MYCOLOGY ABSTRACTS

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Listed alphabetically by first author

* Indicates Poster

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Fungal collections in South Australia—where are they now?

Considerable confusion has been evident for the last 15 years relating to the status and holdings of the fungal herbaria at the Waite Institute, University of Adelaide (ADW) and the State Herbarium of South Australia (AD), especially regarding the important J.B. Cleland material. The collection at ADW has now formally been closed, with non-pathogenic material being transferred to AD and pathogenic material to the New South Wales Department of Agriculture at Orange (DAR). The basis of this and the earlier transfer of most macrofungi to AD is outlined and placed within the context of the history of mycological taxonomy in South Australia. The relationship is discussed between Cleland's main collection at AD and the other significant Australian holding of Cleland specimens at DAR. Difficulties of interpretation of Cleland collections are discussed and the related archives of artwork and correspondence outlined. Comments are made about significant material of other collectors at AD, both within Cleland's herbarium and from other sources, and about the current size and curation of the AD collection.

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Image analysis differentiates spores of allergenic fungal genera and species.

Allergy to some airborne fungi is a major risk for asthma, particularly in drier rural areas. Establishing the relationship between exposure and disease requires simple and accurate methods to enumerate species. We have been investigating the use of computerised image analysis of spores to develop methods which are reliable, rapid and do not require a high level of mycological skill. Spores of 8 species of Alternaria, 4 species of Cladosporium, 3 species of Fusarium and a representative of Aspergillus, Penicillium, Botrytis, Epicoccum, Exserohilum, Ustilago, Coprinus and Psilocybe were examined.

Discrimination was based on seven basic feature measurements obtained from images of individual spores using a high resolution video camera (1000×1000 pixels at 256 grey levels), image processing software (WIT = D2, Logical Vision) and programs developed in-house. Statistical analysis was conducted using Canonical Variance Analysis (CVA) in Genstat.

Based on the seven basic feature measurements it was possible to differentiate the macroconidia and microconidia of the three Fusarium species from conidia of each of the Cladosporium and Alternaria species examined. Within each of these genera it was not possible to differentiate all species from each other, and some species of Alternaria and Cladosporium displayed a degree of overlap. Spores of Epicoccum nigrum were distinct from all others imaged. In contrast, it was not possible to differentiate between spores belonging to Aspergillus and Penicillium, Coprinus and Psilocybe, and Botrytis and Ustilago. Improved differentiation between allergenic fungal genera and species is anticipated following analysis of data gathered with 24 extended feature measurements and 32 Fourier descriptors.

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Mycorrhizal and saprotrophic fungi of remnant woodlands in the Wheatbelt region of Western Australia.

The Wheatbelt region of Western Australia has a dry, warm mediterranean climate with 300-650 mm of rainfall and 7-8 dry months annually. The region lies inland from the wetter tall forest region of south-west Australia. In the Wheatbelt, over 90% of the land has been cleared for agriculture and only scattered remnant patches of indigenous vegetation remain. The region has a range of geographically fragmented vegetation types including

eucalypt woodland dominated by species such as *Eucalyptus capillosa*, *E. loxophleba* and *E. salmonophloia*. Few fungi of this region had been documented before our recent studies on the fungi of remnant patches of indigenous woodland. The studies have yielded a large spectrum of mycorrhizal and saprotrophic species, indicating that fungal diversity in the Wheatbelt vegetation may equal that of wetter eucalypt forests in Australia. Like many other parts of Australia, soils of Wheatbelt woodlands are nutrient-poor. Diversity among mycorrhizal and saproptrophic fungi which are involved in crucial nutrient cycling processes is likely to have contributed to sustainability of the woodlands in the past. Although many Wheatbelt fungal species also occur outside the region, some putatively ectomycorrhizal fungi such as two recently discovered new species of *Torrendia* are currently only known from a few remnant patches of Wheatbelt woodland. The discovery of such fungi adds to the conservation significance of the remnant woodland.

