2010 Prize Winners

The following prizes were awarded to student members presenting at the Australasian Mycological Society Conference at the Sydney Convention & Exhibition Centre, Darling Harbour in Sydney, 4–8 July 2010.

The Australasian Mycological Society established the Dr Jack Warcup Memorial Prize to honour its first patron and to encourage students to present their work at the Society's conferences. The prize of $250 and is awarded for either the best talk or poster presented by a student.

Dr Jack Warcup Memorial Prize

Rachel Graham, University of Southern Queensland. Rachel is a student of John Dearnaley.

After working for several years in disability support, I decided to go to university as a career change. I completed a degree in plant science with Honours at USQ in 2009. During my honours year I looked at the fungal associations of the vulnerable orchid Sarcochilus weinthalii. It was there that my interest in fungi was sparked. I am currently undertaking a PhD looking at the antibiotic potential of endophytic fungi in semi-evergreen vine thickets (dry rainforest). My research interests include the use of fungi as biocontrols, genetics and the importance of fungal biodiversity in ecosystem function. Upon successful completion of my PhD I hope to do a postdoc in one of these areas.

Mycorrhizal associations of the vulnerable epiphytic orchid, Sarcochilus weinthalii

Rachel Graham and John D. W. Dearnaley
Australian Centre for Sustainable Catchments, University of Southern Queensland, Toowoomba QLD 4350, Australia.

The Orchidaceae is the most species abundant family in the flowering kingdom and yet it contains the highest number of vulnerable or endangered taxa. One of the major factors identified which contributes to orchid rarity is a dependency on specific mycorrhizal interactions, usually from fungal species forming a single closely related clade. While the mycological interactions of terrestrial orchids have been well studied over the years, comparatively little is known of epiphytic orchids in this regard. *Sarcochilus weinthalii* is an epiphytic orchid restricted to the Darling Downs region. It has been listed as vulnerable under the EPBC Act 1999, but very little research has been undertaken regarding the species.

This research examined the mycorrhizal associations of *S. weinthalii* across three sites on the Darling Downs, Queensland. The mycorrhizal fungal partner of the species was determined through DNA sequencing and phylogenetic analysis of fungal ITS-DNA regions. Seed germination tests were then used to confirm the mycorrhizal status of the identified fungi.

The results of this study found that *S. weinthalii* interacts specifically with a single species of *Ceratobasidium* and seed colonisation tests showed that seeds would only germinate in the presence of this fungus. The results of this study suggest that the specific mycorrhizal association may be a major restricting factor for *S. weinthalii.*

Australasian Mycological Society Poster Prize

Michael Sivell, University of Sydney. Michael is a student of Dee Carter.

I completed my undergraduate studies in Forensic Biology before moving into the field of membrane proteomics for Honours and fungal proteomics for my PhD. At this point of my scientific career my primary research interest is the development of proteomic techniques and protocols with regard to investigating and understanding fungal pathogenesis. I am not 100% certain about the who, what, where, why and how of my future in science, however I look forward to using and developing my skills in proteomics to gain a better understanding of how things work at the molecular level. I have a great deal of respect for proteomics and have a firm belief that it will form a large part of both my future and the future of science.

Differential expression of proteins in cryptococcal lung infection

M. Sivell[1], B. Herbert[2], C. Hill[1], M. Padula[1], M. Krockenberger[3], D. Carter[4]
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Fungal diseases are an emerging problem worldwide. *Cryptococcus gattii* is an encapsulated fungus that has the potential to act as a primary pathogen, leading to the death of healthy human hosts. The aim of this project is to determine the proteomic changes that occur during cryptococcal infections, both in the host lung and in the pathogen. Differentially expressed proteins may reveal potential biomarkers and provide insight into how the pathogen initiates and maintains infection and how the host lung responds.

This study focuses on the lung proteins using a rat infection model. Fisher rats were inoculated intratracheally with 1×10^7 *C. gattii* cells. Six weeks post inoculation the rats were sacrificed and the lung tissue isolated. Quantitative 2-D gel and 1-D gel proteomics was then performed on whole lung protein and membrane fractions. This revealed the upregulation of a number of lung stress and tissue remodelling proteins and the down regulation of tissue shape control proteins. Significant up-regulation of fatty acid binding protein was also observed. This protein enables the proliferation of the infecting organism in vivo, thus a down regulation would be beneficial for the host. This is an interesting observation as the expression of this protein indicates that *C. gattii* may have the capability to induce the host into doing something that is detrimental to it.

Eukaryotic Cell Young Investigator Award

Eve Chow, University of Queensland. Eve is a student of James Fraser.

I am currently a second year PhD student at the Centre of Infectious Disease Research, School of Chemistry and Molecular Biosciences, University of Queensland. I did my undergraduate Honours year in Dr James Fraser's lab, and continued on to complete my PhD. I am interested in the field of infectious diseases, and my current research focuses on the subtelomeric regions of *Cyrptococcus neoformans* and the microevolutionary events that might occur during

infection that could reveal how the fungus evolves to persist in infection. I am intending to pursue a medical degree after I have completed my PhD, and hope to combine my research with clinical practice.

