

Phenetics and Cladistics

Taxonomy is the science of grouping organisms into different categories according to their physical characters. This grouping or classification should be based on homology, i.e. , the individuals gathered in the same group must share characteristics that have been inherited from a common ancestor . We must keep in mind that systems of classification presented in the past depended on the needs, level of knowledge, philosophical concepts and available technology of the period. Today, systematics aims at developing classifications based on many different criteria as enormous data is now available from several different branches of botany. Data handling to establish relationships between the organisms often makes use of one of the two methods: phenetic methods (numerical taxonomy) and phylogenetic methods (cladistics).

INTRODUCTION

The phenetic classification came into being in the year 1763 and was first given by Michel Adanson. It is a type of classification which is based on the overall similarity of the organisms. It came in an era where advanced methods and technology were not available. In this type of classification groups were made based on a single or few observable characters (easily observed).

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Definition

Phenetics is a type of numerical taxonomy, where organisms are arranged according to the overall similarity of existing organisms based on available characters. This type of classification is termed phenetic classification.

Numerical Taxonomy :-

Definition :->

(Phenetics, taximetry and taxometerics)

- It is a type of classification based on the analysis of various types of taxonomic data (numerical comparison) of equally weighted characters by mathematically or computerized methods and in which individuals are grouped solely on the basis of observable similarities.
- Concept was proposed by Adanson and later in 1963 Seath and Sokal published a book “principles of numerical taxonomy” and attracted scientific community towards numerical taxonomy.
- Basic unit is OTUs

Operation taxonomic Units (OTUs)

- **Any sample, item, individual which is selected / used for analysis is called OTUs.**
- **Basic unit of numerical taxonomy**
- **May be individual, species, genus, family, order, class**
- **In case OTUs is above level of individual then adequate relationship of various forms become essential**

e.g When a genera is OTUs then it should be represented by different species.

Principles of Numerical Taxonomy :-

- i. The more characters the better a given classification will be.**
- ii. Every characters should be given equal weightage (equal weighting)**
- iii. Classification is based on phenetic similarity.**

Methods and procedure of Numerical Taxonomy.

- 1. Selection of taxa (OTUs).**
- 2. Selection of characters or traits**
- 3. Cluster Analysis via computer software**
- 4. Determination of taxonomic relationship between OTUs.**
- 5. Classification on the basis of overall similarities.**

Selection of Characters :-

- Characters which are used are called Unit characters
- Unit character is of two or more states and can be classified into

a) Binary character

A character having only two states and recorded as present or absent

e.g Cell wall: Present/Absent (where cell wall is character and + and - its states)

Coding: Present: + or 1, Absent: - or 0 Missing: N C

b) Multistate character

A character having three or more different states and may be qualitative or quantitative.

e.g Flower color: red, pink, orange, white, yellow

Coding: Can be coded into number using non negative integer

0,1,2,3,4,5,6,7.....

- Rules for selection of unit characters
 1. Included all part of the organism
 2. Not less than 50 characters
 3. Belong to all the stages of life cycle
 4. Due attention given to morphology, physiology, ecology and distributionetc.

- **Character weighting**

Equal weighting: All the characters selected are given equal weightage while creating taxonomic groups and is one of the principle of numerical taxonomy.

Successive weighting: The characters which show the least homoplasy (unique) are identified and given more weightage in the subsequent analysis.

Cluster Analysis

- In this the computer sorts out the OTUs according to their overall similarity i.e according to the number of character in common.
- The software produces a phenogram that is a dedrogram (branching tree diagram) which shows the taxonomic relationship between the taxa.

TECHNIQUES

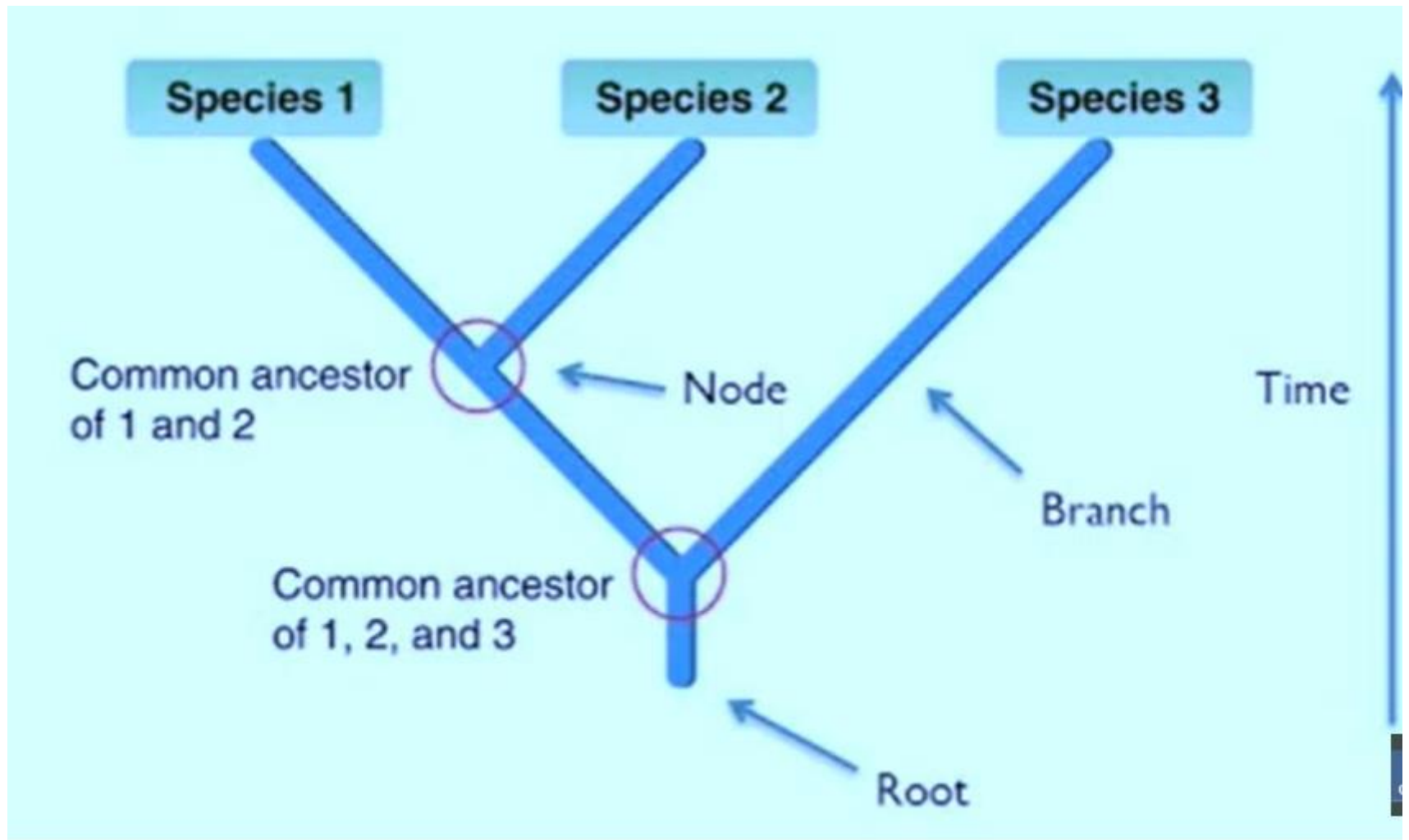
It is a primitive way of classifying organisms. However, phenetics includes the usage of various techniques in order to build relationships among organisms. Clustering and ordination are two ways in which organisms undergo phenetic classification. During phenetic classification, clustering or ordination of organisms takes place based on phenotypes that could be observed by the taxonomist or the scientist.

