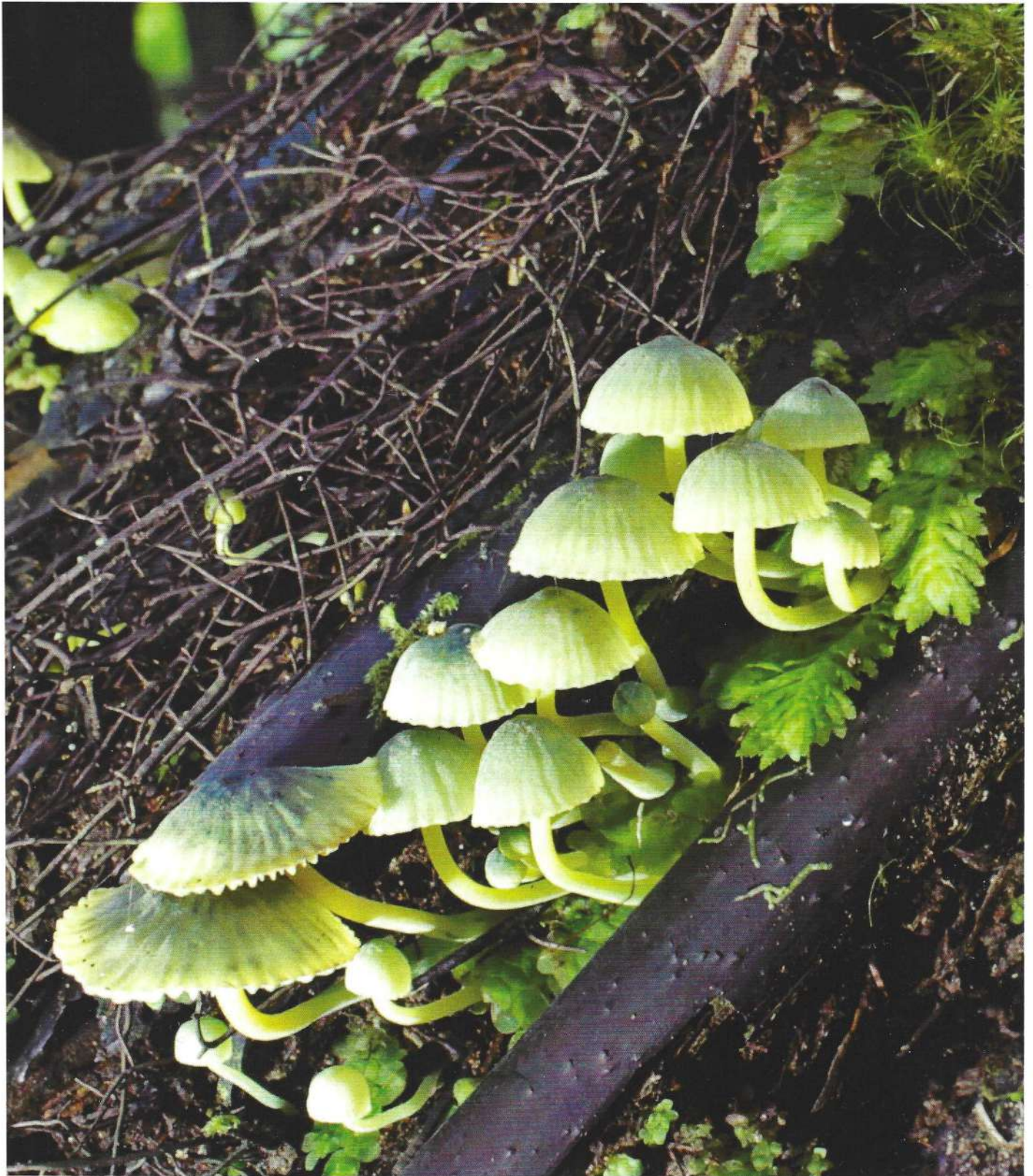


**SCIENTIFIC MEETING OF THE
AUSTRALASIAN MYCOLOGICAL
SOCIETY WITH THE FUNGAL NETWORK
OF NEW ZEALAND
QUEENSTOWN, NEW ZEALAND 3-5 MAY 2016**



PROGRAM AND ABSTRACT BOOK



Invited Plenary Talk I – Abstract

Can we discover better antifungals?

Monk BC

Oral Sciences and the Sir John Walsh Research Institute, School of Dentistry, University of Otago, Dunedin, New Zealand; brian.monk@otago.ac.nz

Abstract. Fungal infections have been estimated to kill 1.4 million people per annum and can have dramatic negative effects on food production. Phytopathogens affect all major crops and fungal infections of humans affect all age groups - the very young, females of reproductive age, the elderly – and especially the immune compromised and those with comorbidities. The use of clinical and field isolates of pathogenic fungi, baker's yeast and a variety of molecular tools have enabled investigation of the biology of many fungal pathogens. Yet this new knowledge has had limited impact in the clinic e.g. the drugs used to treat fungal infections were discovered by the 1980s. Antifungal drug discovery and development by the pharmaceutical industry have been hindered because blockbuster drugs are unlikely and antifungal resistance has been viewed as having a modest impact in the clinic. The agrochemical industry has kept ahead of resistance problems by using mixtures of antifungals and by subtle improvement of antifungals such as the triazole fungicides. The limited efficacy of existing antifungals, the emergence of new fungal threats and the multiple mechanism of antifungal resistance require relevant questions in the laboratory and the exploration of ideas that can yield practical antifungals. Are there “ideal” broad-spectrum antifungal targets? Will knowledge of fungal biology and drug resistance mechanisms help make more effective antifungals? Could the X-ray crystal structures of antifungal targets be used to improve antifungal design? Should antifungals used in the clinic differ significantly from those used in agriculture? These questions will be addressed by discussing old and new antifungal targets.

Symposium I: Medical Mycology – Abstracts

Facing the challenge of emerging fungal infections by dual DNA barcoding

Irinyi L, Khan A, Meyer M & the ISHAM working group for barcoding of human and animal pathogenic fungi

Molecular Mycology Research Laboratory, CIDM, Sydney Medical School-Westmead Hospital, The University of Sydney, The Westmead Institute for Medical Research, Sydney, NSW, Australia; wieland.meyer@sydney.edu.au

Abstract. Correct and fast identification of the causative agents of mycoses is of great importance to enable early diagnosis and targeted antifungal therapy. DNA barcoding offers an accurate, fast, cost-effective, culture independent approach for species identification through DNA barcodes (short standardized sequences). The current official fungal DNA barcode is the internal transcribed spacer (ITS) region. A ultimate quality controlled ISHAM-ITS database of human and animal pathogenic fungi has been established by an international consortium of medical mycology laboratories. The database is available from <http://www.isham.org/> or directly at <http://its.mycologylab.org/>. The gathered data have been used to evaluate the value of the ITS region as a barcode at intra-and inter-species level. Overall, clinically important species show a low intra-species variability and a clear barcoding gap at inter-species level, consequently ITS sequencing can be used for the identification of most of them. However, for the species with more than 1.5% diversity or taxa without a barcoding gap, alternative barcode loci need to be introduced to ensure reliable species identification. To address this issue, potential alternative loci with high level of informativeness and with allegedly universal primer pairs were identified by whole genome comparison of 25 or 70 fungal species, respectively. In a pilot study three new loci and a total set of eight primer pairs were tested for 40 pathogenic fungal species with more than 400 strains, to evaluate their amplification efficiency under standardized laboratory conditions, and the universality of the primers across different taxa. The resulted amplicons were then sequenced and the intra-and inter-species variations were evaluated. The translation elongation factor 1 α gene (*tef1 α*) amplified with the “A133 primers set” proved to be the most promising candidate for an alternative barcode in pathogenic fungi. The amplified region showed less variability at species level than the ITS region and it proved to yield a higher resolution at inter-species level, enabling the separation of numerous closely related/cryptic species such as *Cryptococcus*. As such, the *tef1 α* locus is a promising secondary barcode candidate for the identification of clinically relevant species.

Keywords. Fungal infections, DNA barcoding

Next-Generation Sequencing Multilocus Sequence Typing (NGS-MLST) for detection of multiple *Candida albicans* genotypes in clinical samples

Zhang N & Schmid J

Institute of Fundamental Sciences, Massey University, Palmerston North NZ; n.x.zhang@massey.ac.nz

Abstract. Typing is important for investigating the epidemiology of the pathogenic diploid yeast *Candida albicans*. Multilocus Sequence Typing (MLST) is a reliable, unambiguous, discriminating *C. albicans* typing method, albeit costly. We have developed a next-generation sequencing-based MLST method (NGS-MLST). Using indexed adaptors, NGS-MLST generates MLST data from sets of 96 samples in a single Illumina MiSeq run, at ~35% the cost of conventional MLST. For technical reasons NGS-MLST sequences amplicons slightly shorter than those in conventional MLST, but this has little impact on its discriminatory power (99.8%). The sequences deduced from assembling the ~10,000 reads per amplicon are identical to those obtained by conventional sequencing (tested for 7 loci in 20 strains). Because of cost, to date usually only a single colony per patient sample is MLST typed. This can be misleading, because a site can be colonized by multiple strains. When using NGS-MLST on a single strain, heterozygous polymorphisms are each represented by 50±2% of reads. Allele ratios outside this range should signal presence of multiple strains when NGS-MLST is used on a DNA extracted from multiple colonies from a patient sample. We confirmed this and that genotypes of multiple strains present can usually be reconstructed, an important technological advance.

Keywords. *C. albicans*, Multilocus Sequence Typing (MLST), Illumina MiSeq.

