Afterword

The nature of the scientific method is that the answer to a primary question generally leads to additional questions. Similarly, symposia and workshops organized to answer one set of questions often conclude with the participants considering new questions and reiterating old ones (whether or not the original questions have been answered). The preparation of the symposia published here began with the questions posed in the Introduction to this volume, and ended with the statements and questions listed here:

Multidisciplinary or polyphasic taxonomic studies are the way of the future.

Molecules, morphology, physiology and ecology are all important to fungal systematics. Historically, taxonomy has been the domain of the solitary scientist, alone in a room with a microscope. More and more, groups of scientists with different methodological specializations are collaborating on common questions with carefully selected cultures. Although molecular techniques are now employed in most taxonomic labs, few labs specialize in taxonomic analysis of secondary metabolites, and the number of mycologists doing critical morphological studies is declining at a dangerous rate.

Identification schemes can be devised using any kind of data and need not employ morphology. Classification schemes should be devised using the maximum possible number of different data sets.

How can ecological relationships be included in taxonomic analyses?

Ecological relationships are critical components of evolution and need to be considered in taxonomic and phylogenetic assessments. In this volume, there are many discussions of families and genera that have recognizable ecological patterns. Similarly, in many genera there are examples of sister species competing for an identical niche. There is a general feeling that these ecological relationships have a high taxonomic significance, but relevant ecological parameters must be carefully selected. How can ecological relationships be coded or described so that they can be included in cladistic or phenetic analyses? For example, how can the phylogenetic relationships known to exist between host plants be incorporated in a phylogenetic analysis of plant pathogens?

The methods, philosophies and purposes of cladification and classification are different.

In general, we speak of the identification of monophyletic groups (cladistics) as if it has the same purpose as classical taxonomy, but is this really so? Cladistics does not concern itself with the naming and identification of organisms. From this point of view, the term 'monophyletic taxon' is an oxymoron.

Combining different data sets for analysis usually necessitates the adoption of either cladistic or phenetic analyses as a standard, and the recoding of one type of data to the other. How can this recoding be done without losing information? Is it even appropriate to try?

There is a tendency in contemporary taxonomic literature to accept cladistic, DNA-based gene trees as the final arbiter of phylogenetic relationships, and to reject data sets that do not conform with these relationships as 'phylogenetically uninformative'. Mapping of morphological characters onto cladograms of molecular data is commonly used to test the phylogenetic reliability of morphological characters, but is not suitable for nonhomologous characters.

Can we accept paraphyletic taxa?

This is a major area of conflict between classical and cladistic taxonomists. Cladists reject paraphyletic taxa. Yet, many classical taxa (orders, families, genera) appear to be paraphyletic. Does it make sense to force members of an otherwise monophyletic group into different taxa when one of the nodes in the group undergoes an evolutionary radiation that warrants taxonomic recognition? As long as a mainly morphology-based Linnaean nomenclature forms the basis of communication in mycology, recognition of paraphyletic taxa is inevitable for each collective rank above that of species.

The importance of fungal cultures is increasing.

As fungal taxonomy becomes ever more preoccupied with non-morphological characters, the importance of preserved fungal cultures is enhanced. Thanks to permanent preservation techniques, public culture collections can cope with this high demand. At the same time, the number of cultures of each species needed for a serious examination of species concepts

often exceeds what is available from public collections. The role of field mycologists in collecting, culturing and accurately identifying strains remains critical for the advancement of taxonomic mycology.

New considerations are necessary for morphological studies.

Hiatus taxonomy, in which taxa are separated by discrete, definable phenotypic barriers, is a useful philosophy only in rare cases. The interpretation of continuous variation is the challenge for developing effective taxonomies. With such widespread use of cultures, describing and illustrating the characters of species grown in culture assumes renewed importance. Mycologists should use a diversity of media to maximize phenotypic expressions or stimulate sporulation. Unfortunately, standardization of media has proven to be very difficult, with water and agar quality, and the composition of commonly used extracts (malt, yeast) varying from country to country, and from year to year. Weak or low nutrient media need to be more broadly applied. Taxonomists in temperate latitudes should try lowering the temperatures of their incubators to induce representative morphological structures or stimulate spore germination. Patterns of spore germination are increasingly recognized as being taxonomically informative.

Should standards for molecular and morphological taxonomic studies be encouraged?

The molecular community demonstrated great vision in establishing public databases for nucleic acid and protein sequences, and TreeBASE is now growing as a repository for sequence alignments. Some taxonomists believe that standards need to be developed and applied for minimum required data for morphological descriptions (varying by taxonomic group). Public accessability to both sequences and the fungal material sequenced is of equal importance. Some also see the need for guidelines for DNA sequence alignments and minimum requirements for numerical analysis of genotypic and phenotypic data.

How can we cope with a genus with 100,000 species in it?

Taxonomists sometimes have an intuitive feeling for how many species belong in a genus. Large genera seem to be the result of great ecological success of their morphological/physiological outfit in relation to variable environments. Genera with 100 species or more are rare; there is a smaller number of genera with more than 1000 species. As phylogenetic species concepts result in a more finely dissected species level taxonomy, and if there actually are the number of host specific species for each vascular plant that some estimates suggest, then genera such as *Mycosphaerella* or *Pseudocercospora* could end up with 100,000 species in them. Is contemporary nomenclature too cumbersome to deal with such a volume of species epithets? How can so-defined species be distinguished? Do all these entities need names?

How do we cope with old names?

Many fungal taxa have inadequate or no holotype material, and no ex-type cultures are available. For many teleomorph genera, the anamorph is more informative and represents the only way to accurately distinguish species morphologically. In many such cases, attempts to amplify DNA from minute fruiting bodies or conidiophores have been unsuccessful. How do we approach such taxa? Epitypification is a valid solution that should be more widely applied, but it requires careful examination of authentic material followed by careful selection of a representative culture.

The editors