This issue of Mycological Research News features: Resolving congruence in molecular phylogenies; Common mycorrhizal networks in forests; Soil FungiLog; Saccharomyces cerevisiae provides clues to longevity; Genomic diversity under hypersaline stress and Small scale variation in natural Neurospora populations. An obituary for Stephen T. Moss (1943–2001), President of the Society in 2001, is also included.

This issue includes 11 original papers. These test the efficacy of the relative complexity measure (RCM) in the construction of phylogenetic trees on medically important fungi; reconcile morphological with molecular data in Claviceps; identify the oilseed poppy Peronospora; describe a new sequestrate agaric genus from Australia; recognize polymorphism in the laccase genes of Heterobasidion annosum; demonstrate dsRNA mycoviruses in H. annosum; survey mycotoxins in the Gibberella fujikuroi complex on maize; study the persistence of different Pochonia chlamydosporia strains in roots; describe the development of Cladosporium tenuissimum on Uromyces appendiculatus; examine the fungi associated with southern pine bark beetle Dendroctonus frontalis; and document the behaviour of Piptoporus quercinus in culture.

The following new scientific name is introduced in this part: Barcheria willisiana gen. sp. nov.

DOI: 10.1017/S095375620421958X

IN THIS ISSUE

The first paper in this issue tests the efficacy of a new approach to the construction of phylogenetic trees, the relative complexity measure (RCM), on a variety of medically important fungi. The method, which avoids the need to align sequences prior to analysis, proved to be reliable and robust and can be expected to become increasingly used in mycology (pp. 117–125). Reconciling patterns of morphological variation with molecular phylogenies is not always straightforward. In Claviceps, three different types of conidiogenesis occur, species with appended conidia forming a well-supported clade which may merit recognition as a separate genus (pp. 126–135). Molecular phylogenetic studies have been applied to identification of the oilseed poppy downy mildew pathogen in Tasmania as morphological comparisons were inconclusive; PCR primers for its specific detection have been developed, and ITS sequence data show the species to be better referred to Peronospora crispata than to P. arborescens as which it had previously been identified (pp. 198–205). A new sequestrate genus and species of agarics is described from Australia; nLSU rDNA sequence data place the fungus within a clade including some Agaricus species and also the sequestrate Gyrophragmium duraleii (pp. 206–213).

Two papers concern the conifer pathogen Heterobasidion annosum. Polymorphism in the laccase genes is demonstrated; the more pathogenic race has two types of laccases, and the less pathogenic race one. One of the types in the more pathogenic race was distinct from that in both outgroup species of the genus examined, and also from three other basidiomycete species (pp. 136–148). The transmission of double-stranded RNA mycoviruses in the pathogen has been investigated, and the viruses found to be transferred through basidiospores, which then have reduced germination frequency (pp. 149–153).

Analysis of the production of mycotoxins in 377 isolates of the Gibberella fujikuroi complex from maize in Argentina revealed that most were mating population A (anamorph Fusarium verticillioides) and produced fumonisins (enhanced in ‘female’ fertile strains), but that these compounds were also formed in isolates of mating population D (anamorph F. proliferatum). Mating populations D and also E (anamorph F. subglutinans) also formed beauvericin and fusaproliferin, and the effects of co-occurrences of these and fumonisins are of concern (pp. 154–160).

Pochonia chlamydosporia is well-known for its potential as a biocontrol agent of nematodes, but isolates need to be able to persist as saprophytes to be most efficacious. Here, the persistence of strains in roots with and without tomato or potato plants and with different
strains of the fungus and of nematode infections has been compared, and provides further evidence of intra- and interspecific specialization against different nematodes in the fungus (pp. 161–169). The development of _Cladosporium tenuissimum_ on the bean rust _Uromyces appendiculatus_ has been studied by a wide range of microscopic and cultural techniques; penetration is evidently enzymatic and mechanical, the fungus can empty the contents of the urediospores, produce cladosporol, and appears to synthesize glucanases (pp. 170–182). The interaction of three fungi with the southern pine bark beetle _Dendroctonus frontalis_ has been investigated, and available water found to influence the extent of infections; the results show that water potential may affect the outcome of competitive interactions between the associated fungi, including the beneficial _Ceratocystiopsis ranaculosus_ and the antagonistic _Ophiostoma minus_ (pp. 183–188).

