

COURSE: MSc Part -1

PAPER – 5

TOPIC- Angiosperm (Different topics)

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Topic-1

Numerical Taxonomy

Classification of organisms by a comparison of large numbers of observable characteristics that are given equal value instead of being weighted according to possible evolutionary significance is called as Numerical taxonomy. Also, the analysis of various types of taxonomic data by the mathematical or computerized method is called numerical taxonomy or taximeters.

Adanson a French botanist, was the first to put forward a plan for assigning numerical values to the similarity between organisms. He tried to use as many characters as possible for the classification, and such classifications are recognized as Adansonian principles have developed several methods in taxonomy during recent years, and these methods are all included under numerical taxonomy.

Principles of numerical taxonomy :

Numerical taxonomy is based on certain principles which are also called Neo Adansonian Principle this includes:

- (1) The greater the content of information in the taxa of a classification system, the better a given classification will be.
- (2) Every character has equal weight in creating new taxa.
- (3) The science of taxonomy is viewed and practiced as an empirical science.
- (4) The phenetic similarity is the base of classification.

Unit Characters:

Unit characters are the characters used in numerical taxonomy. According to Sokal and Sneath (1963), unit character is defined as a taxonomic character of two or more states, which within the study at hand cannot be subdivided logically, except subdivision brought about by changes in the method of coding. Only the phenotypic characters are used as unit characters, e.g. presence or absence of an awn in a grass spikelet.

Taxonomic Group:

Estimation of Resemblances:

Most phenetic methods involve taxon-to-taxon distance, similarity or dissimilarity measures. Distance and dissimilarity are sometimes treated as the same thing, though a distinction can be made between them. As the name implies, distance and dissimilarity measure increase with dissimilarity between taxa, while similarity measures decrease with dissimilarity.

Cluster Analysis:

Cluster analysis or clustering is a type of multivariate statistical analysis. It is used to group organisms into separate clusters based on their statistical behaviour. The main objective of clustering is to find similarities between organisms, and then group similar organisms together to assist in understanding relationships that might exist among them.

Advantages of Numerical Taxonomy:

Sneath and Sokal have mentioned the following advantages of Numerical Taxonomy:-

- (1) In comparison with the conventional taxonomy, the data in Numerical Taxonomy are collected from a variety of sources, such as morphology, physiology, chemistry.
- (2) Through Numerical Taxonomy much taxonomic work can be done by less highly skilled workers.
- (3) Because the numerical method are more sensitive in delimiting taxa they provide better keys and classification systems in comparison to the conventional taxonomic method .
- (4) The quality of conventional taxonomy is improved by Numerical Taxonomy as a more and better-described character is used in the latter .

Applications of Numerical Taxonomy:

- (1) Numerical methods are used considerably to study similarities and dissimilarities in bacteria and other microorganisms.
- (2) Several angiospermic taxa are reclassified using numerical methods.

Topic-2

Role of Plant secondary metabolites

Secondary metabolites (SM) are compounds that are not necessary for a cell (organism) to live, but play a role in the interaction of the cell (organism) with its environment. These compounds are often involved in plants protection against biotic or abiotic stresses. Secondary metabolites are from different metabolites families that can be highly inducible in response to stresses. Primary metabolites perform essential metabolic roles by participating in nutrition and reproduction. A few SMs are used as especially chemical such as drugs, flavours, fragrances, insecticides, and dyes and thus have a great economic value. These new technologies will serve to extend and enhance the continued usefulness of the higher plants as renewal sources of chemicals, especially medicinal compounds. A continuation and intensification efforts in this field is expected to lead to successful biotechnological production of specific, valuable and as yet unknown plant chemicals.

