

LABORATORY EXERCISE 1

PHYLOGENY AND CLASSIFICATION

The world has a bewildering array of living things residing on, over and under its surface. This nearly endless variety of organisms has inspired one of them, man, to make something ordered out of a seemingly chaotic situation. He does this in three ways - he identifies, he names and he classifies living things. To a layman, these activities may seem nearly identical, however, they differ a great deal. A person identifies an organism when he recognizes it and shows that it belongs to an already known (and named) group. An organism is named only once, at the time someone observed it and realized that it did not belong to any existing group. Therefore it was a new species, a kind of living thing that was unknown (or unrecognized) before he saw it, and he assigned it a Latin binomial such as *Amoeba proteus*, which refers to the genus and new species of the organism.

Today, before naming a new species, biologists try to learn as much about it as is possible in order to determine whether it is sufficiently different from known species to merit a separate status. It is studied as a population from many viewpoints such as anatomy, physiology, reproduction, embryology, cytology, and even biochemistry. Early investigators considered new species from the standpoint of structure (anatomy) only, and often with only a single animal or a few specimens at hand. Since variation exists within a species, this practice often leads to the naming of poorly delimited species. Although they followed this practice, workers such as Linnaeus in 1758 and Haeckel in 1862 developed the binomial procedure still in use today. They also created a system for arranging the species in hierarchical ranks called taxa (singular-taxon) and this activity is termed classification. Living things most nearly like each other were placed into a species. That species and others like it were grouped into a genus, similar genera went into a family, and so on up a series of even larger and arbitrary taxa. An organism is classified when it is put into any kind of scheme that shows its relation to other living things. Organisms can be classified in many ways, by their color, shape, size, sex, ancestry or anything else. The system of classification in widest use today is a historical one; it has as its basic theme the sequence of evolution of organisms, and it is considered a "phylogenetic" classification. Animals (and plants) are classified in the order in which they are believed to have risen from a single common ancestor. Thus in addition to being a mere cataloguing of organisms, the classification attempts to show the "family tree" of all living things. One must remember that no contemporary organism is the ancestor of any other contemporary organism, since each extant (living) group has nearly as long a history of evolution as any other. Certain groups, however, have changed relatively little; from these and from the remains of genuine ancestors preserved as fossils, the ancestry or organisms can be deduced. On this "family tree" all extant living things have equivalent status at the tips of the branches. It is the stems and branch points that express their evolution. As biologists gain more knowledge, the classification systems are constantly revised and improved, however even the best system possesses some fairly serious gaps in knowledge. For a completely phylogenetic classification, one must know every organism that ever lived on earth, when it lived, what happened to it, and why. The sources for gaining this information are not wholly satisfactory. A study of extant animals is frequently misleading since it is often difficult to discern whether a given characteristic is primitive,

advanced, or the result of a very specialized mode of living. For example, in some animals, the absence of a digestive system is "primitive" and reflects their descent from ancestors that never did have these organs; in others, it indicates a "secondary" loss or "specialization" of animals evolving a parasitic life style. The fossil record is inadequate because (1) some soft-bodied living things such as protozoa, viruses, etc., just don't fossilize; (2) sediments or volcanic ash are necessary to produce fossils, and these have occurred only on parts of the earth's surface; (3) most fossils are under tons of rock and/or water and are hard to obtain or have been destroyed by uplift and erosion. For these reasons, only a fraction of the total knowledge is available so our best phylogenetic classification is far from perfect. However, with these difficulties, there has resulted a workable system that helps to satisfy man's need for orderliness and to reveal the lines of evolution which led to the formation of such diverse creatures from a single type of organism.

A great deal of historical (phylogenetic) information can be obtained from living animals. Remember, all aspects of an animal's morphology, physiology, biochemistry, etc., are the manifestations of the genetic material, the DNA. If two animals are similar, then they must share identical or similar sequences of nucleotides comprising their DNAs. It is extremely unlikely that these similar sequences could have originated by any means other than by having evolved from the DNA of an ancestor common to both animals. Dissimilarities in the two animals (produced by unlike sequences of nucleotides) were produced by evolution in the time elapsed since the common ancestor was alive. Therefore, biological similarity indicates common ancestry, and the degree of similarity, suggests when in geological time (relatively), the ancestor was alive. For example, you share many characteristics with a cat, and fewer of them with a sea star. This can be interpreted as showing that the ancestor you share with the cat existed far more recently than did the animal that gave rise to both you and the sea star. This information can be used to place the branch points in the family tree that includes you and both of your relatives.

Today you'll get a chance to observe and record characters of organisms to use for classifying the organisms using a phylogenetic approach. Using your own observations of specimens, lecture material and/or your textbook, assign a state to each of the 15 study animals for the twelve characters listed on the next page. You can record your data on the character matrix sheet provided.

Characters and character states

1. Cell #:	1-unicellular	2-multicellular	
2. Cell complexity:	1-loose aggregates	2-organized/tissues	
3. # body layers:	0-none	1-two layers	2-three layers
4. Coelom:	0-acoelomate	1-psuedocoelomate	2-coelomate
5. Symmetry:	0-none	1-radial	2-bilateral
6. Skeleton:	0-none	1-exoskeleton	2-endoskeleton
7. Notochord:	0-none	1-present	
8. Hair:	0-none	1-present	
9. Feathers:	0-none	1-present	
10. Blastopore fate:	0-none	1-mouth	2-anus
11. Dermal ossicles:	0-none	1-present	
12. Amniotic egg:	0-none	1-present	

Additional characters and character states

Please develop at least 5 (preferably more) characters that describe the animals we are working with. Remember that the character states need to be ordered in such a way as to reflect the relative “age” of each feature (you may need to make educated guesses here!).

13. _____
14. _____
15. _____
16. _____
17. _____

After you have completed collecting data from the specimens, enter your character matrix into Excel. Next week we will analyze your data using the systematic software, MacClade.

The same animals that your team has just classified, as well as the additional animals, are incorporated in the computer exercise ANIMAL. This exercise is designed to help you learn some of the principles of identification, classification, phylogeny, and taxonomy. In the coming weeks, you should be using the computer extensively to learn this material and to integrate it with your lectures and readings. You will be examined on ANIMAL during 8th or 9th week.