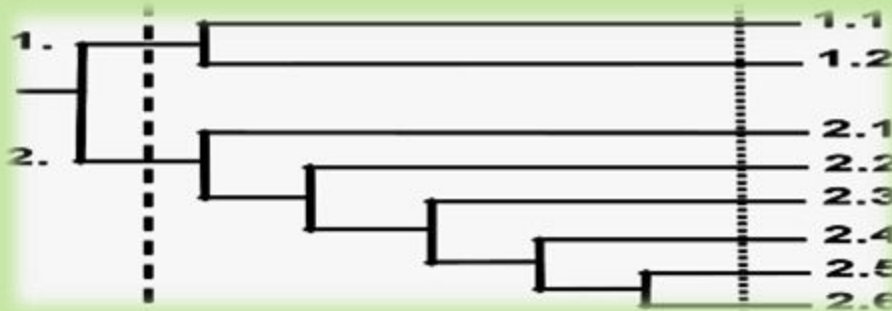




VIDYASAGAR UNIVERSITY

Lecture for 4th Semester Special Paper
(BOT 403A) : **Molecular Systematics**

2. Numerical Taxonomy (Taximetrics)– New Adanson's Classification: Its application in modern Systematics



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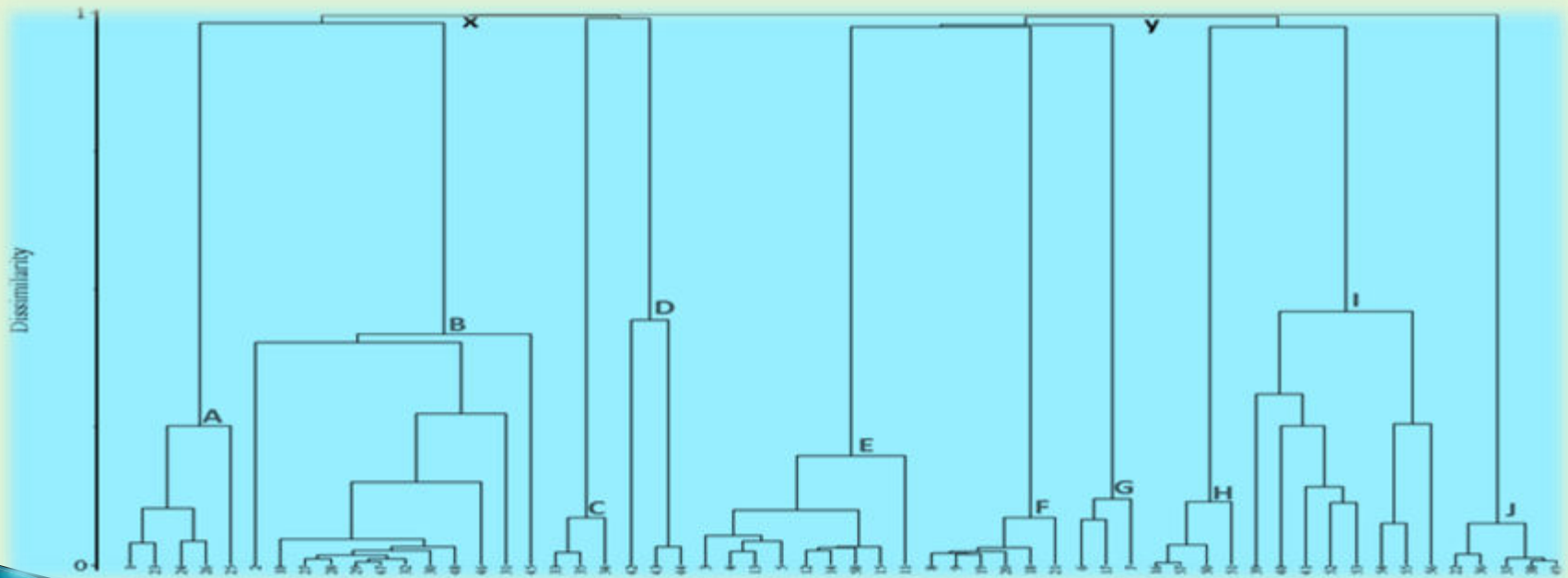
Vidyasagar University

