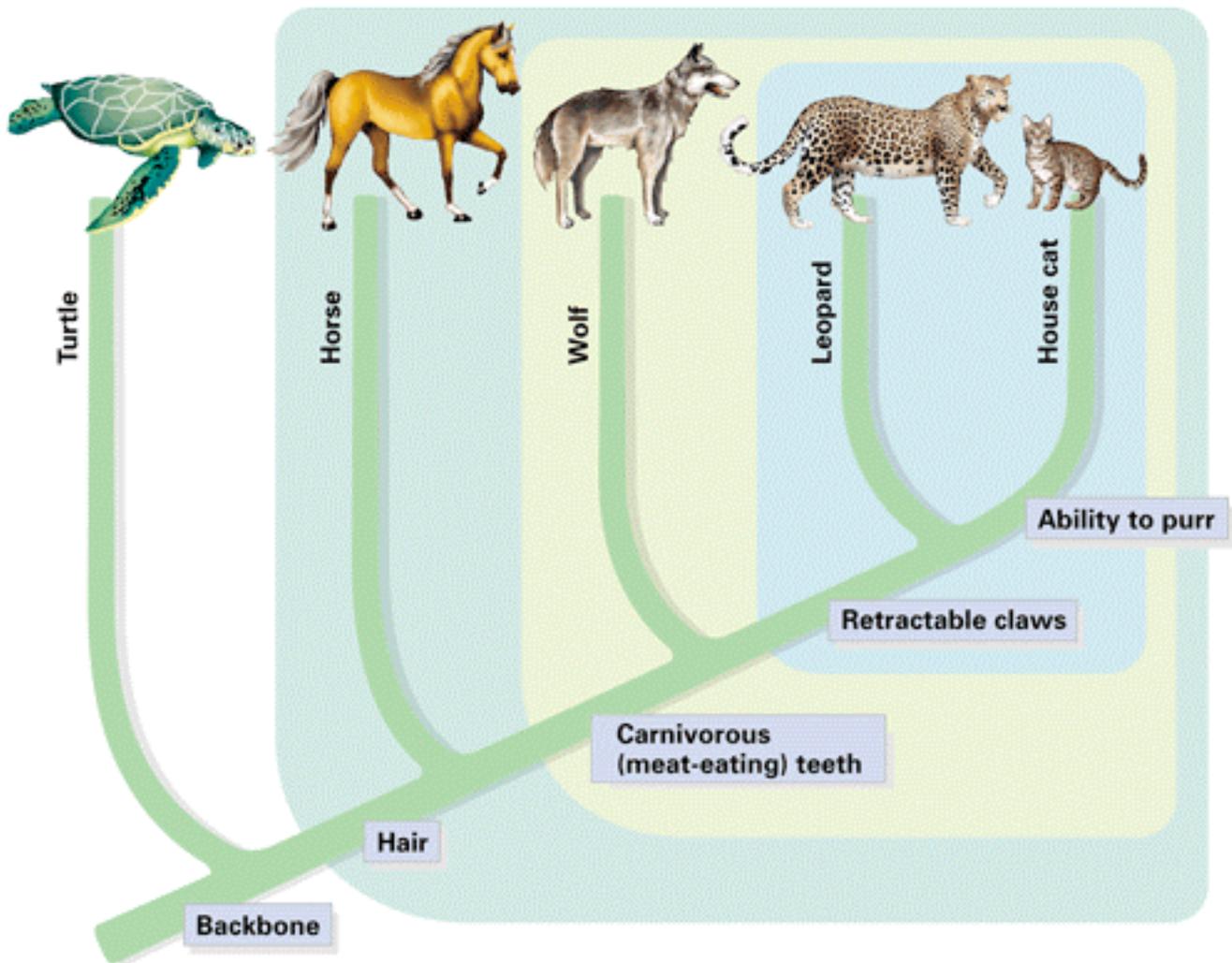


Figure 15-30

This cladogram shows how derived characters can be used to identify clades among certain vertebrates (animals with backbones). All the species shown here share a common ancestor that had a backbone. (Each clade is actually defined by several derived characters, not just one.)