Associations between capsule production, cell size, and clinical outcome in *C. neoformans* and *C. gattii* clinical isolates

Fernandes K¹, Brockway A¹, Campbell L¹, Perfect J² & Carter DA¹

¹*School of Life and Environmental Sciences, University of Sydney, Sydney NSW AU; kyou9292@uni.sydney.edu.au, adam_brockway@hotmail.com, leona.campbell@sydney.edu.au, dee.carter@sydney.edu.au*

²*Department of Medicine, Duke University School of Medicine, Durham NC USA; perfe001@md.duke.edu*

Abstract. Fungal pathogens *C. neoformans* and *C. gattii* both cause severe respiratory and cerebral infections, but while *C. neoformans* tends to infect the immunocompromised, *C. gattii* mainly infects immunocompetent hosts. We examined *in vitro* capsule production in a set of clinical isolates and a set of laboratory derivatives of the *C. neoformans* type strain H99, and analysed correlations between capsule and cell attributes and clinical outcomes or virulence level. Capsule thickness and yeast cell diameter were examined after capsule induction and were found to differ significantly between species, genotypes, and individual strains. *C. gattii* isolates had significantly larger capsules and a greater variation in yeast cells size than *C. neoformans*. In the strains derived from H99, less virulent strains had significantly smaller capsules and produced fewer morphological variants than hypervirulent derivatives. Clinical *C. neoformans* strains frequently had extracellular capsule and produced populations of extremely small (micro) cells, while some very large cells were seen in some of the *C. gattii* strains. A larger yeast cell size was significantly associated with patient death. These results shed light on the complex relationship between cell size, capsule production and virulence that may be relevant during the course of cryptococcal infection.

Keywords. Cryptococcosis, capsule, cell size.

Lessons Learned in a Recent Outbreak of Invasive *Aspergillus* Disease in a Haematology / Oncology Unit.

McKinney W

Mycology Department, LabPlus, Auckland City Hospital, Auckland NZ; wendym@adhb.govt.nz

Abstract. Invasive aspergillosis (IA) is an uncommon but serious complication in Paediatric Haematology/Oncology Units. Over a 7 month period – July 2014-January 2015- there were 7 cases of IA, with 5 cases occurring in January 2015. Ongoing construction within the Star Ship Children’s Hospital started in June 2013. The outbreak was investigated and a number of interventions were put in place. The Infection Prevention and Control Service reviewed the infection prevention practices adhered to during construction and continued to monitor on a daily basis. Air handling in the unit and environmental cleaning were reviewed. Procedures followed for patient transfer to and from the unit were reviewed. Limited air sampling was performed. Interventions included:

- Children identified as high risk were placed on antifungal prophylaxis.
- Air sampling showed high counts of fungal spores at the hospital entrance and in the carpeted corridor leading to the Unit. The carpet was removed. Signage was placed at the ward entrance to remind staff to keep the doors closed.
- Patients were required to wear a mask during transfer to the unit and when moving around the hospital.
- Cleaning within the unit and in the hospital foyers was enhanced.
- A low threshold for diagnostic testing was recommended.

No further cases were identified during 2015. Adherence to best infection practices seems to have played an important role in reducing exposure and hence risk.

Screening Macrofungi for Antibacterial Compounds

Qaraghuli SA, Brown MH, Stroehner UH, Burgoyne LA & Catchside DEA

School of Biological Sciences, Flinders University, Adelaide, SA, AU; qara0003@flinders.edu.au, melissa.brown@flinders.edu.au, uwe.stroehner@flinders.edu.au, leigh.burgoyne@flinders.edu.au, david.catchside@flinders.edu.au

Abstract. The widespread development of resistance to antibiotics amongst bacteria pathogenic to humans has led to interest in finding new antimicrobials. We hypothesised that macrofungi are a likely source of novel antibiotics since their mode of nutrition makes them vulnerable to competition. Amongst the macrofungi, saprotrophs export enzymes to digest macromolecules and must compete with bacteria for the breakdown products and ectomycorrhizal species need to protect the zone of nutrient exchange with plant roots. Accordingly, the production of antimicrobial compounds to control competition for nutrients would provide a competitive advantage to macrofungi. To test our hypothesis, extracts of 170 species have been screened for antibiotics including compounds that block the bacterial efflux pumps that expel antibiotics and compounds that impede the formation of bacterial biofilms. We have screened fruiting bodies and, where possible, also cultures for compounds active against a panel of sixteen bacterial species, including the ESKAPE group of pathogens that cause troublesome hospital acquired infections. We found that a substantial proportion of Australian macrofungi screened do produce antibacterial compounds, including some that inhibit the formation of biofilms or a *Staphylococcus aureus* efflux pump.

Keywords. Macrofungi, antibiotics, biofilms, efflux pumps.

Symposium II: Molecular Mycology – Abstracts

Genes involved in adaptation in *S. cerevisiae* in complex nutrient limited environments

Arderm ZN¹ & Goddard MR²

¹ *School of Biological Sciences, University of Auckland NZ;*
zard001@aucklanduni.ac.nz

² *School of Biological Sciences, University of Auckland NZ;*
Life Sciences, University of Lincoln UK
mgoddard@lincoln.ac.uk

Abstract. The function and adaptive value of genetic sequences depends on environmental conditions, and can be rigorously tested in microbes. Sequencing of microbial experimental evolution populations allows for investigation of the genetic basis of adaptation, and the functions of genes involved. Adaptation of both sexual and asexual populations of *S. cerevisiae* to two complex nutrient limited environments (low carbon with raised temperature, and low nitrogen with raised sodium chloride concentration) was previously investigated, and the end-point populations of these experiments have now been sequenced with an Illumina Hi-Seq. As well as an overview of recent developments in the field I report and discuss some key variants accumulated over the course of 300 generations in these populations, including single nucleotide polymorphisms with different frequencies and effects, and gene duplications in Hxt 4, 6, and 7 in the low carbon environment.

Keywords: Experimental evolution, *Saccharomyces*, genomics, gene duplication

Comparative genomics of a truffle-like fungus *Cortinarius beeverorum* and its close mushroom relative *C. dulciolens*

Orlovich DA¹, Gillard G^{2,3}, Wang X¹, Nilsen AR¹, Brown CM² & Summerfield TC¹

¹Department of Botany, University of Otago, PO Box 56, Dunedin 9054, New Zealand;

david.orlovich@otago.ac.nz

²Department of Biochemistry, University of Otago, PO Box 56, Dunedin 9054, New Zealand

³Present address, Department of Chemistry, Biotechnology and Food Science, Norwegian University of Life Sciences, 1430 Ås, Norway

Abstract. Many fungi show incredible plasticity when it comes to adapting to their environment, one of the most striking examples of this is the convergent evolution of truffle-like fungi. These species attract animal dispersers through strong smells and/or bright colours. Mycologist Ross Beever suggested that in New Zealand, truffle-like fungi evolved to mimic forest fruits that attract ground-dwelling birds like moa, lizards and insects. We sequenced the genomes of two closely related species, the mushroom *Cortinarius dulciolens* and its truffle-like sister species *C. beeverorum*. These genomes are a framework for understanding the underlying causes and mechanisms of the evolutionary transformation from mushroom to truffle in this species pair. We sequenced transcriptomes from stipe and hymenial tissue from three collections of each species to determine levels of gene expression in these tissues. Draft sequences were assembled. Consensus gene models using EvidenceModeller predicted both contained ~10,000 genes, with the mushroom having slightly more. Eighty-eight percent of the gene models in *C. beeverorum* had > 90% similarity (BLAT) with gene models of *C. dulciolens* and 84% of the *C. dulciolens* gene models had >90% similarity to those of *C. beeverorum*. In comparison with the genome of *C. glaucopus*, both *C. dulciolens* and *C. beeverorum* had fewer highly duplicated paralog genes in some ortholog groups, possibly due to the loss of redundant genes. We discovered about 100 highly expressed genes specific to the genome of *C. beeverorum* and eighty highly expressed genes specific to the genome of the mushroom *C. dulciolens*. We will present and discuss the characteristics of the ortholog groups with the highest differences between the truffle-like *C. beeverorum* and the mushroom *C. dulciolens*.

Phosphate acquisition and fungal virulence

Lev S¹, Desmarini D¹, Li C¹, Francis K¹, Sorrel T^{2,3} & Djordjevic J¹

¹Centre for Infectious Diseases and Microbiology, Westmead Institute for Medical Research and Sydney Medical School, University of Sydney at Westmead Hospital, Westmead, NSW, Australia. ²Marie Bashir Institute for Infectious Diseases and Biosecurity, University of Sydney, NSW, Australia. ³Westmead Hospital, Westmead, NSW, Australia; julianne.djordjevic@sydney.edu.au levsophie@gmail.com

Abstract. Inorganic phosphate (P_i) is an essential nutrient which serves as a major component of nucleic acids and phospholipids and the primary means of transferring signalling information (protein phosphorylation) and energy (as ATP). In fungi, intracellular P_i is tightly regulated by phosphate sensing and acquisition (PHO) pathway, which is activated when P_i is insufficient to support growth. PHO pathway activation results in up-regulation of extracellular phosphatases and P_i transporters to enhance P_i acquisition from the environment, but also production of the intracellular enzymes to mobilize P_i from the internal stores. Genes encoding P_i mobilizing enzymes and P_i transporters are collectively regulated by the transcription factor Pho4. PHO pathway function has been extensively studied in the non-pathogenic yeast *Saccharomyces cerevisiae*, however the role of PHO pathway in pathogenic fungi and its contribution to virulence remain poorly understood. We identified the Pho4 encoding gene in an opportunistic human fungal pathogen, *Cryptococcus neoformans*. Mutant in *CnPHO4* (*pho4Δ*) grew markedly slower than the parental strain when P_i was absent or substituted with a more complex source, such as β-glycerol phosphate. We determined that PHO pathway is activated not only in the absence of P_i, but also under conditions mimicking human host (~1 mM P_i), suggesting that PHO pathway responds to yet unidentified host factors. *Apho4* strain was avirulent in the dissemination model of cryptococcosis in mice, assigning PHO pathway a crucial role in virulence in this model. Activation of the PHO pathway is therefore a prerequisite for cryptococcal adaptation to a hostile environment of the mammalian host and disseminated cryptococcosis

Targets Upstream from Lanosterol Biosynthesis Produce Synergy and Prevent Fluconazole Resistance in *Candida glabrata*

Kane A¹, Remyse A², Hibbs D³ & Carter D⁴

¹School of Molecular Biosciences, University of Sydney, Sydney NSW AU; aidan.kane@sydney.edu.au

²School of Molecular Biosciences, University of Sydney, Sydney NSW AU;
arem2618@uni.sydney.edu.au

³Faculty of Pharmacy, University of Sydney, Sydney NSW AU; david.hibbs@uni.sydney.edu.au

⁴School of Molecular Biosciences, University of Sydney, Sydney NSW AU; dee.carter@sydney.edu.au

Abstract withheld for IP reasons

Synergy and antagonism: two sides to drug interactions with iron chelators

Lai, Y-W¹, Pang, I², Campbell, LT¹, Chen, S³, Wilkins, M² & Carter, DA¹.