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(1). Alkaloids are additional class of SMs, which are nitrogenous organic molecules biosynthesized mainly from amino-acids, e.g., tryptophan, tyrosine, phenylalanine, lysine and arginine using many unique enzymes

(2). Many of the most important therapeutic agents are alkaloids. The sites of biosynthesis are compartmentalised at cellular or sub-cellular level. However SMs can be transported long distances and accumulate from their location of synthesis. **Metabolites of Plants and their Role**

(2). Sometimes it is hard to discriminate primary and secondary metabolites. For example, both primary and secondary metabolites are found among the terpenoids and the same compound may have both primary and secondary roles. Secondary metabolites are broad range of compounds from different metabolite families that can be highly inducible in stress conditions. Carotenoids and flavonoids are also involved in cell pigmentation in flower and seed, which attract pollinators and seed dispersers. Therefore, they are also involved in plant reproduction

(3). Plant primary products refer to the compounds of nucleic acids, proteins, carbohydrates, fats and lipids and are related to structure, physiology and genetics, which imply their crucial role in plant development. In contrast, secondary metabolites usually take place as minor compounds in low concentrations. Primary metabolism refers to the processes producing the carboxylic acids of the Krebs cycle. Secondary metabolites, on the other hand, are non-essential to life but contribute to the species' fitness for survival. In fact, these specific constituents in a certain species have been used to help with systematic determination, groups of secondary metabolites being used as markers for botanical classification (chemotaxonomy).

Plants secondary metabolites can be divided into three chemically distinct groups viz: Terpenes, Phenolics, N (Nitrogen) and S (sulphur) containing compounds

I) Terpenes : Terpenes comprise the biggest group of secondary metabolites and are free by their common biosynthetic origin from acetyl-coA or glycolytic intermediates. An immense bulk of the diverse terpenes structures produced by plants as secondary metabolites that are supposed to be concerned in defense as toxins and feeding deterrents to a large number of plant feeding insects and mammals. In Gymnoperms (conifers) α -pinene, β -pinene, limonene and myrcene are found.

(II) Phenolic compounds : Plants produce a large variety of secondary products that contain a phenol group, a hydroxyl functional group on an aromatic ring called Phenol, a chemically heterogeneous group also. They could be an important part of the plants defence system against pests and disease including root parasitic nematodes

(III) Sulphur containing secondary metabolites: They include GSH, GSL, Phytoalexins, Thionins, defensins and alliin which have been linked directly or indirectly with the defence of plants against microbial pathogens. GSH is the one of the major form of organic sulphur in the soluble fraction of plants and has an important role as a mobile tool of reduced sulphur in the regulation of plant growth and development and as a cellular antioxidant in stress responses ,

reported as a signal of plant sulphur sufficiency that down regulates sulphur assimilation and sulphur uptake by roots.

Topic-3

Alpha and omega taxonomy

The term "alpha taxonomy" is primarily used today to refer to the discipline of finding, describing, and naming taxa, particularly species. In earlier literature, the term had a different meaning, referring to morphological taxonomy, and the products of research through the end of the 19th century. William Bertram Turrill introduced the term "alpha taxonomy" in a series of papers published in 1935 and 1937 in which he discussed the philosophy and possible future directions of the discipline of taxonomy. There is an increasing desire amongst taxonomists to consider their problems from wider viewpoints, to investigate the possibilities of closer co-operation with their cytological, ecological and genetics colleagues and to acknowledge that some revision or expansion, perhaps of a drastic nature, of their aims and methods, may be desirable. Turrill (1935) has suggested that while accepting the older invaluable taxonomy, based on structure, and conveniently designated "alpha", it is possible to glimpse a far-distant taxonomy built upon as wide a basis of morphological and physiological facts as possible, and one in which "place is found for all observational and experimental data relating, even if indirectly, to the constitution, subdivision, origin, and behaviour of species and other taxonomic groups". Ideals can, it may be said, never be completely realized. They have, however, a great value of acting as permanent stimulants, and if we have some, even vague, ideal of an "omega" taxonomy we may progress a little way down the Greek alphabet. Some of us please ourselves by thinking we are now groping in a "beta" taxonomy.

Turrill thus explicitly excludes from alpha taxonomy various areas of study that he includes within taxonomy as a whole, such as ecology, physiology, genetics, and cytology. He further excludes phylogenetic reconstruction from alpha taxonomy. Later authors have used the term in a different sense, to mean the delimitation of species (not subspecies or taxa of other ranks), using whatever investigative techniques are available, and including sophisticated computational or laboratory techniques. Thus, Ernst Mayr in 1968 defined "beta taxonomy" as the classification of ranks higher than species.