Studies on the rare oak polypore _Piptoporus quercinus_, a protected species in the UK, have been conducted in artificial culture and basic information on its cultural requirements obtained. In addition, the species was also shown to have poor combative ability, but nevertheless inhibited the extension rate of some other heartrot fungi (pp. 189–197).

DOI: 10.1017/S0953756204229586

RESOLVING INCONGRUENCE IN MOLECULAR PHYLOGENIES

Molecular phylogenies derived from different single-gene data sets are not always the same. For this reason, most researchers now endeavour to compare phylogenies from more than one gene; when the results are supportive, the confidence in the resultant phylogenies is enhanced, but what when they are not? Yeasts are genomically amongst the best studied organisms on Earth, and so comparisons between many more genes in them are possible in comparison to other organisms. In order to test how many genes should be studied to obtain robust trees, Rokas et al. (2003) examined the genome sequence data of seven _Saccharomyces_ species and of _Candida albicans_ (as an outgroup taxon). The authors found 106 orthologous genes that could be compared in this group of species; these were distributed throughout the _S. cerevisiae_ genome on all 16 chromosomes and comprised 127,026 nucleotides, roughly 1% of the genomic sequence and 2% of the total predicted genes. Some of the trees with individual genes were markedly different (cfr their Fig. 1) and provide an example that I can see being widely used in teaching molecular phylogenetics. They conclude that ‘reliance on single or a small number of genes has a significant probability of supporting incorrect relationships for the eight yeast taxa’ (p. 801). In this example, they found that concatenated data sites of 20 genes were sufficient to provide very strong (>95%) bootstrap support for the species tree, many more than regularly used in molecular phylogenetic studies.

While the resources to undertake comparative studies of so many genes may be impractical to secure in routine molecular phylogenetic reconstructions, there is no doubt that comparisons of greater parts of or whole-genomes will become more important in understanding relationships as the technology to facilitate this progresses, a point recently and forcefully made by Austin Burt at the British Society for Medical Mycology and British Mycological Society meeting last March (Whalley 2003). In the meantime, it is clearly important for consumers of the results and researchers in the field to be keenly aware that trees generated from one or a few genes may not be fully representative. Consequently, as much corroborative data as possible from other features, including cell wall polysaccharides, morphology, and secondary metabolites, should be sought to see to what extent they support the trees produced.

This is a paper that all involved in molecular systematics should read. As commented by Gee (2003), ‘the work of Rokas et al. has raised the game of phylogenetic reconstruction to a new level’.


DOI: 10.1017/S0953756204239582

COMMON MYCORRHIZAL NETWORKS IN FORESTS

While it has been recognized that ectomycorrhizas can connect different kinds of plants for around 25 years, and carbon transfer between plant species has been documented using radio-labelling methods (Finlay & Read 1986), the full extent of the phenomenon in nature has only started to become apparent in the last few years (e.g. Visser 1995, Dighton 2003). Now, Kennedy, Izzo & Bruns (2003) have studied the ectomycorrhizal networks on understory and canopy trees in a mixed evergreen coastal forest in northern
Sirtuins are NAD-dependent protein deacetylases, and enzymes of the same family are known in nematodes and humans. Now, Howitz et al. (2003) have screened a number of small molecule libraries in order to identify compounds that could modulate the action of sirtuin. Most efficacious were polyphenols, reservatrol found in red wine, and the plant products butein and fisetin. In the yeast, the reservatrol acts by mimicking calorie restriction by stimulating Sir2, increasing DNA stability, and thereby extending the life-span of yeast cells by 70%; with butein and fisetin, however, the increase in life-span was 31% and 55% respectively. The optimal reservatrol concentration was 2–5 μM, higher levels not providing any additional life-span benefit. However, just how sirtuins function in the ageing process in mammals remains obscure, so potential drug development remains some way off (Finkel 2003). Nevertheless, this new study provides additional evidence of the beneficial health effects of polyphenols, and opens a fresh line of investigation into the effects of polyphenols on age-related human diseases.


