Aggregated retention and macrofungi: a case study from the Warra LTER site, Tasmania

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Abstract

The macrofungi of an aggregated retention coupe harvested and burnt in April 2004 at the Warra long-term ecological research (LTER) site were documented at approximately fortnightly intervals over a period of 16 months between February 2005 and June 2006. In transects of approximately 400 m total length, 167 macrofungal species were recorded in the unharvested aggregates compared to 125 species in the regenerating harvested area, with 63 species common to both. The regenerating area was a source of many saprotrophic fungi and also contained many species that are characteristically opportunistic, appearing after disturbance or fire but not generally seen in forests that have progressed beyond the earliest stage of regeneration. The regenerating area also contained a few species normally associated with mature forest, the presence of which may be attributed to the proximity of mature forest retained in the aggregates. Comparison of the aggregates with an unharvested control coupe sampled at the same intensity and over the same time period indicated lower species richness in the aggregates. This suggests that there are factors present, such as effects of the initial site preparation, opening up of the canopy, and proximity of the surrounding harvested areas, which tend to suppress the full development of the mycota in the aggregates. Nevertheless, the majority of ectomycorrhizal species in the aggregated retention coupe were found only in the unharvested aggregates, indicating that the latter are important reservoirs of ectomycorrhizal fungal diversity, and that they may be expected to show an increased species richness at a later stage of regeneration of the surrounding forest.

Introduction

The Warra silvicultural systems trial was established as a means of assessing a range of alternatives to clearfell, burn and sow (CBS) in Tasmania's lowland wet eucalypt forest (Hickey *et al*. 2001). Ecological assessments have been based on long-term monitoring of the responses to these treatments of vascular plants, non-vascular plants (Kantvilas and Jarman 2004), birds (Lefort and Grove 2009) and litter-dwelling beetles (Baker *et al.* 2009). Out of these assessments, there is growing concensus that aggregated retention (ARN) is a suitable alternative to clearfelling in old-growth forest. A synthesis of these studies (Forestry Tasmania 2009) has concluded that the retained aggregates appear to be functioning as 'lifeboats' (Rosenvald and Lõhmus 2008), in that (at least for beetles and birds) the species assemblages present in aggregates in the first few years following harvest are similar to those present before harvest and/or in nearby extensive unharvested forest. However, responses are species-specific, with some mature-forest species proving to be more resilient than others. They also do not yet demonstrate a

convincing effect of the retained aggregates 'influencing' the successional trajectory of the newly regenerating forest surrounding the aggregates, which is proposed as one of the major ecological advantages of ARN (Forestry Tasmania 2009).

Because of the early promise shown by ARN at Warra, we sought to test the resilience of retained aggregates with respect to a further group of organisms, the macrofungi. Macrofungi were an appropriate choice of study for two reasons. First, fungi are 'arguably among the most important of forest organisms' (Robinson and Bougher 2003): many species are mycorrhizal, influencing plant community structure and succession over decades and centuries (Pascoe and Shipton 1996), while others are saprophytic, playing an important role in releasing and recycling nutrients from dead organic matter (Bougher and Syme 1998). Second, macrofungi have been the focus of previous studies in the Warra silvicultural systems trial area (Gates *et al.* 2005), meaning that the local mycota was already reasonably well-characterised for both mature unharvested and recently clearfelled forest.

In the present study, we examined whether retained aggregates were able to support macrofungal assemblages typical of mature unharvested forest, or whether there was evidence of ecological perturbation brought about by the harvesting of the surrounding forest and the subsequent regeneration burn. We were also interested in whether the retained aggregates might 'influence' macrofungal assemblage composition in the harvested area.