An understanding of the biological meaning of variation and of the evolutionary origin of groups of related species is even more important for the second stage of taxonomic activity, the sorting of species into groups of relatives ("taxa") and their arrangement in a hierarchy of higher categories. This activity is what the term classification denotes; it is also referred to as "beta taxonomy".

Beta (β) taxonomy: Beta (β) taxonomy refers to the arrangement of the species into a natural system of hierarchical categories. Beta taxonomy refers to the delimitation of species using sophisticated, investigative and laboratory techniques, Beta (β) taxonomy refers to the arrangement of the species into a natural system of hierarchical categories. This is done on the basis of easily observable, shared, structural features and evaluation of numerous characters. Thus, β -taxonomy relates to the search of a natural system of classification.

In the community taxonomy is alpha, in between communities is beta and sum of all communities in a region of space is gamma. Broadly speaking, these variations in names come from the interrelationships among species of either a single community or a group of communities

Topic-4

International code of Botanical nomenclature

The International Code of Nomenclature for Cultivated Plants (ICNCP), also known as the Cultivated Plant Code, is a guide to the rules and regulations for naming cultigens, plants whose origin or selection is primarily due to intentional human activity.

The International Code of Botanical Nomenclature (ICBN) is the set of rules and recommendations dealing with the formal botanical names that are given to plants. Its intent is that each taxonomic group ("taxon", plural "taxa") of plants has only one correct name that is accepted worldwide. The value of a scientific name is that it is an identifier; it is not necessarily of descriptive value, or even accurate.

The guiding principle in botanical nomenclature is priority. The ICBN sets the formal starting date of plant nomenclature at 1 May 1753, the publication of *Species Plantarum* by Linnaeus (or at later dates for specified groups and ranks). A botanical name is fixed to a taxon by a type. This is almost invariably dried plant material and is usually deposited and preserved in a herbarium, though can be an image. Some type collections can be viewed online at the websites of the herbaria in question. It was formerly called the International Code of Botanical Nomenclature (ICBN); the name was changed at the International Botanical Congress in Melbourne in July 2011 as part of the Melbourne Code which replaced the Vienna Code of 2005.

Principles, Rules and Recommendations and Provisions for the governance of the code.

A. Division I.

Principles: This division provides 6 Principles which form the basis of the system of Botanical Nomenclature.

These are:

- I. Botanical nomenclature is independent of zoological and bacteriological nomenclature. The Code applies equally to names of taxonomic groups treated as plants whether or not these groups were originally so treated.
- II. The application of names of taxonomic group is determined by means of nomenclatural type.
- III. The nomenclature of taxonomic group is based on the priority of publication.
- IV. Each taxonomic group with a particular circumscription, position and rank can bear only one correct name, the earliest that is in accordance with the Rules, except in specified cases.

V. Scientific names of taxonomic groups are treated as Latin, regardless of their derivation.

VI. The Rules of Nomenclature are retro-active unless expressly limited.

The binomial nomenclature is the system where naming of plants consists of two words — a generic name and a specific name. The first one is the generic name and the second one is the specific name. Both the names together form a binary or binomial name.

In a binomial, only the generic name should start with capital letter and all others in small letters. After selecting the name of a particular plant, it must be added with the name of the author. If the author's name is too long, it should be mentioned in abbreviated form. The names of the plants are written in Latin. The scientific name i.e., the Latin name of Paddy is *Oryza sativa*. The first name, *Oryza* is the generic name and the second name *sativa* is the specific name.

To complete the name, the author's name in abbreviated form should be added at the end. So the complete scientific name of Paddy is *Oryza sativa* L. The L. indicates the name of Linnaeus, who has given the name. Binomials should be typed in Italic type face or in case of handwriting both generic and specific epithet should be underlined separately.

