

Methods of classification

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Systematics= Taxonomy + Evolution

DINC is included in taxonomy

D= Description

I= Identification

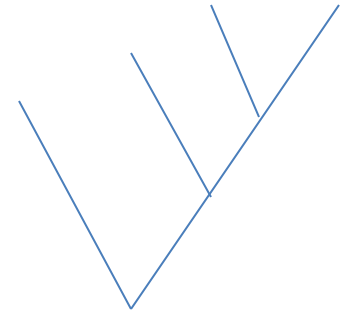
N=Nomenclature

C=Classification

- Systematics aims at developing classifications based on different criteria and, often a distinct methodology is employed for the analysis of data. The two methods are **phenetic methods** and **phylogenetic methods**.
- **Phenetic method** is based on overall similarity and dissimilarity.
- Phylogenetic methods aim at developing a classification based on an analysis of phylogenetic data, and developing a diagram termed **cladogram /phylogenetic Tree/ tree**, depicting the genealogical descent of taxa.
- Biologists practicing this methodology are known as **cladists**, and the field of study as **cladistics**.

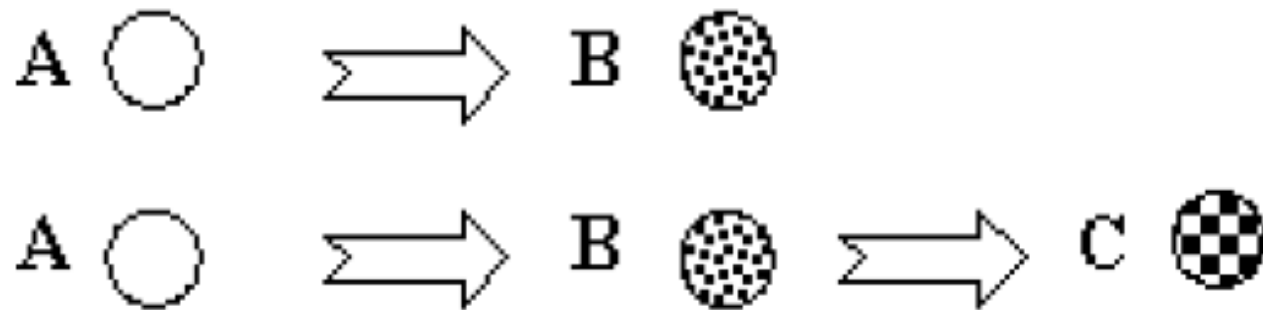
Cladistics

- First proposed by W. Hennig (1950, 1957)
- The term was coined by Mayr (1969)
- It is a branching pattern of evolution.
- method of classifying organisms by common ancestry, based on the branching of the evolutionary family tree.

