Mycological Research News

This issue of Mycological Research News features: Nutrient transfer from birch to liverwort via a fungus; The mycosome hypothesis; Neurospora crassa has twice the genes of Schizosaccharomyces pombe; and Mr Bloomfield’s Orchard (Notice).

Original papers in this issue include one which provides the first visual evidence of condensation and decondensation during mitosis of rDNA in filamentous fungi, and the first ultrastructural study of the ascomata and asci of the primitive ascomycete genus Neolecta. Molecular phylogenetic studies on Phanerochaete spp., Epulorhiza isolates from tropical orchids, and Pleurotus subgen. Coremiopleurotus spp., are presented. Telomeric fingerprinting is shown to be valuable for karyotype estimation in Helicothecia mompa, and heterologous diploid nuclei are demonstrated in that species. Recombination in Beauveria bassiana is explored through the production of heterokaryons.

The effects of light of different wavelengths on branch induction in Gigaspora gigantea are described, and the differential expression of selected genes of Glomus intradices on and near roots is documented. Hypodermal suberization is shown to limit infection in barley roots by Chaetomium globosum, and growth of Collybia fusipes in soil is reduced by soil waterlogging and low oxygen levels.

A new Ascobotryozyma has been discovered associated with nematodes in beetle bore holes in the USA.

The following new scientific name is introduced: Ascobotryozyma cognata sp. nov.

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IN THIS ISSUE

The first paper in this issue is a remarkable study of the condensation and decondensation of rDNA during the different stages of mitosis in two disparate filamentous fungi, Cochliobolus heterosporus and Haematonectria haematococca, using fluorescence in situ hybridisation (FISH) microscopy (pp. 1012–1020). This is the first visual evidence of the cyclic changes rDNA undergoes in filamentous fungi using FISH, and the quality of the photomicrographs makes it clear that this method will have wide applications in the study of chromosomal behaviour in fungi, especially as fungal chromosomes are often too small to be observed in situ. For the first time, light, transmission, and cryo-scanning electron microscopy have been used to study in detail the structure of Neolecta species, already established as amongst the most basal ascomycetes by molecular phylogenetic methods (pp. 1021–1031). The hymenial structure and development are shown to be unique, with ascogenous hyphae branching repeatedly to form asci, and the ascospores released through a split in the apices of the thin-walled asci. The ultrastructural component of this paper was carried out in collaboration with the late Stephen T. Moss, and the quality of the photomicrographs presented is a tribute to his exceptional skills as an electron microscopist.

Three papers address phylogenetic relationships and species concepts within different groups of fungi using molecular approaches. Phanerochaete is found not to be monophyletic on the basis of ITS sequence data, with several common species generally placed in the genus falling outside a core group including P. velutina (pp. 1032–1040). Epulorhiza isolates from tropical orchids in Singapore fell into two groups recognized as species, but considerable infraspecific variation and subgrouping was evident within E. repens, and there were correlations with both hosts and sites (pp. 1041–1049). In Pleurotus subgen. Coremiopleurotus, i.e. those with an Antromycopsis anamorph, mating studies, RAPD analyses and cultural characteristics revealed that P. smithii was not distinct from P. cystidiosus (pp. 1050–1054).

In the violet root rot fungus Helicobasidium mompa, telomeric fingerprinting is shown to be a tool not only for estimating chromosome numbers, but further for the identification of particular strains (pp. 1055–1059). In this same fungus, occurrences of allelic genes coding the G protein alpha subunit have been examined in different strains by RFLP analyses and revealed that one had both homozygous and heterozygous diploid nuclei (pp. 1060–1068). Comparisons of RAPD profiles in the entomopathogen Beauveria bassiana using mutant strains also reveal a complex genetic make-up in that species, suggestive of a range of different recombination mechanisms in play (pp. 1069–1074).
Four papers concern root-infecting fungi. Hyphal branching of the primary germ tube of Gigaspora gigantea is induced by light in the blue to uv-A wavelength range, except in the apical 2 mm; the action spectrum showed that the greatest stimulation was at around 390 nm and 430 nm (pp. 1075–1082). In Glomus intraradices, two genes, Ginmyc1 and Ginth1, are expressed in the external mycelium but not in colonized roots, while a third gene Ginmyc2 was expressed in both; Ginmyc2 and fungal β-tubulin mRNA both increased as root colonization proceeded (pp. 1083–1093). Chaetomium globosum, which has biocontrol potential against plant pathogens, can damage barley roots. However, roots grown in aeroponic culture were not colonized beyond the epidermis, and elegant histochemical studies revealed that this was due to hypodermal suberization (pp. 1094–1102). Growth of the root rot fungus Collybia fusipes has been found to be adversely affected by both soil waterlogging and low oxygen availability; low oxygen also affected the growth of Heterobasidion annosum but not of Armillaria mellea (pp. 1103–1109).

A new ascomycetous yeast, Ascobotryozyma cognata, has been isolated from free-living nematodes associated with beetle and weevil galleries in aspen and willow trees in the USA; it is molecularly and morphologically distinct from A. americana which occurs in the same area (pp. 1110–1120).

