

## Chapt. 25 – Phylogeny and Systematics

### History of Life [See Table 26.1 – YOU DO NOT NEED TO MEMORIZE THE TABLE]

Boundaries between units in the **Geologic Time Scale** are marked by dramatic biotic change

5 Kingdom classification system in use through the late 1900s gave way to Woese's 3 Domains and multiple Kingdoms (Animalia, Fungi, Plantae, multiple Kingdoms of Protists, multiple Kingdoms of Bacteria, multiple Kingdoms of Archaea)

**Taxon (taxa)** = the named **taxonomic unit(s)** at any level in this **taxonomic hierarchy**  
[See Fig. 25.8]

Linnaeus convinced us to use a hierarchical classification system

Darwin provided us with the mechanism by which evolution results in descent with modification

**Taxonomy** – naming & classifying organisms

**Systematics** – naming & classifying organisms according to their evolutionary relationships

**Phylogenetics** – reconstructing the evolutionary relationships among organisms

**Systematic Phylogenetics** – **Systematics & Phylogenetics**

### Macroevolution & Phylogeny

**Phylogenetic tree** – hypothesized genealogy traced back to the last common ancestor (*i.e.*, the most recent) through hierarchical, dichotomous branching

**Cladistics** – the principles that guide the production of phylogenetic trees, a.k.a., **cladograms**

**Phylogenetic tree, phylogeny, or cladogram** [See Fig. 25.9]

**Node** – branch point, speciation event

**Lineage or clade** – an entire branch

A clade is a **monophyletic** group, *i.e.*, an ancestral species and all of its descendents

A **paraphyletic** group consists of an ancestor and some of its descendents

A **polyphyletic** group lacks the common ancestor of species in the group

Taxonomic groups often reflect true clades...

However, tension sometimes exists between taxonomic tradition and cladistic hypotheses...

*E.g.*, If the Class Reptilia is to be monophyletic, birds must be included!

### **How are phylogenetic trees constructed?**

The fossil record is especially valuable, and the only option for many extinct taxa

However, we almost never have a continuous record from one species to the next

Cladistic principles allow us to construct hypothesized phylogenetic trees

Fossils provide morphological data for extinct species, whereas comparisons of multiple types of traits – including molecular – do so for extant species

Similar characters (*e.g.*, morphological, behavioral, molecular, *etc.* traits or features) suggest relatedness...

But, not all similarity derives from common ancestry!

**Convergent evolution** can produce superficially similar traits that lack homology with one another

**Homologous characters** share common ancestry

Lack of similarity among taxa results from **divergence**

**Analogous characters** do not share common ancestry

Similarity among taxa results from **convergence**

As a general rule, the more homologous characters shared by two species, the more closely they are related

Sequences of DNA & RNA (nucleotides) and proteins (amino acids) are used as characters; as a general rule, the more recently two species shared a common ancestor, the more similar their sequences

Each nucleotide can be treated as a character

Character changes (**mutations**) from the ancestral to the derived state include:

**Substitutions**

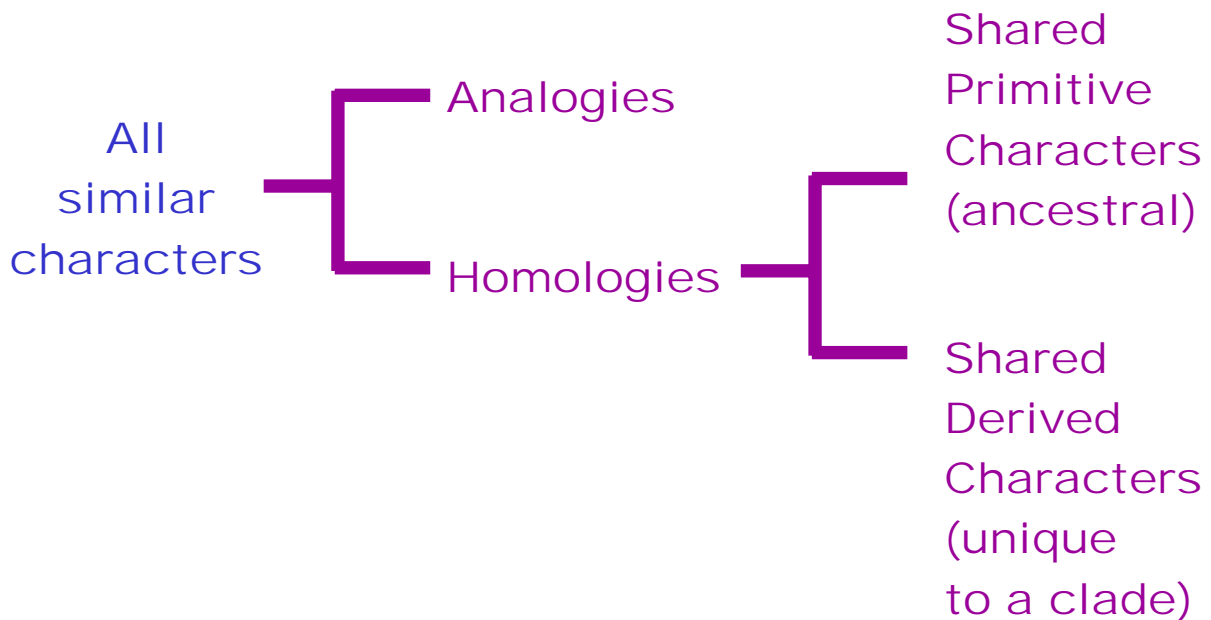
...AGCTCTAGG...  
...AGCTATAGG...

**Insertions**

...AGCTCTAGG...  
...AGCTGATCTAGG...

**Deletions**

...AGCTCTAGG...  
...AGCTCT GG...



By using **shared derived characters** to build a cladogram, the sequence of branching represents the sequence in which evolutionary novelties (**shared derived characters**) evolved

**Ingroup vs. Outgroup [See Fig. 25.11]**

**Ingroup** = the group whose relationships we are trying to resolve

**Outgroup** = a species (or group) known to have an older most recent common ancestor with the ingroup than the ingroup's most recent common ancestor

An outgroup helps identify shared ancestral and shared derived characters (unique to a clade)

**Parsimony & Occam's Razor [See Figs. 25.15, 25.16]**

The most parsimonious tree is the one that requires the fewest evolutionary events (appearance of shared derived characters)

Sometimes the most parsimonious arrangement for one character is not the most accurate overall...

Bird-Lizard-Mammal example.

Don't confuse the age of a **clade** with the age of its component species

The overall trend is increasing diversity, with periodic episodes of **extinction** [See Fig. 26.8]

Asteroid impacts may have caused mass extinction events, *e.g.*, Permian and Cretaceous mass extinction events

**Continental drift** is responsible for many **cladogenic events & biogeographic distribution patterns**

*E.g.*, Proteaceae – a plant family that originated in Gondwana

**Continental drift** results from **plate tectonics** [See Fig. 26.19]

Some **biogeographic similarities** result from **common ancestry (common descent)**

*E.g.*, all bromeliads are found in the New World Tropics & Sub-Tropics

Some **biogeographic similarities** result from **convergent evolution (convergent adaptive modification)**

*E.g.*, cactus of Americas compared to euphorbs of Africa