## TRACING PHYLOGENY (CH. 25)

*Macroevolution* attempts to explain how major adaptive characteristics came into existence.  These characteristics would be the basis for creating new taxa above the species level.

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**Phylogeny**- **evolutionary history of a group of species**; the evolutionary relationships among organisms; the patterns of lineage branching produced by the true evolutionary history of the organisms being considered.
- is used to organize living organisms by looking at ancestors and all descendants; trace evolutionary relatedness
- relatedness based upon fossil evidence, morphological and molecular homologies.
- the science of tracing the history of species and analyzing the diversity and relationships among species is called **systematics**.

The classification and identification of the phylogeny of organisms is part of taxonomy.
- Established by **C. Linnaeus**
- Derived the system of **Binomial Nomenclature**.
  - Each species name consists of 2 parts - Genus & species epithet.
  - names written in Latin
  - determined by discoverer
- **Genus**- group of related species
- **Species**- (*specific epithet*) unique for every organism
  - All species organized within system that groups organisms by related structures, biochemistry.
  - Eg.  related phylogeny.

*Why do we have scientific names written in Latin?*
    Insure that an organism has the same name wherever it is found:
- Bluegill → bream → sun perch → blue sunfish → copperbelly (*Lepomis macrochirus*)
- Striped bass (NY) → Rockfish (Md) (*Morone saxatilis*)
- *M.saxatilis* (Jap.) = *M.saxatilis* (US)

**Taxon**: individual unit of classification system.
- Broadest/most encompassing- Kingdom
- Smallest/most specific- Species/Subspecies

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**Systematics**
- ✓ The goal of systematics is to have classification reflect the evolutionary relationships among organism (phylogeny).
- ✓ Try to classify species into more inclusive taxa base on similarities in morphology (remember **homology** is same structure (*therefore relatedness*) with a different function) and other similarities such as DNA/DNA comparisons [molecular homologies], protein comparisons and molecular clocks.
  - ✓ Comparisons of DNA and amino acid sequences provide a way to measure homologies that are not observed in morphology. **[molecular systematics]**
- ✓ The greater the number of shared homologies, the more closely related the organisms may be.  Most be able to separate homology from analogy.  Remember, analogous structures are those that result from convergent evolution-similar selective pressures working on organisms that are not closely related develop similar results (adaptations)

- ***Cladistics.  Tries to group related organism and their ancestors according to characteristics that they share within in the group.***

**Cladistics** describes branching patterns by examining *derived homologous characters*.

- Cladistics gives us an evolutionary tree called a **cladogram**. A cladogram is made up of many branches called **clades**. Depicts a *hypothetical* branching sequence of lineages leading to the taxa under consideration. The points of branching within a cladogram are called nodes. All taxa occur at the endpoints of the cladogram.
- Each branch in the tree defines a novel homology unique to the members of that clade.
- A cladogram is only as good as the data that is used to produce it.
- *Synapomorphies* (shared derived characteristics) are the basis for cladistics. When constructing cladograms homologies (likeness attributed to shared ancestry) must be differentiated from analogies (similarities due to convergent evolution)

**Cladistics** is a particular method of hypothesizing relationships among organisms. The basic idea behind cladistics is that members of a group share a common evolutionary history, and are "closely related", more so to members of the same group than to other organisms. These groups are recognized by sharing unique features which were not present in distant ancestors. These shared derived characteristics are called *synapomorphies*. It is not just the *presence* of shared characteristics which is important (this would be like analogous structures showing convergent evolution), but the presence of *shared derived* characteristics (homologies). In other words, homologies are used as branch points along the tree. The more homologies organisms share, the more closely related they would be.

> *For example, consider a jellyfish, starfish, and a human; which two are most closely related?*
> The jellyfish and starfish live in the water, have radial symmetry, and are invertebrates, so you might suppose that they belong together in a group. This would not reflect evolutionary relationships, however, since the starfish and human are actually more closely related. In the example above, all three characteristics are believed to have been present in the common ancestor of all animals, and so are trivial for determining relationships, since all three organisms in question belong to the group "animals". While humans are different from the other two organisms, they differ only in characteristics which arose newly in an ancestor which is not shared with the other two.

Whatever scheme you use to reflect the phylogeny of an organism, the species must be grouped into taxa that are representative of only one ancestor. In other words, ideally your cladogram should have members of a given taxa that are derived from only **one** ancestor. This is called a **monophyletic taxon**.
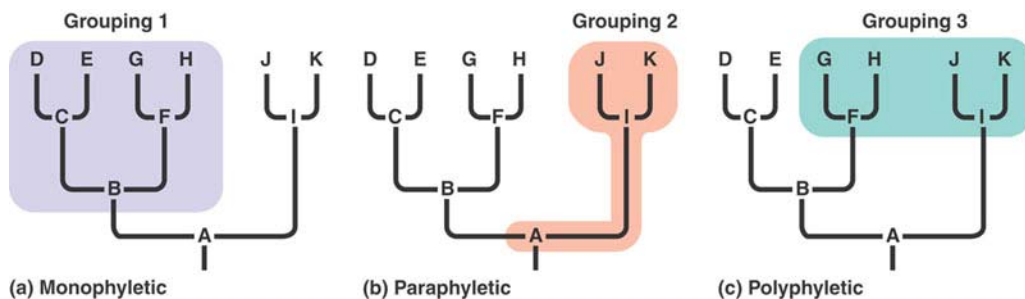


A **polyphyletic taxon** is a taxon that has members that are derived from 2 or more ancestors that are not common to all members of the taxon; usually because the common ancestor lacks the characteristics of the group. In order for species (*figure c above*) to be in the same taxon they must have a common ancestor included (which would be A)

A **paraphyletic taxon** includes some, but not all of the descendants within a group. If A is selected to be part of the taxon, then B must as well.