

## Theses in Australasian Mycology

**Surrogates for cryptogam conservation - associations between mosses, macrofungi, vascular plants and environmental variables.****Sapphire J.M. McMullan-Fisher****Date of acceptance:** February 2008.*School of Geography and Environmental Studies, University of Tasmania, Australia.***Current contact:** PO Box 8083, Hilton, WA 6163, Australia.Email: [sapphire@flyangler.com.au](mailto:sapphire@flyangler.com.au).**Supervisors:** Professor Jamie Kirkpatrick<sup>1</sup>, Doctor Tom May<sup>2</sup>, Doctor Emma Pharo<sup>1</sup>, Professor Richard Coleman<sup>1</sup>.<sup>1</sup> School of Geography and Environmental Studies, University of Tasmania. <sup>2</sup> National Herbarium of Victoria, Royal Botanic Gardens Melbourne, Australia.**URL:** <http://eprints.utas.edu.au/8282/>**Key words:** Conservation surrogates, macrofungi, mosses, vascular plants, environmental variables, Tasmania.**Abstract**

Cryptogams are rarely included in conservation planning and management. This study focuses on two groups of cryptogams, mosses and macrofungi, to test the usefulness of vegetation type, vascular plants and environmental variables, including substrate, as surrogates for cryptogams in achieving satisfactory conservation outcomes.

Sites from four vegetation types (wet forest, heathy woodland, grassy woodland and alpine heath) in the Hobart region of Tasmania were surveyed over a period of several years for vascular plants, mosses and epigeous macrofungi using permanent plots. Repeated sampling of the macrofungi ensured that a reasonable proportion of the taxa likely to be present were recorded. A total of 284 vascular plants, 71 mosses and 233 macrofungi were recorded.

Ordination and Analysis of Similarity both showed that the four vegetation types were significantly different from each other; this pattern was similar for vascular plants, mosses and macrofungi. Congruence between the three taxonomic groups was tested using partial Mantel tests; all pair-wise associations were highly significant, showing highly predictive r-values. There were similarly significant and predictive associations between environmental and substrate variables and biotic groups (vascular plants, mosses and macrofungi, and their various subsets). Canopy cover was the best single predictor of most biotic groups. Combinations of environmental variables had higher correlations



Mycorrhizal macrofungi *Amanita xanthocephala* amongst litter and pleurocarpus mosses *Acrocladium chlamydophyllum*, *Ptychomnion aciculare* and *Thuidiopsis sparsa*.

with biotic groups than single variables. Mosses and macrofungi exhibited high substrate fidelity across time and space. Substrate preferences of macrofungi did not vary among vegetation types, but mosses in wet forest occurred on a wider range of substrates than the same species in other vegetation types.

Iterative, optimisation, fully random and stratified random methods were compared for their effectiveness in the selection of sites for the conservation of vascular plants, mosses and macrofungi. When 10% of sites were selected for reservation there was little commonality in site selection between the three taxonomic groups. When 30% of sites were selected, at least 48% of all taxa were reserved by all approaches tested. The most useful data sets for selecting sites representative of the three taxonomic groups were vascular plants, named species from all three taxonomic groups and sites selected by random with equal proportions of each vegetation type.

The results suggest that coarse scale conservation of vegetation types with reservation of at least 30% of their area should conserve common mosses and macrofungi. However, at the site scale, uncommon taxa of mosses and macrofungi are not concordant with vascular plants. Associations of moss and macrofungal species with particular substrates and microhabitats may assist with site selections for reservation. Particularly for rare species, further research is required on occurrence and substrate and habitat specificity. Taking into account the information now available,

best-practice management decisions for cryptogams should be based on surrogates similar to those tested in this study and should include an understanding of their trophic modes and functions in ecosystems.

### Publications

- McMullan-Fisher, S. J. M., T. W. May, and P. J. Keane. 2002. The macrofungal community and fire in a mountain Ash forest in southern Australia. *Fungal Diversity* **10**, 57-76. [http://www.fungaldiversity.org/fdp/sfdp/FD\\_10\\_57-76.pdf](http://www.fungaldiversity.org/fdp/sfdp/FD_10_57-76.pdf)
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### Coarse woody debris, macrofungal assemblages, and sustainable forest management in a *Eucalyptus obliqua* forest of southern Tasmania.

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**Key words:** macrofungi, soil, wood, litter, ecology, phenology.

### Abstract

This study focussed on two components of the forest ecosystem at a small spatial scale: coarse woody debris (CWD), defined as fallen dead wood  $\geq 10$ cm diameter and  $\geq 1$ m length, and the macrofungal assemblages found on wood, soil and litter in native forest at different times of regeneration since the natural disturbance of wildfire.

The CWD on the forest floor and standing dead wood (stags) in four 50x50m plots (=1ha total area) with differing wildfire histories in a *Eucalyptus obliqua* dominated native wet sclerophyll forest in southern Tasmania, Australia, were quantified and mapped. The CWD volumes obtained were amongst the highest in the world. Analyses showed that although a plot size of 0.25ha was too small to give an accurate measurement of volume, it was large enough to contain dead wood



*Postia punctata*, a common polypore on large diameter wood in the wet eucalypt forests of southern Tasmania.

having attributes that reflected the stand structure resulting from wildfire disturbance. Therefore, a plot's wildfire history can be deduced from the CWD and stags of a 0.25ha plot.