Methods

Sites and site preparation

Two coupes were chosen for this study, both forming part of the Warra silvicultural systems trial, situated at latitude of 43º06´S and longitude of 146º42´E. One of these coupes ('control' coupe WR008J, hereafter known as CON) comprised unharvested mature forest. This is the same coupe used for comparison with clearfelling as reported in Gates *et al.* (2005). The other coupe in the present study was aggregated retention (ARN) coupe WR001E. Both coupes formerly comprised wet sclerophyll forest with no previous history of harvesting. The dominant eucalypt was *Eucalyptus obliqua* L'Hér., and the forest had an understorey of the "G" type (Neyland 2001), containing large amounts of *Bauera rubioides* Andrews, *Gahnia grandis* (Labill.) S.T. Blake and *Melaleuca squarrosa* Donn ex Sm., but lacking *Nothofagus cunninghamii* (Hook.) Oerst. and other rainforest elements. The lack of fire-sensitive rainforest elements and the multi-aged nature of the eucalypts at each site imply that the last wildfire was not stand-replacing; Alcorn *et al.* (2001) concluded that the last fire was about 70 years ago. Both CON and ARN were situated on a gentle to moderate south-facing slope, with CON lying immediately adjacent to the western boundary of ARN. The underlying rock type for both coupes was Quaternary dolerite talus overlying Permian sediments, with water drainage from north to south.

At the time of this study, the ARN coupe (Figure 1) had about 70% of its area harvested, with the remaining 30% retained in eight internal aggregates, the sizes of which ranged between 0.4 and 0.73 ha. Harvesting of this coupe began on 26 March 2003, was completed on 5 August 2003, and a low-intensity regeneration burn was conducted on 20 April 2004. Although the intent was to burn the whole of the harvested area, some parts escaped burning and a mosaic resulted in which the harvested area was burnt to varying degrees. No sowing of seed followed. The interiors of the retained aggregates used in the survey escaped burning, but some parts of their peripheries were singed or scorched.

Survey methods

Macrofungi were surveyed by means of repeated visits to fixed-length transects. Three of the seven aggregates, labelled W (West), C (Centre) and E (East) in Figure 1, were chosen for the survey, as some tracks had already been cut for other research projects. Additional tracks were subsequently cut to give a total transect length of about 400 m across the three aggregates sampled. This total corresponds approximately to the total transect distance in the harvested area, giving approximately equal sampling effort and allowing comparison of the macrofungi of the aggregates and the harvested areas. In CON, the same track was used as that of the previous study (see Gates *et al.* 2005), but instead of using the full 1300 m transect length, only the first 400 m (4 sections) was used, to give comparable sampling effort.

Surveying was done on the same days in ARN and CON, at approximately fortnightly intervals during 35 visits between 8 February 2005 and 16 June 2006. Species of macrofungi seen from the track were recorded, but no diversions were made from the track. There were seven distinct sampling areas in ARN, and a separate list of fungi was made in each area. The three unharvested aggregates comprised a combined sampling unit referred to hereafter as AGG, and the four cleared areas comprised another combined sampling unit, referred to hereafter as HAR. Presence or absence of all species of macrofungi were recorded as formal or "tag" names, along with the substrate on which they appeared and whether the substrate had been burned or escaped burning. Therefore, the following categories resulted: wood burnt, wood unburnt, soil burnt, soil unburnt, litter burnt, litter unburnt, and dung.

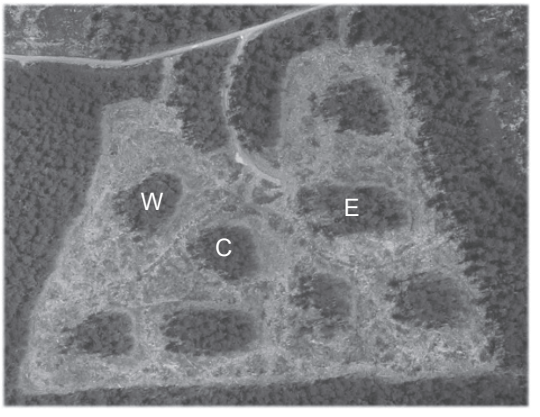

Figure 1. Aerial photograph of the ARN coupe WR001E. The grey areas are the cleared, burnt areas. The three labelled aggregates are West (W), Centre (C) and East (E), having areas of 0.58, 0.50 and 0.73 hectares, respectively. The mature forest coupe WR008J (CON) was located near the western (left) boundary of the ARN coupe (see Gates et al. *2005).*