Therefore, dozens of characters are analyzed before clustering organisms. Then the representation of these characters using graphs takes place. This leads to the grouping of the organisms.

Phenogram

A dendrogram is a diagram representing a tree

Phenogram is a type of dendrogram which is based on phenetic data, used in analysis to show similarity or dissimilarity among specimens or groups of specimens. Lines called phenon lines, drawn at right angles to the dichotomously branching dendrogram, represent lines of percentage similarity of phenetic features between organisms.




Drawbacks

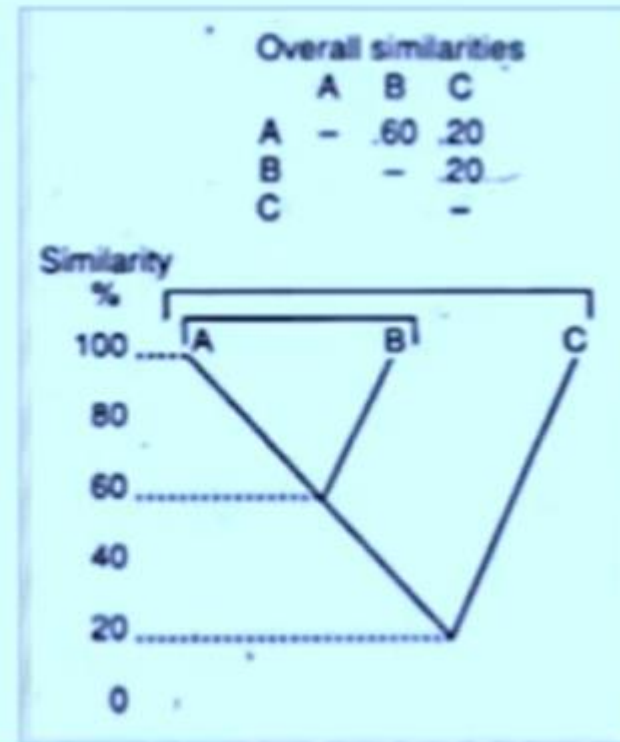
The main drawback of phenetics is that there can be a misinterpretation of organisms into groups as only physical visible characters are considered. This could give false results during the classical clustering process. Therefore, in classifying, it is important to analyze many methods of grouping for accuracy, especially the phylogenetic data of organisms

Phenetics

- Phenetics uses “overall similarity”
- Phenogram/ dendrogram – graphical representation

