required for correct formation of the cell wall. Growth of ΔUth1, but not ΔOtp1/ΔUth1 or ΔOtp1 cells are sensitive to caspofungin, an inhibitor of (1-3)-ß-D- glucan synthase, an enzyme required for cell wall formation. OTP1 is located in the late Golgi and sequence homology predicts it to be a cargo receptor. Results will be discussed in a model encompassing cell wall integrity signalling and the regulation of mitophagy.

id #25626

Invited speaker Thursday

Molecular identification of mycorrhizal Russulaceae fungi

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The Russulaceae is a family of basidiomycetous fungi found in a variety of habitats around the world. While reasonably common in Australian temperate forests, little work has been conducted on this group, with the result that many taxa are undescribed or poorly documented. The aim of this research project is to improve this situation.

The identification of Russulaceae fruiting bodies to species level has many challenges and is predominantly based on characteristics that are highly subjective, changeable, require specialised chemicals, and specialised equipment. A certain amount of expertise is also required. However, even this is no guarantee of consistently obtaining a positive species identification.

Molecular analysis potentially offers a non-subjective method of identification. In particular, the internal transcribed spacer (ITS) region of fungal DNA has been proposed as the primary standard molecular benchmark for identification of fungi. Coupled with access to millions of sequences held in databases such as GenBank, it would seem that molecular identification offers a useful opportunity to streamline and improve the identification of the Russulaceae.

However, this is not always the case, and in sequencing the ITS region of numerous specimens from this family a number of issues have arisen.

This presentation will examine some of the difficulties experienced in the molecular identification of Australian Russulaceae species and discuss some of the potential solutions.

id #25628

Invited speaker Thursday

Modifications to the International Code of Nomenclature in support of modern fungal taxonomy

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Discussions at Nomenclature Sessions during the 10th International Mycological Congress indicated strong support among mycologists for a number of proposals to amend the *International Code of Nomenclature for algae, fungi and plants* (ICN). Such proposals include: (1) changing the conditions for epitypification so that sequenced epitypes can be designated without having to establish that DNA is not recoverable from the holotype, (2) introducing a requirement to register later typification acts such as lectotypification, (3) changing the citation of sanctioned names, (4) prohibiting cross-kingdom homonyms, and (5) ending the priority of sexually typified names. Another change strongly supported by mycologists is to transfer governance so that matters in the ICN peculiar to fungi are dealt with by International Mycological Congresses. Beyond such changes, a proposal should be considered to include in the ICN an article or recommendation dealing with provision of DNA sequence data for new species of fungi, especially in the light of primary and secondary barcodes becoming well-established.

Mandatory registration of names of fungi was introduced in the Melbourne ICN. There is occasional mis-citation of identifiers by authors of fungi names, but otherwise registration has been well-accepted by the mycological community. Nevertheless, there are some issues. Firstly, synchronisation of the three approved registration databases remains problematic. Secondly, it would be ideal if registration databases output all data that is input on registration, in a searchable form, and as web services. This ability to freely recover the protologue and other key information was one of the main reasons for introducing registration in the first place. There is currently much duplication of nomenclatural information across global, national and institutional databases (within Australia, examples are AusFungi, APPD, and individual reference collection databases). Mechanisms to reduce duplication and increase the utility of fungi name databases will be discussed.

id #25605

Invited speaker Thursday

Hunting for antifungal-chelator drug synergy using biological networks

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Invasive fungal infections (IFIs) in humans are difficult to treat. The few effective antifungal drugs available have issues regarding toxicity and long-term effectiveness against drug-resistant strains. It is difficult to develop novel antifungal drugs, thus a promising direction of research is to identify synergistic agents for existing therapy. Iron chelators administered with certain antifungals have been found to improve the clearance of some fungal infections, but the mechanistic role of antifungal-chelator combinations is complex and poorly understood. Using checkerboard assays, we found the iron chelator lactoferrin (LF) was synergistic with amphotericin B (AMB) for *Saccharomyces cerevisiae*. We extracted mRNA from *S. cerevisiae* treated with i) AMB only, ii) a combination of AMB + LF or iii) corresponding matching controls. RNA-seq data were generated using