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EDITORIAL

Dothideomycetes

Since the formal description of Dothideomycetes by Eriksson and Winka in 1997, mainly relying on comparisons of 18S ribosomal sequences, it has become very clear that the important morphological and developmental characters traditionally used in taxonomy of loculoascomycetes, are homoplasious. In fact, without the use of DNA sequence comparisons this class remain virtually indistinguishable from similar loculoascomycete species that now reside in the class Eurotiomycetes. Most recent phylogenetic studies support Dothideomycetes as a single entity with the lichenized Arthoniomycetes as its sister class, but additional relationships in Ascomycota remain uncertain. The data collection of molecular characters has become even more focused recently with genome sequences available from at least 16 genomes at the Joint Genome Institute (http://genome.jgi.doe.gov/dothideomycetes/dothideomycetes.info.html) and more on the way. In addition to this focus on molecular characters there remains a pressing need to expand knowledge about biology, morphology and development of the vast majority of dothideomycetous species and place it in context of molecular driven hypotheses. One factor that will make this challenging is the size and diversity of the class. This very likely is the largest class in phylum Ascomycota with more than 19 000 species and a broad range of ecological roles.

Dothideomycetes are known first and foremost as agents of crop disease with members of this class playing a role in diseases of almost every major monocotyledonous and dicotyledonous crop. In spite of the large body of knowledge on phytopathogens much remains to be discovered about their diversity and closest relatives (see papers on *Cochliobolus*, *Phyllosticta* and *Venturiales* in this volume). In addition to this a large majority of the members in this class are endophytes, epiphytes or saprobes with smaller numbers occurring as lichens and hyperparasites. Several groups, previously defined using morphological characters, still resist efforts at culturing but DNA sampling reveal a surprising range of genetic diversity (see papers on *Microthyriaceae* and *Astrosphaeriella* in this volume). The anamorphs of several dothideomycetous groups are often overlooked and the study on *Tubeufiaceae* in this volume show how careful studies can reveal new genera based on production of distinct anamorphs. Dothideomycetes adapted to aquatic environments have already yielded lineages with distinctive genetic variations and this is expanded for the *Aliquandostipitaceae* and associated species in this volume. The 'sooty molds' is a group with a high level of documented morphological diversity, much of which is highly plastic. Members reside in two classes but a study on dothideomycetous *Capnodiaceae* expands the knowledge of this family in this volume. Finally, lichenized species make up a highly diverse set of species in Dothideomycetes and they are investigated in more detail within this volume.

Previous molecular studies on Dothideomycetes suffer from a shortage of sequences from type or authentic material. Many of the papers in this volume (*Aliquandostipitaceae*, *Astrosphaeriella*, *Capnodiaceae*, *Cochliobolus*, *Microthyriaceae*, *Phyllosticta*, *Tubeufiaceae*) use or discuss type, epitype or authentic sequences or epitypify fresh collections and thus provide data on relationships at various taxonomic levels that can be followed with more confidence than before.

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