¹*School of Life and Environmental Sciences, University of Sydney, Sydney NSW AU;*
yuwen.lai@sydney.edu.au, leona.campbell@sydney.edu.au, dee.carter@sydney.edu.au

²*Systems Biology Initiative, School of Biotechnology and Biomolecular Sciences, University of New South Wales, Sydney, NSW AU;*

i.pang@unsw.edu.au, marc.wilkins@unsw.edu.au

³*Centre for Infectious Diseases and Microbiology Laboratory Services, ICPMR, Westmead Hospital and the University of Sydney, Sydney, AU;*
Sharon.Chen@health.nsw.gov.au

Abstract. There is a paucity of effective, safe antifungal drugs. Fungal cells offer few targets that are not shared by the host, and developing new drugs is hampered by high cost and a relatively limited market. New approaches to treatment are therefore looking to enhance existing antifungals with synergising agents. Iron is essential for all cells, and fungal pathogens with disrupted iron homeostasis are more susceptible to antifungals. We therefore tested a range of iron chelating agents to assess whether they would confer synergy to antifungals commonly used to treat fungal pathogens, with a particular focus on *Cryptococcus*. Synergy was found between amphotericin B (AMB) and the globular chelating protein lactoferrin (LF). However, we also found antagonistic interactions between azole antifungals and some chelators. Interestingly this was confined to strains of *Cryptococcus neoformans* var. *grubii*, and was not seen in *Cryptococcus gattii*, where there was an additive interaction. To understand the molecular basis of antagonism vs. enhanced activity we used RNA-Seq transcriptomics and found an enrichment of transcripts related to drug transport in the *C. neoformans* var. *grubii* strain. This suggests that some chelators can evoke a drug efflux response and cautions against their use in patients receiving azole antifungal therapy.

Keywords. Antifungal, synergy, antagonism, iron chelation, *Cryptococcus*

Symposium III: Plant & Insect Pathogens – Abstracts

How three invasive pathogenic fungi in a species complex share their new host from leaf to continent: oak powdery mildew in Europe

Desprez-Loustau ML¹, Takamatsu S², Massot M¹, Tack AJM³

& RESIPATH partners (Gulden Aday, Johanna Boberg, Thomas Cech, Anne Chandelier, Tamara Corcobado-Sanchez, Tugba Dogmus, Cyril Dutech, Marilia Horta Jung, Thomas Jung, Eugenia Iturriza, Corina Junker, Benoit Marçais, Jonas Oliva, Funda Oskay, Dominique Piou, Venche Talgø)

¹INRA, UMR Biogeco, Bordeaux, FR, AU; Marie-Laure.Loustau@bordeaux.inra.fr

²Faculty of Bioresources, Mie University, Kamihama, Japan; takamatu@bio.mie-u.ac.jp

³Department of Ecology, Environment and Plant Sciences, Stockholm University, Sweden, ayco.tack@su.se

Abstract. Emerging diseases caused by exotic pathogens are on the rise worldwide. Meanwhile, many plant diseases have been shown to be caused by sibling fungal species. Here we focus on the invasion by several exotic fungi within a species complex that causes oak powdery mildew. *Quercus* is the plant genus hosting the largest number of powdery mildew species; in Europe at least four species have been reported: three *Erysiphe* spp. that are most likely of exotic origin, and one possibly native *Phyllactinia* species. The spatial distribution of these species is described here, ranging from the distribution within leaves to the continental scale. The invasive species that caused the devastating epidemics in the early 20th century (*E. alphitoides*) was found as the most prevalent all over Europe. In contrast, *E. quercicola* and *E. hypophylla* were found at lower frequencies, mostly in Southern Europe for the former and in Northern and Central Europe for the latter. Moreover, *E. quercicola* was mostly found on seedlings and *E. hypophylla* on lower leaf surfaces, whereas *E. alphitoides* was distributed irrespective of tree age and leaf surface. These results are consistent with differences in seasonal dynamics between species suggesting that the occupation of the new niche of these three closely related species could reflect niche differentiation during phylogenetic and invasion history.

Keywords. Species coexistence, niche partitioning, biological invasion

Contrasting the sporulation potential of *Phytophthora pluvialis* and *Phytophthora kernoviae* on the foliage of native and introduced hosts in New Zealand

Gardner JF, Dick MA & Williams NM

Forest Protection, Scion, Rotorua, NZ; judy.gardner@scionresearch.com

Abstract. *Phytophthora* species are seldom connected with severe disease of co-evolved plants in their locations of origin. Movement of plants and associated materials around the world has led to distribution of *Phytophthora* in numerous non-native habitats and subsequent frequent disease outbreaks. In New Zealand, both *Phytophthora kernoviae* and *Phytophthora pluvialis*, the causal agent of red needle cast, are present in *Pinus radiata* plantations. Although *P. kernoviae* was described in Great Britain, current research suggests it may have co-evolved with New Zealand native plants while *P. pluvialis* is likely to be native to the Pacific North West of the USA. Variations in the growth and sporulation in relation to lesion development have been observed between susceptible and resistant genotypes of *P. radiata* to these species. Parallels in the pathogenicity and epidemiological implications of both species make an interesting case study contrasting the behaviour of a possibly native versus an introduced pathogen on an exotic host. This will be presented and discussed in contrast to an associated analysis of the sporulation potential of *P. kernoviae* on New Zealand native plant species.

Keywords. *Phytophthora kernoviae*, *Phytophthora pluvialis*, *Pinus radiata*.

Cordyceps and allied genera in New Zealand

Cummings NJ & Glare TR

Bio-Protection Research Centre, Lincoln University, Lincoln NZ; nicholas.cummings@lincoln.ac.nz,
travis.glare@lincoln.ac.nz

Abstract. Arthropod-pathogenic fungi in *Cordyceps* and related genera are an ecologically important but overlooked aspect of fungal biodiversity. Current knowledge of the range of species present in New Zealand is limited, especially in light of major taxonomic revisions in this group. Although morphological characterisation of conidial fungi in *Cordyceps s.l.* has been historically problematic, many species are now well-defined by DNA sequence markers. This talk will discuss identification of New Zealand collections of *Beauveria*, *Isaria*, *Metarhizium*, and other anamorphs of *Cordyceps s.l.* following recent phylogenetic classifications. New evidence is presented for anamorph-teleomorph connections in *Cordyceps* species, including several rarely recorded taxa. Issues surrounding collection, typification, and correct anamorph determination of arthropod-pathogenic fungi will also be discussed.

Keywords. Cordycipitaceae, arthropod-pathogenic fungi, anamorph-teleomorph connections.

Heteroecious rust fungi of New Zealand

Padamsee M & McKenzie EHC

*Systematics Team, Landcare Research, Auckland NZ; padamseem@landcareresearch.co.nz,
mckenziee@landcareresearch.co.nz*

Abstract. The approximately 125 native rust species in New Zealand occur in five genera and three form genera. The three form genera (*Aecidium*, *Caecoma*, and *Uredo*) contain 31 endemic species. Most of the native rusts are thought to be autoecious (non-host-alternating) with only two confirmed heteroecious (host-alternating) species on native plants (*Puccinia caricina* and *Mikronegeria fuchsiae*). In general, experimental inoculations between putative alternate hosts are required to establish whether there is a connection between rust fungi on two unrelated hosts. Such trials can be difficult to conduct with New Zealand rusts as many of them occur on alpine plants, which are difficult to access and may be protected. However, there have been instances elsewhere/overseas in which DNA analyses, in combination with inoculations, were used to confirm alternate hosts for example, with *Puccinia striiformis*. This suggests that DNA analyses alone may suffice to quickly identify alternate hosts. A phylogeny of New Zealand rust fungi was constructed that supported inoculation data establishing *Mikronegeria fuchsiae* as heteroecious, and suggested alternate hosts for *Aecidium ranunculus-lyalli* and *A. otagense*, among others.

Keywords. Life cycle, Pucciniales, systematics.

Challenges in plant disease diagnostics in the era of molecular taxonomy

Toome M, Thangavel R, Ho W & Alexander BJR

*Plant Health and Environment Laboratory, Ministry for Primary Industries, Auckland NZ;
merje.toome@mpi.govt.nz, thangavel.raja@mpi.govt.nz, wellcome.ho@mpi.govt.nz,
brett.alexander@mpi.govt.nz*

Abstract. Accurate identification of exotic fungal and fungal-like plant pathogens is essential to protect New Zealand from biosecurity risks. Therefore, the confirmatory identification of nearly all pathogens that are found from imported plant material or suspected to be recently introduced includes sequence analysis at the Ministry for Primary Industries' Plant Health and Environment Laboratory. While in most cases the identification of fungi and oomycetes can be easily completed, the major challenge is to determine whether these species are new or already present in New Zealand. In the light of their revised taxonomy and as a result of splitting species complexes into separate species, applying new names to earlier records is one of our major challenges. It is essential to verify the identity of earlier reports, which can often be done based on sequence data analysis. Thus, access to the sequence data from earlier collections and submission of isolates to culture collections by various researchers is invaluable to our ability to perform rapid diagnostics in order to ensure informed biosecurity decisions. We present some recent case studies where these challenges have been met, with special focus on plant pathogens in Oomycota.

Keywords. Biosecurity, fungal identification, taxonomic revisions.

Invited Plenary Talk II – Abstract

Multi-kingdom interactions in invasion: plants, fungi and animals

Dickie IA

Bio-Protection Research Centre, Lincoln University, Lincoln, New Zealand; ian.dickie@lincoln.ac.nz

Abstract. Ever-increasing globalisation has led to the current era being described as the “Homocene”, with entirely new assemblages of species dominating ecosystems around the world. One of the most interesting examples of this lies in plant-fungal interaction networks. Recent studies suggest that the successful invasion of multiple tree species (pine, Douglas-fir, alder, willow) in New Zealand is linked to fungal co-invasion. Intriguingly, this co-invasion of North American trees and fungi includes novel interactions with invasive European and Australian mammals, acting as dispersal agents for fungi. The net effects of tree-fungal co-invasions on soil ecosystems are complex, including interactions with soil bacteria, fungi, and nematodes. In particular, pine-fungal co-invasion into native grass/shrub-lands releases recalcitrant N and P, increases available nutrients, and greatly increases bacterial dominance of soil food-webs. These changes in ecosystem function can generate long-lasting legacies, including facilitating invasion by non-native grasses. Our findings highlight that complex interaction networks are involved in driving both plant invasions and their effects in ecosystems. Understanding these complex interactions, and particularly the role of fungi, will be key to managing the novel ecosystems that increasingly dominate the New Zealand landscape.

