

PLANT SYSTEMATICS

Simpson (1961) defined systematic as a scientific study of the kinds and diversity of organisms and of any and all relationship between them.

There are two major means or methods to establish relationship between organism.

1. Phenetic methods – based on a set of phenotypic characteristics of the organisms under study
2. Phylogenetic method – based on evolutionary history or pattern of descent of a group of organisms.

NUMERICAL TAXONOMY OR PHENETICS

Numerical taxonomy is a developing branch of taxonomy which involves the conversion of biological data into numerical form, followed by analysis through computer based program. This type study is also known as Mathematical Taxonomy (Jardine and Sibson, 1971), Taxometrics (Mayr, 1966), Taximetrics (Rogers, 1963), Multivariate morphometrics (Black and Reyment, 1971) and Phenetics.

Definition of Numerical taxonomy:

It is a discipline of taxonomy which is concerned with numerical evaluation of the affinity or similarity between taxonomic units and ordering of these units on the basis of their affinities (Sokal and Sneath 1963). Sneath and Sokal (1973) defined phenetic relationship as similarity based on a set of phenotypic characteristics of the object or organism under study. Phenetic relationship is represented by a computerized diagram, the phenogram.

Principles of Numerical Taxonomy or Taxometrics

The concept of numerical taxonomy is based on ideas proposed by Michel Adanson (1763). He rejected the idea of giving more importance to a certain character instead emphasized to consider all the characters equally. The principles of numerical taxonomy are enumerated below –

1. More the character is taken into consideration, greater the content of information in the taxa is used, better will the classification
2. A priori, every character is of equal weight in creating natural taxa
3. Overall similarity between any two entities is a function of their individual similarities in each of the many characters in which they are being compared.
4. Distinct taxa can be recognised because correlation of characters differ in the groups of organisms under study
5. Phylogenetic inference can be derived from the taxonomic structures of a group and also from character correlations.
6. Taxonomy is viewed and practiced as an empirical science
7. Classification are based on phenetic similarity.

The methodology of Numerical taxonomy

The methodology of numerical taxonomy involve the following steps –

a. Selection of Operational Taxonomic Unit (OTUs):

OTU is the sample from which data is collected. An OTU is defined as the fundamental unit of Numerical taxonomy, the sample from which data is collected. It is actually a plant specimen representing a taxonomic category. Some cautions should be taken in choosing OTUs – firstly OTUs must be well circumscribed and delimited from one another. Secondly the study group itself should be large enough so that all probable closely related OTUs are included in the analysis. It is not advisable however to use genera and higher ranks as OTUs, as the majority of characters would show variation from one species to another and thus would not be possible for comparison.

b. Selection of Unit character:

Character is a feature which varies from one organism to another. An unit character may be defined as a taxonomic character of two or more states. Character states are two or more forms of a character. Generally those features, those are 1. Genetically determined and heritable 2. Relatively invariably within an OTU and 3. Denote clear discontinuities from other similar character and character states should be utilized.

c. Coding of Character

In numerical study huge number of data is handled. Before the data is fed into the computer it should be suitably coded with symbols and numbers and converted into a vector with the help of a data matrix. The coding is of two types –

1. 2-state or binary or presence –absence coding – The 2-state or binary characters are best coded as 0 or 1 for two alternate states. Such a coding is handled very efficiently by computers.

2. Multi-state coding- When the character is represented by more than two character state, the coding process is known as Multi-state coding. It is of two types Qualitative and Quantitative. Qualitative multi-state coding is not entertained while the quantitative ones are reliable since the former is subjective. For better deduction a multi-state character should be converted to a 2-state character. Character like flower colour having 3 character states – like white, red and blue may be converted into 2-state form like white and coloured. The character may be split like flower white vs. not white, flower red vs. not red or Blue vs. Not blue. Such splitting may however give more weight to one original character.

d. Preparation of Data matrix:

The selected unit characters (n) are put horizontally in a coded form and OTUs are put vertically (t). The response of each OTU to each character are coded to form a matrix. Using this matrix a similarity matrix can be calculated, indicating percentage based similarity or simple matching coefficient. A large number of formulae have been proposed by various authors to calculate similarity or dissimilarity (Taxonomic distance) between OTUs – like calculation of similarity percentage, coefficient of association, coefficient of correlation, coefficient of distance.

A data matrix with hypothetical OTUs (t) and character

OTUs (t)	Character with character state				
	Habit Woody = 0 Herbaceous= 1	Leaf character Simple= 0 Compound = 1	Ovary position Superior = 0 Inferior = 1	Carpel Free = 0 United = 1	Fruit type Follicle = 0 Achene = 1
1	1	0	1	0	1
2	1	0	0	1	1
3	0	1	1	1	0
4	1	1	1	0	1
5	0	0	0	1	1

Similarity matrix (with t x t dimension) where both the row and columns represent OTUs.

	1	2	3	4	5
1	100				
2	60	100			
3	20	20	100		
4	80	40	40	100	
5	40	80	20	20	100

e. Cluster analysis

Using the percentage based similarity matrix cluster analysis is done. Cluster analysis is one such method in which OTUs are arranged in the order of decreasing similarity. Today with the help of computer programs branching diagrams with several inclusive clusters are produced, known as Dendrograms. Dendrograms

computed on phonetic features are known as Phenogram. The graphic diagram linking the OTUs in terms of affinity is known as Phenogram.