## Reexamining Traditional Classification :

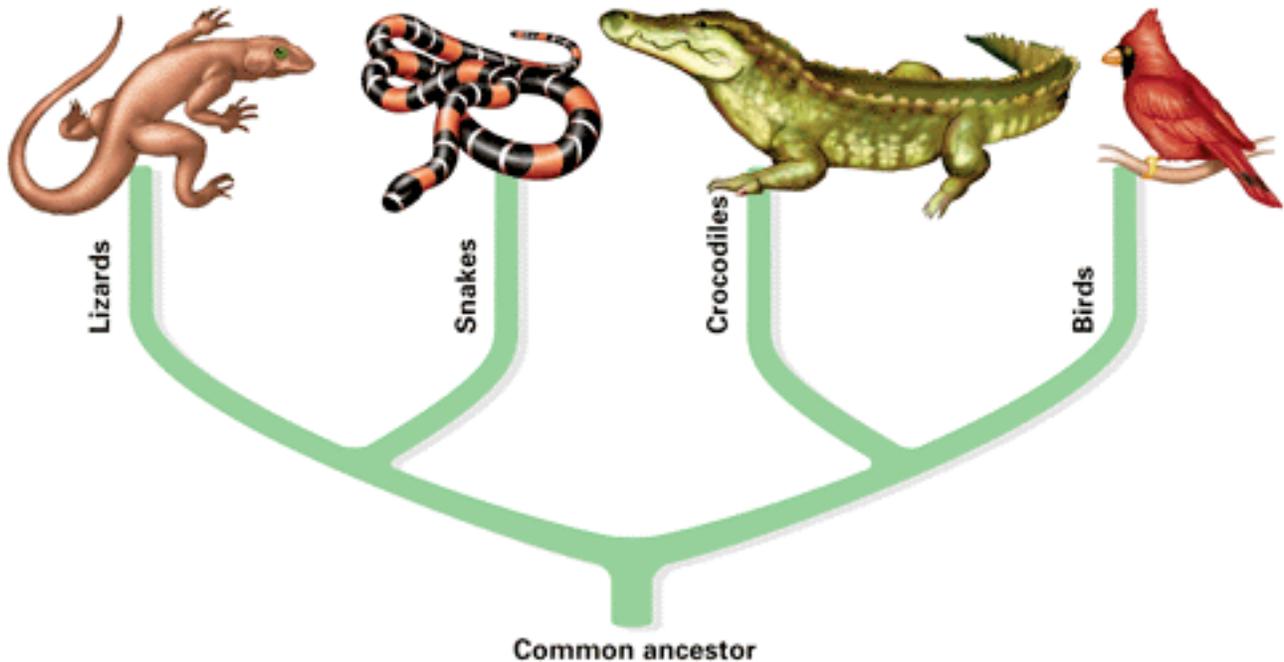


Figure 15-31

Biologists have traditionally placed reptiles and birds in separate classes of vertebrates. However, the tree shown here is more consistent with both fossil record and analysis of derived characters among living species.

## Comparing Classification Schemes

Phylogenetic trees and classifications represent hypotheses about evolutionary history. Like all hypotheses, they are revised to correspond with the discovery of new evidence.

**A Five-Kingdom Scheme** In 1969, American ecologist Robert H. Whittaker proposed a five-kingdom system. In the five-kingdom system, the kingdom Protista contains all eukaryotes that do not fit the definitions of plant, fungus, or animal. Most protists are unicellular. Amoebas and other so-called protozoa are examples. But protists also include certain large, multicellular organisms that are thought to be close relatives of unicellular protists.

**Three Domains** In the last decade, molecular data and cladistics have led to a reevaluation of the five-kingdom system.

A **domain** is a taxonomic category above the kingdom level.

This newer scheme recognizes three basic groups: two domains of prokaryotes—the Bacteria and the Archaea—and one domain of eukaryotes, the Eukarya.

The Bacteria and the Archaea differ in a number of ways.

What is most important to understand here is that classifying Earth's diverse species of life is a work in progress.