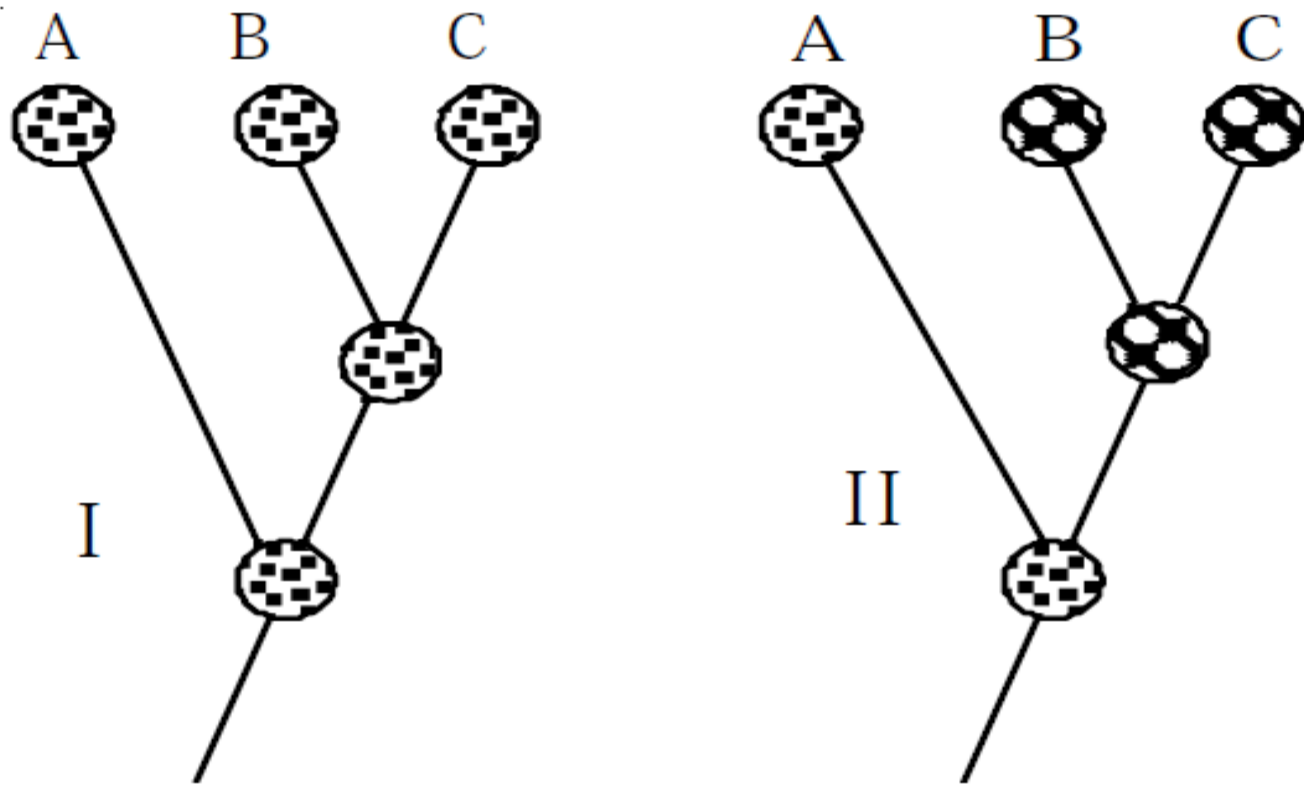


Some important terms

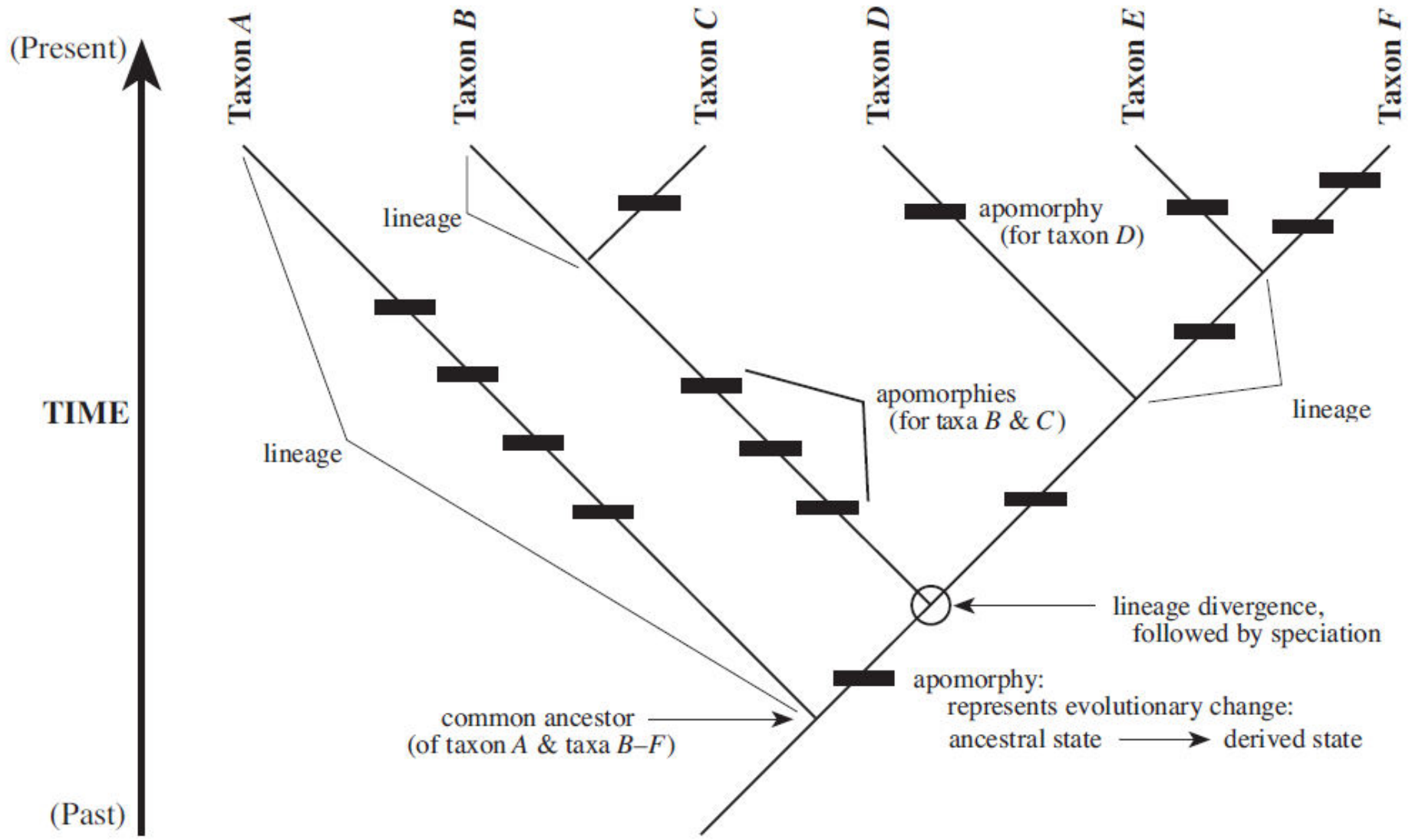
- **Apomorphy**:- A derived or specialised character.
- **Plesiomorphy**: - An ancestral or primitive character.
- **Synapomorphy**: An apomorphy shared by two or more groups which originated in their last common ancestor.
- **Symplesiomorphy**: A character shared by a number of groups, but inherited from ancestors older than the last common ancestor