The major advantage of Numerical Taxonomy:

1. Traditional existing system of classification can be evaluated and revised.
2. It provides exact estimation of affinity
3. Numerical taxonomy has the provision to integrate data from a variety of sources such as morphology, physiology, Phytochemistry, embryology, anatomy, palynology, cytology, Ultrastructure etc. It is very difficult to do by the conventional taxonomy.
4. it provides an excellent frame work of natural relationship among taxa, based on which evolution and interrelationship may be interpreted. It can give a realistic estimation of the process of evolution (Solbrig 1970).
5. Data coded in the numerical form can be used for making description, keys, catalogues, maps and other documents.
6. The method being quantitative, provide greater discrimination and can provide better classification and keys.

The major demerits or disadvantages:

1. It is not so sensitive to convergent process of evolution and to isolating mechanism leading to speciation.
2. The result of numerical taxonomy may not be acceptable to the followers of biological species concept.
3. It fails to discriminate sibling species.
4. Non-relevant characters may be selected for phonetic analysis.
5. The findings are not phylogenetic in interpretation.

PHYLOGENETIC SYSTEMATICS

Phylogenetic systematic or cladistics is that branch of systematic which is concerned with inferring phylogeny. Phylogeny refers to the evolutionary history or pattern of descent of a group of organism. The phylogeny is commonly represented in the form of a graphic representation called Cladogram or Phylogenetic tree, a branching diagram that conceptually represent the best estimate of phylogeny. The lines of a cladogram are known as lineage or clades. Lineages represent the sequence of ancestral-descendant population through time. The point of divergence of one clade into two where the most common ancestor of the two divergent clade is located is termed a Node, the region between two node is called an Internode.

The process of Cladistic analysis

a. Selection of OEUs (Operational Evolutionary Unit) or EU (Evolutionary Unit):

This is the fundamental working unit in cladistics. This is a single plant, taxonomic status of which depends upon the pattern of work undertaken. A unique feature of the Cladistic analysis is that the list of OEUs generally include hypothetical ancestors.

b. Characters and coding:

A list of characters is prepared next and Plesiomorphic (primitive) and Apomorphic (advanced) state of each character is distinguished. Majority of characters are binary characters (with two alternative characters states). In some cases more than two character states may be encountered. Character states for each character are arranged in a sequence known as Transformation series or Morphocline.

c. Polarity:

The first step of character analysis is the determination of polarity. Polarity is the designation of relative ancestry to the character states of a morphocline i.e., whether the character is a derived one (Apomorphic) or ancestral one (Plesiomorphic). Polarity can be determined by in-group and out-group comparison. Comparison may be made within the concerned group (in-group) or relatives of out-group. If two character states of a character are

found in a single monophyletic group, the character state that is also found in a sister group is likely to be Plesiomorphic and that found only within the concerned monophyletic group is likely to be Apomorphic.

In case where the character has 3 states (Leaf simple → pinnately lobed → Pinnately compound). The coding may be accordingly be done, as '0' for most primitive character state (simple leaf), '1' for intermediate character state (pinnately lobed leaf) and '2' for most advanced character state (Pinnately compound leaf).

It is often assumed that whereas the same character state may arise more than once within a group between closely related species (Parallelism) or between remotely related species (Convergence).

4. Preparation of data matrix:

After the coding of character states a data matrix is prepared. OEUs including a hypothetical ancestral last in the row are enlisted in vertical series and the characters with coded character states are arranged horizontally.

5. Measurement of distance between the two OEUs

The data matrix can be used for calculating the distance (and consequently the similarity) between every pair of OEUs including the hypothetical ancestor. One method of calculating distance involves calculation of the number of apomorphic character state common between the pair of Concerned OEUs, ignoring the possession of Plesiomorphic character states in common.

6. Construction of Cladogram

Most cladistic analysis yield numerous cladograms that are equally most parsimonious. Parsimony is the principle that the simplest explanation that can explain the data is to be preferred. In the analysis of phylogeny, parsimony means that a hypothesis of relationship that requires the smallest number of character changes is most likely to be correct. A consensus tree is a cladogram derived by combining the features in common between two or more cladogram. The consensus tree can be derived in different ways –

1. Strict consensus tree – Involve the monophyletic groups that are common to all the tree.
2. Majority-rule consensus tree – It shows all the groups which appear in a majority of tree.
3. Semi-strict consensus tree – It indicates all the relationships supported by both type of trees or any one these, but not contradicted by any.

7. Cladogram analysis:

A cladogram represent an evolutionary diagram. Wiley (1981) defines Cladogram as “a branching diagram of entities where the branching is based on inferred historical connections between the entities as evidenced by synapomorphies. Taxa in a truly phylogenetic system should be monophyletic. It has been found that Synplesiomorphy (possession of primitive character-states in common by two or more taxa) does not necessarily indicate monophyly. Synapomorphy (possession of derived or apomorphic character-states in common by two or more taxa) is reliable indicator of monophyly.

The methodology of phylogenetic systematic generally presumes the dichotomous or polytomous splitting of taxa. However reticulation in evolution of plant may happen, the hybridization of two previously divergent taxa forming a new lineage. Most standard phylogenetic analysis do not consider reticulation and would yield an incorrect cladogram if such process had occurred. A typical cladistic analysis may involve the use of the DNA sequence from one or more gene plus the use of morphological data. The strict consensus tree of this combined analysis generally represent the best estimate of Phylogenetic relationship of the group studied. Cladogram represent an estimate of the pattern of evolutionary descent, both in terms of recency of ancestry and in the distribution of derived (apomorphic) character states.

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