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Urban bushland fungi at Kings Park and Botanic Garden, Perth, Western Australia.

Located close to the centre of metropolitan Perth, Kings Park and Botanic Garden has nearly 300 hectares of eucalypt and banksia bushland in addition to botanic gardens and recreation/tourist areas. Major management concerns for the Park bushland include weed invasion, fire, and restoration of bushland plant communities. The bushland is an important refuge for many fungi and about 50 species had been recorded there up until the end of 1996 including numerous new species, e.g. Phylloporus clelandii Watling published as new to science in 1991. Our recent research on the biodiversity and ecology of fungi in Kings Park has identified many species of fungi not previously recorded in the Park, including some that are new records for Western Australia, e.g. Coprinus picaceus—the 'magpie fungus'. Fungi can form a crucial part of the natural processes of any bushland. Fungi contribute to the health of the Park bushland ecosystem by capturing, storing, releasing and recycling essential nutrients. Some of the major roles of fungi include: (a) mutually beneficial relationships (mycorrhiza) with trees and other plants; (b) decomposition of organic matter and capturing/recycling mineral nutrients; (c) attacking living plants or producing wood rots. The diversity of fungi in Kings Park is significant because unique physiological attributes of each fungal species probably help perpetuate the woodland, as well as aid its recovery in the face of environmental pertubations. The biodiversity of fungi at Kings Park, their specific roles, and the potential uses of fungi in restoration of bushland plant communities have yet to be fully assessed.

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Revision of New Zealand polypore fungi.

In the most recent (1965) monograph of polypore fungi of New Zealand and Australia, Cunningham described 242 species. Since then, taxonomic concepts in this group have altered, especially at the generic level, with incorporation of new characters such as type of rot. Only 39 (16%) of the species' names used by Cunningham are accepted today.

Revision of New Zealand polypore fungi is in progress for publication in a new series, *Fungi of New Zealand*. The work is based mainly on Cunningham's collections along with our more recent collections deposited in the New Zealand Fungal Herbarium (PDD). About 170 species are currently recognised from New Zealand. Cunningham arranged these in 26 genera, although today they are considered to represent 60 genera. About half of the genera contain only one New Zealand species, and only a single genus, *Australoporus*, is endemic to the region.

Several PDD collections of polypore fungi bear misapplied Northern Hemisphere names. Among such collections we recently discriminated four new species in the genera *Postia* (PDD collections as *Poria albolutescens*), *Diplomitoporus* (as *Tyromyces mollis*), *Polyporus* (as *Polyporus udus*) and *Dichomitus* (as *Poria leucoplaca*). The new species of *Polyporus* and *Dichomitus* are characterised by occasionally unit to multiseptate basidiospores, a feature newly recorded within the order Aphyllophorales, and apparently also unknown in the Agaricales. Septation appears to be confined to older spores, especially those dispersed from the tubes.

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Relative competitive ability of homokaryons and heterokaryons.

The relative interspecific competitive abilities of mycelial homokaryons and heterokaryons of four species of wood decay fungi (Peniophora sp. 1., Peniophora sp. 2, Pereniporia medula-panis, Aleurodiscus lividocoeruleus) were assessed. It was found that there was no simple relationship between nuclear status and competitive ability. The homokaryon of Peniophora sp. 2 was competitively superior to its heterokaryon, whereas the homokaryon of Peniophora sp. 1 was inferior to its heterokaryon. A hierarchy of competitive abilities of each strain revealed that P. medula-panis' homokaryon Peniophora sp. 1 heterokaryon Peniophora sp. 1 heterokaryon Peniophora sp. 2 homokaryon Peniophora sp. 2 heterokaryon Peniophora sp. 1 homokaryon. This experiment showed that homokaryons as well as heterokaryons have the potential to influence community structure through competitive effects.

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Congruence between molecular and morphological characters in three Australian species of Russula.

