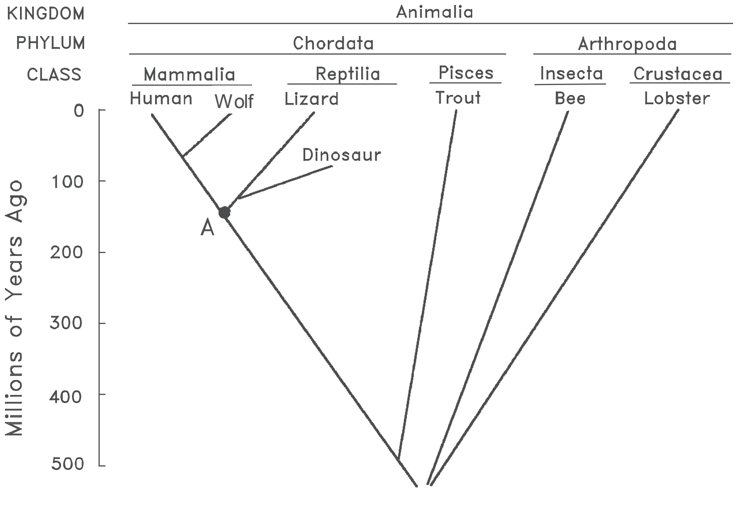
15. Classification And Evolution

As a consequence of Darwin's work it is now recognized that taxonomic classifications are actually **reflections of evolutionary history**. For example, Linnaeus put humans and wolves in the class Mammalia within the phylum Chordata because they share certain characteristics (e.g. backbone, hair, homeothermy, etc.). We now know that this similarity is not a coincidence; both species inherited these traits from the same **common ancestor**. *In general, the greater the resemblance between two species, the more recently they diverged from a common ancestor.* Thus when we say that the human and wolf are more closely related to each other than either is to the honeybee we mean that they share a common ancestor that is not shared with the honeybee.

Another way of showing the evolutionary relationship between organisms is in the form of a **phylogenetic tree**:

Figure 15.1
Phylogenic Tree



The vertical axis in this figure represents time. The point at which two lines separate indicates when a particular lineage split. For example, we see that mammals diverged from reptiles about 150 million years ago. The **most recent common ancestor** shared by mammals and reptiles is indicated by the point labeled A. The horizontal axis represents, in a general way, the amount of divergence that has occurred between different groups; the greater the distance, the more different their appearance.

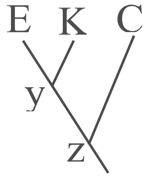
Note that because they share a fairly recent ancestor, species within the same taxonomic group (e.g. the class Mammalia) tend to be closer to each other at the top of the tree than they are to members of other groups.

Several types of evidence can elucidate the evolutionary relationship between organisms, whether in the form of a taxonomic classification (Table 15.1) or a phylogenetic tree (Figure 15.1). One approach, as already discussed, is to compare living species. The greater the differences between them, the longer ago they presumably diverged. There are, however, pitfalls with this approach. For example, some species resemble each other because they independently evolved similar structures in response to similar environments or ways of life, not because they share a recent common ancestor. This is called **convergent evolution** because distantly related species seem to converge in appearance (become more similar).

Examples of convergent evolution include the wings of bats, birds and insects, or the streamlined shape of whales and fish. At first glance it might appear that whales are a type of fish. Upon further examination it becomes apparent that this resemblance is superficial, resulting from the fact that whales and fish have adapted to the same environment. The presence of hair, the ability to lactate and homeothermy clearly demonstrate that whales are mammals. Thus, the taxonomist must take into account a whole suite of characteristics, not just a single one.

The fossil record can also be helpful for constructing phylogenetic trees. For example, bears were once thought to be a distinct group within the order Carnivora. Recently discovered fossils, however, show that they actually diverged from the Canidae (wolves, etc.) fairly recently. The use of fossils is not without its problems, however. The most notable of these is that the fossil record is incomplete. This is more of a problem for some organisms than others. For example, organisms with shells or bony skeletons are more likely to be preserved than those without hard body parts.

When there are three or more species in a genus you must decide which two of the species share a common ancestor not shared by the other(s). The diagram below indicates that species E and K are more closely related to each other than either is to C. We hypothesize that E and K have a common ancestor (y) that is not shared by C. Similarly, two genera that more closely resemble each other than they do other genera presumably share a common ancestor. Thus, even in the absence of a fossil record it is possible to develop a phylogenetic tree. We can even infer what a common ancestor like y might have looked like.

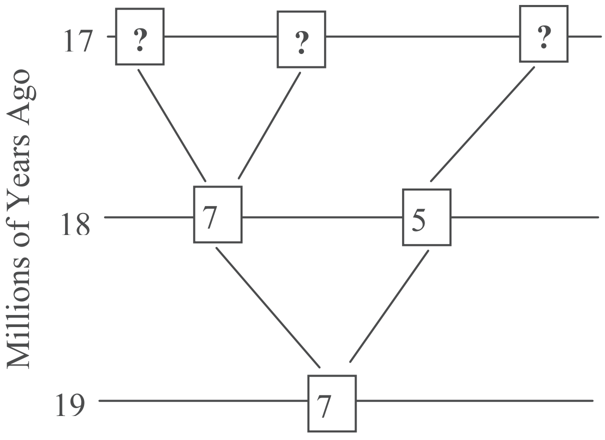


3. THE PHYLOGENY OF CAMINALCULES

Using a large sheet of paper, construct a phylogenetic tree for the Caminalcules. Use a meter stick to draw 20 equally spaced horizontal line on the paper. Each line will be used to indicate an interval of one million years. Label each line so that the one at the bottom of the paper represents an age of 19 million years and the top line represents the present (0 years).

Figure 15.2

Arranging your piles



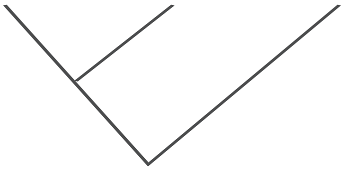
Cut out all the Caminalcules (including the living species). Put them in piles according to their age (the number in parentheses). Beginning with the oldest fossils, arrange the Caminalcules according to their evolutionary relationship. Figure 15.2 shows how to get started.

Hints, Suggestions and Warnings

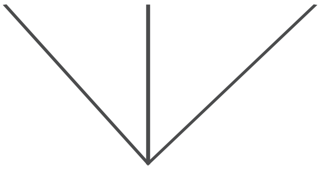
a. Draw lines faintly in pencil to indicate the path of evolution. Only after your instructor has checked your tree should you glue the figures in place and darken the lines.

b. Branching should involve only two lines at a time:

Like This



Not Like This



c. Some living forms are also found in the fossil record.

d. There are gaps in the fossil record for some lineages. Also, some species went extinct without leaving any descendants (remember the dinosaurs, Figure 15.1).

e. The Caminalcules were numbered at random; the numbers provide no clues to evolutionary relationships.

f. There is only one correct phylogenetic tree in this exercise. This is because of the way that Joseph Camin derived his imaginary animals. He started with the most primitive form (#73) and gradually modified it using a process that mimics evolution in real organisms. After you complete your phylogeny compare it with Camin's original.