Bio1B   **Evolution section (Thomson)**   **Sept 28, 2003**   **Fall 2003**

lecture 2: Systematics and cladistics (ch. 23:425-437)

- **Systematics and cladistics (summary of topics)**
  - Describe the broad features of the branching relationships of life on earth
  - Explain the weaknesses of the hierarchical Linnaean classification system
    (Kingdom. phylum or division, class, order, family, genus, species
  - Describe and apply the basic methodology of cladistics
  - Contrast ancestral and derived traits
  - Contrast homologous and analogous traits

- **Why do we want to draw evolutionary relationships?**
  - Intrinsic interest in knowing the relationships of all life forms.
  - When we have a good knowledge of the "tree of life" we can study the genetics of new
    innovations, e.g., the same gene is involved in fin development in "fish" and limb
    development in tetrapods.
  - If an important drug, e.g., in treatment of cancer, is only available from a plant species that
    is rare, one can look at closely related plants to see if there is an abundant species from
    which the drug can be obtained.
  - If a feature such as antifreeze in some Arctic and Antarctic species of fish can be shown
    from an evolutionary tree to have evolved independently in these two regions, we can
    study the molecular basis of these innovations to see if they use a similar molecular
    solution (they do in this case), or have evolved entirely different solutions. Similarly with
    other convergent traits such as giving birth to live young, adaptations for living in desert,
    or other harsh, conditions.
  - Knowing the genetic relationships of taxa can be important in study of the biogeography of
    living and fossil forms found in the same area. The study of closely related species on
    different continents can provide information on continental drift.
  - In the study of behavioral traits, one needs a good evolutionary tree on which to map the
    trait and determine convergences versus shared ancestry.

• Systematics

Linnaeus: developed systematic naming of animals and plants

taxonomy: hierarchical classification system—
kingdom, phylum or division, class, order, family, genus, species (see Figure 23.11 of textbook)
(King Philip Calls Out For a Good Soup)

- Note that the hierarchical classification system is primarily used for convenience, and there is a great deal of variation between groups with regard to how closely organisms need to be related to be considered in the same family or order, etc. An avian family may have a more recent common ancestor than a family of flowering plants, or vice versa (see page 343 of the textbook), and similarly with genetic variation.

- Taxonomy is in a state of flux. We currently use a combination of cladistics (see below) for drawing evolutionary relationships while retaining also some features of Linnaean nomenclature.

taxon (taxa): any named taxonomic group, such as the family Felidae, or the genus *Homo*, or the species *Homo sapiens*

systematics: study of biological diversity and its evolution

phylogeny: "Tree of life": branching relationships among species, showing which species shares its most recent common ancestor with which other species

homologous: same evolutionary origin, but may now differ in structure and function. When considering evolutionary relationships, we look for homologies, these can be based on morphology, embryology, genetics, and fossil evidence (see Figures1.2 and 23.2 of the book).

analogous: similar structure and function but different evolutionary origins (see Figure 23.2 of the textbook). Analogies can confuse us when considering evolutionary relationships (also see convergent evolution).

convergent evolution (convergence): the independent evolution of similar features by two or more groups. Also, a synonym for analogy.

- Similar adaptations are independently acquired through, e.g., living in the same type of environment, adopting the same diet, or defending against similar predators.

- One examples of convergent evolution is the streamlined bodies of some marine animals, e.g., sharks, icthyosaurs (extinct marine reptile of the Mesozoic), and dolphins (more examples will be considered in the next lecture). Also see Figure 23.8 in the textbook.

reversion (reversal): reappearance of ancestral characters that have been absent in intervening generations

homoplasy: possession by two or more species of a similar or identical character state that has <u>not</u> been derived by both species from their common ancestor; embraces convergence and evolutionary reversal

Weaknesses of Linnaean classification:
- With plants, Linnaeus often used characters that were convergent, i.e., although they looked similar, they were cases of convergent evolution, and did not reflect close genetic relationship. Historically with plants there have been continual arguments as to which is the most important character to base classification on.
- There are no consistent rules to determine when a new genus (or family, order, etc.) is warranted.
- While the Linnaean system is hierarchical it does not describe the evolutionary (genetic) relationships within a group, e.g., all families within an order.
- Further, it can lead to "paraphyletic groupings," e.g., placing humans (*Homo sapiens*) in a separate family (Hominidae) means that the family Pongidae (orangutans, gorillas, and chimpanzees) is a paraphyletic grouping (see below for definition).
- Similarly, the class Reptilia is paraphyletic since birds are not included. Dinosaurs (class Reptilia) are more closely related to birds, which are in a different class (Aves), than they are to turtles which are in the same class. Class Reptilia should have been divided into separate classes for turtles, lizards, snakes, crocodiles, etc.