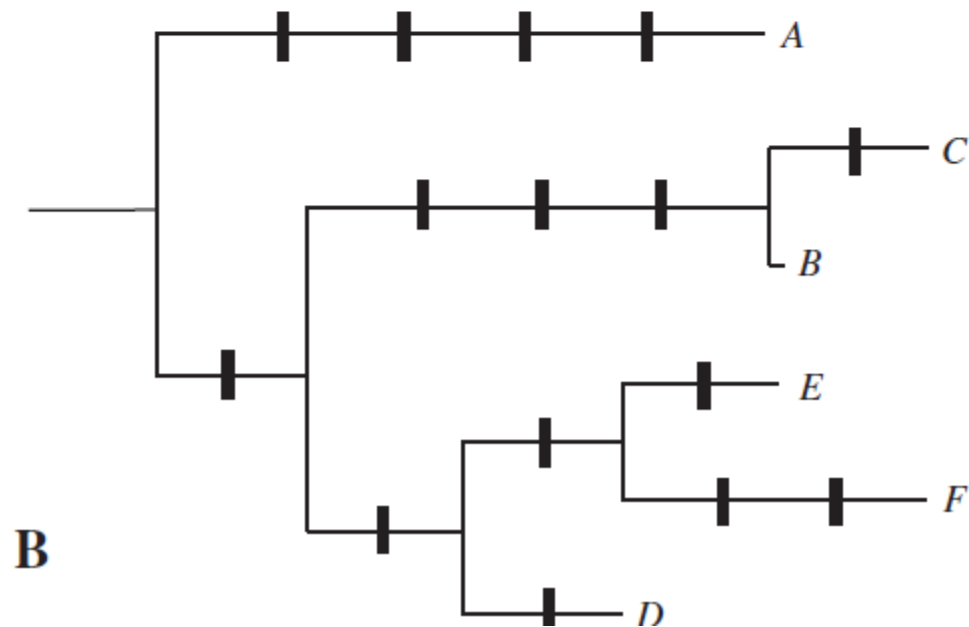
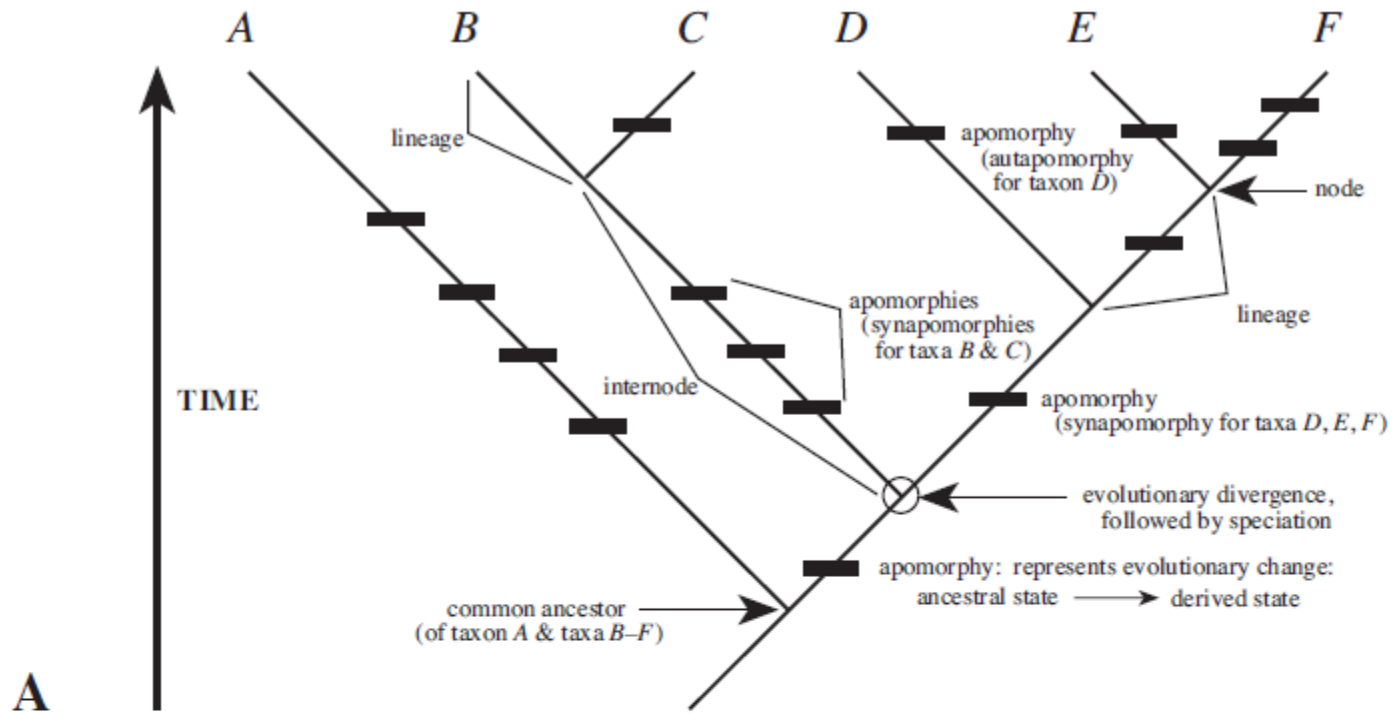