2nd April, 2020

Numerical Taxonomy

(Taximetrics)– New Adanson's

Classification: Its application in modern Systematics



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Content:

- Meaning of Numerical Taxonomy
- Principles of Numerical Taxonomy
- Merits of Numerical Taxonomy
- Demerits of Numerical Taxonomy
- Applications of Numerical Taxonomy

Numerical Taxonomy

Numerical taxonomy or taximetrics, nowadays frequently and perhaps more appropriately referred to as phenetics, refers to the application of various mathematical procedures to numerically encoded character state data for organisms under study.

What is Numerical Taxonomy?

Classification of biological species is one of the important concerns while studying taxonomic and or evolutionary relationships among various species.

Classification is either based on only one / a few characters known as “Monothetic”, or based on multiple characters known as “Polythetic”.

➤ It is obviously much more difficult to classify organisms on the basis of multiple characters rather than a few characters.

➤ The traditional approaches of taxonomists are tedious.

➤ The arrival of computer techniques in the field of biology has made the task easier for the taxonomists.

Numerical taxonomy is a system of grouping of species by numerical methods based on their character states. It was first initiated by Professor Peter H. A. Sneath et al.

Thus, it is the analysis of various types of taxonomic data by mathematical or computerized methods and numerical evaluation of the similarities or affinities between taxonomic units, which are then arranged into taxa on the basis of their affinities.

According to Heywood the numerical taxonomy may be defined as the numerical evaluation of the similarity between groups of organisms and the ordering of these groups into higher ranking taxa on the basis of these similarities.

❑ The period from 1957 to 1961 saw the development of first methods and of theory of numerical taxonomy.

❑ Plants as we all know are classified based on their characters.

❑ It was Michel Adanson, a French botanist, who for the first time put forward a plan for assigning numerical values to the similarity between organisms and proposed that equal weightage should be given to all the characters while classifying plants.

❖ He has used as many characters as possible for the classification, and such classifications came to be known as Adansonian classifications.

❖ Numerical taxonomy was however largely developed and popularized by Sneath and Sokal.



The application of **Adansonian principles** and use of modern methods and electronic data-processing techniques, have helped in the evolution of several new classifications of plants during the past few decades.

➤ Before going further I would like to clear the difference between two common terms, namely, “Classification” & “Identification”.

➤ When the organisms are classified on the basis of like properties, then it is called Classification, and after the classification, when the additional unidentified objects are allocated, then it is known as Identification.

➤ The purpose of taxonomy is to group the objects to be classified into natural taxa.

➤ Conventional taxonomists equate the taxonomic relationships with evolutionary relationships, but the numerical taxonomists defined them as three kinds:

- **Phenetic:** based on overall similarity.
- **Cladistic:** based on a common line of descents.
- **Chronistic:** temporal relation among various evolutionary branches.

Principles of Numerical Taxonomy:

Numerical taxonomy involves two aspects:

(a) Construction of Taxonomic Groups:

(b) Discrimination of the Taxonomic Groups:

(a) Construction of Taxonomic Groups:

i. In numerical taxonomy, first, individuals are selected and their characters spotted out.

There is no limitation to the number of characters to be considered.

However, the larger the number of characters, better is the approach for generalization of the taxa.

ii. The resemblances among the individuals are then established on the basis of character analysis, which can often be worked out with the help of computers, the accuracy of which depends on the appropriateness in character.

The best way to delimitate taxa is, to utilize maximum number of characters, with similar weightage given to all of them.

(b) Discrimination of the Taxonomic Groups:

- ❖ **When the taxonomic groups chosen for the study show overlapping of characters, discrimination should be used to select them.**
- ❖ **Discrimination analysis can be done by various techniques, specially devised for such purposes.**
- ❖ **Numerical taxonomy is thus, based on certain principles, also called neo Adansonian principles.**

Following seven principles of numerical taxonomy have been enumerated by Sneath and Sokal:

(i) The greater the content of information in the taxa, and more the characters taken into consideration, the better a given classification system will be.