- **Cladistics**

cladistics: the members of a group in a cladistic classification share a more recent common ancestor with each other than with the members of any other group
- Our aim is to use cladistics to describe the evolutionary relationships of all living and fossil species. We use anatomical, developmental, and genetic data (see Table 23.1 and Figures 23.5 and 23.7 in the textbook) on living and fossil species, to draw evolutionary relationships in a systematic and unbiased way.
- In cladistics, we use new traits shared by all descendants of a common ancestor (synapomorphies) to determine monophyletic groupings which include the common ancestor and all descendants.

clade: a group of organisms that have <u>all</u> evolved from a common ancestor, includes the common ancestor and all its descendants e.g., vertebrate amniotes (see below). A synonym for monophyletic group (see below).

common ancestor: assuming a single origin of life, then any two taxa have a most recent common ancestor

node: a branch point, it represents a common ancestor at the time of divergence into two or more lineages

cladogram: a graphical depiction of phylogenetic relationships

sister groups (or taxa): two groups with the same immediate common ancestor

plesiomorphic: an ancestral trait, sometimes (inappropriately) termed primitive

symplesiomorphic: an ancestral character shared by several species (we usually do not use this term, but imply it when we say plesiomorphic)

apomorphic: a derived (new) trait, sometimes (inappropriately) termed advanced

synapomorphies: shared apomorphies (derived) characteristics. To draw a phylogenetic tree, we look for synapomorphies

autapomorphy: a derived character state possessed by only <u>one</u> of the taxa under consideration. Autapomorphies demonstrate the uniqueness of a taxa but they don't help identify clades.

monophyletic group: a taxon is monophyletic if a single ancestor gave rise to <u>all</u> species in that taxon and to <u>no</u> species placed in any other taxon
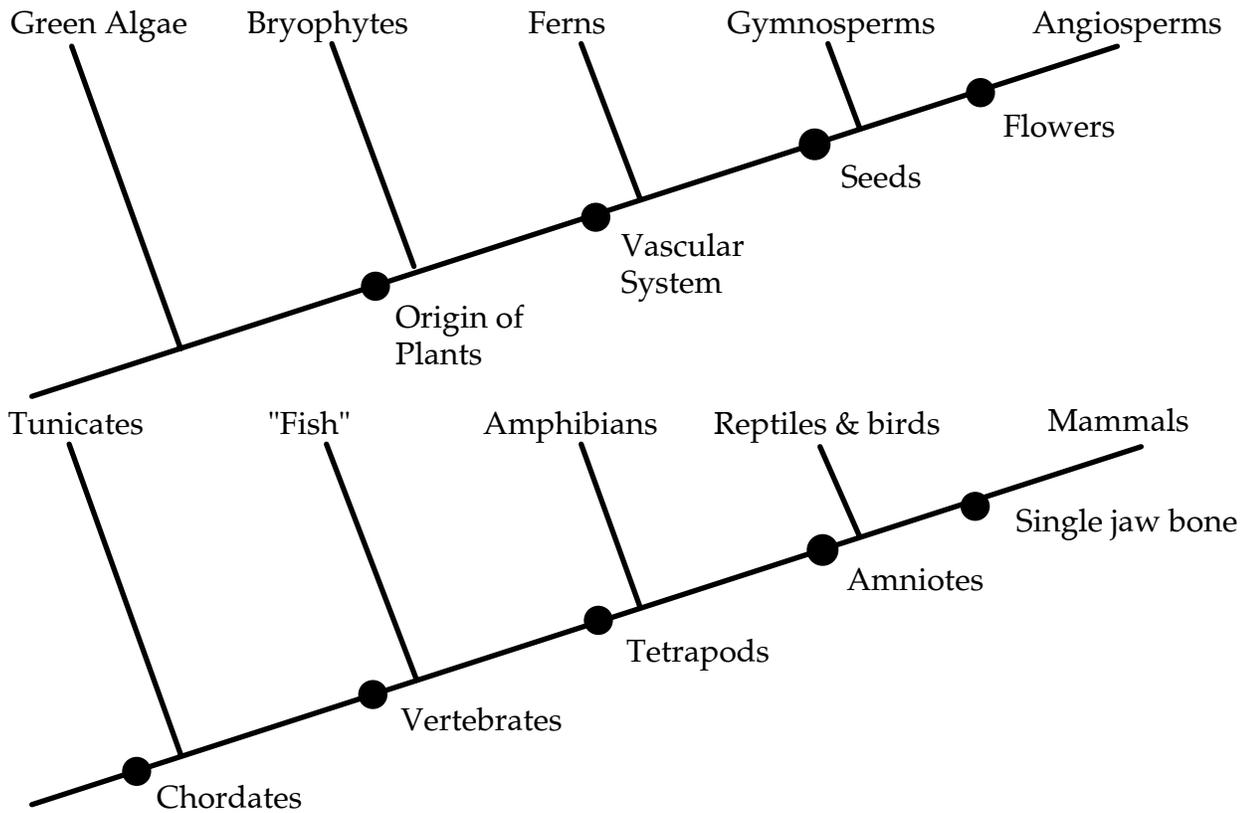
paraphyletic group: a paraphyletic taxon <u>excludes</u> species that share a common ancestor that gave rise to the species included in the taxon. The class "Reptilia", excluding birds, is a paraphyletic grouping.