Homology between characters (or character states). In the first example, character A is plesiomorphic and B is apomorphic. In the second example, B is apomorphic in relation to A but plesiomorphic in relation to C as all three belong to an evolutionary transformation series.



Homology between two organisms B and C. In diagram I, similarity is due to symplesiomorphy as the character was unchanged in the previous ancestor. In II, it is due to synapomorphy as the previous ancestor had a plesiomorphic character and the two now share a derived character.





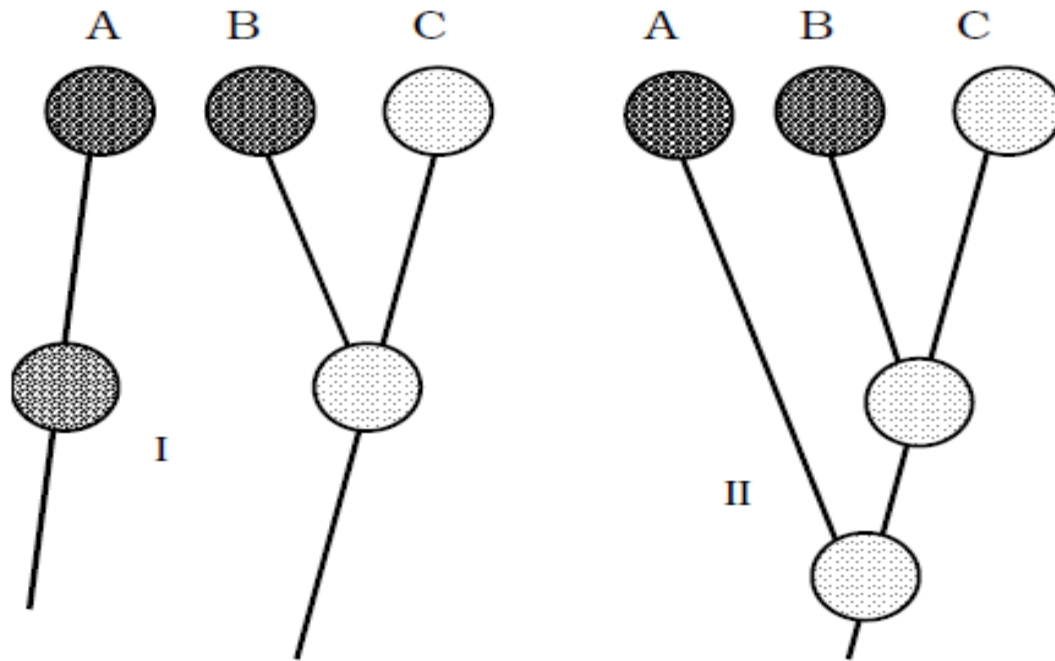
Principle of parsimony- the most likely evolutionary route is the shortest hypothetical pathway of changes that explains the pattern under observation.