(ii) Every character should be given equal weightage in creating new taxa.

(iii) The overall similarity between any two entities is a function of the individual similarities in each of the many characters, which are considered for comparison.

(iv) Correlation of characters differ in the groups of organisms under study. Thus distinct taxa can be recognized.

(v) Phylogenetic conclusions can be drawn from the taxonomic structure of a group and from character correlations, assuming some evolutionary mechanisms and pathways.

(vi) The science of taxonomy is viewed and practiced as an empirical science.

(vii) Phenetic similarity is the base of classifications.

How is the classification do by Numerical Taxonomy?

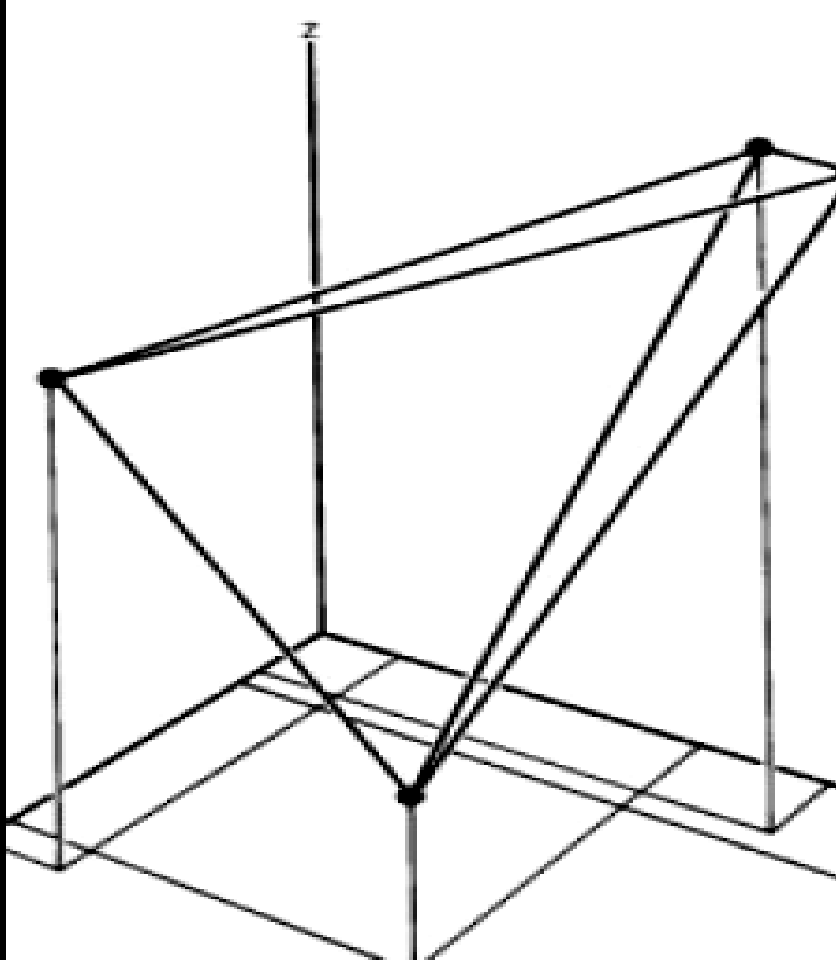
The objects to be classified are known as Operational Taxonomic Units (OTUs).

They may be species, genera, family, higher ranking taxonomic groups, etc.,

The characters are numerically recorded either in the form of appropriate numbers or may be programmed in such a way that the differences among them are proportional to their dissimilarity.

Lets say, a character called 'hair-ness of leaf', it may be recorded as:

- hairless = 0
- sparsely haired = 1
- regularly haired = 2
- densely haired = 3



OTUs (black dots) represented in a multidimensional space.

Such a numerical system imply that the dissimilarity between densely haired and hairless is 3 times than that of sparsely haired and hairless.

❑ The other method of implementing numerical taxonomy is that the characters are always represented by only two states, i.e., 0 for the absence and 1 for the presence of a particular character.

❑ This method is usually implemented in the field of microbiology.