The genus Russula is comprised of putatively ectomycorrhizal species some of which are commonly found in Australian forests. Intraspecific variation in morphological characters of basidiomes of Russula clelandii, R. 'multicolor' and R. persanguinea were compared. Russula clelandii has a relatively high level of variation in macrocharacters (particularly cap, gill and stipe colour) and microcharacters (particularly encrustations, shape and gelatinisation of pileipellis elements). The variation is somewhat broader than indicated in the original species' description. Among the species examined, R. persanguinea showed least morphological variation across a broad spectrum of geographical and ecological sites. Molecular characters may help to discriminate between genetic and environmental factors in producing the observed high level of intraspecific morphological variation. While DNA sequencing is often used as a source of molecular characters, the expense of this procedure reduces the number of specimens that can be processed. PCR RFLPs, while providing less resolution than direct sequencing can be applied to a large number of specimens. We amplified the ITS region of nuclear rDNA and digested the product with several restriction enzymes. Russula persanguinea which is widely distributed in Australia, and the apparently Western Australian restricted R. 'multicolor' showed no intraspecific variation. Russula clelandii collections showed intraspecific variation which did not reflect either geographic or forest association or morphological characters. The restriction sites will be mapped to enable systematic analysis. Other regions (e.g. mitochondrial LSU rDNA) will also be analysed. Further molecular analysis may refine the acceptable morphological concept of this species.

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Biodiversity of Microfungi associated with palms in the tropics.

The mycobiota of several palm genera have been examined within tropical rainforests in Australia, Brunei, Ecuador and Hong Kong. There were three aims to this survey: 1) to identify the saprophytic, and to a lesser extent, parasitic Ascomycetes living on these hosts; 2) to record the endophytic, parasitic and saprophytic fungi on a small number of individuals of two species of *Licuala*, and; 3) to establish numbers of tropical fungi associated with palms, and to compare these with global estimates of tropical fungi.

The ascomycetes on decaying palm tissues were a diverse assemblage distributed among nine orders, 28 families, 79 genera and 202 species. Eight of the genera, and 95 of the species, are new to science. The Hyponectriaceae dominate the saprophytic mycobiota, accounting for 46.2% of the collections identified. The predominance of this family is largely attributed to the genus *Oxydothis*, which comprised 33.1% of all saprophyte collections. Host proximity was found to have a greater influence on the distribution of the palm fungi than host relatedness. Comparison of the mycobiotas of Australia, Brunei and Hong Kong, revealed distribution patterns that were more consistent with climatic factors, than those of host distribution or past biogeography. The estimated numbers of fungi in the tropics will need to be reconsidered based on these results.

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Biogeographic relationships of Southern Hemisphere Rhytismataceae.

Earlier studies showed that the Rhytismataceae of New Zealand comprised two biogeographically and biologically distinct groups: 1) species known also from tropical Asia and/or tropical America, all found on a wide range of host plants; and 2) species known only from New Zealand, or from New Zealand and Tasmania, most restricted to a single host genus or family.

Biogeographic relationships of the Australasian representatives of this family will be updated following recent collecting in cool-temperate and tropical rainforest in mainland Australia, and in southern South America. Although each region has several putatively endemic species, the discussion will focus on those shared between more than one region.

Despite the level of sampling being lower in Australia and South America than in New Zealand, some conclusions can be drawn. The broadly distributed tropical species found in the north of New Zealand are also common in Australian subtropical rainforests. Many more species are shared between Australia and New Zealand than are shared between either Australia and southern South America, or New Zealand and southern South America. All of the species shared between two or more of the temperate Southern Hemisphere regions are host-specialised. Several of the most common species in southern South America are also found in the temperate Northern Hemisphere.

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Fungal invaders.

The ectomycorrhizal Amanita muscaria and the wood-rotting Favolaschia calocera are both known to have been introduced to New Zealand in historically recent times. Both species are invading native forests at some sites, unusual for fungi introduced to New Zealand.