Taxa in a truly phylogenetic system should be monophyletic.

Homoplasy- similarity due to parallelism or reversal of character states
e.g. Spines of cacti and euphorbs.

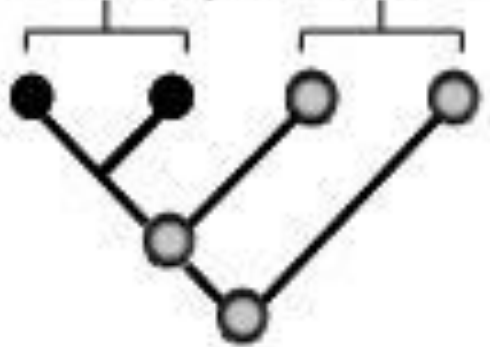
Parallelism - independent occurrence of similar changes in groups with a common ancestry
e.g. development of vessels in Gnetales and dicotyledons,
two species *Ranunculus tripartitus* and *R. hederacea* have a similar aquatic habit and dissected leaves and have acquired these characters by parallel evolution

Convergence - increasing similarity between two distinct phyletic lines, either with regard to individual organ or to the whole organism
e.g. 'switch habit' (circular sheath at nodes) in *Equisetum*, *Ephedra* and *Polygonum*

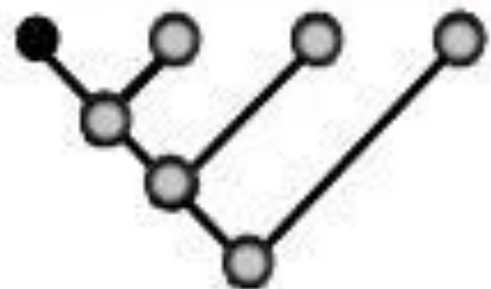


Examples of convergence (I) and parallelism (II) between organisms A and B. In convergence, similarity is between organisms derived from different lineages. In parallelism, the ancestor is common but both A and B have evolved an apomorphic character independently. In both cases, similarity represents false synapomorphy. Dissimilarity between B and C in both diagrams is due to divergence.

