

platelet functions prothrombin time, activated prothrombin time and factor estimation⁸. In the present study, mean age of the patients was 9.1 ± 5.6 years. Sixty per cent of the cases were males and the rest were females. Only one patient was educated whereas 80% parents were uneducated and were not fully aware about the disease. Eighty per cent of the cases were known cases of bleeding disorders (3 haemophilia and 1 VWD) whereas one was diagnosed after admission. None of the patients had provided a proper past history of bleeding episodes to the doctor nor any attempt was made by doctor to elicit this relevant history. In our study, 100% patients had complication following surgical intervention and in one case it was life threatening. None of the parents were educated regarding the disease and the first aid nor did they attend any awareness camp. In our case series of five patients the doctor did not suspect or elicit proper history of

bleeding disorder in the patients. None of the patients underwent investigations for bleeding profile prior to surgery. HFI is active since 1983 and sponsoring treatment and education of children with haemophilia. Efforts of HFI, awareness and following the WFH guidelines in India are small steps towards harmonizing care of the people with bleeding disorder in the country until evidence-based practice is possible.

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On phylogenetic classification of fungi *sensu lato*: are we closing doors for morphotaxonomists?

Phylogeny remained speculative for very long, never had any role in classification and often formed the last chapter of mycological textbooks^{1,2}. With the emergence of molecular techniques, suddenly it is taking the front seat. The other criteria employed for elucidation of fungal classification and rearrangement of various taxa/groups other than morphology and ontogeny include biosynthetic pathways, genetic basis, scanning electron microscope (SEM) for surface ornamentation, transmission electron microscope (TEM) for internal structure and presence/absence of organelles, cell wall composition, etc. Apart from beautiful diverse morphological characters for which fungi are known, taxonomists also used host association (parasitism, saprophytism/commensalism), serological reactions, anamorph–teleomorph connections and sexuality as parameters in taxa differentiation.

Fungi play an important role in ecosystem functions³, therefore we need documentation/classification of these.

Thus we enter the field of taxonomy, where the taxonomists play a central role with a herculean task at hand while 'inventorying the biodiversity of this planet'. Hawksworth estimated 1.5 million species of fungi based on 1:6 ratio of plant and fungi of the most extensively studied piece of land, the British Islands. But later he revisited his conservative estimate with a more sound basis of known plant species (270,000), the vast number of unknown insect species (5–30 million), the increasing number of fungi plant ratio in specific geographical regions and the possibility of more fungi in tropical/polar regions than in temperate regions and arrived at the estimate of 9.9 million species⁴. The large number of devoted morphotaxonomists could discover only 100,000 species of fungi. Tropics contain more than 50% of biodiversity, including fungi, but have less number of mycologists^{5–6}.

A glance through the recent mycological journals *Mycological Research* and *Mycologia* reveals that the entire tradi-

tional fungal classification is like an Iranian carpet turned upside down due to the phylogenetic/molecular analysis based classification. A few examples of groups will clarify this statement. In fact, almost all the groups have been phylogenetically reshuffled/rearranged. The traditional aplanospore/zygospore (presence or absence) forming fungi, earlier placed in Zygomycota now treated in subphylum Mucoromycotina, Kickxellomycotina, Zoopagomycotina and Entomophthoromycotina of fungi as *insertae sedis*⁷ (not placed in any phylum). In the phylum Ascomycota^{7,8}, the order Erysiphales earlier treated in Pyrenomycetes now treated in Leotiomycetes and Meliolales earlier in the same class as Erysiphales are now placed in Sordariomycetes *inc. sed.* Braun and Takamatsu⁹ as a result of rDNA ITS sequences synonymized well-known teleomorph morphology based distinguishable genera *Uncinula* (appendages curved apically), *Microsphaera* (appendage branched apically) and *Sphaerotheca* (appendages myceloid

with single ascus/ascomata) to *Erysiphe* and *Podosphaera* respectively¹⁰. This is most disastrous at a time when an excellent comprehensive morphological criteria-based monograph on Erysiphales appeared recently¹⁰. Similarly, several smuts of the order Ustilaginales, class Ustilaginomycetes, subphylum Ustilaginomycotina are now placed in Microbotryales, class Microbotryomycetes^{7,11} of the subphylum Pucciniomycotina, i.e. along with rusts in the class Pucciniomycetes^{7,12,13}.

Similarly, the traditional orders of Chytridiomycetes: the Blastocladales¹¹ and a newly discovered group of rumen parasites, mitochondria lacking organisms under Neocallimastigales^{7,14} are now treated each as subphylum of Kingdom Fungi, Blastocladiomycota and Neocallimastigomycota. But these are only tips of an iceberg. Morphotaxonomists now appear to have been shifted to the backseat as parataxonomists. Various molecular methods at times give contradictory results¹⁵. After much contradiction, we now classify Microsporidia^{7,16} as Phylum Fungi. Even if there is closeness at molecular level (>95%), the expression of this difference in morphology is a matter of great appreciation which took >900 m.yr, when fungi separated from animals, 500 m.yr which separated Basidiomycota from Ascomycota and 600 m.yr for Endogonales and Glomerales separation¹⁷ and for expression of characters and further refinement for ecological adaptation and survival. Thus, grouping the organisms with taxonomically appreciable characters, by which we distinguish the present day fungi as species/genera is the essence of morphology-based classification. To put the 'concept and future strategy' in a more straight way, phylogenetic classification is good to investigate genealogical relationships, but the identification, naming and classification should be based on the structure we see under microscopes, otherwise this would turn out to be a 'terminator-gene' for the world over morphotaxonomists and their superb taxonomic publications¹⁸⁻²⁴.

Sexual reproduction and parasexuality are the means of exchange of genetic material/traits, which took a million of years to shape the characters of the genera/species or higher taxa as per adaptation pressure. If molecular biologists/taxonomists are engaged in unfolding the cryptic species²⁵⁻²⁷, the agenda of mapping of fungal diversity will be sidelined and many of the novel¹⁸⁻²⁴ fungi will be lost before being discovered/documentated, where we require expert manpower with little facilities for cataloguing the morphological-based genera/species or higher taxa.

In view of these facts, a critical appraisal is necessary before shelving the morphotaxonomic treatment of taxa. Moreover, it is a fact that we are working with less than 10% of fungi known to date with the industrious efforts of morphotaxonomists who have produced superb monographs¹⁸⁻²⁴. The more we stick to phylogeny, the more we lose the biodiversity of fungi due to climate change, habitat destruction and deforestation through fire and flood. We still have 90% unexplored biodiversity of fungi to document. Now, are we closing the doors for morphotaxonomists with their simple classical refined concepts, when we still have a long way to go?

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