**DOIs: 10.1017/S0953756204249589**

**SOIL FungiLog: UNDERSTANDING FUNGAL FUNCTIONAL DIVERSITY**

The problems of understanding fungal diversity in soil, in relation to both the species living there and ecological functions, are well-known. Now Sobek & Zak (2003) have devised a procedure to enable ecologists to determine the roles fungi play in providing structure and stability ecosystem services in soil. The idea is developed from the FungiLog method devised previously to evaluate fungal functional diversity in plant litter (Dobranic & Zak 1999). In Soil FungiLog, spores are first removed to ensure that only actively growing fungi are considered. Microtiter plates with wells containing different carbon-containing substrates are inoculated with a mixture of the soil organic matter, water agar, antibiotics, and dimethylthiazole-diphenyl-tetrazolium bromide, and colour changes noted after incubation at 25 °C for 120 h with an automated plate reader; different particle densities are used. Substrate activity and richness are estimated by measuring changes in optical activity in the wells, and the results are subjected to stepwise discriminant-function analysis and other approaches. The procedure was tested for soils from two areas in the USA, with different degrees of disturbance and supporting distinctive plant communities; the method successfully discriminated between sites with different disturbance histories. Even though the system does not provide direct information on relative species-richness, comparative ecological function information is generated. The method clearly has the potential to ensure a fuller and more meaningful integration of fungal data into ecological comparisons between soils.


**DOIs: 10.1017/S0953756204259585**

**SACCHAROMYCES CEREVISIAE SIRTUINS PROVIDE CLUES TO LONGEevity**

In *Saccharomyces cerevisiae*, lifespan is increased by an enhanced activity of the sirtuin Sir2, something promoted by calorie restriction (Lin, DeFossez & Guarante 2000). Sirtuins are NAD+-dependent protein deacetylases, and enzymes of the same family are known in nematodes and humans. Now, Howitz et al. (2003) have screened a number of small molecule libraries in order to identify compounds that could modulate the action of sirtuin. Most efficacious were polyphenols, reservatrol found in red wine, and the plant products butein and fisetin. In the yeast, the reservatrol acts by mimicking calorie restriction by stimulating Sir2, increasing DNA on those of the canopy. Further studies involving radioactively labelled compounds are now desirable to confirm that nutrient flow occurs between the different trees.
GENOMIC DIVERSITY UNDER HYPSALINE STRESS

Strains of *Aspergillus versicolor* from the shoreline to a depth of 280 m in the hypersaline Dead Sea, which can have to 340 g l$^{-1}$ dissolved salts (about ten times that of seawater), have been compared by Kis-Papo et al. (2003). Using > 600 bp AFLP markers, genomic diversity in both the coding and non-coding parts regions was found to be positively associated with hypersaline stress, culminating in the Dead Sea surface, but progressively dropping into only a few adapted genotypes through the 50–280 m deep water column. Further, a comparison with isolates from non-saline environments placed the saline ones in a different clade. Noting similarities between these results and the positive correlation between sexual reproduction and stress in fungi already reported by Grishkan et al. (2002; see Mycological Research News, *Mycological Research* 107(1): 2, January 2003), Kis-Papo et al. conclude that the results from *A. versicolor* corroborate the general biological niche-width environmental theory of genetic diversity, i.e. that genomic diversity and sex levels are positively correlated with stress gradients, except in the most extreme situations where only a few adapted genotypes can survive.


SMALL-SCALE VARIATION IN NATURAL NEUROSPORA POPULATIONS

Within two weeks of fires in the Everglades, FL, USA, in May 1999, extensive swards of conidial *Neurospora* colonies developed on a wide range of burned plants, with thousands of individual tufted conidial colonies noted in a single 1000 m$^2$ area. Powell et al. (2003) made a detailed study of these populations with remarkable results. Species and mating types were assigned based on crossing behaviour, and genetic variation assessed by direct sequencing of PCR products at two loci (het-c and frq). They found four species (*N. crassa*, *N. intermedia*, *N. sitophila* and *N. tetrasperma*) and more than ten genetically distinct individuals on three burned stems of sugarcane, and up to three different species and six different haplotypes on a single stem. However, individuals were not distributed randomly and adjacent nodes on the same stem were most likely to be colonized by the same haplotype, suggesting that there was substantial below-surface vegetative spread of mycelium after initial colonization. This study demonstrates the power of molecular methods to contribute to our knowledge of *in situ* colonization by fungi, especially in being able to determine the holomorphs with only superficially very similar anamorphs present, and further the need to be aware that even in sampling colonies very close to one another or even on the same stem, what seem to be very similar colonies may not necessarily represent the same species! It will be interesting to see whether the fresh studies of *Neurospora* isolates in Europe now being undertaken following the fires in the summer of 2003 (Jacobsen 2003) show similar complexities.