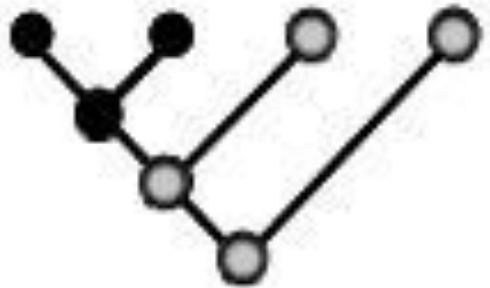
Apomorphy Plesiomorphy



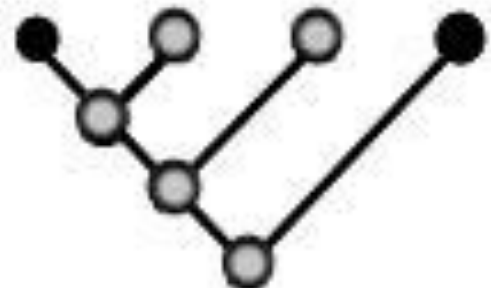
Autapomorphy



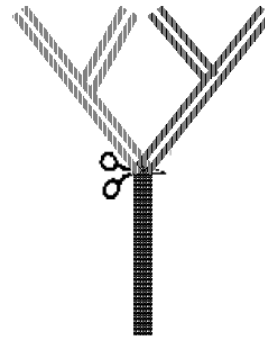
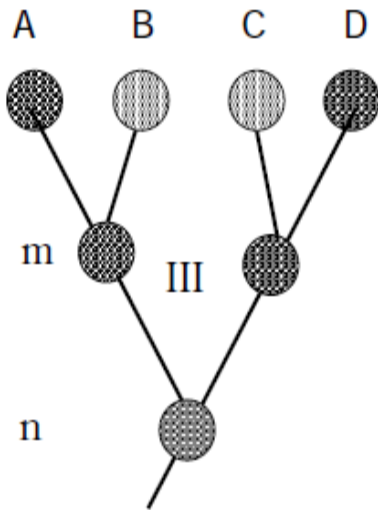
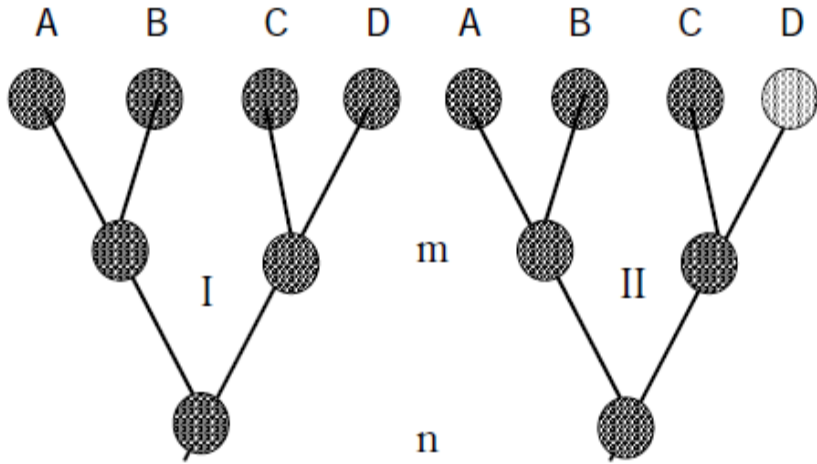
Synapomorphy



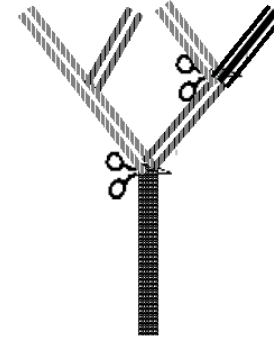
Homoplasy



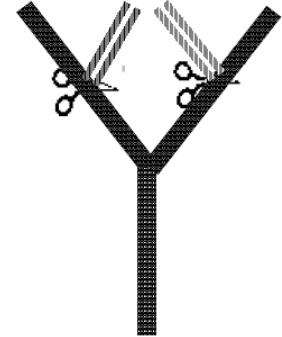
Ancestral trait (○)
Derived trait (●)



