EDITORIAL NEWS

Fast-track publication

The popularity of Mycological Research as the major outlet for original work in all aspects of mycology and the number of sound papers received in 1999 led to increasing time lags between acceptance and appearance in print. Action taken by the Editors in 2000 has had a dramatic impact on this situation. Most articles received in 2001 are expected to appear 6–7 months after acceptance, with ones which Editors consider merit particularly rapid publication appearing in 3–4 months. Such fast-track publication has already been achieved for some items in the later issues of 2000 and one is included in this part (pp. 5–15). This rapid publication facility places Mycological Research at the forefront of the timely dissemination of state-of-the-art novel research to mycologists world-wide. If you have results that may merit the fast-track treatment, and are of international interest, make Mycological Research your first choice for submission in 2001. An increase in the number of topical papers of wide interest is expected to result in an increase in the impact factor accorded to Mycological Research.

Sequence alignments

The Instructions and Guidelines to Authors published in January 2000 (Mycological Research 104 (1): 119–127) did not provide specific advice on the publication of sequence alignments. As these can take a considerable amount of space, published alignments will be strictly limited. Contributors of papers with sequence data are, however, expected to deposit sequences in GenBank (http://www.ncbi.nlm.nih.gov/Genbank/) and where appropriate to place alignments in TreeBASE (http://www.herbaria.harvard.edu/treebase/) or other publically accessible databases. The availability of sequence and alignment data to Editors and Referees, is, however, often critical to the assessment of the soundness of papers using such approaches. Recognizing that all authors may not wish to make their data public before papers are accepted, copies of pertinent sequences and alignments should be included with submissions specifically for the use of Editors and Referees and marked ‘not for publication’. The collections in which voucher specimens and/or cultures of sequenced material are deposited must be cited for all sequenced material (see Mycological Research 104 (6): 642–644, June 2000).

Contacting the Executive Editor

The Executive Editor is privileged to be serving as an Invited Professor in the Departamento de Biología Vegetal II of the Universidad Complutense de Madrid until June 2001, supported by the Ministerio de Educación y Cultura and Catedrático FBBV (Fundación del Banco Bilbao-Vizcaya). The main address for Mycological Research and the receipt of manuscripts during this time continues to be that of MycoNova in Hendon where the main files remain and from which papers are distributed to Editors. New manuscripts for submission should not be sent to Madrid; any sent first to Madrid will experience some otherwise avoidable delay in
processing. After the reviewing process, manuscripts recommended for publication by the Editors are being returned to Madrid, and corrected proofs are also to be sent to the Madrid address. Editors and authors needing to reply to Madrid are supplied with self-adhesive address labels. These arrangements have been in operation since July 2000 with no resultant delays in production. However, authors may sometimes experience up to two weeks wait to receive a formal acknowledgement of the safe receipt of their papers.

In case of urgency, in addition to ‘myconova@btinternet.com’, e-mails should also be copied to ‘davidh@euimos.sim.ucm.es’ to ensure the quickest possible response. Items for consideration for inclusion in Mycological Research News can be sent as e-mail attachments in Microsoft Word to both electronic addresses.

Authors requiring updates as to the current state of refereeing and processing submitted papers may contact the appropriate Editor directly. In order to facilitate this, e-mail addresses are being included on the inside front cover of each issue from January 2001.

IN THIS ISSUE

Several key molecular papers are included in this issue. The specificity of primers used to detect glomalean arbuscular mycorrhizal fungi has been examined; most previously published prove not to be reliable at the level they have been applied and have sometimes also picked out other fungi, and three Glomus clades are distinguished which represent different families (pp. 5–15). In the ascomycetes, the Agryrales prove to merit recognition at the ordinal rather than the family level, and to belong to the Lecanoromycetes (pp. 16–23). The identification of dark septate endophytic fungi has been addressed by inter-simple-sequence-repeat-anchored PCR which proves to be a powerful tool providing strain- and taxon-specific markers and can be expected to be widely used in future (pp. 24–32). Rhizoctonia solani AG-1 1A isolates from rice have been compared with other anastomosis groups by pectic zymograms and A+T-rich DNA RFLP methods; different anastomosis groups had distinct patterns, and within AG-1 1A lesser degrees of variation were found in material from different countries (pp. 33–40). Molecular and morphological approaches are used to reassess the relationships of nine species of the ascomycete genus Paraphaeosphaeria which appears to be polyphyletic and to merit restriction to a narrower group (pp. 41–56). Further, the pseudoflower-forming rust Uromyces pisi s. lat. on Euphorbia cyparissias has been found to belong to several different species on the basis of ITS sRNA sequences, some of which are microcyclic; the region sequenced is expected to be widely used in future studies (pp. 57–66).

