

Major advances in fungal systematics during last few years are;

- (i) Recognition of five kingdom systems instead of three kingdom system.
- (ii) Data analysis techniques of phylogenetic systematics
- (iii) Development and application of molecular techniques in mycology.
- (iv) Additional discoveries of new taxa, including fossils.

Kingdoms

Previously, there were three kingdoms i.e. Prokaryotes (Monera), Animals and plants (in plants fungi were also studied). Now, new classification has recognised new two kingdoms, and now, five kingdoms are being used, these include;

- (i) Prokaryotes (Monera)
- (ii) ~~Animalia~~ Animalia
- (iii) Plantae
- (iv) Fungi
- (v) Protista

To further understand the taxonomy, following terminologies must be kept in mind.

ch-3

Monophyletic group:-

Groups that contain an ancestor and all its descendants.

Phylogenetic relationship:-

A classification having evolutionary relationship is called phylogenetic relationship.

Taxa (Taxon - sing):-

The names of groups of organisms, all correspond to monophyletic lineages

Phylogeny:-

is hypothesis of genealogy of a group of organisms and their hypothetical ancestors. The relationship is represented by diagrammatically, by phylogenetic tree

Sister group:-

Relationships for closely related lineages that share a more recent common ancestor with each other than they do with other lineages. For example animals and plants have close lineage with fungi, so they are

Sister group.

Polyphyletic group:-

Groups that do not share a close common ancestor.

Paraphyly :-

A group that has common relatives of an ancestor.

Characters:-

A character is any attribute or feature of an organism that can serve as a basis for comparison with other organisms. The different expressions of a character are known as character states. Mycologists use many types of characters to contribute to their evolutionary studies. These includes;

- (i) Morphological characters
- (ii) Anatomical "
- (iii) Ultrastructural "
- (iv) Biochemistry "
- (v) Nucleic acid "

Characters are the basis of building a tree. All the characters mentioned above should be considered to ~~provide~~ phylogenetic analysis for classification studies.

In morphological studies, we study basic shape of the thallus and form, colour, and size of a spore-producing structures. In anatomical studies, hyphal tissues, the arrangement of asci or basidia and sterile structures within spore-producing structures, and hyphal structures are studied. Now with the availability of electron microscopy, deep studies of morphological and anatomical characters are possible. For example, nuclear division studies, internal structures of cell organelles and ascus wall structure can easily be studied. For biochemical characters, different techniques are available, that includes ; chromatography, protein electrophoresis and further other techniques are available for bio-chemical characters. New molecular techniques, for example Polymerase chain reaction (PCR) and other latest are being used for studying genetical characters.

Constructing and Evaluating Tree

characters are building blocks of phylogenetic tree. There are many methods by which phylogenetic tree may be built and evaluated. These namely;

- Maximum parsimony.
- Maximum likelihood.
- Distant methods.

Many versions of these methods are available in computer softwares (packages) through which these phylogenetic trees can be constructed and evaluated.

1- MAXIMUM ~~PARS~~ PARSIMONY

is a method, in which those characters are taken to construct a tree which can not be shared with other organisms or having less character state changes. In maximum parsimony, monophyletic ~~character~~ ^{groups} are defined by characters not by shared ~~character~~ ancestors. Maximum parsimony have one draw back, sometimes it gives misleading information in classifying

organisms when characters are markedly different.

2-MAXIMUM LIKELIHOOD

Maximum likelihood is another method to construct and evaluate a tree. The maximum likelihood method takes all those characters having maximum likelihood. This method takes all those characters having maximum same nucleotide sequence. Hence, this method is based on genotypic, not phenotypic. This method has draw back, it demands an explicit model to compare the nucleotide or amino acid sequence characters.

Now new methods have come, known as Robust Method. These are the methods, which can use any type of data to construct and evaluate the phylogenetic tree. Robust methods have also the ability to recover the tree by using data of new characters.

Specific Concept:

3- Distance and Phenetic Method:-

Distance method is based on overall similarity of the characters being compared between the taxa. However, this method causes problems, where conflicting occurs between the characters. Yet, discrete characters can be analysed to build a tree.

Species Concept:-

This method is being used to define different species or name different species.

Three methods are being used to define species

- I - A morphological species concept.
- II - " Biological species concept.
- III - " Phylogenetic species concept.

I - A morphological species concept is based on morphological characters alone.

II A biological species concept is based on natural population or populations of individuals that are actually or potentially interbreeding and isolated reproductively from each other.

III A phylogenetic species concept is based upon genealogical relationships. This method is most common in mycology systematics.

Evaluation within the fungal groups

Presently, to evaluate fungal groups, the method being mostly used, and is most reliable is, use of DNA sequence analysis and ultra-structural features. On the basis of these two tools, most of the groups previously were being considered in kingdom fungi, are now been placed in separate group i.e protists. So the only way for the evaluation of fungal groups is, use of biotechnology and molecular biology, and electron microscopy.