Monophyly



Paraphyly

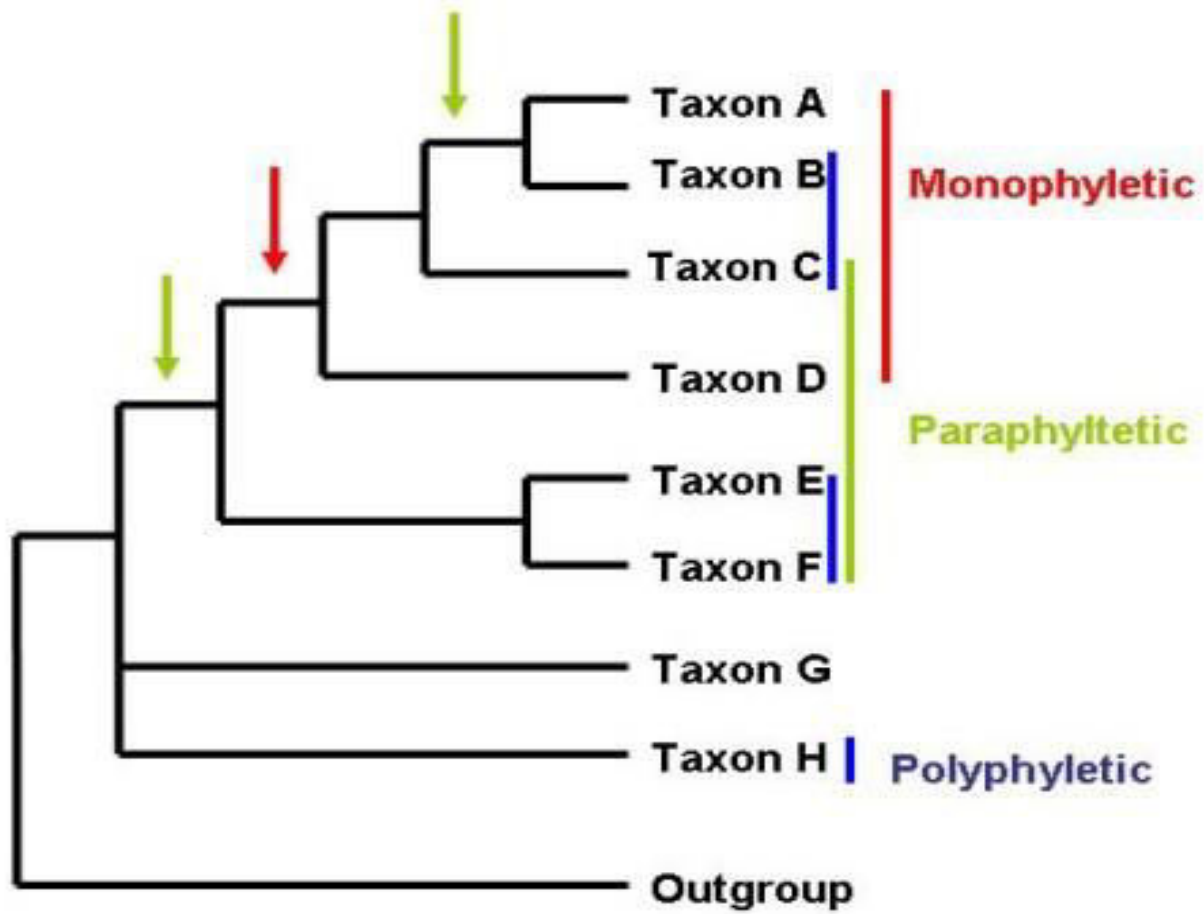


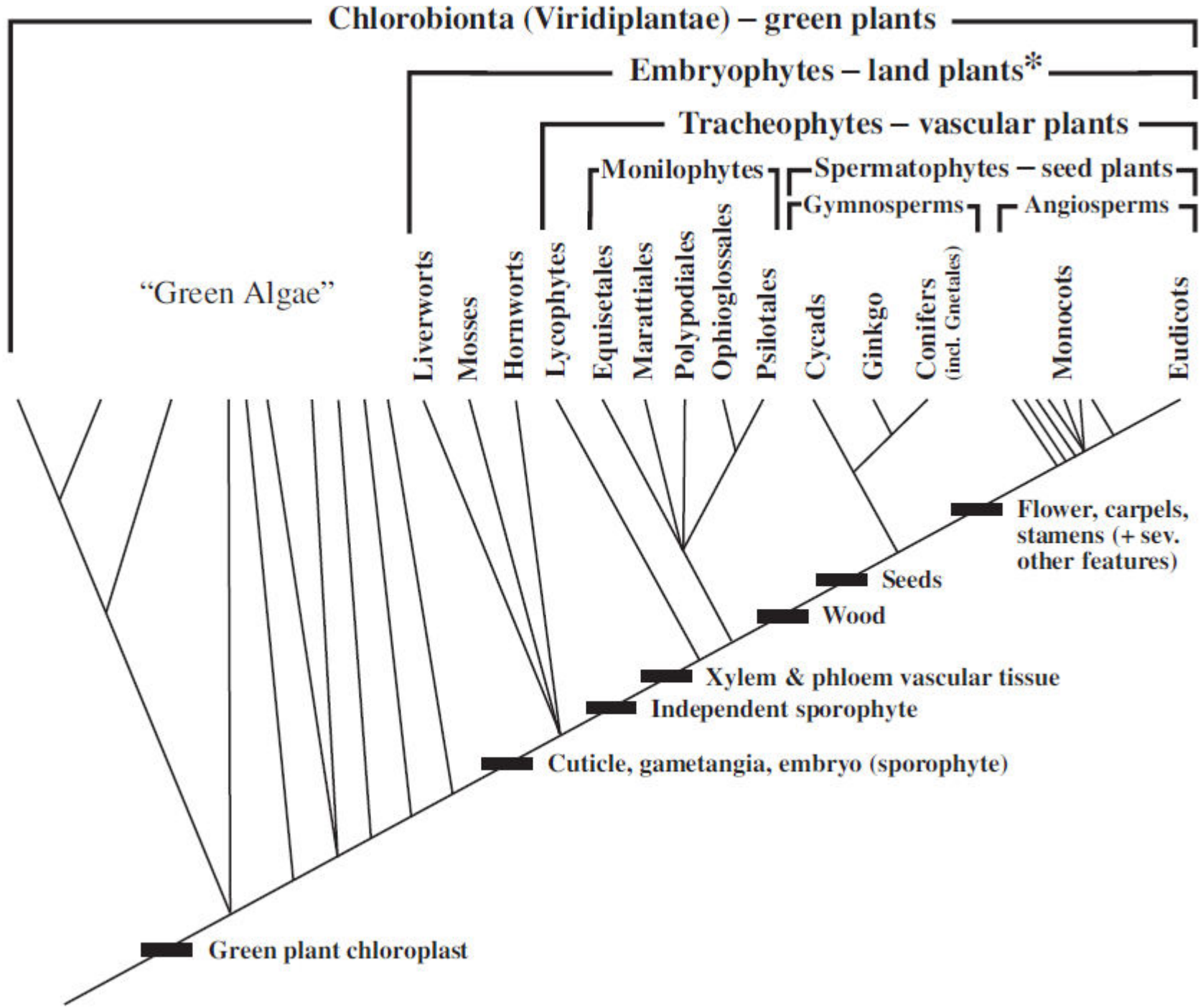
Polyphyly

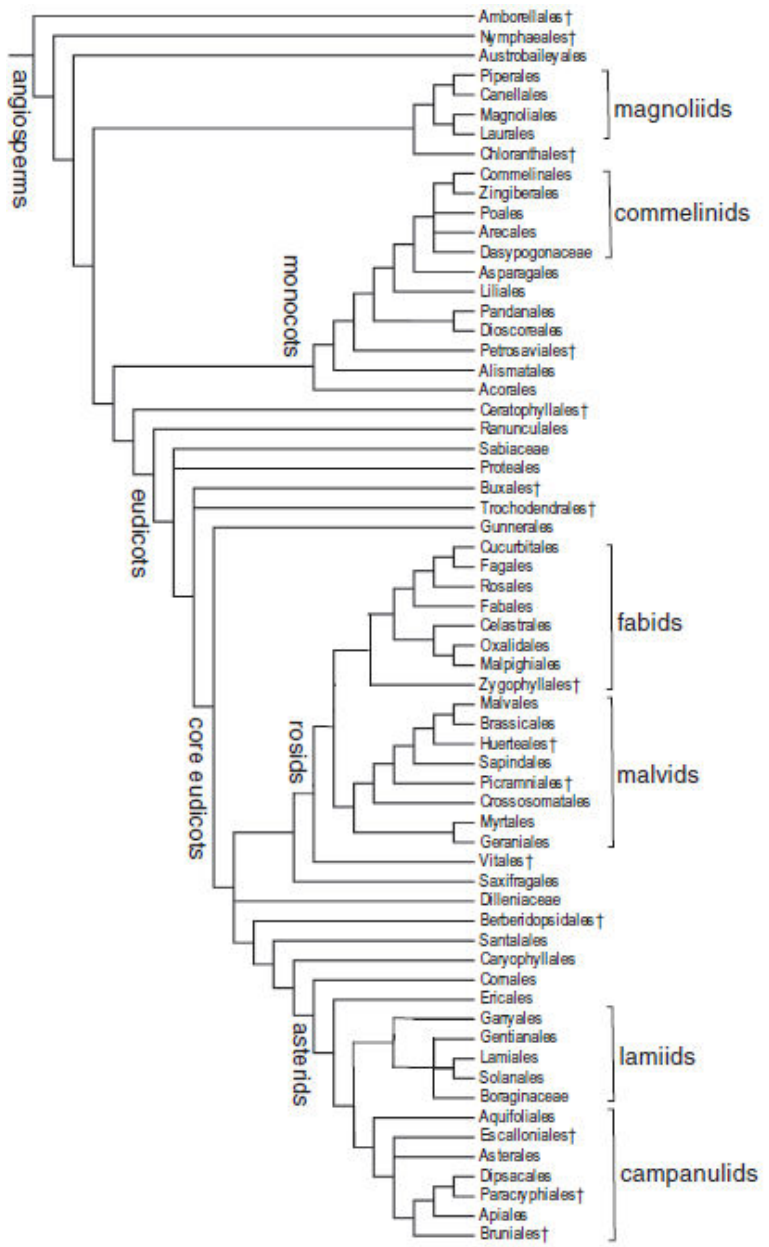
All descendants of a common ancestors are included.

All descendants of a common ancestors are not included

a group with two or more (i.e., multiple) ancestors, but not including the true common ancestor of its members







Basic steps in constructing cladograms-

1. Selection of taxa(sp.= OTU/EU)
2. Selection of characters
3. Homology
4. Morphocline (character state network, red to pink to white)
5. Data matrix preparation(Binary)

Methods to construct an evolutionary tree (phylogenetic inference)

- **Maximum parsimony:** The selection of the simplest phylogenetic tree requiring the least number of substitutions from among all possible phylogenetic trees as the most likely to be the true phylogenetic tree.
- **Maximum likelihood:** For this method, protein sequences are much more reliable than the DNA sequences.
- **Neighbour-joining:** A simplified version of the minimal evolution method. An evolutionary distance is computed for all pairs of sequences, and a phylogenetic tree is constructed from pair wise distances by using the smallest distances by inferring a bifurcating tree.