

WHAT'S IMPORTANT IN CHAPTER 26

Concepts 26.1, 26.2, and 26.3 are all important, and are summarized here.

Taxonomy - the theory and study of classifications

Binomial nomenclature - giving a two-word name to each species, like *Homo sapiens*

Linnaean (hierarchical) taxonomy - the traditional taxonomy of "groups within groups"

Domain - largest grouping (includes kingdoms as subgroups)

Kingdom

Phylum (sometimes called "division" among plants) (plural: phyla)

Class

Order

Family

Genus (plural: genera)

Species (same spelling in singular and plural)

Phylogeny - an evolutionary family tree

Phylogenetics - the study of phylogenies

Systematics - the study of how evolution (and phylogenetics) relates to classification (and taxonomy)

Taxon - a group (like a family or phylum) at any level of a classification

Lineage - a succession of species

Branch point (dichotomy) - splitting of a lineage into two branches (See Fig. 26.5 in Campbell)

Polytomy - splitting of a lineage into more than two branches

Sister taxa - the two taxa corresponding to the two branches of a dichotomy

Clade - a branch and all of its sub-branches and sub-sub-branches

NOTE: Ideally, a taxon in a classification should correspond to a clade in the family tree

Cladistics - the practice of constructing family trees first, then basing classifications upon them

Homology - resemblance that reflects ancestry (e.g., human arm, whale flipper, bat wing, dog foreleg)

Analogy - resemblance that reflects similar adaptation or use (e.g., wings of birds, bats, and insects)

Homoplasy - misleading resemblance by analogy, not indicative of common ancestry

Monophyletic - a taxon that includes its common ancestor and all its descendants (see Fig. 26.10)

Paraphyletic - a taxon that includes a common ancestor and some but not all of its descendants

Polyphyletic - a group rejected from taxonomy because it is derived from several different ancestors; the common ancestor of ALL its members lies outside the group

MAKING A PHYLOGENY (see page 543 in Campbell):

To make a phylogeny of a group (the "ingroup"), begin by comparing it to a closely related "outgroup".

Traits or conditions found in the "outgroup" are considered ancestral; other conditions are "derived".

Shared derived characters are evidence that the species sharing the character trait belong to a clade, but **shared ancestral characters** do not.

TRY TO BUILD A PHYLOGENY that has the fewest changes ("transitions") from an ancestral to a derived condition. This usually requires us to assume that the transition happened only once, in the ancestor of all the species sharing the derived trait. Usually, most characters will form a consistent pattern, but occasionally we may need to assume that a shared derived trait originated independently twice, or that it was lost among some descendants. "Maximum parsimony" and "maximum likelihood" are two methodologies (or computer algorithms) for constructing phylogenies from a data matrix like the one in Fig. 26-11(a) or a series of DNA sequences. Fig. 26.15 shows a well-explained example.

Concept 26.6 is important and should be easy to understand.

Concepts 26.4 and 26.5 are less important-- reading them just once should suffice.