Keywords. Invasive species, networks, co-invasion, *Pinus*, *Pseudotsuga*

Symposium IV: Fungal Ecology – Abstracts

Scattered far and wide: the biogeography of the fungal communities in the roots of the dune grass *Ammophila arenaria*

Johansen R¹, Johnston P², Mieczkowski P,³ Perry, GLW⁴, Robeson MS⁵, Vilgalys R⁶, & Burns BR¹

¹*School of Biological Sciences, University of Auckland, Auckland, NZ; rjoh103@aucklanduni.ac.nz*

²*Landcare Research, Auckland, NZ; JohnstonP@landcareresearch.co.nz;*

³*Department of Genetics, University of North Carolina, Chapel Hill, NC, USA; miecz001@med.unc.edu*

⁴*School of Environment, The University of Auckland, Auckland, NZ; george.perry@auckland.ac.nz*

⁵*Fish and Wildlife Conservation Biology, Colorado State University, Fort Collins, Colorado, U.S.A.; Michael.S.Robeson@colostate.edu*

⁶*Department of Biology, Duke University, Durham, NC 27708, USA; fungi@duke.edu*

Abstract. The biogeography of cryptic fungal communities in natural systems is poorly understood. Native to Europe, the dune grass marram (*Ammophila arenaria*) has been transported around the world. We explore the fungal communities in the roots of marram, and in alternative host grasses, in dunes in the United Kingdom, Australia and New Zealand. The communities have been characterised using next generation sequencing on the Illumina MiSeq platform. Our data show a range of fungi can tolerate the harsh dune environment and occupy marram roots across the globe. While some taxa are shared widely amongst different dune systems, spatial heterogeneity occurs within and between countries. Geographic distance between sites does not predict community similarity. These findings suggest that many dune taxa are not dispersal limited across large scales, but rather filtered out of the community by environmental conditions. The most diverse fungal community in marram is found in New Zealand, despite the plant being non-native in this country. Host species influence over fungal community composition is minimal. This study demonstrates that next generation sequencing can be a powerful tool for characterizing whole fungal communities, and that invasive plants can have relationships with species of fungi with ranges extending across thousands of kilometres.

Keywords. Invasive plant, next generation sequencing, biogeography

Quantifying Separation and Similarity in a *Saccharomyces cerevisiae* metapopulation

Knight SJ¹ & Goddard MR^{1,2}

¹*School of Biological Sciences, University of Auckland, Auckland NZ; s.knight@auckland.ac.nz*

²*School of Life Sciences, University of Lincoln, Lincoln UK; mgoddard@lincoln.ac.uk*

Abstract. Determining population processes occurring in microbes can help our understanding of their evolutionary histories and potential future trajectories. Despite their undisputed importance both commercially and scientifically, we have a poor understanding of microbial population biology and ecology. Here we report an in-depth quantitative analysis of population structure and migration in the budding yeast *Saccharomyces cerevisiae* to provide a more detailed account of the population processes occurring in microbes. Over 10 000 isolates were collected from native plants, vineyards and spontaneous ferments of fruit from six major regions spanning 1000 km across New Zealand. From these, hundreds of *S. cerevisiae* genotypes were identified and a suite of analytical methods were employed to provide a comprehensive quantitative analysis of both population structure and rates of migration. Within each geographic region no genetic differentiation was detected, even between populations inhabiting native forests and vineyards; however at distances greater than ~100 km, varying degrees of population structure were observed. This is complemented with estimates of bidirectional migration rates between geographic regions which correlate with the movement of fruit by the New Zealand wine industry. This suggests anthropogenic activities may influence microbial population patterns and diversity and in turn may influence their potential evolutionary trajectories.

Keywords. *Saccharomyces cerevisiae*, population genetics, ecology.

Plant responses to endophytic fungi and their effects on herbivorous insects

Rostás M¹, Raad M¹, Maag D^{1,2}, Cripps M³, Silcock P⁴, Kandula D¹, Müller C⁵ & Glare T¹

¹Bio-Protection Research Centre, Lincoln University, New Zealand

²Fundamental and Applied Chemical Ecology, University of Neuchâtel, Switzerland

³AgResearch Ltd., Lincoln, New Zealand

⁴Department of Food Science, Otago University, New Zealand

⁵Department of Chemical Ecology, Bielefeld University, Germany

Abstract. Communities of fungal endophytes are ubiquitous in above and below-ground tissues of probably all plants, where they live without causing any visible symptoms. Endophytes and plants have been found to interact on the molecular and biochemical level and, depending on the fungal species (or isolate) involved, the outcome of such interactions may even be beneficial to the colonized plant, leading to enhanced growth and stress tolerance. Plants and herbivorous insects also form intricate relationships and because plant chemistry is crucial for herbivore development and behaviour, endophyte-mediated responses may change the outcome of such plant-insect interactions. To shed some light on this question we studied the plant responses to three endophyte species with significantly different life histories: a ubiquitous, facultative root-colonizer (*Trichoderma atroviride*), a well-known insect pathogen (*Beauveria bassiana*), which was only recently described as capable of endophytic colonization, and the obligate shoot-colonizing grass endophyte *Epichloë uncinatum*. This talk will highlight some of the metabolic and transcriptional changes each fungus causes and will focus on the possible induction of plant defences against insects. Furthermore, data will be presented that demonstrate changes in volatile root compounds due to endophyte colonization and how this can affect the foraging behaviour of a soil insect. We conclude that endophytes interact directly with plants and indirectly with higher trophic levels thus playing important roles in the ecosystem. Understanding the mechanisms of these multitrophic interactions may help to manipulate crop plants for more sustainable pest and pathogen management.

The increased abundance and activity of *Cortinarius* sp. is associated with shrub spread on Arctic tundra as climate warms

Deslippe, JR¹, Hartmann², Grayston SJ³, Mohn MM⁴, Simard SW³.

¹ School of Biological Sciences, Victoria University of Wellington, Wellington, New Zealand; julie.deslippe@vuw.ac.nz

² Forest Soils and Biogeochemistry, Swiss Federal Research Institute WSL, Zuercherstrasse 111, CH-8903 Birmensdorf, Switzerland Martin Hartmann; martin.hartmann@microbiome.ch

³ Department of Forest and Conservation Sciences, Faculty of Forestry, 2424 Main Mall, University of British Columbia, Vancouver, Canada; sue.grayston@ubc.ca; suzanne.simard@ubc.ca

⁴ Department of Microbiology and Immunology, Life Sciences Institute, University of British Columbia, Vancouver, Canada; wmohn@interchange.ubc.ca

Abstract. Climate warming is leading shrub expansion in Arctic tundra but the role of ectomycorrhizal (ECM) fungi in this process is poorly understood. In experiments focused on *Betula nana*, the shrub increasing in Alaska, we assessed the effect of warming on the ECM community and used ¹³CO₂ labelling of plants to elucidate the potential for carbon (C) transfer through ECM networks. Results indicated a prominent role for *Cortinarius* spp. in the response of *B. nana* to warming and to the existence of mycorrhizal networks (MN) involved in interplant C-transfer but only among *B. nana*. We then applied stable isotope probing (SIP) of microbial phospholipid fatty acids (PLFA) and fungal DNA to identify the fungi involved in C-transfer. PLFA-SIP revealed 7 times the ¹³C enrichment of fungal than bacterial PLFAs, confirming a dominant role for a direct MN pathway in C transfer among *B. nana*. DNA-SIP-pyrosequencing data indicated that a single OTU belonging to *Cortinarius* sp. was unique in being highly enriched in ¹³C, providing strong evidence that MNs of *Cortinarius* sp. facilitate C transfer among *B. nana*. Symbiosis with *Cortinarius* sp. may provide *B. nana* a competitive advantage over co-occurring species, facilitating its expansion in Arctic tundra as climate warms.

Keywords. Arctic tundra, shrub expansion, climate warming, ectomycorrhizal fungi, DNA-SIP, PLFA-SIP, stable isotope probing, *Betula nana*.

Do mycorrhizal interactions influence invasion success of *Eucalyptus* in New Zealand?

Tourtellot SG, Hulme PE & Dickie IA

Bio-Protection Research Centre, Lincoln University, Lincoln 7647, Canterbury, New Zealand;
samuel.tourtellot@lincolnuni.ac.nz

Abstract: Ectomycorrhizal (EM) mutualist limitation can be a barrier to the success of plants introduced into novel areas. Several introduced EM plant species have required the introduction of compatible fungal mutualists from their native range for both establishment, and in some cases invasion. It is unclear, however, whether this is always true. We propose four mechanisms by which an EM plant may overcome EM mutualist limitation: (i) reliance on introduced fungi from the plant's native range; (ii) forming effective novel associations with indigenous fungi; (iii) benefiting sufficiently from alternative mutualisms, *e.g.*, Vesicular-arbuscular mycorrhiza (VAM); and/or (iv) an ability to prosper without such mutualists. We test these by comparing the *in situ* fungal mutualist communities and *in vitro* growth responses of four invasive and four non-invasive Australian *Eucalyptus* species in New Zealand. We found that, despite the close bio-geographical association between the biota of the two countries, *Eucalyptus* exhibited relatively depauperate EM fungus communities and a strong preference for its native Australian fungi. Additionally, invasive species relied less on EM fungi than non-invasive species and showed increased benefit from VAM as alternative mutualists. The insights our research provide into the mycorrhizal ecology of plant introductions and invasions will be discussed.

Keywords. Mycorrhiza, *Eucalyptus*, mutualisms, biological-invasions.