We have initiated a programme to determine the distribution of these two species in New Zealand's native forests, and to ask the questions: what are the biological consequences of these invasions? and, what characteristics allow some exotic fungal species to invade indigenous ecosystems? Although these species are not plant pathogens, they have the potential to displace native species from the communities in which they occur, to disrupt natural fungal successions in these communities, and perhaps to disrupt the food chains of indigenous invertebrates.

McGee, P.A. School of Biological Sciences, University of Sydney, NSW 2006.

Problems with taxonomy of Glomus (Glomales: Zygomycota).

The arbuscular mycorrhizal fungus Glomus mosseae (Nicol. & Gerd.) Gerd. & Trappe is found in agricultural soils around the world. Considerable variation is found within the functional attributes within the fungus, even when the fungal isolates are extracted from one soil type from one locality. Other species examined have similar functional variation. The current taxonomy of this group of fungi uses a phylogenetic species concept. However, the species derived using the concept do not allow functionally predictable information to be inferred. One consequence of the lack of predictability is that a different system of taxonomy will be developed, leading to further confusion.

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The distribution of species and communities of Australian fungi.

Known species of Australian fungi are mostly widespread geographically and in regard to host and habitat. Species with restricted distributions are almost always represented by single or few collections, and in most

cases further collections are predicted to considerably enlarge their distributions. For Victoria, very few of the macrofungi known from more than five collections are endemic to restricted geographic areas at the scale shown by vascular plants. The macrofungal assemblages of south-eastern and south-western Australia also overlap considerably. The limited collecting and taxonomic study of Australian fungi may be the reason that common and widespread species predominate among those that are known. There are predicted to be at least 20 times as many species of Australian fungi as already described. It is vital to establish how many localised species are to be expected among the undescribed species. Thorough taxonomic revision (and distribution surveys) of selected higher taxa is a basis for predictions of how many species have restricted distributions. The mycoflora of single sites is potentially very diverse. This diversity, coupled with the need for repeated sampling, makes studying macrofungal communities difficult. Assessments are urgently required of the congruence of fungal and vascular plant communities; to thus establish the effectiveness of existing reserves in conserving fungi—especially the species yet to be described. For a selection of 50 distinctive species of macrofungi, the FUNGIMAP scheme has provided a rapid increase in distribution data. Extension of FUNGIMAP and the establishment of an Australian Network of Sites for Monitoring Fungal Biodiversity is proposed as the most efficient method of rapidly improving knowledge of the distribution of species and communities of fungi in Australia.

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Dynamic functional morphology in mushrooms—how mushrooms make mushrooms.

Morphogenesis is not simply a matter of playing out a predefined genetic programme. Expression of developmentally important genes is epigenetic and place- and time-dependent. Gene expression relies on previously-formed tissue structures and is consequently dependent on the overall context into which the developmentally regulated gene product(s) is (are) inserted. The 'overall context' includes chemical, electrical and structural/mechanical tensions. Though research on fungal developmental biology is regrettably sparse, homologues and analogues of all of the mechanisms known in animals and plants can be found in fungi. Key words at each stage of development in fungi are: competence, induction and change. Developmental change occurs when the competent tissue is induced. Each developmental step takes the tissue to a higher order of differentiation. Most differentiated hyphal cells require reinforcement of their differentiation 'instructions'. This reinforcement is part of the context within which they normally develop. Another common feature of fungal morphogenesis is its compartmentalisation into a collection of 'sub-routines' which are distinct genetically and physiologically. These sub-routines can be recognised at the levels of organs, tissues, cells and cellular components. Sub-routines may run in parallel or in sequence. When played out in their correct order the morphology which is normal to the organism under consideration results. If some of the sub-routines are disabled (genetically or through physiological stress), the rest may still proceed. Partial execution of developmental sub-routines produces an abnormal morphology but may allow a crop of spores to be formed. Homologous sub-routines can be recognised in different fungi, and gross differences in morphology can then be related to the different ways in which homologous sub- routines are executed. Flexibility in expression of developmental sub-routines illustrates that tolerance of imprecision is an important attribute of fungal morphogenesis.