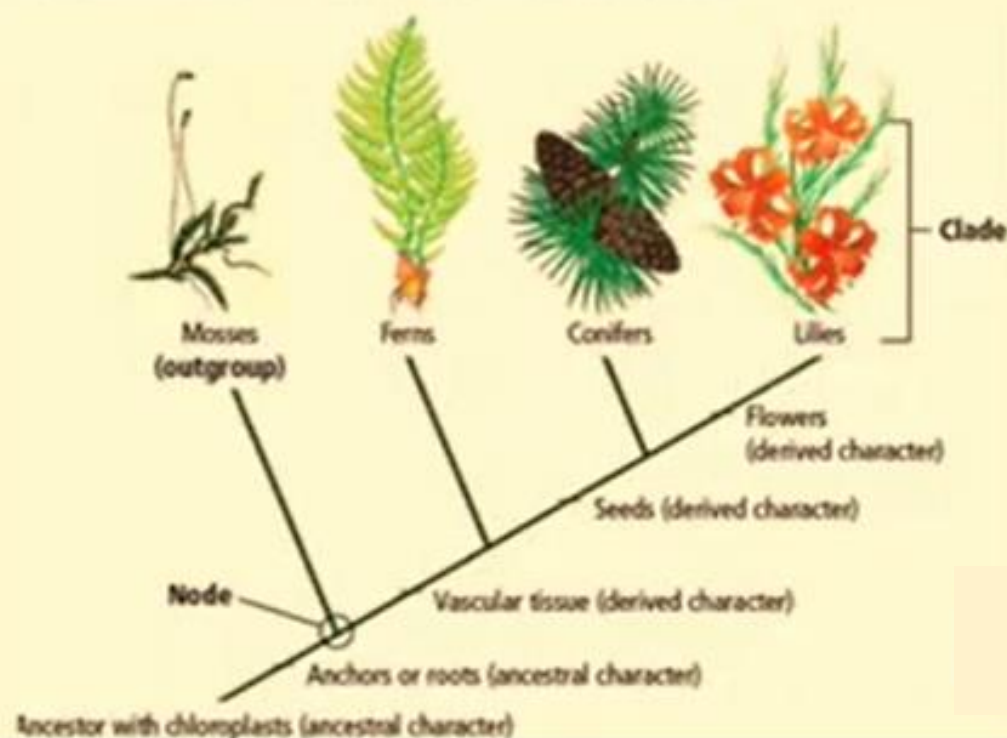


Species	Characters				
	1	2	3	4	5
A	0	0	0	0	0
B	1	1	0	0	0
C	1	0	1	1	1



What is Cladistics?

- Will Henning (1966).
- It is method of Taxonomy
- **Clade** is Greek word means **Branch**
- Classification in which organisms are categorized in groups (**Clades**) based on the most recent common ancestor.



Definition of Terms

- **Cladistics** – (from ancient Greek, *klados*, "branch"; originally called **phylogenetic systematics**) is a taxonomical technique for arranging organisms according to how they branch in the evolutionary tree of life.

NONVASCULAR BRYOPHYTES

VASCULAR SEEDLESS PLANTS

VASCULAR SEED PLANTS



Hornworts



Liverworts



Mosses



Club mosses



Ferns



Gymnosperms



Angiosperms

CLADOGRAM

Green algal ancestor

Evolution of cuticle, multicellular gametangia, multicellular embryos

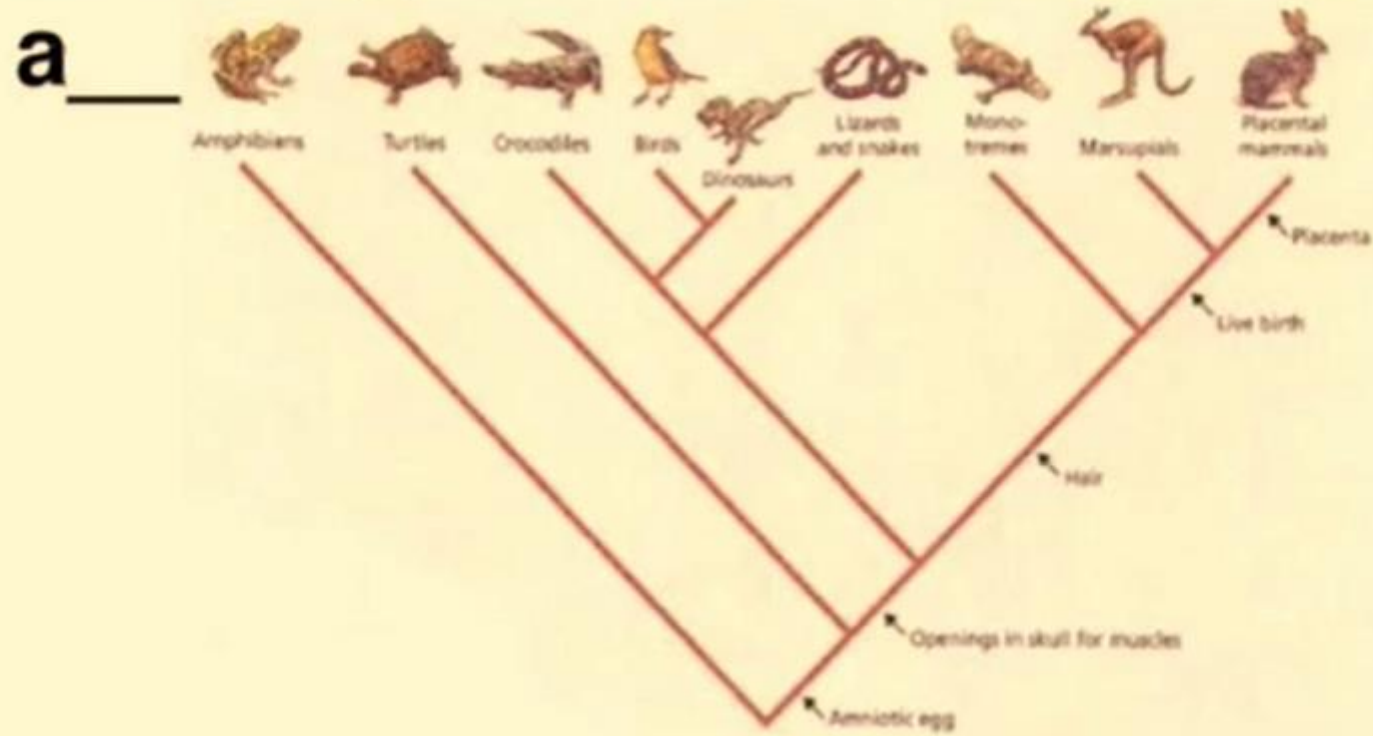
Evolution of dominant sporophyte, vascular tissue

Evolution of seeds

Which are more closely related?
Ferns and Liverworts or Ferns and Gymnosperms?