Mycorrhizal fungi associated with marri in Western Australia: a comparison between a field and glasshouse trial

Sapsford SJ, Paap T, Hopkins A, Hardy GESTJ & Burgess TI

School of Veterinary and Life Sciences, Murdoch University, Perth WA AU; s.sapsford@murdoch.edu.au

Abstract. Marri is a keystone tree in Western Australia, however, a canker disease has caused population decline. Disease incidence is high in areas of anthropogenic disturbance such as roadside reserves, especially those adjacent to cleared land. At these sites there is no observed recruitment of marri. The pattern of decline and symptoms observed suggest a complex interaction of factors including nutrient imbalance and loss of mycorrhiza. The aim of this study was to determine changes in communities of mycorrhizal fungi on adult trees, along an anthropogenically disturbed gradient from road edge to intact forest and the ability of seedlings to grow and form mycorrhiza with soil collected along the gradient. Fine roots were collected from soil samples collected from 5 transects and then the soil was used in a glasshouse bioassay trial where seedlings were grown for 4 months. The marri seedlings were harvested and the fine roots collected. Next generation sequencing was carried out on the fine roots collected from transect soil, as well as the roots from the glasshouse trial. Mycorrhizal communities changed across the gradient both from roots of adult trees and from the seedling baits. These changes were both in taxonomic groups and functional composition.

Keywords. *Corymbia calophylla*, mycorrhizal fungi, next generation sequencing.

Symposium V: Fungal Conservation – Abstracts

Fungal Conservation: Global efforts

McMullan-Fisher SJM

School of Geography and Environmental Studies, Private Bag 78, Hobart, TAS 7001 AU and Royal Botanic Gardens Victoria, Birdwood Avenue, Melbourne, Victoria 3004, AU; sapphire.mcfish@gmail.com

Abstract. Conservation biology is a branch of scientific study that aims to protect and restore species, their habitats and ecosystems, with all their complex biotic interactions, to be healthy and functional. Many conservation societies started in the 1980's when it became clear that rates of extinction could not be reduced nor populations restored without conservation actions. Fungal conservation is rarely considered by most conservation groups so to fill this gap the *International Society for Fungal Conservation* (ISFC), was established in 2010. It was the first society anywhere in the world to be “entirely devoted to protecting these beautiful and wonderful organisms”. Much conservation funding is currently tied to lists of endangered species; this is problematic as there are very few fungi listed when compared to the lists of animals and plants. There have been other recent global conservation efforts with the Global Fungi Red List Initiative aiming to list 300 species on the IUCN Red List of Threatened Species. As part of these efforts two species from Oceania were successfully listed in Feb 2016. Collaboration and focus appears to be important in improving conservation efforts by including fungi. Ideas for future conservation actions will be raised.

Keywords. Conservation biology, fungi, collaboration

Threat-status listing of fungi in Australia and future directions for fungal conservation

May TW

Royal Botanic Gardens Victoria, Birdwood Avenue, Melbourne, VIC 3004, AU; tom.may@rbg.vic.gov.au

Abstract. There are currently 45 species of fungi, including lichenised fungi, that are formally listed under state and territory legislation in Australia – 23 in Tasmania (all lichens), 10 in Western Australia, nine in New South Wales (and one ecological community) and three in Victoria; but none listed nationally. In addition, a single species of fungus that occurs in Australia (*Claustula fisheri*) is included in the current IUCN Red List of Threatened Species. There are further species suggested for listing, such as in taxonomic monographs or state advisory lists. The rationale and mechanisms for increasing the formal listing of fungi on global, national and regional threat status lists will be discussed. It is desirable to increase support for community groups, such as Fungimap and regional fungal studies groups, to make nominations. Consideration will also be given to general strategies for improving the conservation status of fungi at a global scale, including potential for extension of the current Global Strategy for Plant Conservation to become a Global Strategy for the Conservation of Plants, Algae and Fungi. The vital role of fungi in mutualisms also needs to be acknowledged, such as by extending Seed Banks to become Seed+Fungi Banks, encompassing mycorrhizal fungi.

Keywords. Conservation, threat-status listing, legislation.

Impact on fungal conservation of the global trade in beneficial mycorrhizal fungi – a New Zealand example

Buchanan PK¹, Lebel T², Cooper JA³ & Pennycook SR¹

¹Landcare Research, St Johns, Auckland 1072, New Zealand; buchananp@LandcareResearch.co.nz,
pennycooks@LandcareResearch.co.nz

²Royal Botanic Gardens Victoria, Plant Sciences & Biodiversity, Melbourne, Victoria 3004, Australia;
teresa.lebel@rbg.vic.gov.au

³Landcare Research, Lincoln 7608, New Zealand; cooperj@LandcareResearch.co.nz

Abstract. Mycorrhizal fungi benefit associated plants through increased absorption by roots of water and minerals, aiding drought resistance and also providing resistance to disease. Agricultural practices to enhance mycorrhizal development include minimal tillage, reduced fertiliser, and addition of mycorrhizal inocula. These inocula are marketed as global commodities for nurseries and plant restoration initiatives, with both VAM and ECM species prepared as amendments to soils. Overseas, key mycorrhizal species have been identified as amenable for mass production and incorporation as mixtures into mycorrhizal inocula, including ectomycorrhizal species of *Pisolithus* and *Scleroderma*. These inocula are then sold widely, crossing trade borders where their beneficial role may outweigh biosecurity questions about composition and biosafety. This paper explores, from a New Zealand perspective, regulations applying to imported exotic mycorrhizal inocula, verification of product composition, and the potential for negative impacts to arise from competition between newly imported and native species of mycorrhizal fungi. The composition of imported inocula will be compared and contrasted with New Zealand's fungal diversity that includes three native species of *Pisolithus* and several native and exotic species of *Scleroderma*.

Keywords. Mycorrhizal inocula, *Pisolithus*, *Scleroderma*, Biosecurity.

Fungal and bacterial communities in Ultramafic Substrates in New Caledonia, Implications for Ecological Conservation and Restoration

Gourmelon V¹, Maggia L^{1,2}, Powell J³, Gigante S¹, Hortal S³, Gueunier C⁴, Letellier K¹ & Carriconde F¹

¹*Institut Agronomique néo-Calédonien (IAC), Axe 2 "Diversités biologique et fonctionnelle des écosystèmes terrestres", BP 18239, 98800 Nouméa, New Caledonia; gourmelon@iac.nc, maggia@iac.nc, gigante@iac.nc, letellier@iac.nc, carriconde@iac.nc*

²*CIRAD, UMR AGAP, 98800 Nouméa, New Caledonia, laurent.maggia@cirad.fr*

³*Department of Soil Biology & Genomics, Hawkesbury Institute for the Environment, Sydney NSW AU; Jeff.Powell@westernsydney.edu.au, s.hortalbotifoll@westernsydney.edu.au*

⁴*Société Le Nickel (SLN) – Groupe ERAMET, Département Environnement, BP E5, 98848, Nouméa, New Caledonia; C.GUEUNIER@eramet-sln.nc*

Abstract. New Caledonia is defined as a biodiversity hotspot according to its high concentration of endemic species and anthropogenic threats that impact this diversity. In this context, it appears essential to establish conservation and restoration actions. Microorganisms are known to be involved in numerous ecological processes and they thus could play central role in such actions. For this, we studied soil fungal and bacterial diversity in different plant formations representing a potential vegetal succession on New Caledonian ultramafic substrates. Four different plant formations (degraded soils, *Tristaniopsis* spp. maquis, monodominant *Nothofagus aequilateralis* rainforests and mixed rainforests) in two different sites were retained. To assess soil microbial diversity in each of these plant formations, a high-throughput sequencing approach was used. Our main results showed a difference in microbial community structures between each plant formation type and to a lesser extent between sites. These communities were also linked to floristic composition and edaphic parameters. Furthermore, a correlation between soil fungal and bacterial communities has been observed. Overall, our data suggest complex interactions between plants, edaphic parameters and different groups of microorganisms in structuring soil microbial communities. These results will allow us to define biological indicators for further conservation and restoration programs.

Keywords. New Caledonia, ultramafic substrates, plant formation, fungal community, bacterial community, high-throughput sequencing

Red Lists – Science or Politics?

Leonard PL ¹

¹*Queensland Mycological Society*
PO Box 1193, Buderim 4456, Queensland
patbrenda.leonard@bigpond.com

Abstract. The IUCN Red Lists were introduced to focus attention on rare and threatened species. The assessment criteria focussed on scarcity and threat. Data to determine these is poor for fungi. This talk addresses what strategies might be adopted to protect fungal biodiversity in the light of poor scientific knowledge. Four approaches are compared: do nothing, wait for the science to catch up, protect the habitat and list and be damned. The focus should be on selecting fungal candidates with different biological roles in a full range of habitats. This will fulfil the IUCN's aim of improving management plans for species survival and might possibly lower extinction rates.

Keywords. Red list, fungi, conservation.

Arbuscular Mycorrhizae of a restored New Zealand wetland across hydrological gradients

Coles A

School of Biological sciences, Victoria University of Wellington, NZ.
colesalex@myvuw.ac.nz

Abstract. Wetlands are unique and valuable ecosystems that provide habitat for many of our threatened native flora and fauna, and crucial ecosystem services to humans including water filtration, flood control, and carbon sequestration. New Zealand has lost over 90% of former wetland areas and many of those that remain are in a degraded state. Wetland restoration projects often focus on planting native vegetation, however survival rates of trees are variable. Elsewhere, the reestablishment of trees is contingent upon positive biotic interactions, but little is known of the biotic interactions of wetland plant species. Over 80% of wetland plants in New Zealand form symbioses with arbuscular mycorrhizal fungi (AMF) however we know almost nothing of their role in wetland restoration success. In this study the AMF communities on *Phormium tenax* (Harakeke) are characterised and compared across a hydrologic gradient of a Wairarapa wetland restoration site, during winter and summer. I test the hypothesis that AMF diversity and biomass is greatest in older restoration stages during summer and lowest in inundated early restoration stages during winter. I will discuss the methods used to identify and quantify AMF communities and how examining AMF diversity sheds new light on their importance in wetland restoration success.

Keywords. Arbuscular mycorrhizal fungi, restoration ecology, wetland restoration.