Potential antagonists of the banana crown rot pathogen Colletotrichum musae were tested against 36 isolates, and the most satisfactory biocontrol occurred when different antagonistic fungi were applied together (pp. 67–76). An evaluation of Epicoccum purpurascens for the biocontrol of Sclerotina head rot in sunflower showed that while conidia of the fungus reduced the incidence of the disease in glasshouses they were less effective on field-grown plants; extracted secondary compounds had no such effect (pp. 77–84).

Variation of Pythium irregulare isolates from cereals, medic and sub-clover studied by RFLP methods showed most to be heterozygous and that outcrossing occurs, but that pathogenicity varied between hosts, although some were not necessarily most pathogenic on the host from which they originated (pp. 85–93). Studies on Cryphonectria cubensis, which causes a destructive canker on Eucalyptus in South Africa, revealed little genetic diversity suggesting sexual reproduction was absent; however, isolates belonging to different vegetative compatibility groups differed in their ability to cause lesions (pp. 94–99). Following on from earlier work on endopolygalacturonase coding genes in species of Fusarium from Pinus (Mycological Research 104(11): 1341–1346, November 2000), the highest polygalacturonase activity was found in F. oxysporum and F. moniliforme which could contribute to their pathogenicity (pp. 100–104).

In a study of the ability of ericoid mycorrhizal endophytes from Woollsia pungens and Hymenoscyphus species to grow on different amino acids as sole nitrogen sources, Woollsia isolates grew least well on lysine, but the Hymenoscyphus isolates showed no such strong responses (pp. 105–111). A mathematical model for the intraspecific competition of two species of Coprinus has been tested experimentally; competition caused a change in growth rate and while the model generally estimated weights it did not always correctly predict the outcomes (pp. 112–118).

The ultrastructure of the conidiomata of Tubakia dryina is documented in detail (pp. 119–121), and notes on the ascomycete genus Cresporhaphis provided together with the description of a new species from Spain and a key to the seven species now known (pp. 122–126).

NEW PHYTOPHTHORA LINKED TO SUDDEN DEATH OF OAKS

Diseases of plants caused by species of Phytophthora plague agriculture and forestry worldwide (Erwin & Ribeiro 1996). Even the most infamous and longest-known phytophthor disease agent, potato late blight (P. infestans), is currently reappearing in the form of new, virulent strains (Goodwin 1999, Moore 2000). Trees are among the types of plant attacked; oaks in Europe have been suffering dieback that has been attributed to P. quercina (Jung et al. 1999), and oaks
southern Mexico have been dying from infection of their roots by *P. cinnamomi* (Tainter et al. 2000). Now a team of scientists in California, has reported that a species of *Phytophthora* is likely to be responsible for the sudden death of common forest oaks in that state (http://camfer.cnr.berkeley.edu/oaks/). Tanoaks (*Lithocarpus densiflorus*), coast live oaks (*Quercus agrifolia*) and black oaks (*Q. kelloggii*) in several areas in California are dying in large numbers. It is projected that the disease, termed ‘Sudden Oak Death’, will impact wildlife by reducing the acorn supply that serves as a staple in coastal central and northern California, and by increasing fire hazards in dry seasons.

The initial symptoms of the disease are wilted shoots and loss of colour in mature leaves; this is followed by death of the foliage, which remains attached to the branches. The inner bark and sapwood are watery and release red sap from lesions in the bark (images are provided at the website cited above). David M. Rizzo and Matteo Garbelotto of the University of California at Davis and Berkeley, respectively, are leading the microbiological investigation of the sudden-death syndrome. In the early summer of this year, Rizzo and Garbelotto discovered that although a black-stromatic ascomycete (*Hypoxylon* sp.) and wood-boring beetles are associated with the disease, the probable primary disease agent is a species of *Phytophthora*. Sporangia of the *Phytophthora* are produced in the red ooze from diseased trees, and mycelia are present in the bark and phloem. Zone lines demarcate the extent of oomycotic invasion. Current evidence suggests that only one species of *Phytophthora* is involved, and it has been isolated from several disease locations, from root crowns to spots higher than 2 m from the ground. Rizzo and Garbelotto have found that sporangial morphology and rDNA information indicate that the sudden-oak-death *Phytophthora* is not the same as *P. quercina*; however, its rDNA ITS base sequences are 98 % similar to *P. lateralis*, from which it differs morphologically. Garbelotto is investigating whether the sudden-oak-death species might be a hybrid between *P. lateralis* and another *Phytophthora*. Rizzo and Garbelotto plan to formally publish their findings, along with information from other members of the oak-death research team (entomology, pathology, remote sensing, forestry; see website cited above) in 2001.