CLADISTICS

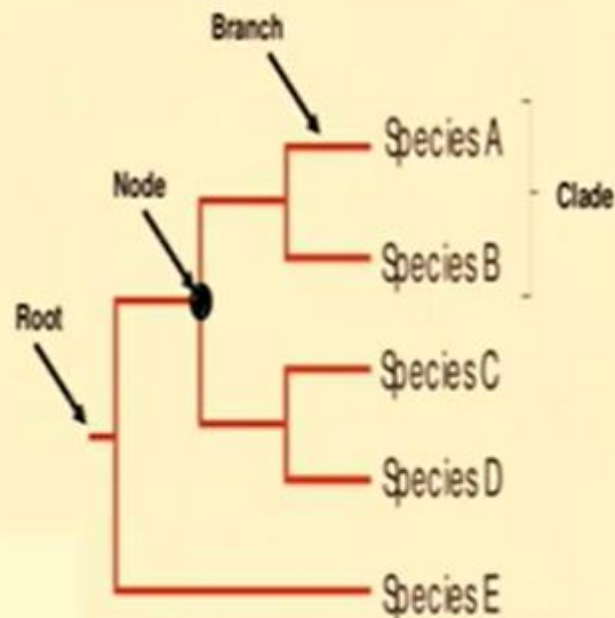
Cladistic relationships are shown in a diagram called **CLADOGRAM**

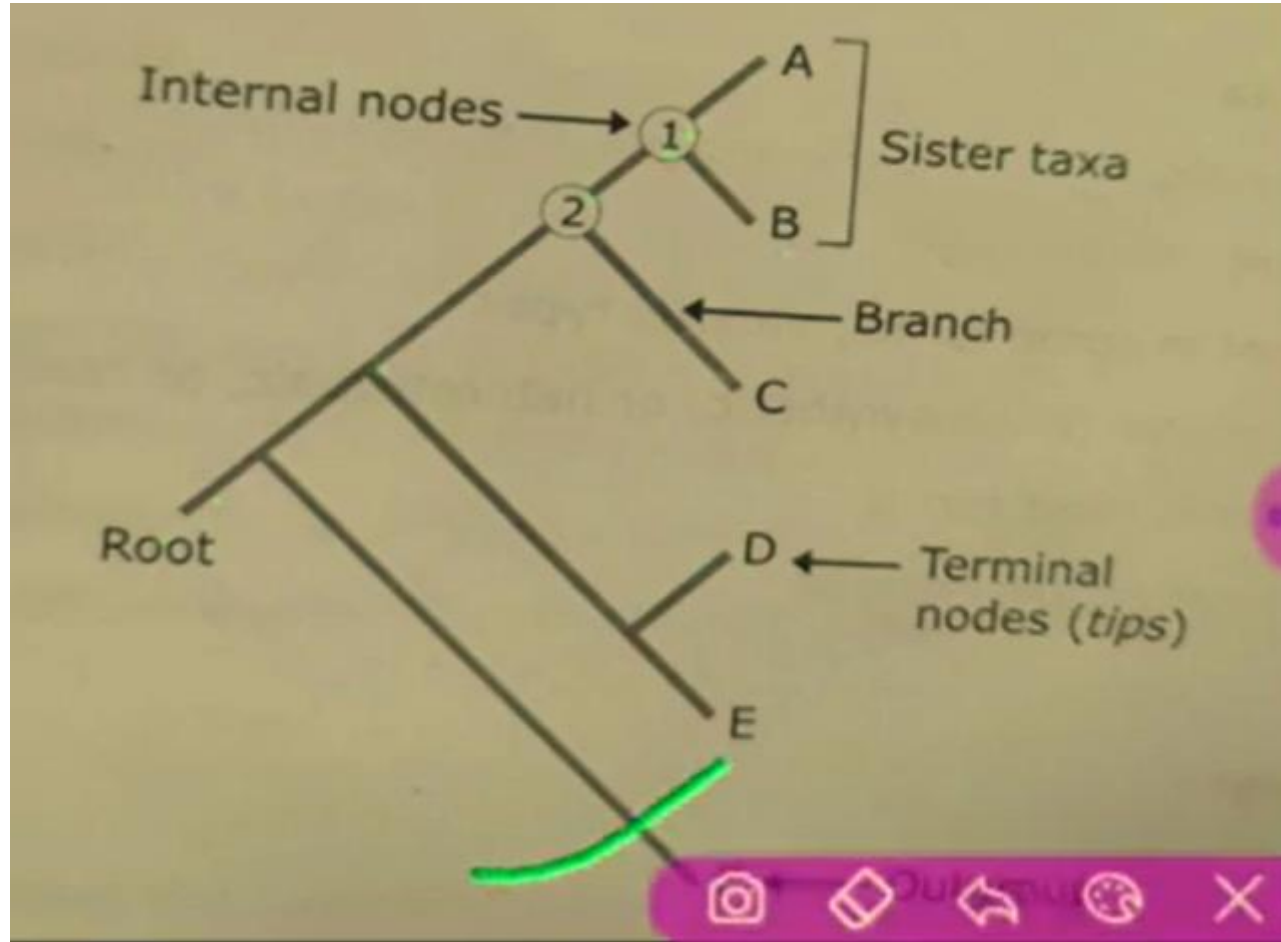


Cladogram

- It is evolutionary tree showing point at which lineages derived from common ancestral forms.

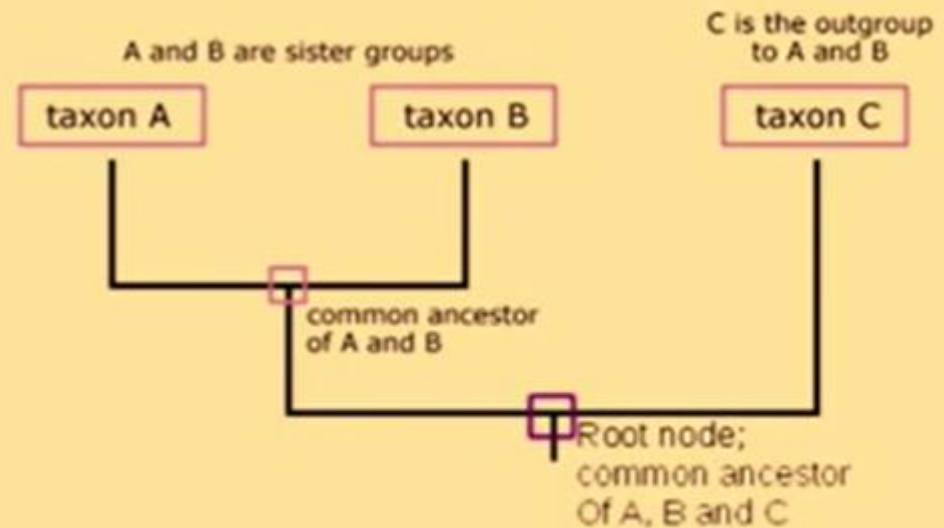
- **Node** - a branch points based on homologous, shared derived traits
- **Root** - the common ancestor of all taxa
- **Branch** - defines the relationship between the taxa in terms of descent and ancestry
- **Branch length** (scaled trees only) - represents the number of changes that have occurred in the branch