The substrates wood (dead wood and standing trees), soil and litter in each plot were surveyed for macrofungal fruit bodies at approximately fortnightly intervals for 14 months. A total of 849 macrofungal species was recorded from 1ha of native forest. Wood supported 410 species of which 295 were on CWD but not exclusively, i.e. a few species were found on CWD and soil or on CWD and litter. The majority of the remaining species on wood was supported by 'other dead wood' (a category containing dead wood that did not fit into CWD), which contained many species not in common with those on CWD. It was concluded that macrofungal species richness on CWD is not affected by decay class; however, length or surface area explained between 45-48% of the variation in species richness.

Of the 495 species found fruiting on soil, 330 were known to be ectomycorrhizal and 165 were considered decomposers. In addition, 146 species of macrofungi were associated with litter. It was found, using temperature and rainfall data, that the appearance of fruit bodies is seasonal but not directly attributable to rainfall events. There was a better correlation using the indigenous peoples' concept of three seasons than when using the four European-based seasons.

In essence, each plot contained a distinctive mycota, reflecting its chronosequence history, site



characteristics (e.g. soil type, soil pH) or microclimate. To maintain the macrofungal diversity associated with the differing plots, a mosaic of multi-aged stands in the managed forest landscape is needed to provide inoculum for the reestablishment of macrofungal communities in forests at different times of regeneration. In addition, reserves should be as large as possible (at least 1ha) to encompass the variability (due to site characteristics, vegetation type, etc.) in the forest landscape and the associated macrofungal diversity as evidenced by the appearance of fruit bodies. This has particular implications for the silvicultural treatment of ARN (aggregated retention) where the retained aggregates provide refugia for macrofungal assemblages associated with the pre-treatment forest type. The results of the study also suggest that there should be some coupes assigned to longer rotations to provide a continuum of dead wood sizes and decay classes in the forest landscape, thereby maintaining associated macrofungal diversity.

### Publications

- Gates GM, Mohammed C, Wardlaw T, Ratkowski DA, Davidson NJ 2011. The ecology and diversity of wood-inhabiting macrofungi in a native *Eucalyptus obliqua* forest of southern Tasmania, Australia. *Fungal Ecology* 4, 56-67.
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Declining *E. delegatensis* forest in north-eastern Tasmania.

## Eucalypt Dieback and Ectomycorrhizal Community Ecology of *Eucalyptus delegatensis* Forest, Tasmania, Australia..

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**Key words:** Forest decline, fire, fungi, soil chemistry, vegetation, Cortinariaceae, Russulaceae phenology.

### Abstract

Ectomycorrhizal (ECM) fungi underpin critical ecosystem processes which affect tree health. Eucalypt decline is widespread throughout Australia and has been linked to altered fire regimes and associated changes in mycorrhizal communities. This thesis explores ECM fungal communities in relation to eucalypt health, understorey vegetation and soil chemistry, and furthers our understanding of ECM ecology and factors important to the maintenance of a healthy forest ecosystem.

Twelve plots with known disturbance histories were established in eucalypt forest across Tasmania, with either rainforest or dry sclerophyll understorey. ECM fungal sporocarps, root tips and soil samples were collected during a three-year period. Fungal species were identified through DNA sequencing and phylogenetic analysis. Understorey vegetation, soil and eucalypt foliage chemistry and eucalypt crown condition data were collected from each plot. Primary crown dieback was the most effective method for the measurement of eucalypt health. Multivariate statistical analyses were used to explore the relationships among ECM communities, eucalypt health, vegetation and abiotic variables.

*E. delegatensis* forest with rainforest understorey was more likely to be affected by severe eucalypt decline and had higher concentrations of soil inorganic nitrogen (N) and eucalypt foliar N, lower concentrations of soil and eucalypt foliar phosphorus (P), than forest with sclerophyll understorey. As forest declined in



Species of Cortinariaceae found in north-western Tasmanian dry sclerophyll eucalypt forest.

health there was a shift from N limitation to P limitation. Soil chemistry was important in explaining the ECM communities of eucalypt forest. Soil pH, total soil N, soil organic carbon and soil P were significant in predicting ECM communities in distance-based multiple linear regression models. Available soil nitrate and P were significant in predicting ECM community richness and showed that high richness was associated with low available soil nitrate or P. Northern hemisphere studies which show that changes in soil chemistry, especially mineral N, can strongly influence ECM species richness, species composition and community structure corroborate the likely influence of soil N on the ECM communities of *E. delegatensis* forest.

Similar to other Australian forests the Cortinariaceae were highly diverse and were the most species-rich family. The Helotiales, Russulaceae and Thelephoraceae were important additional components. ECM communities differed between moderately and severely declining forest. The Cortinariaceae had high species richness in healthiest sites while the Russulaceae and Thelephoraceae were rich in forest affected by severe decline.

This is the first study to find a strong correlation between ECM fungal communities and the status of eucalypt

forest health. The results support the model that in the absence of fire, premature decline of temperate Australian eucalypt forests is closely linked to changes in soil chemistry, understorey vegetation and ECM communities.

### Publications

- Horton BM, Close DC, Wardlaw TJ, Davidson NJ 2011. Crown condition assessment: An accurate, precise and efficient method with broad applicability to *Eucalyptus*. *Austral Ecology* **36**, 709-721 doi:10.1111/j.1442-9993.2010.02206.x.
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