Topic-5

Chemotaxonomy

Nature which consists of so many variabilities of living components of the environment possesses useful, harmful and inactive chemical constituents. The classification based on these chemical constituents is known as chemotaxonomy. All the living components of the environment produce secondary metabolites that are derived from primary metabolites. The chemical structure of the secondary metabolites is often specific and restricted to taxonomically related organisms. The classification of plants on the basis of specific class of secondary metabolites and their biosynthetic pathways constitutes chemotaxonomy. Its study is helpful to taxonomist, phytochemists and pharmacologists to solve selected taxonomical problems.

Chemotaxonomy, also called chemosystematics, is the attempt to classify and identify organisms (originally plants) according to confirmable differences and similarities in their biochemical compositions. Chemotaxonomy-based plant selection is a prerequisite for the successful natural product research. Due to difficulty in PCR amplification, molecular markers are very often inapplicable for yew extracts. More importantly, the gene variations cannot represent the variations at the metabolite level that are closely related to the manufacturing process of taxanes. Novel classifications based on metabolic analysis are thus highly desirable. During the past 20 years, some substantial quantitative and qualitative variations among different *Taxus* species have been found using modern analytic techniques (van Rozendaal et al., 2000; Wang et al., 2011). However, there was no practical chemical classification that can be applied to yew species identification. The systemic analysis of yew constituents is a big challenge, due to the numerous constituents from different classes and varying metabolite levels caused by many nongenetic factors such as developmental stage, climate, elevation, and slope exposure. As a rapid, cost-efficient, and popular analysis method, HPLC (high-performance liquid chromatography) fingerprinting has been regarded as the first choice for medicinal plant identification and quality control (Lu et al., 2005; Xie et al., 2006). A holistic approach of fingerprint analysis, profile similarity-based clustering, and choice of taxonomic markers capable of capturing the greatest chemical variations is proposed for *Taxus* classification (Ge et al., 2008b). Thirty samples representing eight *Taxus* species are collected and analyzed, and the fingerprint-based data are extracted and processed by hierarchical cluster analysis (HCA) and principal component analysis (PCA). Based on the PCA loadings, 12 chemical constituents, identified by LC–mass spectrometry (MS), are selected as the chemotaxonomic markers that can be used to establish a more sensible classification. Eight studied species are divided into six well-supported groups, and most samples can be assigned to the correct species. Traditional chemotaxonomic and chemosystematic studies are frequently used to infer relationships among plant taxa, by using the average concentration of several preselected compounds (van Rozendaal et al., 1999). However, they could not be used to examine the variations within species and may result in wrong conclusions in cases where the intraspecific variation is large (Becerra, 2003; Wink, 2003). In contrast, profile-based classification can investigate variations within and among species by

comparison of fingerprints (Vieira et al., 2003). Moreover, the fingerprint similarity-based taxonomy, which relies on the ratio of selected constituents, can improve the misclassifications caused by large quantitative differences.

Chemotaxonomic Classification- The phenolics, alkaloids, terpenoids and non-protein amino acids, are the four important and widely exploited groups of compounds utilized for chemotaxonomic classification. These groups of compounds exhibit a wide variation in chemical diversity, distribution and function. The system of chemotaxonomic classification relies on the chemical similarity of taxon]. Three broad categories of compounds are used in chemotaxonomy:

1 **Primary metabolites:** Primary metabolites are the compounds that are involved in the fundamental metabolic pathways. Most of the primary metabolites are of universal occurrence and utilized by the plant itself for growth and development. These compounds are ubiquitous in nature and hence play little role in chemotaxonomic classification.

2 **Secondary metabolites:** Secondary metabolites are the compounds that usually perform non-essential functions in the plants. They are used for protection and defense against predators and pathogens. These compounds are of restricted occurrence and hence very useful for chemotaxonomic classification.

Comparison of the protein banding patterns as a basis for chemotaxonomic classification:

In recent times protein banding patterns obtained by gel electrophoresis, have been focused on the problem of identification of critical taxa, their relationship and taxonomic status. Considerable variation in protein complements has been recorded at the level of species and genus, and even between the same plants in different populations. These form evidence upon which taxonomic systems may be founded, tested or demolished.