NUTRIENT TRANSFER FROM BIRCH TO LIVERWORT VIA A FUNGUS

The role of mycorrhizal fungi in nutrient transfer from trees to fungi and vice versa, and of such fungi acting as conduits for photosynthetic products from one tree or plant to another, are well known. Now a further dimension of complexity has been demonstrated experimentally. Cryptothallus mirabilis (‘Ghostwort’) is a widespread non-photosynthetic liverwort living underground, usually under mosses and plant litter on the upper soil layers. The liverwort has been known to be mycorrhizal for almost 85 years, and coiled aggregates of hyphae (‘peletons’) are conspicuous inside the liverwort’s cells (cfr Boullard 1988). However, the identity of the fungi involved has been obscure, and experimental relationships on nutrient transfer had not been carried out.

Now, Bidartondo et al. (2003) have determined by molecular phylogenetic studies that the fungal partner of C. mirabilis is a species of Tulisanella, occupying a separate clade from other species in GenBank and with T. asymmetrica as its sister group. Further, they demonstrated in microcosm experiments that it was necessary for the liverwort to interact with the fungus to grow, and that the Tulisanella transported 14C administered to birch seedlings from the seedlings into the liverwort thallus. The liverwort was in effect living parasitically (‘epiparasitically’) off the birch seedings, exploiting the ability of the fungus to form an ectomycorrhizal association with the liverwort by using it as a transport system.

This is a fascinating example of how complex and interdependent interorganismal relationships can be. It is not known if other mycorrhizal liverworts which do have chloroplasts can benefit by making links through their partners to trees. Further, not all liverworts have Tulisanella species as partners. While Aneura pinguis also has a Tulisanella, liverworts of the Jungermanniales have just been demonstrated as having partners in the Sebacinaeae (Kotte et al. 2003).

The MYCOSOME HYPOTHESIS

It far from usual for mycologists to be confronted with a totally novel concept. Atsatt (2003) claims that under stress Auerobasidium pullulans forms ‘mycosomes’, minute reproductive propagules able to live and reproduce within senescent plastids in plant cells. Mycosomes are described as wall-deficient and 0.1–1 μm diam, and able to develop into larger structures, notably naked protoplasts, yeast-like cells, or membrane-bounded thylakoid-containing sphaerules (within which mycosomes reproduce). The structures, which are documented by numerous brilliant colour, uv-light, and TEM micrographs, are certainly most unusual and not easily explained away. The author claims that mycosomes can be produced by both asco- and basidiomycetous fungi, including species of Candida, Cryptococcus, Rhodotorula, and Trichosporon, and also some unidentified fungi. They occurred in at least 25 host genera, including cyanobacteria, cyccas,
diatoms, ferns, flowering plants, green algae, and mosses.

Peter Atsatt, of the University of California at Irvine, is not new to producing thought-provoking questions (Atsatt 1988), but if confirmed the mycosome hypothesis could have wide implications for the cryptic persistence of pathogenic fungi inside potential hosts. The hypothesis now requires critical testing using in situ DNA species-specific probes to establish whether his remarkable interpretation of the micrographs presented is correct. Were it to be substantiated it would open up whole new areas of enquiry into the transmission and persistence of plant diseases.


**NEUROSPORA CRASSA HAS TWICE THE GENES OF SCHIZOSACCHAROMYCES POMBE**

Neurospora crassa has become the third fungus to have its complete genome sequenced, and the first filamentous fungus to have been (Galagan et al. 2003). The ‘high quality draft’ reveals that the entire genome consists of about 40 megabases and some 10000 protein-coding genes. This compares with a ‘mere’ 4876 in Schizosaccharomyces pombe (Wood et al. 2002), and is only about 4000 short of the number in the fruit-fly Drosophila melanogaster (Adams et al. 2000). Amongst the genes, ones involved in red-light photobiology, secondary metabolite production, and Ca$^{2+}$ signalling have been recognized. Further, the Neurospora has a remarkable array of defence mechanisms, stated to be the widest known in any eukaryotic organisms and including repeat-induced point mutation (RIP). The analysis suggests that RIP has had a fundamental role in genome evolution, reducing the rate of creation of new genes through duplication and resulting in a genome with a lower proportion of closely related genes than is usually the case in other organisms sequenced. The project involved 70 authors from 32 laboratories in Australia, Germany, Israel, the UK, and USA. The completion of this sequence will ensure that Neurospora and the information resulting from it will remain at the forefront of basic genetic research as it has for over 60 yr.


**MR BLOOMFIELD’S ORCHARD²**

**Notice**

Nicholas P. Money, author of Mr Bloomfield’s Orchard: The mysterious world of mushrooms, molds and mycologists (Oxford University Press, New York, 2002), regrets that a passage in the book involving pathogenic fungi caused unintended offence to Jack Fisher. The author’s reflections on laboratory life introduced some inaccuracies about Jack’s work, and should not be read as an unfavourable commentary on Dr Fisher’s research.

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