Soil fungi in urban Melbourne grasslands – it is not about time since fire

Egidi E¹ & McMullan-Fisher SJM^{1,2}

¹Franks Lab, Environmental Microbiology, Department of Physiology, Anatomy and Microbiology, School of Life Sciences, La Trobe University, VIC 3086, AU; eleonora.egidi@gmail.com

²School of Geography and Environmental Studies, Private Bag 78, Hobart, TAS 7001 AU and Royal Botanic Gardens Victoria, Birdwood Avenue, Melbourne, Victoria 3004, AU; sapphire.mcfish@gmail.com

Abstract. Frequent burning is commonly undertaken to maintain diversity in temperate grasslands of southern Australia. How burning affects below-ground fungal community diversity remains unknown. We show, using a fungal rDNA metabarcoding approach (Illumina MiSeq), that the fungal community composition was influenced by fire regimes (frequency) but not time-since-fire. The project was designed expecting fire effects, as repeated burning has been shown to be a key factor in plant diversity. Preliminary analyses showed that for the total 613 taxa with reliable reads, the similarity between samples was lower than expected with most sites with around 80% Bray-Curtis dissimilarity. To explore the total variation observed in the Fire Frequency treatment, the low frequency taxa were left out, leaving the “common” OTUs. When re-analysed, these ‘core’ taxa returned the same significant correlation, implying that the change in composition is mainly related to changes in relative abundance of the most common species. Fungal community composition and diversity have been explored further by separate analyses of fungal phyla to investigate the patterns of diversity. These Analysis of Similarity showed that fungi of phylum Glomeromycota were most strongly correlated to different Fire Frequencies (global $R=0.42$, $P=0.3\%$), suggesting that the observed differences may be driven by the shift in the plant community composition following different fire regimes.

Keywords. Metabarcoding, soil fungi, diversity

Symposium VI: Systematics – Abstracts

Austral *Austroboletus*: an Update

Fechner N¹, Bonito G², Lebel T³ & Halling R⁴

¹Queensland Herbarium, Mt Coot-tha Road, Toowong, Brisbane, QLD AU
nigel.fechner@science.dsitia.qld.gov.au

²Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing,
MI 48824 USA; bonito@msu.edu

³National Herbarium of Victoria, Royal Botanic Gardens, South Yarra, VIC AU;
teresa.lebel@rbg.vic.gov.au

⁴Institute of Systematic Botany, New York Botanical Garden, Bronx, NY 10458 USA; rhalling@nybg.org

Abstract. *Austroboletus* is a well-characterized genus of Boletaceae (Basidiomycotina, Boletales). Ornamented spores with a pinkish vinaceous colour in deposit along with an alveolate to heavily reticulated stipe are diagnostic features. The majority of species are found in countries of the western Pacific, both north and south of the equator. There are approximately 15-16 species known from Australia (14) and New Zealand (2). Exact numbers from New Caledonia, Papua New Guinea, Malaysia, and Indonesia are wanting. Continued field exploration has uncovered further diversity and documented additional distribution patterns. Further, the field work promoted the development of a finer resolution/augmentation of the diagnostic characters. Molecular phylogenetic analyses have helped to refine species concepts.

Keywords. Boletaceae, phylogeny, diversity.

Macrofungi Collections Consortium

Thiers BM¹, & Halling RE¹

¹*Herbarium and Institute of Systematic Botany, New York Botanical Garden, Bronx, NY 10458 USA;*
bthiers@nybg.org; rhalling@nybg.org

Abstract. The Macrofungi Collections Consortium (MaCC) consists of 40 U.S. institutions that collectively have digitized and shared collection information from about 1.5 million specimens of mushrooms, truffles, polypores and discomycetes, along with approximately 25,000 images of living collections. The data generated through this project will allow researchers to address the questions: To what extent do the diversity and distribution of macrofungi determine the diversity and distribution of the organisms with which they form commensal or symbiotic relationships, and by extension, how will changes in macrofungal diversity and distribution affect those organisms and ultimately human affairs? These data are shared through the Mycoportal (<http://mycoportal.org/portal/index.php>). A parallel project, the Microfungi Collection Consortium (MiCC) began in July 2015, is now contributing equivalent information about microfungi, and by 2018, all three million fungal collections in the U.S. will be digitized and available worldwide. Both the MaCC and the MiCC projects are funded by The National Science Foundation. We hope that this resource will support fungal research worldwide and will stimulate similar national initiatives in other countries.

Keywords. Herbaria, digitization, specimens.

Six under-collected or rare small black discomycetes (Pezizales, Ascomycota) from South Australia

Catcheside PS^{1,2} & Catcheside DEA²

¹*State Herbarium of South Australia, Plant Biodiversity Centre, P.O. Box 2732, Kent Town, SA 5071, AU;*
pam.catcheside@sa.gov.au

²*School of Biological Sciences, Flinders University, P.O. Box 2100, Adelaide, SA 5001, AU;*
david.catcheside@flinders.edu.au

Abstract. Small black disc fungi, discomycetes, are not commonly collected, possibly because of the problems they present. They are cryptic, usually cannot be identified without detailed microscopy, relevant literature is often scant and molecular sequences with which to compare collected specimens may not be available. During fifteen years of surveying the macrofungi in South Australia, the authors have collected a number of small, black, saucer-shaped fungi from a number of genera. These include under-collected *Sphaerosoma trispora*, *Marcelleina atroviolacea*, *Plectania platensis* and *Plicaria ?alveolata*. The rare *Boudiera areolata* grows as a small black lump on moist soil; a larger, undescribed fungus consists of an irregular, black shallow crust covering a chambered cone of brittle, waxy, grey-black tree-like pillars. Descriptions of macro- and microscopic characters, known distribution in Australia and molecular data are presented.

Keywords. Black disc fungi, under-collected, rare, distribution.

Toward true diversity of Korean milkcaps

Lee H, Oh SY & Lim YW

School of Biological Sciences, Seoul National University, Seoul, Korea;
hodoo1@snu.ac.kr, syoh@snu.ac.kr, ywlim@snu.ac.kr

Abstract. The genera *Lactarius* Pers. and *Lactifluus* (Pers.) Roussel are well-known ectomycorrhizal fungi which produce latex when cut or bruised. Approximately 500 species have been reported worldwide from these two genera and 52 species were reported in South Korea thus far. The taxonomy of Korean milkcaps was largely based on morphological comparison to European and North American species. As numerous recent studies have shown that Asian fungal species are not conspecific to western species, we decided to re-evaluate Korean milkcap taxonomy and diversity to estimate the milkcap diversity in Korea. We analysed ITS sequences obtained from 574 specimens and NGS data from 94 soil samples of both deciduous and coniferous forest in Korea. Surprisingly, we found 84 species of milkcaps from dried specimens and 16 more MOTUs through NGS data analysis. Overall, we confirmed 100 species of milkcaps in Korea. In order to further understand milkcap diversity in Korea, we aim to collect specimens only observed from NGS data analysis and increase NGS sequencing depth by using milkcap specific primers.

Keywords. Milkcap, Diversity, NGS

Ecology, morphology and molecular biology: delimiting fungal species through integrative taxonomy

Fernández-López J, Martín MP, Dueñas M & Tellería MT

Real Jardín Botánico, Consejo Superior de Investigaciones Científicas, Madrid, Spain; jflopez@rjb.csic.es,
maripaz@rjb.csic.es, mduenas@rjb.csic.es, telleria@rjb.csic.es

Abstract. The genus *Schizopora* has been traditionally studied as poliporoid or corticioid groups, but little is known about the phylogeny between and within their species. Currently, new methods like molecular biology have demonstrated that classical approaches of morphological or biological species concepts have failed in the task of describing the actual diversity in many corticioid fungi. In this study, we address the internal structure of the species *S. radula* genus using four nuclear molecular markers (ITS, LSU, RPB2 and EF1-alpha) combined with morphological study in more than 50 specimens around the world. Moreover, we assess the evidence of ecological differentiation through ecological niche analysis. Our results show that internal biodiversity of *S. radula* is higher than those described by exclusively morphological characters and their distribution patterns indicate that ecological conditions could model the evolution of these white rot fungi. This study raises new questions and causes a rethink of the hypothesis "Everything is everywhere, but environment selects" in this organisms, and the underestimation of fungal biodiversity due to these cryptic species.

Keywords. *Schizopora radula*, cryptic species, ecological niche modelling.

Species diversity of *Leucocoprineae* (Agaricaceae) from China and Molecular Phylogeny of the Tribe

Ge Z-W & Yang ZL

Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, China; zaiweige@gmail.com

Abstract. Specimens of putative *Leucocoprineae* collected from China were examined. As a result, forty species were identified which belong to five genera of this tribe, including five species within *Chlorophyllum*, one species within *Clarkeinda*, twenty one species within *Leucoagaricus*, six species within *Leucocoprinus* and seven species within *Macrolepiota*. All identified species were described and illustrated in detail, and differences between similar species are provided and discussed. A key to the genera of the *Leucocoprineae* and keys to the species belong to the studied genera were provided. Based on sequence data from the nuclear ribosomal large subunit gene (nLSU), the internal transcribed spacer (ITS), and the mitochondrial ribosomal small subunit gene (mtSSU), phylogenetic trees of *Leucocoprineae* were reconstructed. The results show that *Leucocoprineae* is not monophyletic, with *Agaricus*, the type genus of tribe *Agariceae*, and its allies derived from the *Leucocoprineae* clade and formed the sister clade to *Chlorophyllum*. Revised genera *Chlorophyllum* and *Macrolepiota* formed a monophyletic group of their own respectively, while genera *Leucoagaricus* and *Leucocoprinus* are shown to be artificial, with species of either genus shifted from one to another.

Keywords. Agaricales, *Leucoagaricus*, *Leucocoprinus*, Taxonomy, Phylogeny.

Australasian roll-rims: a revision of *Austropaxillus* and *Gymnopaxillus*

Lebel T¹, May T¹, Robinson R², Bonito G³, Cooper J⁴

¹Plant Sciences & Biodiversity, Royal Botanic Gardens Victoria, Melbourne VIC AU; teresa.lebel@rbg.vic.gov.au

²Science and Conservation Division, Department of Parks and Wildlife, Manjimup WA AU; richard.robinson@dpaw.wa.gov.au

³Plant, Soil & Microbial Sciences, Michigan State University, East Lansing MI USA; bonito@msu.edu

⁴Systematics, Landcare Research Co, Lincoln NZ; cooperj@landcareresearch.co.nz

Abstract. The family Serpulaceae comprises several brown-rot taxa and the more recently evolved ectomycorrhiza forming southern hemisphere genera *Austropaxillus* (mushroom, 5-8 spp.) and *Gymnopaxillus* (truffle-like, 2-4 spp.). Considerable confusion reigns in Australasia over species boundaries and names in the two genera, their geographic distributions, and specificity of the plant-host association. Analysis of a 3-gene dataset and morphological characters, supports circumscription of seven described species (*A. infundibuliformis*, *A. muelleri*, *A. mcNabbii*, *A. nothofagi*, *A. squarrosus*, *G. vestitus* and *G. nudus*), five undescribed species (three mushroom and two truffle-like), and the sinking of *Austropaxillus* into *Gymnopaxillus* (which is the older name). Host plant associations do appear to be geographically important (ie. *Nothofagus* versus *Leptospermum* in New Zealand, or *Allocasuarina* versus *Nothofagus* or *Eucalyptus* in Australia).