Species names

As the taxonomy of the Australian macrofungi remains poorly known, with the majority of species still to be validly named, we used a mixture of validly described species and "tag" names, the latter for unnamed, but readily recognised, species. Names of validly described species of the Basidiomycota were taken from May and Wood (1997), May *et al.* (2003) or from the interactive, updated list of fungi on the Royal Botanic Gardens Melbourne website (www.rbg.vic.gov.au). As no Australian catalogue of Ascomycota exists at the present time, the names used in this paper for those species are based on those that are in current use by Australian authors or that can be searched on websites such as the Index Fungorum (www.indexfungorum.org/Names/Names.asp) or Landcare Research, New Zealand (nzfungi.landcareresearch.co.nz/html/mycology.asp). All species new to the authors were macroscopically and microscopically described, and drawings and photographs were made. Representative material was collected wherever possible and deposited in the Tasmanian Herbarium (HO) as voucher material for this study.

In this study, we ascribed each basiomycetous species to one of two

life mode categories, "decomposer" (to encompass both saprotrophic and parasitic species), and "ectomycorrhizal" (the latter being predominantly found on soil). Because most ascomycetous taxa remain unidentified to species level and are of uncertain life mode (e.g. Tedersoo *et al.* 2006), we retained them in a third category, Ascomycota.

Statistical methods

Fungal species records from each visit were converted to presence/absence data. For this purpose, at any visit, tabulations of unduplicated records were used: species appearing in more than one component part of a sampling unit were counted only once for that unit. As the macrofungi of all three sampling units were recorded at each of the 35 visits, paired-sample t-tests were used to test the null hypothesis of no difference in species richness between AGG and HAR, between AGG and CON, and between CON and HAR.

To establish the relationship between species numbers and sampling intensity, the Mao-Tau estimator in EstimateS (Colwell 2005) was applied to the species lists from the 35 visits to each sampling unit. The Mao-Tau estimator is a theoretical estimator for "sample-based rarefaction" (see Colwell *et al.* 2004) that effectively removes seasonality and random variation among visits, producing a smooth species accumulation curve charting the effect of repeated visits.

Differences among species assemblage compositions were visualised using non-metric multidimensional scaling (MDS), employing the Bray-Curtis measure of dissimilarity, but without any further standardisation or transformation. MDS was performed using the program Primer 6 (2006). Formal testing of differences in assemblage composition among the sampling units was done using canonical analysis of principal coordinates (CAP) (Anderson and Willis 2003), using the program of the same name, available as freeware from the home page of M.J. Anderson of the University of Auckland (http://www.stat.auckland.ac.nz/~mja/).

Chi-square tests were conducted to examine whether the ratio of basidiomycetous ectomycorrhizal species to basidiomycetous decomposer species is the same for all sampling units.

Results

Species identification

Of the 387 species recorded during the survey, 179 species (46.3%) are formally described, with the remainder bearing tag names only. All species found are listed in alphabetical order in Appendix 1, without regard to their taxonomic position, which is in a constant state of flux.

Species richness and frequency distributions

As 35 visits were made to each of the three sampling units AGG, CON and HAR, a species could have been recorded a maximum of 105 times. The full frequency distribution (Figure 2) shows that, of the total of 387 species recorded, 162 (41.9%) were recorded once only, 57 (14.7%) were recorded twice, 28 (7.2%) were recorded three times, and so on. Overall species richness was higher in AGG (167 species from 494 records) than in HAR (125 species from 550 records), with both parts of ARN combined (229 species from 1044 records) being less rich than CON (288 species from 942 records).

Figure 3 shows how the number of species observed for each treatment varied by visit. The pairwise t-test based upon these visits gave a non-significant difference between the species numbers in HAR and AGG ($t = 1.64$, $df = 34$, $P = 0.110$), suggesting that the two components of ARN are about equally species-rich at any given point of time. Highly significant differences were obtained, however, between the control coupe and the component parts of ARN

(CON vs. AGG, t = 7.22, df = 34, P < 0.0001; CON vs. HAR, t = 6.31, df = 34, P < 0.0001). In all three of these t-tests, the residuals were close to being normally distributed.