❑ After that, all the characters and the taxonomic units are arranged in the form of the data matrix and the similarity among all possible pairs of OTUs is computed based on the considered characters.

❖ The similarity (more specifically, dissimilarity) is the distance between OTUs is represented in a multidimensional space, where the characters can be visualized as the coordinates.

❖ The objects that are very similar are plotted close to each other and those which are dissimilar are plotted farther apart.

❖ Then these straight lines are computed.

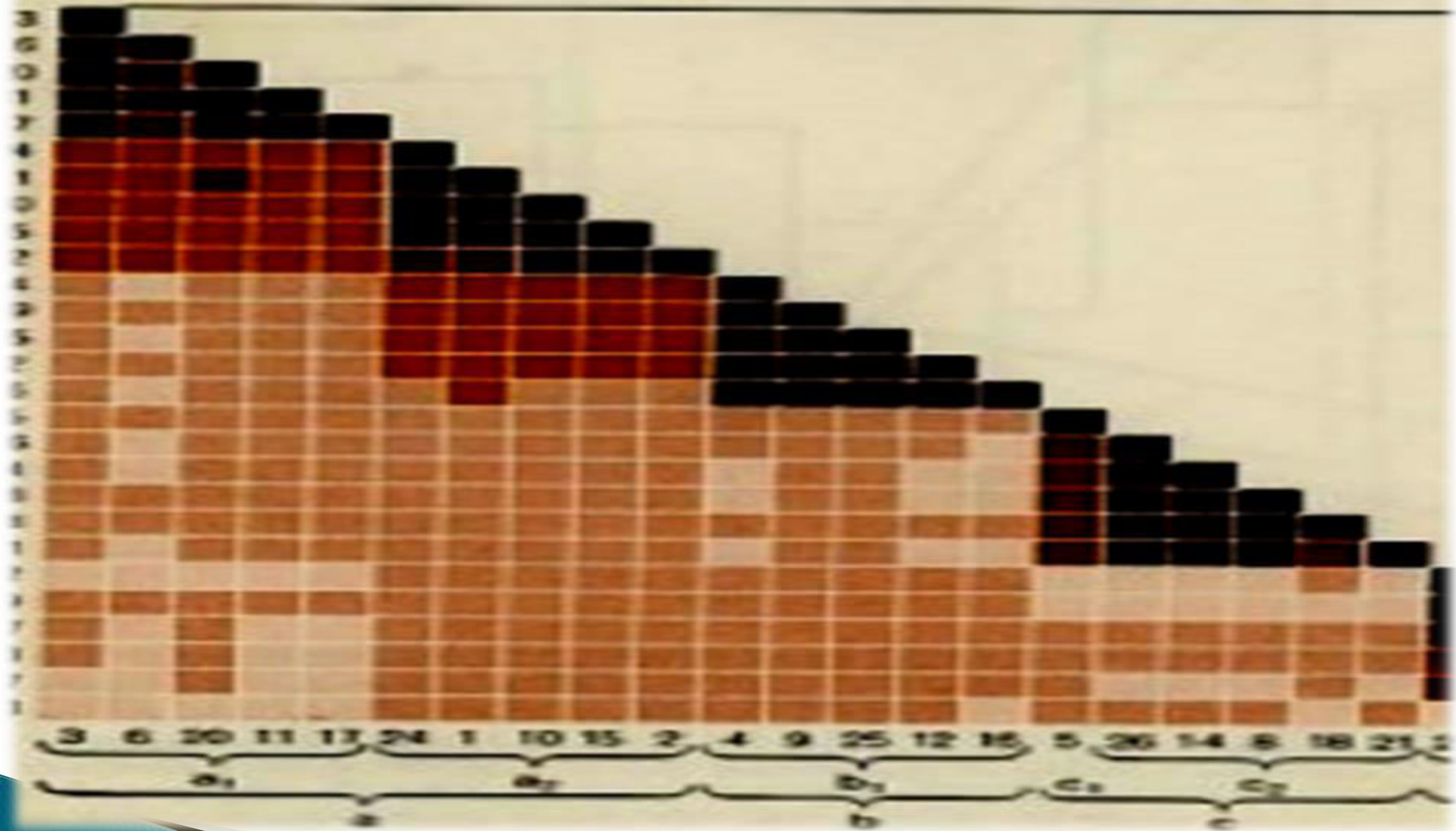
❖ The similarity among the OTUs is calculated by 'similarity matrix' having few color schemes, where the dark-shaded areas are highly similar.