Keywords. Ectomycorrhizal fungi, truffle-like fungi, Australasia.

Posters – Abstracts

Molecular identification of fungal endophytes in *Dipodium roseum* roots

Boddington M¹, Lebel T², Leonard P³ & Dearnaley JDW¹

¹Faculty of Health, Engineering & Sciences, University of Southern Queensland, Toowoomba QLD AU; morwenna.boddington@usq.edu.au, john.dearnaley@usq.edu.au

²National Herbarium of Victoria, Royal Botanic Gardens Melbourne, VIC AU; teresa.lebel@rbg.vic.gov.au

³PO Box 1193 Buderim QLD AU; patbrenda.leonard@bigpond.com

Abstract. *Dipodium* or hyacinth orchids are large, fleshy, terrestrial orchids commonly seen in summer in Australian woodlands. Most species have limited chlorophyll, appear to be non-photosynthetic and rely on mycorrhizal fungi for their nutrition. Previous molecular investigations of the endophytic fungi of roots of *Dipodium variegatum* and *Dipodium hamiltonianum* have shown that the orchids are largely colonised by members of the ectomycorrhizal basidiomycete family, the Russulaceae. The fact that these plants consistently grew close to the base of *Eucalyptus* and *Callitris* trees suggested that the orchids acquire carbon and minerals from the tree host via an ectomycorrhizal connection. In the current project the fungal endophytes of *Dipodium roseum* were investigated for the first time. Orchid roots were sampled from multiple sites over two seasons in southern Queensland, Australia. DNA was extracted from colonised roots and isolated pelotons of the orchid. PCR amplification was conducted using ITS1F and ITS4 primers and following DNA purification, sent for Sanger sequencing at the Australian Genome Research Facility. BLAST searches of returned sequences against the GenBank database revealed a variety of fungi colonising the roots of *D. roseum*. This included a number of fungi not previously found as root endophytes of Orchidaceae species.

Keywords. *Dipodium*, Russulaceae, endophytic fungi.

Where do Tropical Endophytes Call Home: Does Host Really Matter?

Bransgrove, K¹, Crayn, D² & Abell SE¹

¹ Australian Tropical Herbarium and College of Marine and Environmental Science, James Cook University, Cairns QLD AU; kaylene.bransgrove@my.jcu.edu.au; sandra.abell@jcu.edu.au

² Australian Tropical Herbarium, James Cook University, Cairns QLD AU; darren.crayn@my.jcu.edu.au

Abstract. Fungal endophytes are a highly diverse group of fungi that asymptotically inhabit all plant parts. Their beneficial impact on plant health is well documented and development of the anti-inflammatory/antibiotic-like secondary metabolites they produce for agricultural and human health purposes is a burgeoning field of research. To facilitate this, we require an understanding of endophyte communities and how they vary between hosts. To evaluate the host specificity of foliar endophytes from tropical rainforest trees, leaves were collected from three, distantly related, plant genera with differing successional strategies (*Elaeocarpus*, *Endiandra*, *Normanbya*), the epiphytes removed, total genomic DNA extracted and the ITS1 region of the endophyte community sequenced using Illumina next generation sequencing. We detected a total of 421 fungal species from 250 genera in 55 families. While ascomycetes dominated the endophytic flora, host species significantly ($p \leq 0.05$) affected the composition of endophyte communities within. Endophyte communities of *Elaeocarpus* (early successional) and *Normanbya* (palm, late successional) were more similar to each other than to that of *Endiandra* (late successional). This illustrates that to understand endophyte biodiversity in tropical plants, irrespective of application, a broad taxonomic and phylogenetically distant host range and many ecological niches need to be examined.

Keywords. Endophyte, host specificity, rainforest.

Identification of a Pathogen Affecting Oil Palm in Sarawak, Malaysia

Hill RA¹, Cummings N¹, Walker M¹ & Agbayani F²

¹ Bio-Protection Research Centre, Lincoln University, Lincoln, New Zealand; robert.hill@lincoln.ac.nz

² Grand Perfect Sdn Bhd, Bintulu, Sarawak, Malaysia; flor@grandperfect.com.my

Abstract. A petiole wilt disease was first observed affecting oil palm (*Elaeis guineensis*) in the Sibuan area of Sarawak in 2013. The disease has now spread widely in this area and has also been recorded in the Miri district. Disease symptoms were observed as a progressive die-back of the leaf, beginning with the tip and making its way down towards the petiole, with lesions also present along the leaf stem. The disease eventually results in the destruction of the entire leaf and ultimately destroys fruiting capacity in infected plants. Pure cultures were isolated from lesions on diseased oil palms. The pathogen was identified as *Ceratocystis paradoxa* based on morphological characteristics and DNA sequence data. The species has a wide distribution in the tropics and has been previously reported from oil palm, causing the diseases known as dry basal rot in Africa, and common spear rot in Indonesia. The pathogen also causes black seed rot in sprouted oil palm seeds, which has resulted in major economic losses in oil palm production in Nigeria. Biological control using endophytic *Trichoderma* may provide a means of controlling the disease in oil palm.

Keywords. *Ceratocystis paradoxa*, *Elaeis guineensis*, oil palm.

Mycelia Obsession: developing a benchmark for Scientific Mycological Illustration for Illustrators

Elliott M¹, Weekes T² & Llewellyn A³

¹*School of Design Communication and Information Technology, University of Newcastle, Newcastle NSW AU; maree.elliott@uon.edu.au*

²*School of Design Communication and Information Technology, University of Newcastle, Newcastle NSW AU; trevor.weekes@newcastle.edu.au*

³*School of Design Communication and Information Technology, University of Newcastle, Newcastle NSW AU; anne.llewellyn@newcastle.edu.au*

Abstract. Scientific botanical illustration is well known by illustrators and information is readily available. However, very little is known about scientific mycological illustration for illustrators. So what information does an illustrator need to collect to achieve a scientific mycological illustration? To answer this question one must look at the field and laboratory methodologies of mycologists. The two key processes for collecting important information for mycologists are the field and laboratory processes. By combining the data the fundamental characteristics of fungi is revealed and used for identification. The key process for the illustrator is the studio process. The methods of the illustrator and the mycologist come together when the illustrator links all the essential information collected in the field and the laboratory to produce an accurate scientific mycological illustration equal to that of a scientific botanical illustration. The by-product of all these processes is a dried specimen and spore print with field and laboratory notes suitable for depositing into a herbarium. Considering how little is known about fungi compared to plants I believe illustrators have an obligation to deposit their specimens with a herbarium. Following are the processes that I consider important for Scientific Mycological Illustrators. They are:

- Field:
- Laboratory:
- Studio:
- Herbarium:

Keywords. Scientific mycological illustration, fieldwork, laboratory work

Genomic analysis of *Epicoccum purpurascens* (Didymellaceae, Ascomycota): insight into a widespread saprophytic species to reveal its biotechnological potential

Fokin M¹, Weir B², Fleetwood D³ & Villas-Boas SG¹

¹ *School of Biological Sciences, University of Auckland, Auckland, NZ; mikhail.fokin@gmail.com, s.villas-boas@auckland.ac.nz*

² *Landcare Research, Auckland, NZ; WeirB@landcareresearch.co.nz*

³ *Biotelliga Limited, Auckland, NZ; Damien@biotelliga.com*

Abstract. *Epicoccum purpurascens* (syn *E. nigrum*) is a very common saprophytic species with a worldwide distribution. Although two revisions of Didymellaceae have been published recently expanding the definition of the *Epicoccum* genus, very little is known about the intraspecific phylogeny of *E. purpurascens*. Numerous strains of this species have been used for mining bioactive compounds, but these studies often lack genetic identification of the strain. In total, more than 60 compounds have been isolated from *E. purpurascens*, but almost nothing is known about their biosynthetic pathways and associated genes. We have carried out a meta-analysis of the literature on secondary metabolites reported for *E. purpurascens* coupled with the reconstruction of intraspecific phylogeny tree based on NCBI and our own datasets. To identify genes involved in the biosynthesis of bioactive compounds, we have sequenced, assembled and annotated the full genome of *E. purpurascens* SVB-F1 strain. We have discovered more than 30 putative secondary metabolite gene clusters predicted to encode pathways for major classes such as polyketides, non-ribosomal peptides and terpenes. Further studies in comparative genomics, transcriptomics and metabolomics of *E. purpurascens* will contribute to functional characterisation of known compounds and discovery of new ones.

Keywords. Genomics, secondary metabolites, phylogeny.

Density and diversity of the aeromycota in urban Sydney and their relationship with environmental parameters

Irga PJ¹ & Torpy FR¹

¹ *School of Life Sciences, University of Technology Sydney, Sydney NSW AU; peter.irga@uts.edu.au, fraser.torpy@uts.edu.au*

Abstract. A comprehensive survey of airborne fungi within urban Sydney, and the factors that are associated with fungal species distribution and density is lacking. This study determined the diversity and abundance of culturable outdoor airborne fungal concentrations in urban Sydney. Several sites with a range of environmental characteristics were sampled for culturable airborne fungi and a range of physiochemical air quality variables monthly for one year. Through multivariate analysis, the primary factors associated with fungal species diversity, propagule density and species distribution were identified. Grass as a component of urban forestry was associated with higher total spore density. As has been the case with research from other cities, there were major seasonal changes in the species distribution detected; although samples from most months were dominated by *Cladosporium* spp. and *Alternaria* spp. Pathogenic fungi were sparsely distributed in the data set, although *Aspergillus* spp. including *A. fumigatus* was detected in several samples. Further, the investigation indicated the potential contribution of senescent leaves to the diversity of airborne fungal propagules during the season of autumn.

Keywords. Airborne fungi, bioaerosols, seasonal; allergy, risk assessment.

What AMF communities are found within kauri roots?