Phylogenetic Tree

- A visual representation of the relationships between different organisms, showing the path through evolutionary time from a common ancestor to different descendants.
- Phylogenetic trees are hypothesized reconstructions of evolutionary history.



Monophyletic group

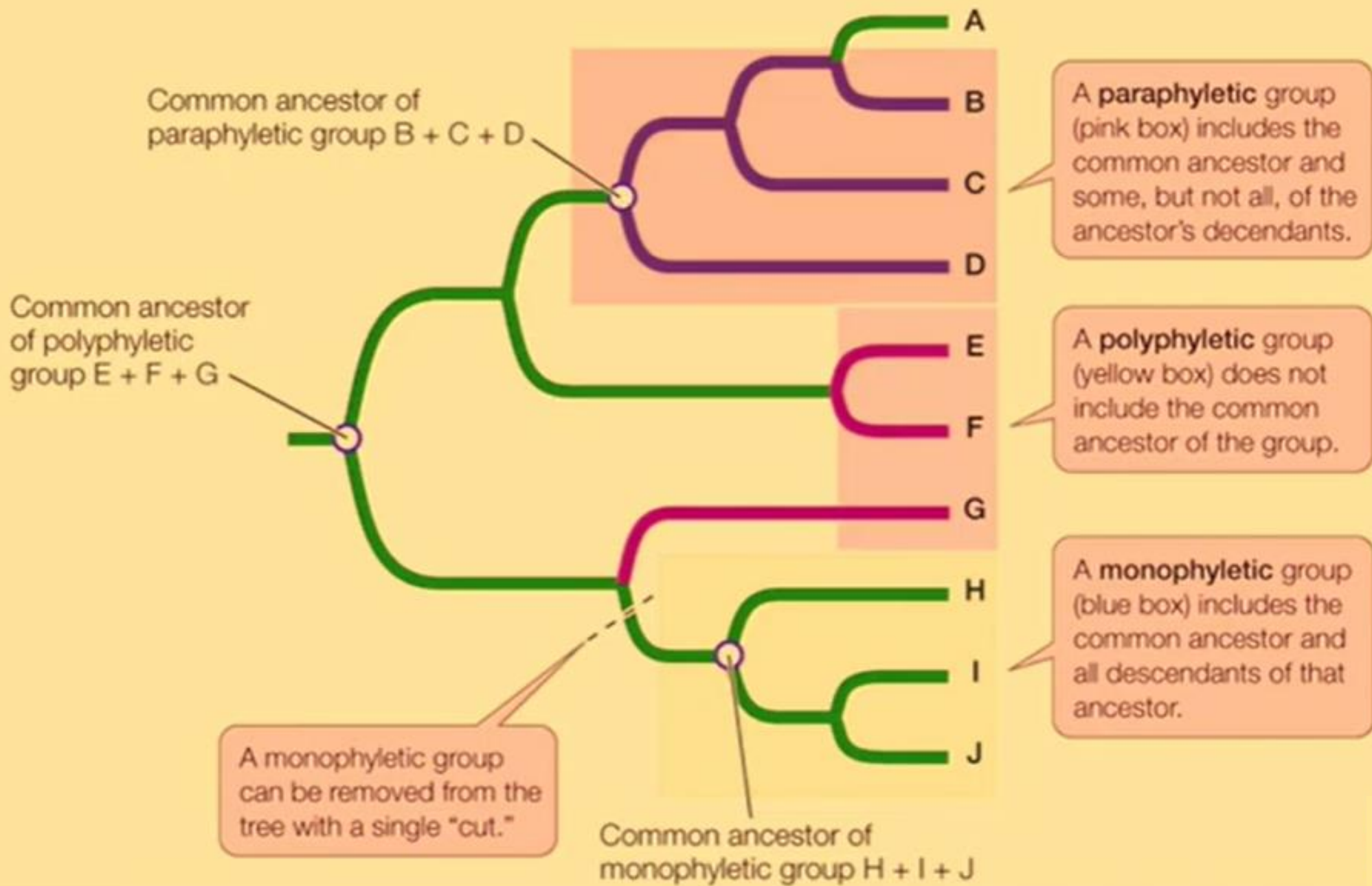
- It is made up of an ancestor species and all its descendants

Paraphyletic groups

- It includes the common ancestor but not all of its descendants.

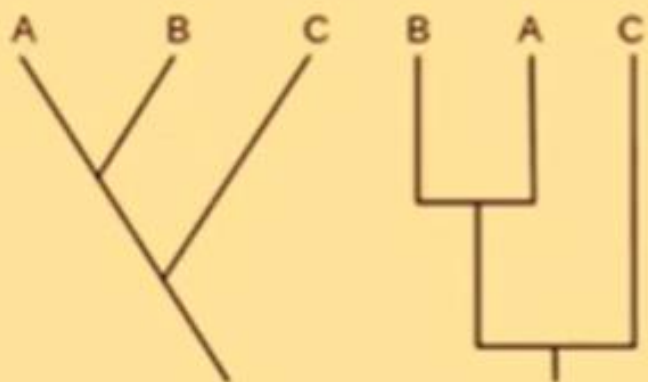
Polyphyletic group

- It does not includes the common ancestor but includes descendants.