❖ This matrix is then rearranged to get the clusters of similar OTUs. The results of numerical taxonomy are generally represented in the form of phenograms.

2nd April, 2020

DISSIMILARITY (PHENETIC DISTANCE)

.09-.48
 .49-.88
 .89-1.28
 1.29-1.68



MERITS OF NUMERICAL TAXONOMY:

According to Sokal and Sneath, numerical taxonomy has the following advantages over conventional taxonomy:

a. The data of conventional taxonomy is improved by numerical taxonomy as it utilizes better and more number of described characters.

The data are collected from a variety of sources, such as morphology, chemistry, physiology, etc.

b. As numerical methods are more sensitive in delimiting taxa, the data obtained can be efficiently used in the construction of better keys and classification systems, creation of maps, descriptions, catalogues, etc. with the help of electronic data processing systems.

Numerical taxonomy has in fact suggested several fundamental changes in the conventional classification systems.

c. The number of existing biological concepts have been reinterpreted in the light of numerical taxonomy.

d. Numerical taxonomy allows more taxonomic work to be done by less highly skilled workers.

Demerits of Numerical Taxonomy:

Numerical taxonomy can however prove to be disadvantageous from the following points of view:

- a. The numerical methods are useful in phenetic classifications and not phylogenetic classifications.
- b. The proponents of “biological” species concept, may not accept the specific limits bound by these methods.

c. Character selection is the greatest disadvantage in this approach. If characters chosen for comparison are inadequate, the statistical methods may give less satisfactory solution.

d. According to Steam, different taxonomic procedures may yield different results.

A major difficulty is to choose a procedure for the purpose and the number of characters needed in order to obtain satisfactory results by these mechanical aids.

It is necessary to ascertain whether a large number of characters would really give satisfactory results than those using a smaller number.

Applications of Numerical Taxonomy:

Numerical taxonomy has been successfully applied in the following studies:

a. Study of similarities and differences in bacteria, other micro-organisms and several animal groups.

b. Delimitation of several angiospermic genera like *Oryza*, *Sarcostemma Solarium*, and other groups including Farinosae of Engler and a few others.

c. In the study of several other angiospermic genera including Apocynum, Chenopodium, Croton, Cucurbita, Oenothera, Salix, Zinnia, wheat cultivars, Maize cultivars, etc.

d. Phytochemical data from seed protein and mitochondrial DNA RFLP studies has been numerically analyzed by Mondal et al. to study the interspecific variations among eight species of Cassia L. Based on the results of electrophoretic patterns, the degree of pairing affinity (PA) or similarity index was calculated by the following formula, according to the method of Sokal & Sneth and Romero Lopes et al.:

Separate dendograms expressing the average linkage were computed using the cluster method UPGMA, which showed that the eight species could be placed into two categories or clusters with *C. alata*, *C. siamea*, *C. fistula* and *C. reginera*, all being trees or large shrubs and characterized by the absence of foliar glands on petiole or rachis and presence of dense axillary terminal racemes greater than 30 cm long, being clustered into one group, whereas the other four species, i.e., *C. occidentalis*, *C. sophera*, *C. mimosoides* and *C. tora*, forming the other cluster, all being herbs or undershrub's and characterized by the presence of short corymbose racemes less than 10 cm long and with foliar glands, either on petiole or rachis.

