

# Introduction to Botany. Lecture 37

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## 1 Questions and answers

## 2 Methods of taxonomy

- Expertise
- Cladistics
- Likelihood
- Phenetics



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## 2 Methods of taxonomy

- Expertise
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# Previous final question: the answer

Why sporophyte is better than gametophyte?



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Why sporophyte is better than gametophyte?

- Diploid heterozygotes with lethal gene will survive
- Organisms with more chromosomes have bigger potential for recombinations
- Diploids have heterosis (“hybrid vigour”)



# Methods of taxonomy

## Expertise



# Experts

- Experts produce classifications based of their exclusive knowledge about groups. First taxonomic expert was Carolus Linnaeus (XVIII century).
- Experts use variety of methods, including phenetics, cladistics, general evolutionary approach, their ability to reshape available information and their intuition.
- Their goal is to create the “mind model” of diversity and then convert it to classification.



# Methods of taxonomy

## Cladistics





# Steps 1–4

- 1 The goal of analysis is creation of evolutionary history tree (“cladogram”) which become a basis of classification
- 2 We need to start with determining “players”—all subtaxa of bigger group. In our case, it will be three families:  
**Alphaceae**  
**Betaceae**  
**Gammaceae**
- 3 Create descriptions of these three groups:  
**Alphaceae:** Flowers red, petioles short, leaves whole, spines absent  
**Betaceae:** Flowers red, petioles long, leaves whole, spines absent  
**Gammaceae:** Flowers green, petioles short, leaves dissected, spines present
- 4 Separate individual characters (we will need  $2N + 1$  characters where  $N$  is number of studied taxa):
  - (1) **Flower color**
  - (2) **Petiole size**
  - (3) **Dissection of leaves**
  - (4) **Presence of spines**



# Step 5: character coding

- 5 **Polarization of characters:** every characters should have at least two characters states where 0 is a primitive, **plesiomorphic** state, 1 is advanced, **apomorphic** state:
- (1) Flower color green—0; red—1
  - (2) Petiole size small—0; big—1
  - (3) Dissection of leaves absent—0; present—1
  - (4) Absence of spines—0; spines present—1
- 5a These states are usually applied on the base of:
- (a) Historical evidence (e.g., from fossils)
  - (b) Developmental evidence
  - (c) Comparative evidence (from all available taxa)
- 5b If we do not have this information, we need to find **outgroup** which is primitive by definition. In our case, we will employ outgroup:  
**Omegaceae**: Flowers green, petioles short, leaves whole, spines absent.



# Step 6: character table

## 6 Character table

	1	2	3	4
Alphaceae	1	0	0	0
Betaceae	1	1	0	0
Gammaceae	0	0	1	1

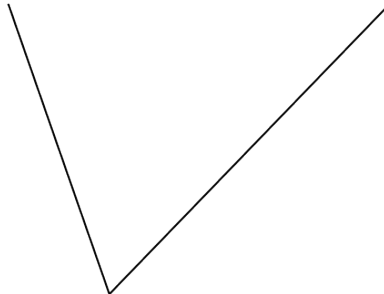
[Omegaceae has all zeroes]



# Step 7: starting the tree

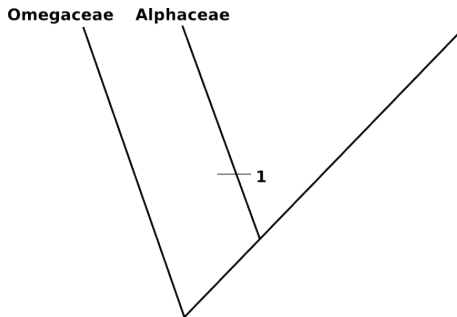
7 Tree is always started from outgroup:

**Omegaceae**

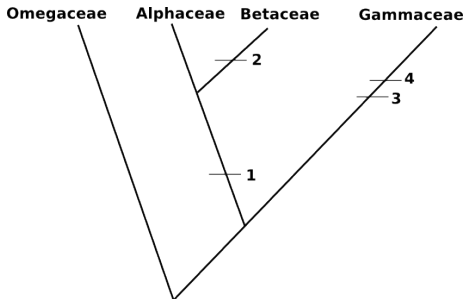


## Step 8: first branch

- 8 Then, the most primitive ingroup (Alphaceae) is attached as a first branch:



9a Then, the more and more advanced taxa are attached. If there is a choice, we can end up with multiple trees. In our case, Betaceae and Gammaceae have equal number of synapomorphies but Betaceae have only one character different from Alphaceae so we attach it there, and finally we attach Gammaceae:

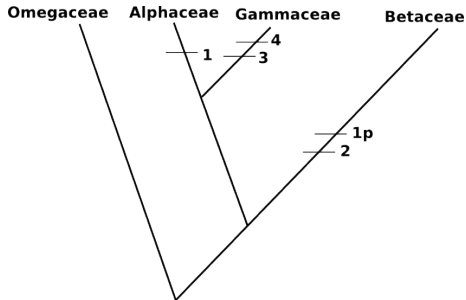


The tree has 4 evolutionary events (length= 4)



# Step 10: principle of parsimony

- 9a If we attach taxa in other way (saying, Gammaceae to Alphaceae), the resulted tree may be one step longer:



“p” are *parallel* characters (homoplasies). There are five events (length= 5).

We may also end up with tree length= 6, or with tree which includes character *reversal*, but all of them are longer than tree on previous slide.

- 10 We need to choose the shortest, most **parsimonious** tree. Second tree has 5 events, first tree has 4 events. Consequently, we prefer the first tree. Many computer programs produce all possible trees and then choose shortest.



# Step 11: resulted classification

11 We can now use chosen tree as a source of classification, e.g.:

## **Order Alphales**

1. Family Alphaceae
2. Family Betaceae

## **Order Gammales**

1. Family Gammaceae





# Methods of taxonomy

## Likelihood



# Likelihood

- Likelihood methods are based on evolutionary models (how characters are evolving, what is a probability of transformation)
- This methods is especially applicable for the analysis of DNA sequences



# Methods of taxonomy

## Phenetics



# Steps 1–6

- 1 The goal of phenetics (or numerical analysis) is creation of dendrogram which become a basis of classification. Phenetics consider characters as **all equal** and **do not employ any evolutionary assumptions**.
- 2–4 Same as in cladistics: (2) decide which taxa we will need, (3) assess their descriptions, (4) extract characters
- 5 Similar to cladistics, but codes (0 and 1) may be specified arbitrarily, and we do not need outgroup
- 6 Character table is the same



# Step 7: matrix of similarity

## 7 Matrix (or table) of similarity

	Alphaceae	Betaceae	Gammaceae
Alphaceae	1		
Betaceae	0.75	1	
Gammaceae	0.25	0	1

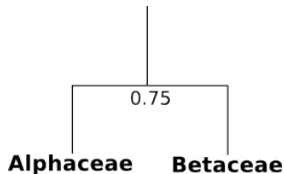
Every cell has a value of similarity  $K$ :

$$K = \frac{\text{number of matching characters}}{\text{number of all characters}}$$



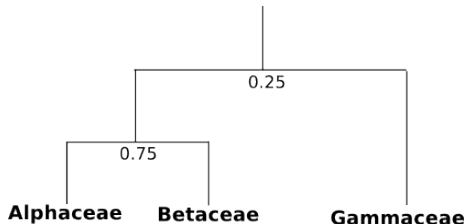
## Steps 8: starting a dendrogram

- 8 First, we need to connect the closest taxa, Alphaceae and Betaceae:



## Step 9: making a dendrogram

9 Then attach other taxa which are closest to to previous group:



# Step 10: classification

- 10 Betaceae and Alphaceae are closer, so we can unite them in one order:

## **Order Alphales**

1. Family Alphaceae
2. Family Betaceae

## **Order Gammales**

1. Family Gammaceae





# Final question (3 points)



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Why our cladistic and phenetic classifications are identical?



# Summary

- Expert methods are based on the mind models of diversity
- Cladistic methods are based on character polarization and parsimony
- Phenetic methods are based on equality of characters and similarity matrix



# For Further Reading



J. E. Bidlack, Sh. H. Jansky.

*Stern's introductory plant biology*. 12th edition.

McGraw-Hill, 2011.

*Chapter 13.*



Th. L. Rost, M. G. Barbour, C. R. Stocking, T. M. Murphy.

*Plant Biology*. 2nd edition.

Thomson Brooks/Cole, 2006.

*Chapter 18.5.*