Smoothed species accumulation curves are shown in Figure 4, calculated using the Mao-Tau estimator, with their standard errors. In no case does the number of species

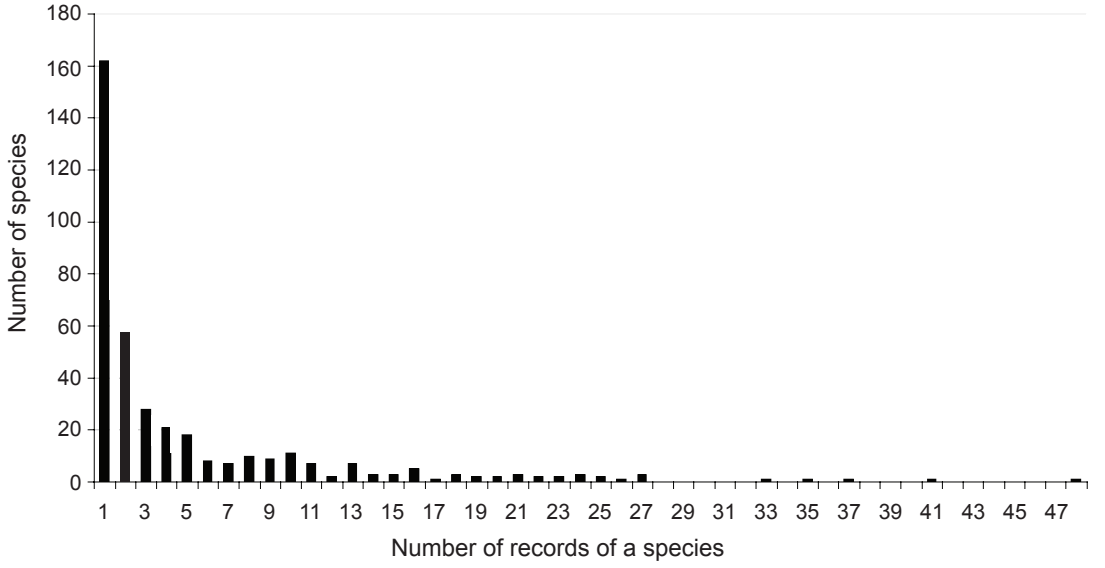

Figure 2. Frequency distribution of sampling for the 387 species of fungi recorded during the study. The ordinate represents the number of species having the number of records given by the abscissa. A record implies the species was recorded at one of the 35 visits to one of the three sampling units AGG, CON or HAR separately.

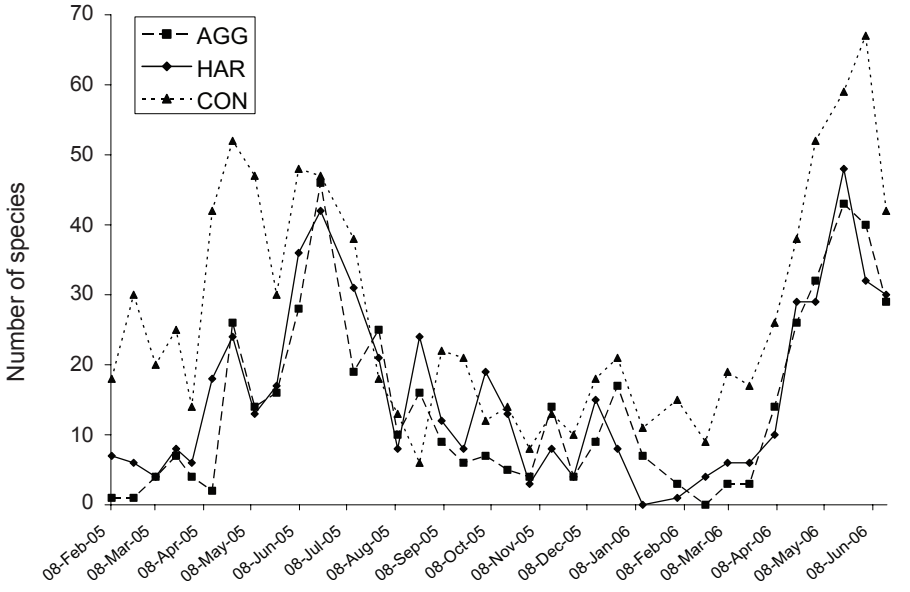

Figure 3. Variation in the number of species of macrofungi recorded on separate visits to each of three sampling units.

approach an asymptote, indicating more species would be detected by more visits in each case.