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Preliminary studies on the Australian Phyllachoraceae (Fungi, Ascomycota).

The Phyllachoraceae are a conspicuous component of the mycoflora often producing black, shiny 'tar spots' on both economically important cultivated and native plants. This project endeavours to monograph the biodiversity of the Phyllachoraceae (excluding Glomerella and Colletotrichum) in Australia. Detailed recent publications of Phyllachora in Australia include studies on graminicolous hosts by Parbery (1964, 1967) and on the host family, Leguminosae by Cannon (1991). Several smaller papers by Swart (1965, 1981, 1982, 1988, 1989) and Hyde & Pearce (1993, 1996), Pearce & Hyde (1993a, b, c, 1994a, b, 1995a, b) and Pearce, Hyde & Shivas (1995) dealt with specific species of Phyllachora. No attempt has previously been made to document the biodiversity of this family in Australia. In January, 1996 when this project commenced, 90 species from 8 genera were recognised in Australia. To date, we have identified c. 103 species in 13 genera, including 1 new

genus, 6 new species and several new species' records for Australia. A series of inoculation experiments have been commenced to ascertain the host specificity of *Phyllachora callistemonis*, *P. hakeicola* and *P. queenslandica*. Since host identification has in the past been an important character in classification of *Phyllachora* to species' level, the reliability of this character is being examined. This talk aims to present some of the genera found in Australia, and the taxonomic characters used in their identification.

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DMI fungicide resistance in Uncinula necator in Australian vineyards: detection and development of new tools.

Powdery mildew of grapevine, caused by the obligately biotrophic fungus, *Uncimula necator*, is the most economically important disease of grapevines worldwide. Infection of shoots and berries reduces grape quality and yield. *Uncimula necator* reproduces both asexually and sexually, however, the relative importance of sexual reproduction in contributing to variation in Australia is unknown. A functional sexual stage creates significant opportunities for variation within *U. necator*, *e.g.* the development of new pathotypes and reduced sensitivity to demethylation inhibiting (DMI) fungicides. DMIs inhibit one metabolic site within the organism, and can be applied as protective sprays when sulphur applications are inadvisable. Lack of disease control due to resistance to DMIs has been reported in Europe and USA and there is circumstantial evidence that resistance is occurring in Australian vineyards. We will develop a bioassay for fungicide resistance to determine sensitivities of *U. necator* isolates from different viticultural regions in Australia to DMIs such as Bayfidan® (triadimenol), Topas® (propiconazole) and Rubigan® (fenarimol). However, present bioassay techniques are slow, and molecular markers have potential for rapid detection of resistance. Molecular markers (RFLP and PCR) have been developed for characterising the genetic diversity of *U. necator*. These markers will be screened for ability to detect DMI resistance and additional markers will be developed as required. The information gained from these studies will contribute to the development of improved disease management strategies.

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Molecular and phenotypic characterisation of Phomopsis viticola in Australian vineyards.

Phomopsis cane and leaf spot disease of grapevine, caused by Phomopsis viticola (Sacc.) Sacc., can lead to significant yield losses. The objective of this research is to develop phenotypic and molecular markers to study the genetic variation in natural populations of P. viticola and the relatedness of the two main taxa of this fungus that occur in Australia. A greater understanding of the epidemiology and population dynamics of this pathogen will contribute to the development of improved disease management.

DNA libraries of taxon 1 and taxon 2 isolates were constructed in the plasmid vector pUC19. The libraries contained clones specific for each taxon, as well as clones that identify variation between isolates. A putative taxon 2 specific probe (4 kb) and four putative taxon 1 specific probes (3.5, 3.6, 3.8 and 3.9 kb) were identified. A potential use of taxon specific sequences is for the detection of *P. viticola* in symptomless grapevine tissue. In addition, microsatellite probes and cloned sequences identified genetic variation within and between viticultural regions. All probes identified differences between taxon 1 and taxon 2.

