**Taxonomy: Classifying Life**

One of the hypotheses Charles Darwin put forth in his book, *On the Origin of Species*, was that all modern organisms derive from a single common ancestor, and that differences between organisms today resulted from evolutionary changes that occurred as species diverged from one another. This theory is referred to as **the theory of common descent**. According to this theory, all modern organisms can be arranged in a “family tree” or phylogeny, that describes their relationship to each other. The theory of common descent is now well accepted as the best explanation for the origins of modern species.

Biologists who study the evolutionary history of living organisms are called **systematists**. One of the generalizations of the science of systematic is that organisms that share more features are more closely related than organisms that organisms that share fewer features. By this reasoning, systematists think that shared features might have been present in the common ancestor of the organisms. Shared features among species that occur as a result of the species’ shared relationships are known as homologies. Phylogenies are created by systematists based on their investigation of the homologies among species.

Testing hypotheses of evolutionary relationship is especially important because not all similarities among organisms are homologies. In other words, two organisms that appear similar might not have similar features because they have a common ancestor, Instead similar environmental conditions experienced by two distantly related organisms might favor the evolution of similar structures or features. Shared characteristics that arise as a result of shared environmental conditions are known as **analogies**. For example, dolphins appear superficially similar to sharks, with their streamlined bodies, lack of body hair, and generally gray color. These similarities are analogous, however, and reflect their similar lifestyles as ocean predators. Dolphins are actually more closely related to other mammals, such as otters and humans, than they are to sharks and fish. Dolphins and other mammals are similar because dolphins breathe air (rather than have gills), produce hair, and provide milk for their young. Distinguishing between homology and analogy is one of the most difficult tasks a systematist faces.

At least 1.7 million species of living organisms have been discovered, and the list grows longer every year (especially of insects in the tropical rain forest). How are they to be classified?

Ideally, classification should be based on **homology**; that is, **shared characteristics that have been inherited from a common ancestor**. The more recently two species have shared a common ancestor,

* the more homologies they share, and
* the more similar these homologies are.

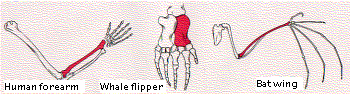
Until recent decades, the study of homologies was limited to

* anatomical structures and
* [pattern of embryonic development.](http://users.rcn.com/jkimball.ma.ultranet/BiologyPages/R/Recapitulation.html)

However, since the birth of molecular biology, homologies can now also be studied at the level of

* [proteins](http://users.rcn.com/jkimball.ma.ultranet/BiologyPages/T/Taxonomy.html#ProteinSequences) and
* DNA

Anatomical homology

The figure shows the bones in the forelimbs of three mammals: human, whale, and bat (obviously not drawn to the same scale!). Although used for such different functions as throwing, swimming, and flying, the same basic structural plan is evident in them all. In each case, the bone shown in color is the **radius**.

Body parts are considered **homologous** if they have

* the same basic structure
* the same relationship to other body parts, and, as it turns out,
* develop in a similar manner in the embryo.

It seems unlikely that a single pattern of bones represents the best possible structure to accomplish the functions to which these forelimbs are put. However, if we interpret the persistence of the basic pattern as evidence of inheritance from a common ancestor, we see that the various modifications are adaptations of the plan to the special needs of the organism. It tells us that **evolution is opportunistic**, working with materials that have been handed down by inheritance.

Exercise 1

Phylogenies are often presented graphically in the form of a tree diagram. On these trees, all of the modern organisms are found at the tops of the branches. The junctions between branches lower down on the tree represent common ancestors to these modern organisms. Junctions near the top of the tree represent more recent common ancestry than junctions near the base of the tree.

A C C CC

E B

D

Species A and C

are very similar,

therefore, they are

closely related.

This junction represents Species E and B look the least like

The ancestor of these two the others. Therefore, they must

species (A,C) share a very ancient ancestor with

species A, C, and D.

* 1. Draw your family’s phylogenetic tree.

It can be helpful to understanding a phylogenetic tree to relate it to relationships that you already know about.

Fill in the following table, as best you can:

|  |  |
| --- | --- |
| **Relationship to you** | **Name of Person** |
| A. Self |  |
| B. Full sibling (brother or sister) |  |
| C. First cousin |  |
| D. Parent (from 1st cousin’s side of family) |  |
| E. Grandparent (father or mother of parent listed) |  |

Using the information from the table, fill in the following tree:

A: \_\_\_\_\_\_\_\_\_\_\_\_\_ B: \_\_\_\_\_\_\_\_\_\_\_\_\_ C: \_\_\_\_\_\_\_\_\_\_\_\_\_\_

D: \_\_\_\_\_\_\_\_\_\_\_\_\_\_

E: \_\_\_\_\_\_\_\_\_\_\_\_\_\_

* 1. Answer the following questions:

1. Who is the common ancestor of all the individuals on the tree?

2. Why does the diagram place only you, your sibling, and your cousin at

the branch tips?

3. How is this tree different than those produced by biologists attempting to determine the evolutionary relationship among species?

**Cytochrome c** is part of the respiratory chain down which electrons are passed to oxygen during cellular respiration. Cytochrome c is found in the mitochondria of every aerobic eukaryote — animal, plant, and protist. The amino acid sequences of many of these have been determined, and comparing them shows that they are related.