Han, V¹, Padamsee, M², & Burns, B.R.³

¹*School of Biological Sciences, University of Auckland, New Zealand; vhan016@aucklanduni.ac.nz*

²*Landcare Research, Auckland, New Zealand; padamseem@landcareresearch.co.nz*

³*School of Biological Sciences, University of Auckland, New Zealand; b.burns@auckland.ac.nz*

Abstract. Arbuscular mycorrhizal fungi (AMF) form symbiotic relationships with the roots of more than 80% of all land plants. Arbuscular mycorrhizal fungi (AMF) are highly beneficial to plants where they provide enhanced nutrition to the host plant in return for photosynthates. Other benefits of AMF include increased resistance to pathogens, including *Phytophthora*, in some cases. *Agathis australis* (New Zealand Māori name kauri) is both an ecologically and culturally important (taonga) species to New Zealand. It is the only endemic member of the Araucariaceae found in New Zealand. Arbuscular mycorrhizal fungi have been observed to inhabit the roots of kauri, specifically the nodulated parts of the root. The function of AMF in kauri roots are still unknown, however, it has been speculated that they may provide increased nitrogen uptake and possibly in phosphorous uptake as well. Currently, PTA, now known as *Phytophthora agathidicida* (PA), are destroying our kauri forests. By using both root staining techniques as well as next generation DNA 454 sequencing, AMF within kauri roots may be able to be characterised. Differences and similarities between infected and uninfected roots will also be looked at. Results will hopefully reveal slight differences and similarities and future studies can be done on them.

Keywords. Arbuscular mycorrhizal fungi, kauri, 454 sequencing.

Phylogenetic diversity of *Polyporus sensu lato* (Polyporales, Basidiomycota) in Korea

Lee H¹, Kim CM², Lim YW¹

¹*School of Biological Sciences, Seoul National University, Seoul, South Korea; hodoo1@snu.ac.kr,*

ywlim@snu.ac.kr

²*National Institute of Biological Resources, Environmental Research Complex, Incheon, South Korea;*

snebull@korea.kr

Abstract. *Polyporus Micheli* ex Adans are wood rotting fungi, which produce stipitate basidiocarps with dimitic hyphal system and cause white rot. Most species of *Polyporus* grow on dead wood but several species are found on living substrates such as grass or bamboo roots. Traditionally, they were divided into six subgroups by morphological distinction without given ranks. Recent phylogenetic analysis showed that *Polyporus sensu lato* is separated into at least five well-defined clades as follows: *Dendropolyporus*, *Favolus*, *Neofavolus*, *Polyporellus*, and *Polyporus*. Eleven species of *Polyporus* have been recorded in Korea to date. In order to investigate phylogenetic diversity of *Polyporus sensu lato* in Korea, *Polyporus* specimens deposited in several herbaria in Korea were re-evaluated by multi-gene phylogeny and morphology. Thirteen species of five genera were confirmed. Two species are newly reported in Korea and four species are potential new species. Their phylogenetic relationship and distinctive characters are discussed.

Keywords. *Polyporus*, wood rotting fungi, multi-gene phylogeny.

Cortinarius majestaticus: a new name for *Descolea majestatica*

Orlovich DA & Anderson TP

Department of Botany, University of Otago, PO Box 56, Dunedin NZ; david.orlovich@otago.ac.nz

Abstract. In describing *Descolea majestatica* in 1971, Horak noted that this species shares many morphological similarities with both *Descolea* and members of the genus *Rozites* (now synonymised with *Cortinarius*), and suggested *D. majestatica* may be intermediate between the two genera. Evidence from Bayesian and maximum parsimony phylogenetic analyses, and the Shimodaira-Hasegawa test, indicates that *D. majestatica* is nested within the genus *Cortinarius*, related to an unnamed Argentinian *Cortinarius* (Trappe 26352) and not to other species of *Descolea*. The poster will present the evidence supporting the transfer of *D. majestatica* to *Cortinarius*.

Keywords. *Cortinarius*, phylogenetic analysis.

Molecular identification and phylogenetic analysis of stipitate hydroid fungi from southwestern Australia

Robinson RM^{1,5}, Stefani F², May TW³ and Syme K⁴

¹Department of Parks and Wildlife, Manjimup, WA, AU; richard.robinson@dpaw.wa.gov.au

²MycoDiagnostic Inc., Québec, QC, CA; fstefani@mycodiagnostic.com

³Royal Botanic Gardens Victoria, South Yarra, VIC, AU; tom.may@rbg.vic.gov.au

⁴1874 South Coast Hwy, Shadforth, WA, AU; katrinasyme@gmail.com

⁵Present address: 17 Woodhurst Road, Seven Mile Beach, TAS, AU

Abstract. Stipitate hydroid fungi are an artificial group from a diverse range of families and orders. In Australia they have gained little attention, but in other regions of the world many species are known to be rare or threatened. Phylogenetic analysis of the Internal Transcribed Spacer region of 81 samples of Australian stipitate hydroid fungi, predominantly from south-west Western Australia, revealed 17 clades; 10 in *Phellodon*, four in *Hydnellum*, two in *Hydnum* and one *Sarcodon*. In addition, there were two singleton phylogenetic taxa of *Phellodon*. The position of the Australian species was compared to species from nearby regions, especially New Zealand, and elsewhere in the world. Nearest matches to existing sequences were most often to species from New Zealand.

Keywords. Stipitate hydroid fungi, Phylogenetic analysis, Western Australia.

On populations of ectomycorrhizal fungi introduced to the Bonin Islands

Sheedy EM¹ & Hosaka K²

¹Department of Botany, National Museum of Nature and Science, Tsukuba, Ibaraki JP;
biz.sheedy@gmail.com

²Department of Botany, National Museum of Nature and Science, Tsukuba, Ibaraki JP;
khosaka@kahaku.go.jp

Abstract. The Bonin (Ogasawara) Islands are oceanic islands located approximately 1000 km south of Tokyo. There are no known native ectomycorrhizal (ECM) plants or fungi on these islands. *Pinus luchuensis* (Ryukyu Pine) has a native distribution in the Ryukyu Islands of Japan. However, in 1899 this ECM tree and associated ECM fungi were introduced to the Bonin Islands, where they successfully invaded. The aim of this project is to investigate population genetics of *Suillus granulatus* and *Lactarius akahatsu*, the two most frequently fruiting ectomycorrhizal fungi on the Bonin and Ryukyu Islands. Over 200 and 100 collections respectively of *S. granulatus* and *L. akahatsu* individuals were made in 2015, including collections from the two inhabited Bonin Islands (Chichijima and Hahajima) and from potential source islands in the Ryukyu Archipelago (Amami, Okinawa, Ishigaki and Miyako). Populations will be analysed by using restriction enzymes to reduce the genome complexity (eg. restriction-site associated DNA) and finding single nucleotide polymorphisms (SNPs) through next-generation sequencing. Results are expected to indicate lower genetic diversity in the non-native, compared to native, range. The results from this study will provide useful information about ECM fungi introduced to new areas, particularly where no native ECM plants and fungi were previously present.

Keywords. Genotyping-by-sequencing, introduced species, phylogeography.

The International Collection of Microorganisms from Plants (ICMP)

Weir BS, Paderes E & Petterson M

Landcare Research, Private Bag 92170, Auckland, New Zealand weirb@landcareresearch.co.nz

Abstract. The International Collection of Microorganisms from Plants (ICMP) is New Zealand's national culture collection of living Bacteria, Fungi, and Chromists. The collection and associated databases, considered 'Nationally Significant' by the government, are in part publically funded. The ICMP holds 20,000 cultures predominantly from plant, soil, and water in the natural environment, as well as important reference and type cultures of the world's plant pathogenic fungi and bacteria. All cultures are databased and available online at <https://SCD.LandcareResearch.co.nz> Cultures are available for a fee to cover retrieval costs. New accessions into the collection are welcome, and recommended when publishing papers on microbes to provide a stable permanent resource for future researchers. The cultures are preserved under liquid nitrogen or in freeze dried ampoules. The ICMP containment and transitional facility conforms to enhanced PC2 Containment criteria, with generic permits to import quarantine and unwanted organisms into New Zealand.

Keywords. preservation, cultures, collections.

Getting ready for Myrtle Rust

Ho W & Alexander BJR

Plant Health and Environment Laboratory, Ministry for Primary Industries, P.O. Box 2095, Auckland 1140, New Zealand; wellcome.ho@mpi.govt.nz; brett.alexander@mpi.govt.nz

Abstract. Myrtle rust (*Puccinia psidii*) is a highly invasive fungal pathogen which infects species within the plant family Myrtaceae. It is spreading around the globe with fairly recent incursions in Australia, New Caledonia, Indonesia and South Africa. The incursion in Australia has cost the Australian government millions of dollars to manage this rust. While myrtle rust is currently absent in New Zealand, it is anticipated that this pathogen may arrive through the prevailing winds from Australia, as a contaminant of imports, or on passengers' clothing. Myrtle rust is considered to be a major economic threat to New Zealand's 22 thousand hectares of *Eucalyptus* forests, feijoa (*Acca sellowiana*) crops and manuka honey industry as well as to high value environmental assets such as the iconic Pōhutukawa (*Metrosideros excelsa*), Rātā (*Metrosideros robusta*) and Mānuka trees (*Leptospermum scoparium*). In preparation for the arrival of this invasive pathogen, the Ministry for Primary Industries' Plant Health and Environment Laboratory (PHEL) in collaboration with other crown research agencies has developed a range of diagnostic tools to facilitate the early detection of this pathogen. This includes a myrtle rust specific real-time PCR test that provides greater sensitivity and significantly quicker results than the previously published nested PCR test and a DNA barcoding database to ensure accurate identification of Myrtaceae plants. PHEL is also currently developing a lateral flow device for rapid field testing during investigations, and to facilitate long term disease management by industries and relevant agencies.

Keywords. Biosecurity, myrtle rust, preparedness.

Lipophilic Drug Derivatives Inhibit Growth of Major Fungal Pathogens

Kane A¹, Taing W², Hanrahan J³, Hibbs D⁴ & Carter D⁵

¹School of Molecular Biosciences, University of Sydney, Sydney NSW AU; aidan.kane@sydney.edu.au

²Faculty of Pharmacy, University of Sydney, Sydney NSW AU; wlia8715@uni.sydney.edu.au

³Faculty of Pharmacy, University of Sydney, Sydney NSW AU; jane.hanrahan@sydney.edu.au

⁴Faculty of Pharmacy, University of Sydney, Sydney NSW AU; david.hibbs@uni.sydney.edu.au

⁵School of Molecular Biosciences, University of Sydney, Sydney NSW AU; dee.carter@sydney.edu.au

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