Some the methods used for classification on the basis of chemotaxonomy are:

a. Protein electrophoresis. This process also helped in establishing a close relationship between *Vicia* and *Lathyrus*.

b. DNA RFLP- Interspecific variations among eight species of *Cassia* (Caesalpinaceae) were evaluated on the basis of seed protein and mitochondrial DNA RFLP by gel electrophoresis as well as pollen protein patterns.

c. Amino acid sequence: Comparison of amino acid sequences of homologous proteins from different taxa has also provided a powerful tool for evolutionary and systematic studies. The degree of similarity in the amino acid sequence is presumably proportional to the degree of genetic relationship.

d. Analysis of isoenzymes and alloenzymes — Electrophoresis of enzymes can reveal two distinct types of genetically controlled variation in enzyme phenotype. Alloenzymes are different

forms of a particular enzyme that are coded by a single gene locus but by more than one different allele, each coding for a slightly different amino acid sequence, which have difference in mobility during electrophoresis.

e. Isoenzymes — They are different forms of the same enzyme formed from genes at different loci.

f. Nucleic Acids: The potentiality of the huge amount of phylogenetic information comprising the base sequences of cellular nucleic acids has been recognized relatively. It has now become possible to sequence any form of DNA from any plant. The relative homology of DNA or RNA of various plants is useful in a taxonomic study and as a possible screening method for inter-fertility of species.

g. Ribosomes, which are essential for protein synthesis, are ubiquitous and virtually abundant in the vast majority of plant cells. All ribosomes are composed of a larger and a smaller subunit, each in turn comprising a RNA molecule (rRNA), the size of which, vary between plants, and a number of protein molecules. It is the rRNA that has made a considerable impact on molecular taxonomy as they have domains with different average rates of nucleotide substitution. For example, Pollard noted the specificity of ribosomal RNA in cabbage, cauliflower, celery, corn and parsnip and showed that 28S and 18S ribosomal RNA from these taxa have distinct base compositions, which are characteristic of the species.

Further, restriction fragment analysis of cpDNA can help distinguish between potentially single or multiple origins of hybrid taxa. For example, presence of two quite different chloroplast genomes in the hybrid species *Aegilops triuncalis*, indicates that it has arisen through two hybridization events, one with *A. caudate* as the female parent and one with *A. umbellulata*.

Topic-6

Natural system and Phylogenetic system of classification

Many systems of classification of angiosperms have been proposed by many taxonomists from time to time. This is divided into three categories:

i. Artificial Systems based on superficial features.: These systems of classification were based on one or few morphological characters. Theophrastus (370 – 285 BC), a Greek philosopher, in his book *Historia Plantarum* classified about 480 plants into four groups on the basis of their habit-herbs, undershrub's, shrubs and trees. Carolus Linnaeus (also called Carl Linnaeus) (1707-1778), a Swedish naturalist in his book *Species Plantarum* (1753) classified 7300 species of plants into 24 classes, mainly on the basis of number, union and length of stamens. For example, he described the classes as Monandria (1 Stamen), Diandria (with 2 stamens), Triandria (with 3 stamens) and so on Polyandria (with 20 or more stamens). This system is commonly known as sexual system of classification.

ii. Natural systems based on form relationships. In these systems the organisms are classified on the basis of their natural affinities (i.e. the basic similarities in the morphology) rather than on a single character for determining the affinities.

(i) A.L. de Jussieu (1748-1836) published a natural system of classification of plants in his book *Genera Plantarum secundus ordines Naturales Disposita*. The plants were divided into three main groups, i.e. Acotyledones (plants without cotyledons). Monocotyledones (plants with one cotyledon) and Dicotyledones (plants with two Cotyledons)

(ii) A.P. de Candolle (1778-1841) a French botanist published *Theorie elementaire de la Botanique* in which he classified about 58,000 species into 161 families. He divided plants into two major groups i.e. cellulares (non-vascular plants) and vasculares (vascular plants).

(iii) Bentham and Hooker's Classification:

The most important and the last of the natural systems of classification of seed plants was proposed by two British taxonomists George Bentham (1800-1884), a self trained botanist, and Joseph Dalton Hooker (1817-1911), the first director of the Royal Botanical Garden, Kew (England). Their monumental work which took about quarter of a century for completion was described in three volumes of *Genera Plantarum*, published in Latin during July 1862 and April 1883. Bentham and Hooker's system of classification is still used and followed in several herbaria of the world. It is still the best system of classification followed in India.