Human cytochrome c contains 104 amino acids, and 37 of these have been found at equivalent positions in every cytochrome c that has been sequenced. We assume that each of these molecules has descended from a precursor cytochrome in a primitive microbe that existed over 2 billion years ago. In other words, these molecules are **homologous**.

The first step in comparing cytochrome c sequences is to align them to find the maximum number of positions that have the same amino acid. Sometimes gaps are introduced to maximize the number of identities in the alignment (none was needed in this table). Gaps correct for [insertions and deletions](http://users.rcn.com/jkimball.ma.ultranet/BiologyPages/M/Mutations.html#insertions) that occurred during the evolution of the molecule.

This table shows the N-terminal 22 amino acid residues of human cytochrome c with the corresponding sequences from six other organisms aligned beneath. A dash indicates that the amino acid is the same one found at that position in the human molecule. All the vertebrate cytochromes (the first four) start with glycine (Gly). The [Drosophila](http://users.rcn.com/jkimball.ma.ultranet/BiologyPages/D/Drosophila.html), wheat, and yeast cytochromes have several amino acids that precede the sequence shown here (indicated by <<<). In every case, the heme group of the cytochrome is attached to Cys-14. and Cys-17 (human numbering). In addition to the two Cys residues, Gly-1, Gly-6, Phe-10, and His-18 are found at the equivalent positions in every cytochrome c that has been sequenced.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Molecular homology of cytochrome c** | | | | | | | | | | | | | | | | | | | | | | | |
|  |  | 1 |  |  |  |  | 6 |  |  |  | 10 |  |  |  | 14 |  |  | 17 | 18 |  | 20 |  |  |
| Human |  | Gly | Asp | Val | Glu | Lys | Gly | Lys | Lys | Ile | Phe | Ile | Met | Lys | Cys | Ser | Gln | Cys | His | Thr | Val | Glu | Lys |
| Pig |  | - | - | - | - | - | - | - | - | - | - | Val | Gln | - | - | Ala | - | - | - | - | - | - | - |
| Chicken |  | - | - | Ile | - | - | - | - | - | - | - | Val | Gln | - | - | - | - | - | - | - | - | - | - |
| Dogfish |  | - | - | - | - | - | - | - | - | Val | - | Val | Gln | - | - | Ala | - | - | - | - | - | - | Asn |
| Drosophila | **<<<** | - | - | - | - | - | - | - | - | Leu |  | Val | Gln | Arg |  | Ala | - | - | - | - | - | - | Ala |
| Wheat | **<<<** | - | Asn | Pro | Asp | Ala | - | Ala | - | - | - | Lys | Thr | - | - | Ala | - | - | - | - | - | Asp | Ala |
| Yeast | **<<<** | - | Ser | Ala | Lys | - | - | Ala | Thr | Leu | - | Lys | Thr | Arg | - | Glu | Leu | - | - | - | - | - | - |

We assume that the more identities there are between two molecules, the more recently they have evolved from a common ancestral molecule and thus the closer the kinship of their owners. Thus the cytochrome c of the rhesus monkey is identical to that of humans except for one amino acid, whereas yeast cytochrome c differs from that of humans at 44 positions. (There are no differences between the cytochrome c of humans and that of chimpanzees.)

### Phylogenetic trees (cladograms)

With such information, one can reconstruct an evolutionary history of the molecule and thus of their respective owners. This requires

* using the [genetic code](http://users.rcn.com/jkimball.ma.ultranet/BiologyPages/C/Codons.html#dna_codons) to determine the minimum number of nucleotide substitutions in the DNA of the gene needed to derive one protein from another and
* a powerful computer program to search for the shortest paths linking the molecules together.

The tree corresponds quite well to what we have long believed to be the evolutionary relationships among the vertebrates. But there are some anomalies. It indicates, for example, that the primates (humans and monkeys) split off before the split separating the kangaroo, a marsupial, from the other placental mammals. This is certainly wrong. But sequence analysis of other proteins can resolve such discrepancies.

Cytochrome c is an ancient molecule, and it has evolved very slowly. Even after more than 2 billion years, one-third of its amino acids are unchanged. This conservatism is a great help in working out the evolutionary relationships between distantly-related creatures like fish and humans.

Exercise 2 Cytochrome C Comparison Lab

1. Compare the amino acid sequence of cytochrome C in various organisms

a. Mark the amino acids which are different. Use the example below to show

you how.

------GDVAKGKKTFVQKCAQCHTVENGGKHKVGPNLW

-**GV**GDV**E**KGKK**I**FVQ**R**CAQCHTVE**A**GGKHKVGPNL**H**

b. Count and record the total number of differences (7)

2. Make a branching tree (cladogram) using the data provided:

a. The two most closely related species have the fewest differences in amino

acid sequence. Place the two most closely species on the two shortest branches of the tree.

species 1 species 2

b. Place the next two closest species on the next shortest branches.

species 3 species 4

c. Place the species which is the next closest on the next longest branch. Continue

until all the species have been placed.

3. Answer the following questions:

a. How many cytochrome c amino acid sequences differences are there between chickens and turkeys?

b. Make a cladogram for chickens, penguins and turkeys.

c. Predict the number of cytochrome c amino acid sequence differences you would expect to see between

i. horse and zebra

ii. donkey and zebra

What other information did you use to make this prediction?

d. List three other things used to determine how organisms are related to each other.

e. Explain why more closely related organisms have more similar cytochrome c.