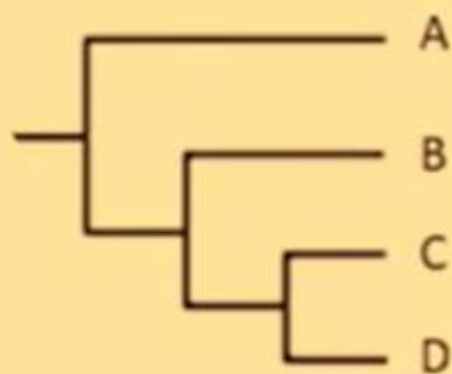


REPRESENTATION OF PHYLOGENETIC TREES

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Vertical
Cladogram



Horizontal
Cladogram

This representation is well suited for both rooted and unrooted trees, and such trees are most easily understood. The branches connecting the taxa are separated by a vertical line (of an arbitrary length). The midpoint of the vertical line indicates the internal node (representing the hypothetical common ancestor of these taxa, which are not available at the present time) between two taxa being connected.

Types of Trees

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- In **rooted trees** a single node is designated as a **common ancestor**, and a unique path leads from it through evolutionary time to any other node.
- **Unrooted trees** only specify the relationships between nodes and say nothing about the direction in which evolution occurred.
- Roots can usually be assigned to unrooted trees through the use of an outgroup.



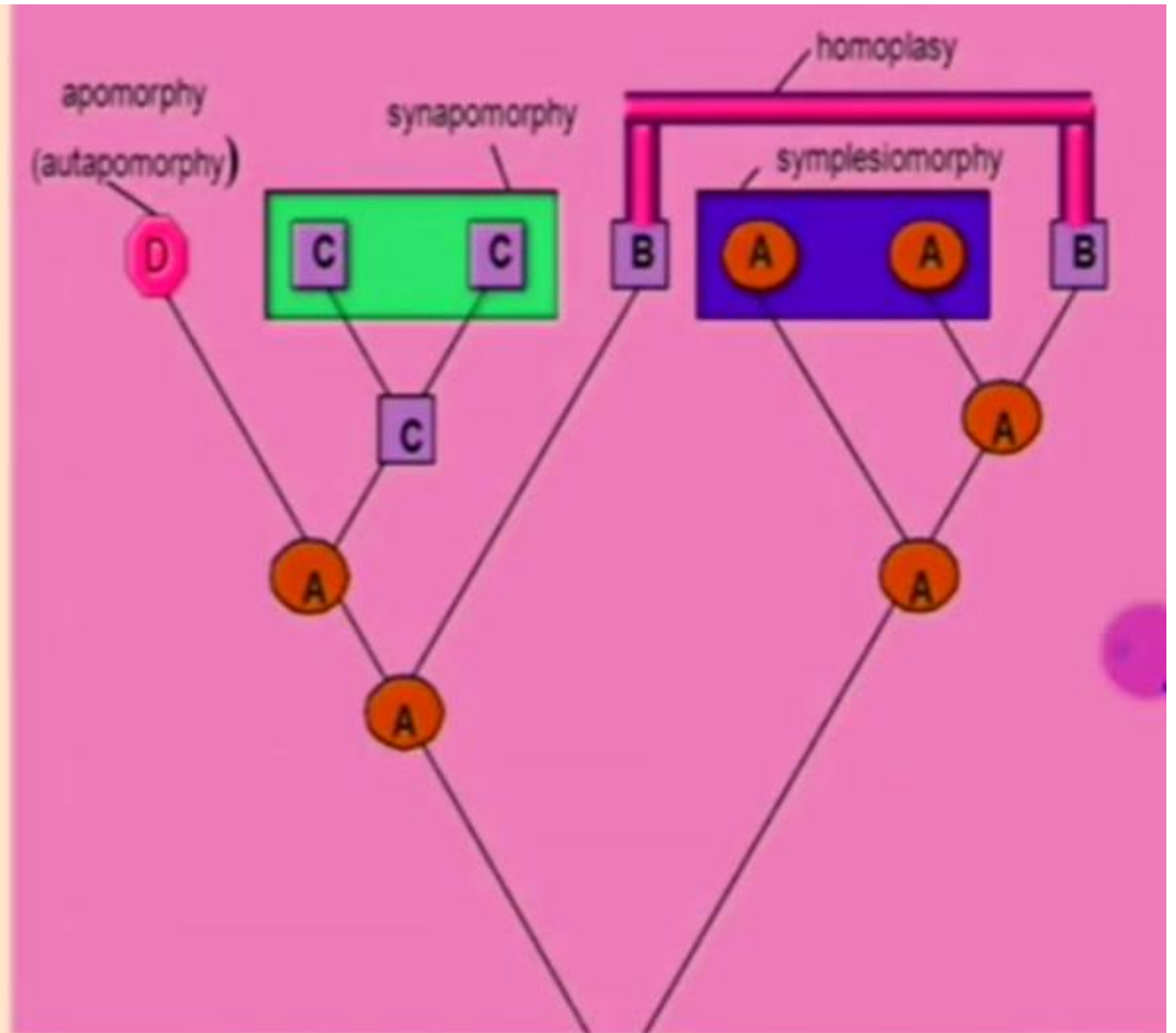
Synplesiomorphy- Character state is common between two organisms is present in immediate common ancestor and ancestor's ancestor.

Synapomorphy- Common character state between two organism present in recent common ancestor but not in ancestor's ancestor.

Apomorphy- They are evolutionary novelties that is evolved character not drive character so they are advance character.

Plesiomorphy- The drive character from ancestor so it is primitive character.

Homoplasy- it is a character shared by a set of species but not present in their common ancestor.