Assemblage composition

Figure 5 depicts the first two axes of a three-dimensional MDS configuration applied to the presence-absence fungal lists for each of the visits to AGG, CON and HAR. This unconstrained ordination had a "stress" measure of 0.13, and shows a clear separation between the mature forest CON and the harvested areas HAR, with the unharvested aggregates AGG sandwiched between the two.

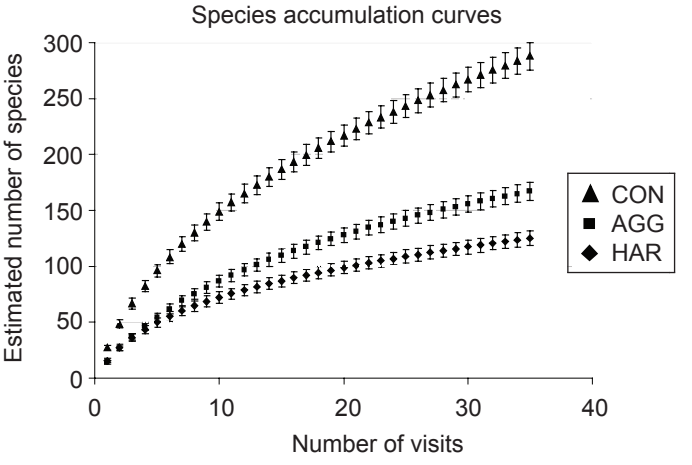

Figure 4. Species accumulation curves for the three sampling units calculated using the Mao-Tau estimator on the species lists from the 35 visits. The bars represent standard errors.

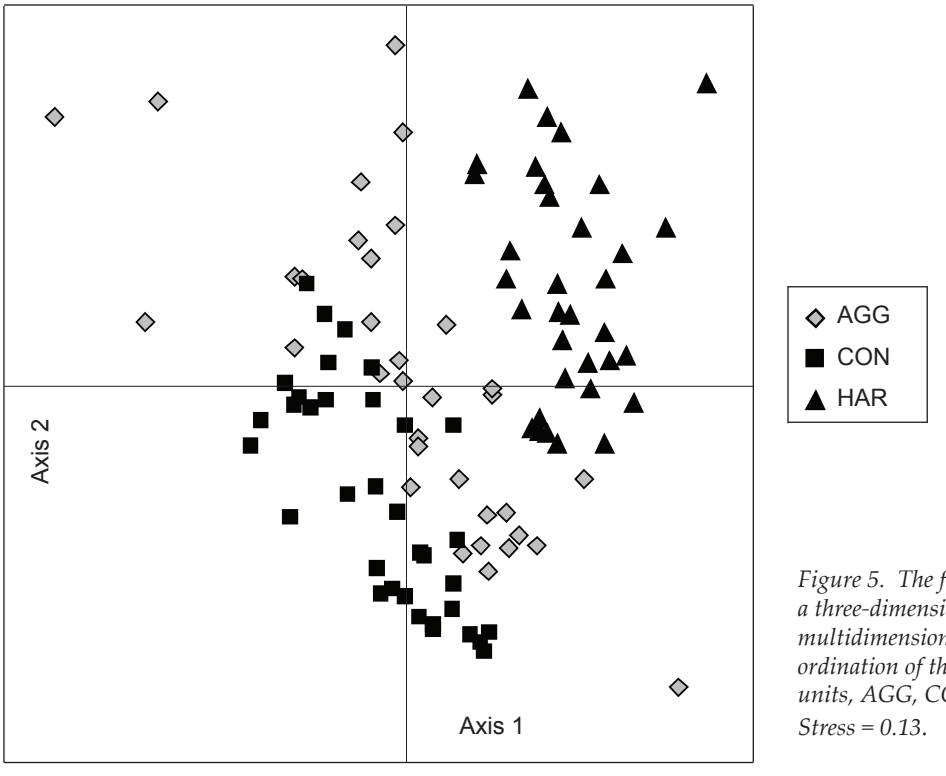

Figure 5. The first two axes of a three-dimensional nonmetric multidimensional scaling ordination of the three sampling units, AGG, CON and HAR. Stress = 0.13.