Number of fungi

in the world, so far, 1.5 million species of the fungi have been reported, while < 70,000 species have been recognized. It means still almost 14,30,000 species are to be discovered. From this, it is quite evident that less work is being done on systematic studies of fungi. Less studies have been conducted in tropical and temperate regions of the world on systematic aspects, this is the reason why less number fungi have been discovered, yet.

Fossil fungi :-

Fossil fungi, is a new method for systematists for data collection of genealogy and evolution. Fossil fungi studies help the systematists to collect information about the origin of fungi. For example, one study tells that "bracket fungi" came out from the teeth of the lung-fish. Following are the key fungal fossils emphasizing key earliest reports of taxonomy groups.

1-Proterozoic :- A period of 1800-1900 million years ago (MYA). Gives little information

Ch-3

about the origin of the eubryotes. However, little information has been given about the early protists or the probaryotes.

2- Cambrian:- Dates back to 570 MYA.

These fossils give little information about the vertebrates and invertebrates, but no information about the fungi.

3- Ordovician:- Dates back 505 ^{My} years ago.

Gives information about the fungus present in marine.

4- Silurian:- Dates back 430.

Give information about the origin of ascomycota. Silurian also give information about the oomycete associated with the marine life.

5- Devonian:- (408 MYA)

Give information about the fungi and their hosts. The fossil wood tells about the ascomycetes and basidiomycetes. This information also has evidence of conidia (asexual spore).

6- Carboniferous:- (360 mya)

These fossils have information about the chytridiomycetes, zygomycetes, ascomycetes and basidiomycetes. Further, also tell about the different phenomenon and

Structures of the fungi

7- Permian :- (286 mys)

In these fossils no information has been found about the fungi. However, much information has been given about the insect, plants and animals.

8- Triassic :- (245 mys)

It is the time of dinosaurs and mammals; gymnosperms and ferns were the common plants. Information about the fungi and their structure is present in these fossils. Maximum evidence about the structure of fungi i.e. ascomycota is very clear among these fossils. Structures like, ascocarp, and ascocarp with ostiole has also been found in this period.

9, 10- Mesozoic and Cenozoic :- (144 and 66 mys)

Have lots of information about the fungi. Fruiting bodies found in these fungi are just like the fungi present in these days. Fruiting bodies; shelf fungi, puffballs, and ostiolate fossils have been found in these

Indicator fossils

Microfossils with organic walls are termed as indicator fossils. These fossils

have helped little about the identification of fungi. However, indicator fossils have helped the systemists to study the environment of the fungi. Thus far, the indicator fossils have also helped in making hypothesis of evolution of fungi.

Nomenclature

Giving of names to the organisms is termed as nomenclature. Nomenclature rules are formulated by the "International code of Botanical nomenclature". International Botanical Congress is held every year in which new names are given to newly discovered individuals or species. Also, if objection arises from the scientists on previous those names are also rejected. A committee on fungi, give names to the fungi. This Committee is constituted by the congress officials.

Rules are important to mention here, which are applied to typification, use of priority, and citation of authorities.

- Ch 13

Typification - Designating a specimen (a collection, dried culture, or slide mount). Designation of a type specification is a requirement for a new species to be considered as validly published. A type specimen is the ~~specie~~ basis for a genus (called the type species of the genus), and genus might be the type of a family (called the type genus of the family). All of these taxa thus are linked to the type specimen. Photographs, drawings and sometimes, DNA samples are used to represent species or used in typification.

PRIORITY :-

Helps to determine the correct name for a taxon. For example, if a single species is described by two mycologists (or in a few cases, more than once by the same mycologist), the species described first is said to have priority, and its name may be taken up as a correct name. Sometime, if two mycologists have given name to the species and research paper of one mycologist published first than the other one, then priority will be given to that

Ch-3

Name which has published first.

Authority:-

Usually we have seen non-~~italic~~ name at the end of the fungal name. For example, Mucor corymbifer Cohn, here Cohn is the authority. Cohn was the scientist who first given name to this fungus. So, authority means the scientist name abbreviation at the end of technical name of the fungus. If latter on, some changes occurred in fungal name, then these are written after the authority. For example, Mucor corymbifer Cohn was latter on placed in Absidia by the scientist Saccardo and Trotter in 1912. Now, the authority name will come in parentheses and new scientist name will be placed after parentheses. Now this fungus name will be written as, Mucor corymbifer (Cohn) Sacc & Cor'et¹³, Trotter.

Further, there are many provisions in naming fungi. If fungi are in association with, e.g. symbiotic relationship, then at the time of giving name, fungal component is considered. Similarly, if fungi

Have many morphological forms (Pleomorphic) then names are given to the fungi on the basis of spore type. If ^a fungus has all its forms (Holomorphic), then the name is given on the basis of sexual form or stage.

To giving name to the fungi is really tough. At the time of Congress of International Code of Botanical Nomenclature, very hot discussions took place. The journal TAXON deals with the names or nomenclature of fungi. If any change comes to fungus name, that is also noticed or reported in the same journal i.e. TAXON.

The End