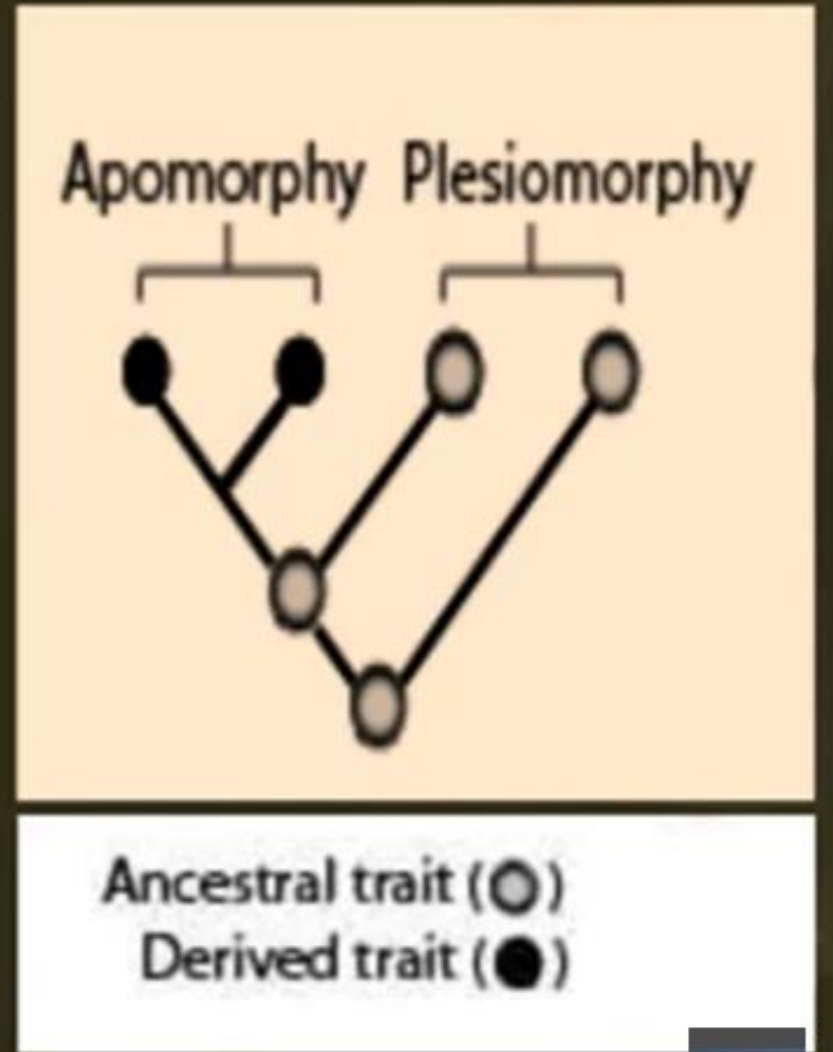


CHARACTERS IN PHYLOGENETIC TREES

APOMORPHIC CHARACTERS :-

If any character present in descendent but not present in its ancestor.

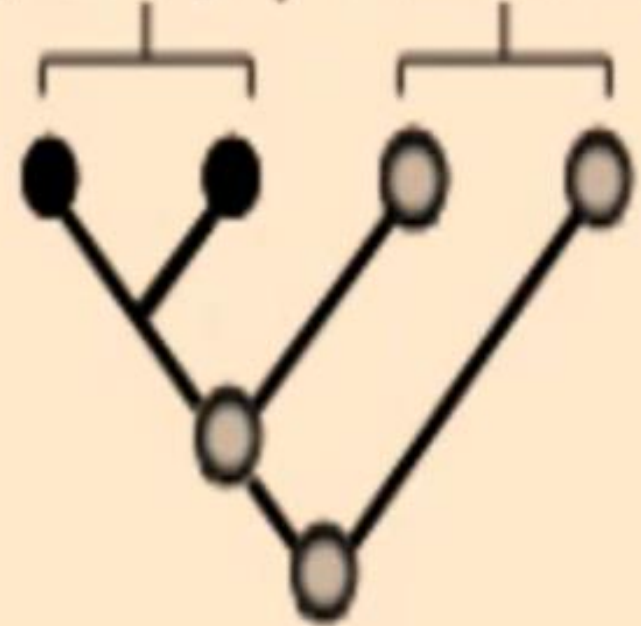
Any character which is being evolved after a speciation event is known as apomorphic characters. Also known as advanced character, derived character and apomorphy.



PLASIOMORPHIC CHARACTERS :-

- If a character present in last common ancestor then is called plasiomorphic character.
- Also known as primitive character, and ancestral character.