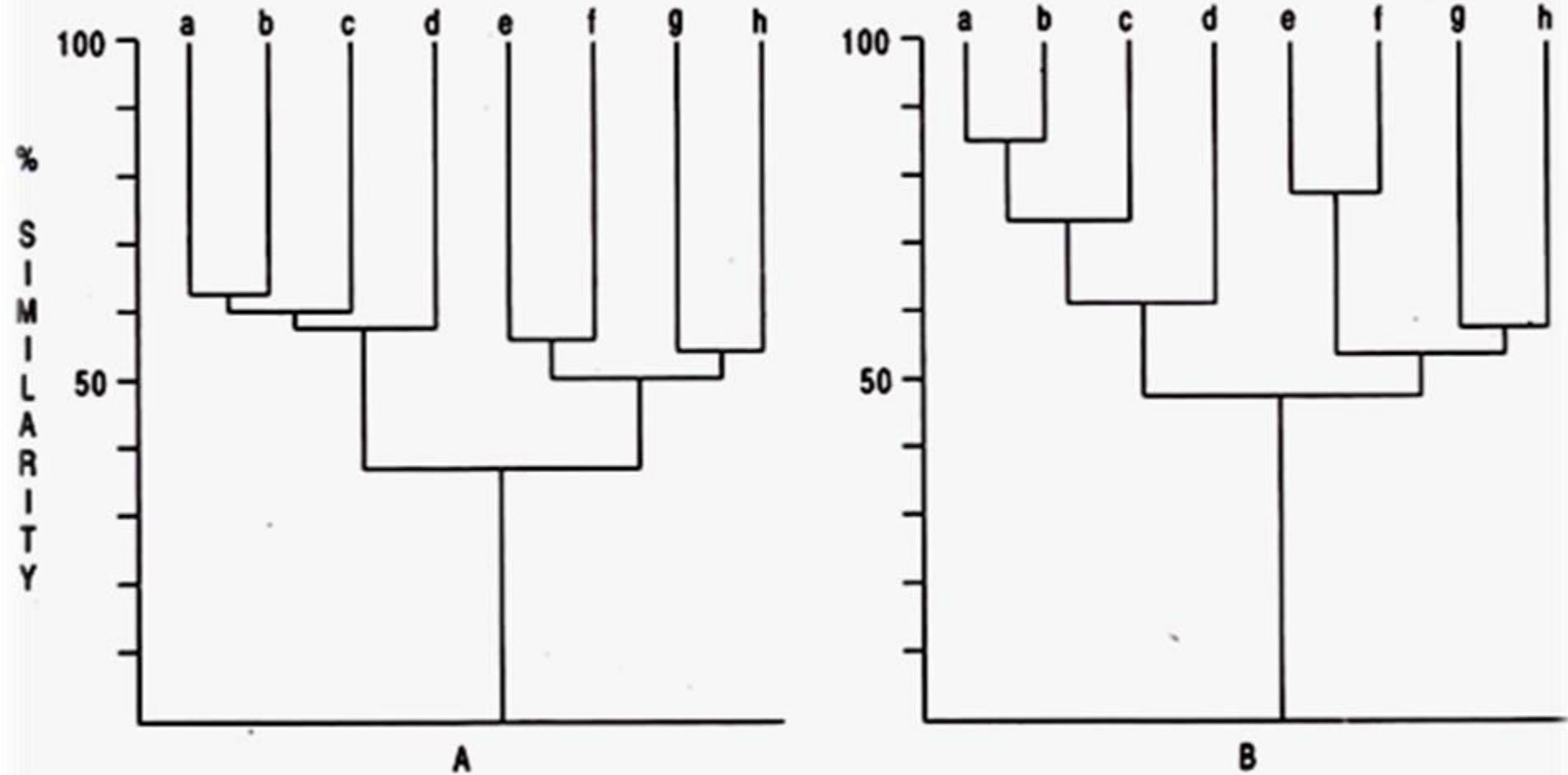


Fig. 9.6 : Dendrogram representing the 'average linkage' relationship among the eight species of *Cassia* shown by (A) seed protein electrophoresis and (B) mtDNA restriction fragments (a) *C. occidentalis*, (b) *C. sophera*, (c) *C. mimosoides*, (d) *C. toro*, (e) *C. alata*, (f) *C. siamea*, (g) *C. fistula*, (h) *C. siamea*

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We shall overcome!!!!!!!

#SAVE FROM CORONA

Stay Home

Save your Life

Save your Family

Save your Society

Save your Country

Save your beautiful Planet

THANK YOU