Salient Features of Bentham and Hooker's system:

1. It is a classification of only the "seed plants" or phanerogams.

2. They described 97,205 species of seed plants belonging to 7,569 genera of 202 families starting from Ranunculaceae up to Gramineae.
3. They classified all the seed plants into 3 groups or classes i.e. Dicotyledons (165 families), gymnosperms (3 families) and monocotyledons (34 families).
4. They included disputed orders among Ordines Anomali which they could not place satisfactorily.
5. Monocotyledons were described after the dicotyledones.
6. The dicotyledons were divided into 3 Divisions (Polypetalae, Gamopetalae and Monochlamydeae) and 14 series. Each series again divided into cohorts (modern orders) and cohorts into orders (modern families).
7. Creation of the Disciflorae, a taxon not described by the earlier taxonomists.
8. Among the Monochlamydeae, major taxa, like the series, were divided on the basis of terrestrial and aquatic habits.
9. Polypetalae carries 82 families, 2610 genera & 31,874 species. Gamopetalae carries 45 families 2619 genera & 34,556 species. Monochlamydae includes 36 families, 801 genera & 11,784 species. Similarly Monocotyledons consist 34 families, 1495 genera and 18,576 species.

Merits of Bentham and Hooker's System:

1. Each plant has been described either from the actual specimen or preserved herbarium sheets so that the descriptions are detailed as well as quite accurate.
2. The system is highly practical and is useful to students of systematic botany for easy identification of species.
3. The flora describes geographical distribution of species and genera.
4. The generic descriptions are complete, accurate and based on direct observations.
5. Larger genera have been divided into sub genera, each with specific number of species.
6. Dicots begin with the order Ranales which are now universally considered as to be the most primitive angiosperms.
7. Placing of monocots after the dicot is again a natural one and according to evolutionary trends.
8. The placing of series disciflorae in between thalami florum and calyciflorae is quite natural.
9. The placing of gamopetalae after polypetalae is justified since union of petals is considered to be an advanced feature over the free condition.

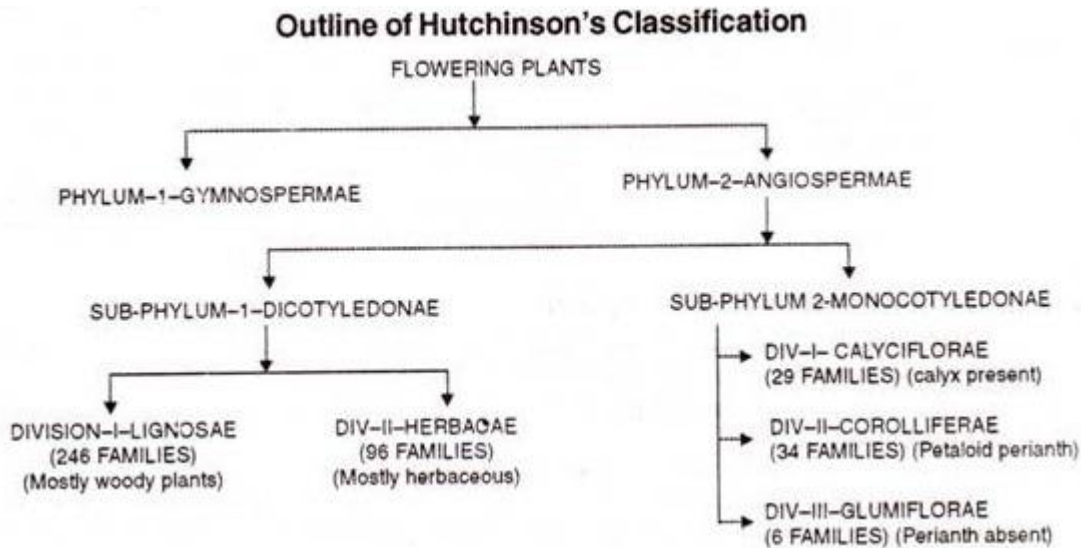
Demerits of Bentham and Hooker's System:

1. Keeping gymnosperms in between dicots and monocots is anomalous.
2. Subclass monochlamydeae is quite artificial.
3. Placing of monochlamydeae after gamopetalae does not seem to be natural.
4. Some of the closely related species are placed distantly while distant species are placed close to each other.
5. Certain families of monochlamydeae are closely related to families in polypetalae, e.g. Chenopodiaceae and Caryophyllaceae.
6. Advanced families, such as Orchidaceae have been considered primitive in this system by placing them in the beginning. Placing of Orchidaceae in the beginning of monocotyledons is unnatural as it is one of the most advanced families of monocots. Similarly, Compositae (Asteraceae) has been placed near the beginning of gamopetalae which is quite unnatural.
7. Liliaceae and Amaryllidaceae were kept apart merely on the basis of characters of ovary though they are very closely related.
8. There were no phylogenetic considerations

Phylogenetic system of Classification

John Hutchinson (1884-1972):

John Hutchinson was a British botanist associated with Royal Botanic Gardens, Kew, England. He developed and proposed his system based on Bentham and Hooker and also on Bessey. His phylogenetic system first appeared as "The Families of Flowering Plants" in two volumes. The first volume contains Dicotyledons (published in 1926) and second volume contains Monocotyledons (published in 1934). He made several revisions in different years. The final revision of "The Families of Flowering Plants" was made just before his death on 2nd September 1972 and the 3rd i.e., the final edition, was published in 1973.



The following principles were adopted by Hutchinson to classify the flowering plants:

1. Evolution takes place in both upward and downward direction.
2. During evolution all organs do not evolve at the same time.
3. Generally, evolution has been consistent.
4. Trees and shrubs are more primitive than herbs in a group like genus or family.
5. Trees and shrubs are primitive than climbers.
6. Perennials are older than annuals and biennials.
7. Terrestrial angiosperms are primitive than aquatic angiosperms.
8. Dicotyledonous plants are primitive than monocotyledonous plants.
9. Spiral arrangement of vegetative and floral members are primitive than cyclic arrangements.
10. Normally, simple leaves are more primitive than compound leaves.
11. Bisexual plants are primitive than unisexual plants and monoecious plants are primitive than dioecious plants.
12. Solitary flowers are primitive than flowers on inflorescence.
13. Types of aestivation gradually evolved from contorted to imbricate to valvate.

14. Polymerous flowers precede oligomerous flowers.
15. Polypetalous flowers are more primitive than gamopetalous flowers.
16. Flowers with petals are more primitive than apetalous flowers.
17. Actinomorphic flowers are more primitive than zygomorphic flowers.
18. Hypogyny is considered as more primitive from which perigyny and epigyny gradually evolved.
19. Apocarpous pistil is more primitive than syncarpous pistil.
20. Polycarpy is more primitive than gynoeceium with few carpels.
21. Flowers with many stamens are primitive than flowers with few stamens.
22. Flowers with separate anthers are primitive than flowers with fused anthers and/filaments.
23. Endospermic seeds with small embryo is primitive than non-endospermic one with a large embryo.
24. Single fruits are primitive than aggregate fruits

Merits and Demerits Merits:

1. Hutchinson proposed the monophyletic origin of angiosperms from some hypothetical Proangiosperms having Bennettitalean characteristics.
2. He made a valuable contribution in phylogenetic classification by his careful and critical studies.
3. Monocots have been derived from Dicots.
4. According to him, the definitions of orders and families are mostly precise, particularly in case of subphylum Monocotyledones.

Demerits:

1. There is undue fragmentation of families.
2. Too much emphasis is laid on habit and habitat. Thus, creation of Lignosae and Herbaceae is thought to be a defect reflecting the Aristotelean view.
3. The origin of angiosperms from Bennettitalean-like ancestor is criticised by many, because the anatomical structures of the early dicotyledons are not tenable with such ancestry.

Students are further advised to prepare notes on families given in the provided SLM

Also prepare notes on some important plants of economic importance