Apomorphy Plesiomorphy

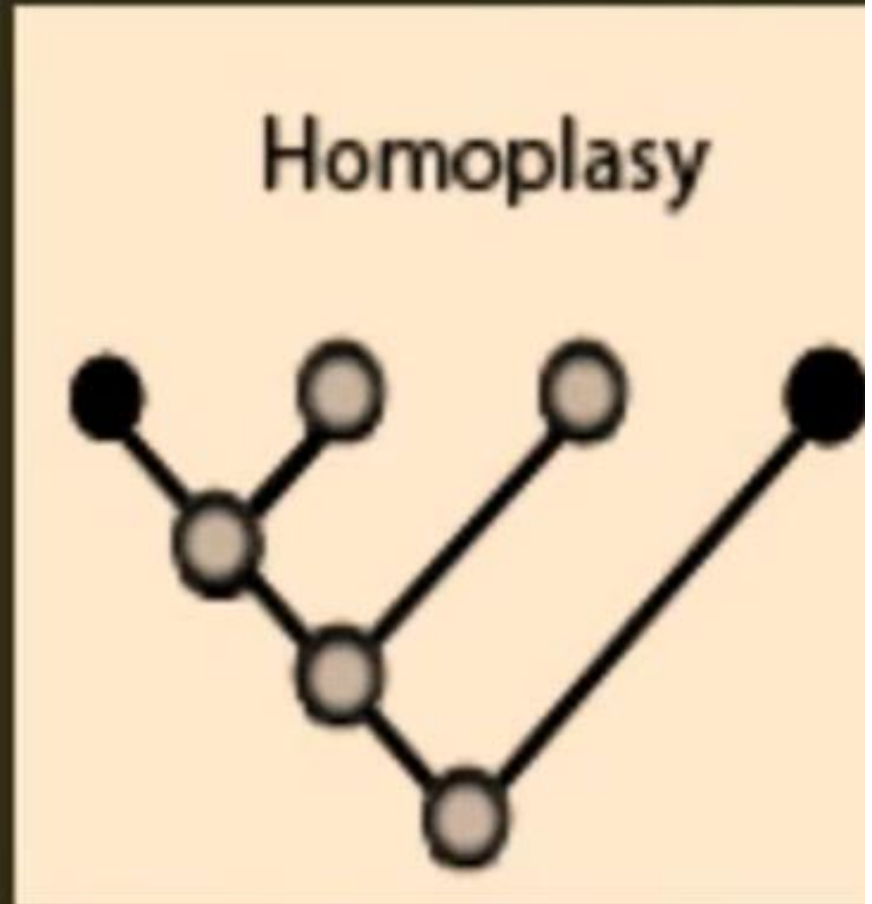


Ancestral trait (○)

Derived trait (●)

HOMOPLASY-

- These character are not present in their ancestor,they evolved by chance.
- It is an advance or apomorphic character.
- They formed as a result of convergent evolution.
- Eg.wings in birds and insects.



Ancestral trait (○)

Derived trait (●)

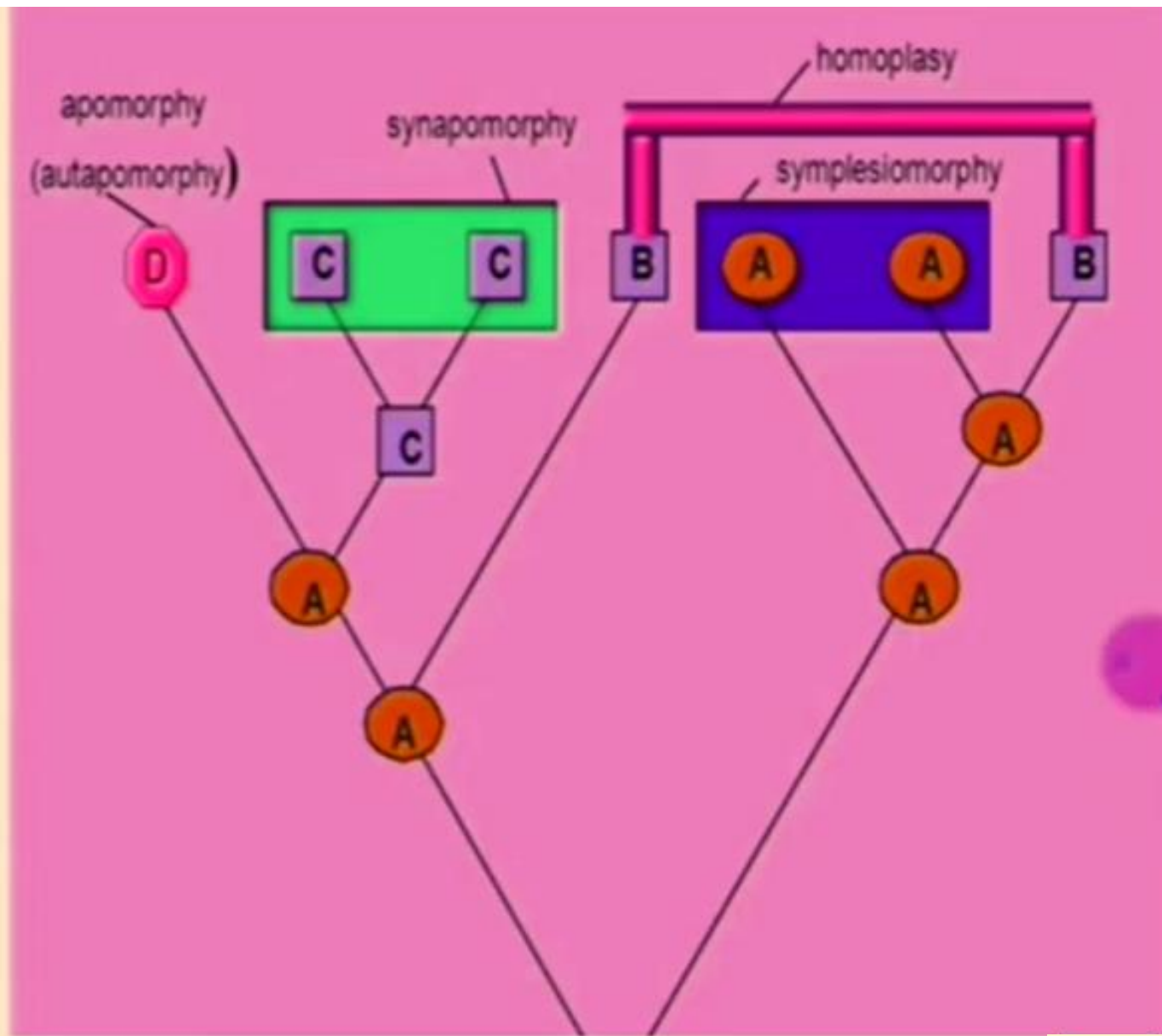
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AUTAPOMORPHY -

- In phylogenetics, an autapomorphic feature is a developed characteristic which is specific to a taxon. It is therefore not present in any other taxon.

Autapomorphy



Ancestral trait (○)

Derived trait (●)

THANK YOU