Gene amplification as a mechanism of microevolution in the subtelomeres of *Cryptococcus neoformans*

Eve Chow, Carl Morrow and James Fraser
Centre for Infectious Disease Research, School of Chemistry and Molecular Biosciences, University of Queensland, Australia.

The subtelomeric regions of diverse organisms ranging from protists to fungi undergo a much higher rate of rearrangement than is observed in the rest of the genome. We have investigated whether similar genetic changes occur in the subtelomeres of the fungal human pathogen *Cryptococcus neoformans* to contribute to infection. Comparative bioinformatic analyses of the subtelomeric regions of three sequenced *Cryptococcus* genomes have shown that these genomic features are generally syntenic, although there are genes in the subtelomeres of some isolates that are absent in others. Using molecular techniques we have characterised the differences in one of these regions, the right telomere of chromosome 3, revealing the presence of a gene amplification event in a number of clinical isolates. Involving a gene encoding an arsenite-efflux transporter (ARR3), the 3,177 bp amplicon existed in a tandem array of 1 to 15 copies, and occurs exclusively in strains belonging to *C. neoformans* var. **grubii** subclade VNI A5. Strains bearing the amplification displayed dramatically enhanced resistance to arsenite that correlated with the copy number of the repeat. The origin of this increased resistance was verified as being transport related by functionally complementing an arsenite transporter mutant of *Saccharomyces cerevisiae*. Further supporting this role, *C. neoformans* experimental evolution in the presence of increasing concentrations of arsenite yielded strains with additional ARR3 amplification that accounted for up to ~1% of the genome, conferring resistance to arsenite to concentrations greater than 30 mM.

Beyond identifying fungal isolates that are highly resistant to arsenite, these studies describe the first reported instance of microevolution via gene amplification in *C. neoformans*. Together, these results support the hypothesis that adaption through gene amplification may be an important mechanism that *C. neoformans* employs in response to environmental stresses such as those encountered during infection.

Visiting graduate student scholar infungal systematics and evolution: University of Tennessee

A visiting graduate student scholar is sought to engage in research in fungal systematics and evolution at the University of Tennessee. The research will take place in the laboratory of Dr. Brandon Matheny and is funded by the National Science Foundation award REVSYS: Revision of Australian Inocybaceae: studies in systematics and evolution of ectomycorrhizal Agaricales from the southern hemisphere (DEB0949517). The position includes a six-month stipend and funds for travel. Graduate student applicants from Australia or graduate students involved with research on Australian fungi are particularly encouraged to apply, but applicants from elsewhere will be considered. The time period for support is scheduled between 1 September 2011 and 31 March 2012. Consideration will be given to split the six-month stipend into two to support two visiting graduate students for three months of support. The University of Tennessee provides a stimulating atmosphere in ecology and evolutionary biology due to a mix of internationally known faculty members, numerous junior faculty, and immediate proximity of NIMBioS, the National Institute for Mathematical and Biological Synthesis. Opportunities to sample diverse fungi abound due to the proximity of the Great Smoky Mountains, the Cumberland Plateau, and a variety of habitats in the Tennessee River Valley. Applications should include a CV, a proposed research statement of not more than one page, and a list of two references to contact. Applications should be sent to Dr Brandon Matheny at pmatheny@utk.edu.

Vale Ross Beever (1946–2010)

Dr Ross Beever passed away peacefully on 3 June 2010 after a short battle with bowel cancer. Ross' scientific interests and influences were wide-ranging. His studies on phosphorus uptake in the fungus *Neurospora crassa* led him to co-author a review (1981, *Advances in Botanical Research* **8**, 127–219) of phosphorus uptake, storage and utilisation in fungi. This was a significant synthesis of knowledge at the time, and it stimulated much new research on phosphate utilisation by fungi. Ross' expertise in fungal genetics resulted in numerous publications on the plant pathogen *Botrytis cinerea,* and in him pursuing the question "why fungi like sex?". Ross led the discovery that cabbage tree decline in New Zealand was caused by a phytoplasma, and his careful elimination of other potential causative agents (in the face of public and political opposition) is testament to his tenacity, scientific rigour and strength of character. Ross was passionate about truffle-like fungi. Those who forayed with him were always impressed by how willing he was to share his knowledge about fungi, and indeed to talk on any subject, in a friendly, encouraging way with thoughtful enthusiasm, and his ideas had a strong foundation in his incredibly broad expertise in fungal and plant biology. Ross and Jessica Beever have both played an immeasurable role in nurturing younger generations of scientists, and all of those who have come under their infectious spell of enthusiasm will be sharing the pain of this sad loss with Jessica, to whom we offer our most heartfelt condolences. Ross was farewelled at a service in Auckland on 10 June 2010, where a standing-room-only crowd recognised Ross as a world-famous scientist, and celebrated the close and loving relationships he had as husband to Jessica and as brother, father, grandfather, mentor, colleague or friend to all those with whom he so generously shared his life.

David Orlovich