Mycelial incompatibility studies showed that 28 taxon 1 isolates fell into eight putative vegetative compatibility groups (VCGs). A dark interaction zone was present when incompatible isolates were paired on potato dextrose agar. The taxon 2 isolates (16) were compatible with each other, and those tested (5) were incompatible with taxon 1 isolates.

Mating studies of taxon 1 are in progress. Paired isolates produced perithecia *in vitro* on autoclaved, unsprayed Chardonnay canes. Interpretation of the mating type data is complicated because several isolates appear to be self compatible.

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Relationships among the species of Mycosphaerella from foliage of species of eucalypts.

Almost 30 species of *Mycosphaerella* (Dothideales: Mycosphaerellaceae) have been described from eucalypt leaves. Many of these species were first described from countries to which eucalypts (species of *Angophora*, *Corymbia* and *Eucalyptus*) had been introduced for forestry plantations or amenity plantings. Careful collecting has shown that almost all these apparently exotic species also occur on eucalypts in Australia. There is little evidence species of *Mycosphaerella* from Myrtaceae other than members of the *Eucalyptus* alliance (*sensu* Briggs & Johnson) infect eucalypts. The characters used to distinguish species (*e.g.* ascospore size and shape, ascospore germination patterns, anamorphs) are reviewed, and possible relationships between the described species are discussed.

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Ammonia fungi in the jarrah forest of Western Australia and parallelism with other geographic regions of the world.

Ammonia fungi are a chemoecological group of fungi with greatly enhanced mycelial and fruiting activity in the presence of ammonium nitrogen compounds. Under natural conditions ammonia fungi occur in specialised ecological circumstances such as near animal corpses or other NH₄ nitrogen depositions. A succession of various ammonia fungi may also be induced by artificial application of ammonium nitrogen such as in the form of urea. The fungal succession relates to specific changes in soil factors such as pH, moisture and levels of ammonium ions. Certain species of Deuteromycetes (e.g. Ambylosporium botrytis) are stimulated shortly after application of ammonium and they are usually followed in turn by various Ascomycetes (e.g. Ascobolus denudatus) and Basidiomycetes (e.g. Lyophyllum tylicolor). Ammonia fungi include decomposer and mycorrhizal species and are therefore an important components of microbial nutrient cycling in forest ecosystems. They have been recognised in many parts of the world such as Japan, Europe and New Zealand. In Australia, the presence of ammonia fungi has been speculated due to the occurrence of the 'ghoul fungus'-Hebeloma aminophilum which is always found close to carcasses of kangaroos, snakes and other sizeable animals. To determine whether a successional range of ammonia fungi occurs in Australia, experimental applications of urea and subsequent monitoring of fungal activity and soil conditions were recently undertaken in the Jarrah (Eucalyptus marginata) forest of Western Australia. The applications induced successions of ammonia fungi related to specific changes in soil conditions which parallel observations recorded in other parts of the world.

RETIREMENT OF PROFESSOR DAVID HAWKSWORTH

Professor David Hawksworth has taken early retirement from the International Mycological Institute with effect from 1 January. He will act as a Special Adviser in Mycology to CABI Bioscience, and will also be able both to complete existing responsibilities and to pursue his research interests in ascomycete (including lichens) systematics, bioindication, bio-nomenclature and nature conservation.

THE ORIGIN OF THE TERM 'BIODIVERSITY'

I have long had the impression that biodiversity was a word invented at a political rather than biological level. Recently I encountered the origin of the term, described in E.O. Wilson's foreword to Biodiversity published on the proceedings of the national Forum on BioDiversity, Washington, D.C., 21–24 September 1986, published 1988.

He notes that the 'National Forum on BioDiversity and thence this volume were made possible by the cooperative efforts of many people. The forum was conceived by Walter G. Rosen, Senior Program Officer in the Board on basic Biology—a unit of the Commission on Life Sciences, National Research Council/National