Plant identification and classification = Plant Systematics = Plant Taxonomy

**Binomial nomenclature** - Each species has a two word latin name consisting of its genus and species names. These words are always underlined or italicized when written.

“System” wherein newly discovered species can be sorted into groups by shared traits. Linnaeus called his system the “Sexual System”, because he used the presence or absence and number of sexual parts as the basis for classification.

**Classification** - the sorting of things into groups and the assigning of names to those groups; biological classification is **hierarchical** – groups nested within groups.

**taxon** (plural – taxa) - taxonomic group at any hierarchical level (could be a species, genus, family, etc.) – **taxonomy**: description, naming, & classification of organisms.

**Artificial classification** - with no regard for evolutionary relationships (e.g., any classification of things other than living things would have to be artificial).

**Natural classification** - reflecting evolutionary relationships. Darwin was the first to suggest that any classification of life should be “genealogical” and would naturally be hierarchical; now we call this “phylogenetic”.

Much of the Linnaean system is still intact, because the characters he used are good indicators of evolutionary relationships.

**Phylogeny** = Pattern of evolutionary history among species Phylo- from phylum (Greek – tribe) and –genetic (from origin or genesis)

The phylogeny of a group of organisms is a real thing, but we can only hope to estimate that pattern in a phylogeny reconstruction.

**Phylogenetic classification** = hierarchical ordering of taxa according to phylogenetic relationships consisting of a nested set of ever more inclusive groups. A more explicit term than “natural” classification. Goal is to identify a nested, hierarchical, set of **monophyletic** groups.

Example of dynamic nature of classification with respect to new understandings of phylogeny: tree formerly known as *Chamaecyparis nootkatensis* was shown to not be related to other species of *Chamaecyparis* in study of Cupressaceae phylogeny (Gadek et al. 2000; American Journal of Botany), thus creating a
problem for the taxonomy, because the genus *Chamaecyparis* is no longer monophyletic. Discovery in 2002 (Farjon et al. 2002; Novon) of a new species of conifer in Vietnam shown to be the closest living relative of *Chamaecyparis nootkatensis*. Conclusion that these two species should be included in a new genus, *Xanthocyparis: Xanthocyparis vietnamensis* and *Xanthocyparis nootkatensis*.

**Phylogeny reconstruction/phylogenetic inference (cladistics)** – the process by which we deduce evolutionary relationships.

**Monophyletic group** - a group of species that includes an ancestral species and all of its descendants (identified by synapomorphies = homologies).

**Paraphyletic group** - ancestor and some, but not all, descendants.

**Polyphyletic group** - a group of species in which the common ancestor does not belong to the group.

How do we go about identifying groups and relationships? We look for **similarities**. In systematics we call similar structures **characters** (a variable trait in the group under study), and variations in those structures **character states** (alternate forms of a character).

For example: CHARACTER = skin covering; CHARACTER STATES = 1) keratin scales, 2) feathers, 3) hair

The term we use for a character that arose with the evolution of the group and is shared due to common ancestry is **homology**. A character is a hypothesis of homology. "Homology - similarity in two or more organisms that can be traced back to the same feature in the common ancestor of those organisms." (Mayr 1969).

Example: wings on birds, also wings on bats, but NOT wings on birds AND bats. When we talk about ‘homology’ as evidence for relationship, we must refer both to a trait and a group of organisms. This provides a ‘level of universality’ for that homology.

For example: feathers are a homology for birds, and keratin structures as skin covering is a homology for all Amniotes (birds, mammals, and ‘reptiles’).

To know for sure that a character is a homology, we need to know the relationships among the species that share the character.

**Sources of data**: any comparative data (e.g. morphology, cytology, behavior, DNA sequences, etc.)

Similarities can reflect 3 different relationships:

1) **Shared derived similarity** (synapomorphy) Example: Feathers on birds - these evolved at the time birds first arose

2) **Shared ancestral similarity** (symplesiomorphy) Example: keratin scales on reptiles - these are transformed into feathers in birds

In these examples, feathers are evidence of monophyly in birds, but scales are
NOT evidence of monophyly in reptiles.

3) **Convergent similarity** (homoplasy) - similarity due to evolution in parallel in two different organisms (convergent evolution). Example: wings on birds and bats - another term for this is parallel evolution.

These kinds of similarity correspond to the three kinds of groups: shared derived --> **monophyly**, shared ancestral --> **paraphyly**, convergent --> **polyphyly**.

How do we know whether a similarity we observe is a synapomorphy (derived state) or a symplesiomorphy (retained ancestral similarity)? This is called **Polarity** (= evolutionary direction) and there are several criteria that have been used to determine whether a trait is derived or ancestral.

The method that is applicable most uniformly and has the fewest problems is outgroup comparison - inference from distribution of character states in sister group. For a character with 2 or more states, the state occurring in the outgroup is ancestral (for a multi-state character, this is only effective for establishing the most primitive state).

Once we know the polarity we can construct a tree from the characters. This is called **cladistic analysis**.

Sometimes there is conflicting evidence when convergence (or reversal or loss) occurs in the evolution of a character. Then we need a means to resolve the conflict. We can do this by invoking the principle of parsimony - the principle that the explanation requiring the least change is preferred.

Simple example of 3 characters, two of which agree. We choose the tree that best fits the data.

![Characters](image)

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Draw the three possible rooted trees supported by these characters and show the distribution of changes inferred.