Steve Newell

*Marine Institute, University of Georgia, Sapelo Island, Georgia 31327, USA.*

E-mail: newell@uga.edu

---

**PHYLOGENY OF AGARICALES RE-EXAMINED**

The standard reference for classifying gilled mushrooms is *The Agaricales in Modern Taxonomy* (Singer 1986). Singer explicitly excluded from the *Agaricales* any ‘gasteromycetes’ including secatoid agaric relatives. Additionally, he purposely incorporated virtually all gilled mushrooms in his monograph, leading him to include the *Polyporaceae*, where he classified *Pleurotus* and *Lentinus*, and the suborders *Russulineae* and *Boletineae*. Subsequently, the ‘*Agaricales*’ have been subjected to intensive phylogenetic analysis at Duke University (Durham, NC). Hibbett & Vilgalys (1993) first showed that *Lentinus* in Singer’s sense was polyphyletic and largely outside of the *Agaricales* proper as was *Pleurotus*. This has led to research on polpores and other aphyphloralean fungi by Hibbett & Donoghue (1995) revealing a primarily agaricoid clade (*Agaricales* or ‘euagarics’) excluding the *Russulineae* (distantly related) and *Boletineae* (a sister group). Simultaneously, research on boletes and their relatives in Berkeley (CA) independently reached the same conclusions (Bruns et al. 1998) and established that secatoid taxa were in fact nested within such clades. Hibbett went on to demonstrate that puffballs (‘*Lycoperdales*’) are ‘euagarics’ (Hibbett et al. 1997), as are various coral fungi (Pine, Hibbett & Donoghue 1999).

Emphasizing nuclear large subunit ribosomal DNA (nLSU-rDNA) sequence data, research at Duke University covered more agarics and their relatives, including *Coprinus s. lat.* (Hopple & Vilgalys 1999), *Omphalina s. lat.* (Lutzoni 1997), *Lepiota s. lat.* (Johnson & Vilgalys 1998), *Amanita* (Drehmel, Moncalvo & Vilgalys 1999) and *Pleurotus s. lat.* (Thorn et al. 2000).

Now all this LSU data has been incorporated in one large analysis of 154 taxa (Moncalvo et al. 2000), concentrating on agarics. Much of this new paper is devoted to the methodology for handling large datasets, which involves various forms of compromise given the enormous amount of computational time testing for congruence. The results are intriguing. There is little support for some agaric families such as the ‘*Tricholomataceae s. lat.*’, which is spread over much of the trees, while other ‘families’ are either nested within other ‘families’ or have emerged as newly recognized entities. There is a *Mycena* and allies clade, a *Lyophyllum* and allies clade, an amaenitoid clade, a *Pleurotaceae* clade, an *Agaricaeaceae* clade (but including the type of *Coprinus*, i.e. *Coprinaceae s. str.*), and a 90% residual ‘*Coprinaceae*’ clade (excluding the type but including *Psathyrella*).

Using LSU data, there is little or no support for families such as the * Cortinariaceae, Hygrophoraceae, and Strophariaceae*. Many genera are strongly supported as monophyletic (e.g. *Agaricus, Amanita, Hygrophorus s. str., Pleurotus, Tricholoma*) but many others are poly- or paraphyletic (e.g. *Collybia s. lat., Marasmius*, and even *Gymnopilus s. str.*). Many genera are
orphaned, without being placed in recognized families. One of the more spectacular revelations is a ‘clade X’ of omphalinoid fungi (‘Omphalina’ rossella and Rickenella sp.) which nests outside the main agaric clade. This landmark paper sets the stage for a major reclassification of the agarics, in lockstep with research by Hibbett, Bruns, and others in this rapidly changing field.


Scott A. Redhead

Systematic Mycology and Botany, Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, Central Experimental Farm, Ottawa, Ontario K1A 0C6, Canada.
E-mail: redheads@em.agr.ca

PERMANENT SLIDES

In a recent note Agerer et al. (2000) stress the importance of depositing vouchers on which any type of mycological research is based, and such deposit has been made a prerequisite for publication in Mycological Research. Obviously, the value of vouchers depends on their usefulness even after decades of storage, and dried specimens, in particular microscopic ascomycetes, often no longer show critical features, such as ascii, hamathecia or ascospore appendages. Therefore, permanent microscope slides are of paramount importance to preserve delicate structures. However, microslides are often prepared without the necessary care and valuable dissected type material becomes useless, if it is not permanently sealed. We would like to draw attention to our note in The Mycologist (Volkmann-Kohlmeier & Kohlmeier 1996) in which we describe a method by which microscope slides can be permanently sealed.


Jan E. Kohlmeier & Brigitte Volkmann-Kohlmeier

Institute of Marine Sciences, University of North Carolina at Chapel Hill, Morehead City, NC 28557, USA.
E-mail: jbkohlm@email.unc.edu