polyphyletic group: a polyphyletic group includes two or more taxa, but not the common ancestor of those taxa. The members of a polyphyletic group are grouped by <u>false synapomorphies</u> - i.e., their similarities are analogous rather than homologous.
If we grouped dolphins and sharks based on their physical similarity of a streamlined body adapted for speed in a marine environment, we would be forming a polyphyletic grouping.

outgroup: among the states of a character found in the members of a monophyletic group, the <u>ancestral</u> character state is the one that is most widely distributed among taxa <u>outside</u> this group (unless there is contrary evidence). These latter taxa are called <u>outgroups</u> and their features provide valuable information for inferring relationships among the members of the monophyletic group under study.

stem group and **crown group:** (used especially in discussing taxa with a fossil record), a stem group is an ancestral clade from which a crown group with new derived characteristics has evolved

monophyletic groupings for living taxa: if one just looks at modern taxa of bacteria and archae, then monophyletic groups can be defined. Similarly, for living species the class "Reptilia" could be subdivided into monophyletic groups of turtles, snakes, lizards, crocodiles (including respectively their most recent common ancestor). When we talk about the paraphyletic grouping "dinosaurs" or "fish" (which includes jawless, cartilagenous, and bony fishes), we use the quote marks to denote that we know we are talking about a paraphyletic grouping.

Green Algae   Bryophytes   Ferns   Gymnosperms   Angiosperms

Flowers

Seeds

Vascular
System

Origin of
Plants

Tunicates   "Fish"   Amphibians   Reptiles & birds   Mammals

Single jaw bone

Amniotes

Tetrapods

Vertebrates

Chordates

chordates: notochord present - long flexible rod - dorsal hollow nerve cord

vertebrates: backbone in all vertebrates is very similar (fishes, amphibians, reptiles, birds, mammals)

tetrapods: a vertebrate possessing 2 pairs (i.e., 4) limbs - amphibians, reptiles, birds, mammals

amniotes: a vertebrate possessing an amnion (an extra embryonic membrane) surrounding the embryo (reptiles, birds, mammals)

Choice of traits in a cladistic analysis: a cladogram is only as good as the traits used to construct the branching points. However, it does provide us with a potentially unbiased way to determine evolutionary relationships. If we use enough traits, and consistently see the same relation ships, we can be pretty certain of the accuracy of the cladogram.

• One must be careful to avoid as much as possible including in the analysis traits which are convergent, or at least to use enough traits and parsimony so that we can detect convergences (see Figures 23.1 and 23.8).

• Also one has to be careful that adaptations have not obscured homologies.

• Remember too that in the outgroup there is also evolution via cladogenesis and anagenesis and synapomorphies defining monophyletic groupings. Usually however these traits will differ from those defining the taxa under study.

• The choice of the outgroup is important, one wants to use the closest sister taxa when possible. Still, the assumption that the outgroup retains the ancestral trait may not always be correct. Often more than one outgroup taxon is used.

• Living sister taxa are always more closely related to each other than to the living outgroup taxon.

• A cladogram shows relative time, but not absolute time.

• Every species is a mixture of ancestral (plesiomorphic) and new (apomorphic) traits. No species per se is more primitive, it may however retain the ancestral trait with respect to the group being studied.

• We traditionally put the trait before the node defining the most recent common ancestor of the taxa under consideration. We assume there are fossil forms we have not found yet that fall within this monophyletic grouping and these may predate the taxa under consideration.

fossils on cladograms: we can never tell whether or not a fossil form was in a direct lineage leading to current species