Table 1. Classification table summarising the results of a CAP analysis on the fungal species lists from 35 visits each to the three sampling units, AGG, CON and HAR. Fungi were recorded on 103 of these 105 visits. Classification is based upon the "leave-one-out" principle. Total correct = 101/103 = 98.1%. Misclassification error = 1.9%.

	Classified into group				
Original group	AGG	CON	HAR	Total	% correct
AGG	33	1	0	34	97.1%
CON	0	35	0	35	100.0%
HAR	1	0	33	34	97.1%

Table 2. Numbers of macrofungal species observed in the present study, classified by substrate and by sampling unit.

Substrate		AGG	CON	HAR
Soil	SB	na	na	38
	SUB	89	158	29
Wood	WB	na	na	47
	WUB	57	104	62
Litter	LB	na	na	16
	LUB	20	28	21
Dung		3	4	3
Total		167	288	125

AGG = aggregates; CON = control; HAR = harvested areas; SB = soil, burnt; SUB = soil, unburnt; WB = wood, burnt; WUB = wood, unburnt; LB = litter, burnt; LUB = litter, unburnt; na, not applicable.

Some overlap occurs between AGG and CON. The results of CAP, which formally tests the hypothesis that there are no differences among the species assemblage compositions in the three sampling units, are summarised in a classification table (Table 1). Using the "leave-one-out" rule, only two of the 103 visits in which fungi were recorded were misclassified, and the permutation test of 99,999 trials yielded a P-value of 0.00001. These results suggest substantial differences in the species assemblage compositions in the three sampling units.

Seasonality

Figure 3 shows that production of macrofungal fruiting bodies was strongly influenced by season, with high species numbers occurring from late April to the end of July (autumn and winter), and low numbers occurring between January and March (summer).

Substrate

The macrofungal species observed were classified by substrate and sampling unit. Because some species occurred on more than one substrate, the entries do not sum to the column totals. For HAR, the records on soil, wood and litter are divided into whether the substrate was burnt or not. In this sampling unit, there were more species on wood, both burnt and unburnt, than on either burnt or unburnt soil. No fungi were observed in the hot, calcining burn that was sporadically present in portions of the regeneration area, with fungi on burnt soil only being observed in areas that escaped this hotter burn. In AGG and CON, where the substrates were unburnt, a majority of the species were found on soil, with a further high proportion being found on wood. In all sampling units, only a relatively small number of species were found on litter or dung.

Life mode

The species in each of the sampling units were classified by their phylum,

Table 3. Numbers and proportions of macrofungal species classified by phylum, life mode and sampling unit.

Phylum/Life mode	AGG	CON	HAR
Ascomycota	7 (4.2%)	20 (6.9%)	11 (8.8%)
Basidiomycota decomposers	103 (61.7%)	160 (55.6%)	105 (84.0%)
Basidiomycota ectomycorrhizal	57 (34.1%)	108 (37.5%)	9 (7.2%)
Total	167	288	125

AGG = aggregates; CON = control; HAR = harvested areas

and also for Basidiomycota by life mode (Table 3). There was a strong correlation between life mode and the substrate (not shown). Decomposers were mostly on dead, dying and decaying wood or on litter. Those that were in soil may be decomposing litter remnants in the humus. Omitting Ascomycota, for which life modes are uncertain, HAR, with only nine ectomycorrhizal species, had a much smaller proportion of these species than AGG or CON, and the ratio of ectomycorrhizal species to decomposer species was not the same for all sampling units ($\chi^2 = 39.8$, df = 2, $P < 0.0001$). The unharvested sampling units AGG and CON did not have different proportions of ectomycorrhizality ($\chi^2 = 0.92$, df = 1, $P = 0.34$, not significant). The disparities in macrofungal species richness in the combinations of phylum and life mode are visualised in Figure 6, a series of Venn diagrams for the three sampling units. Fig. 6a shows the total species numbers, and the other three parts show the species numbers for the various phylum/life mode combinations. Two major

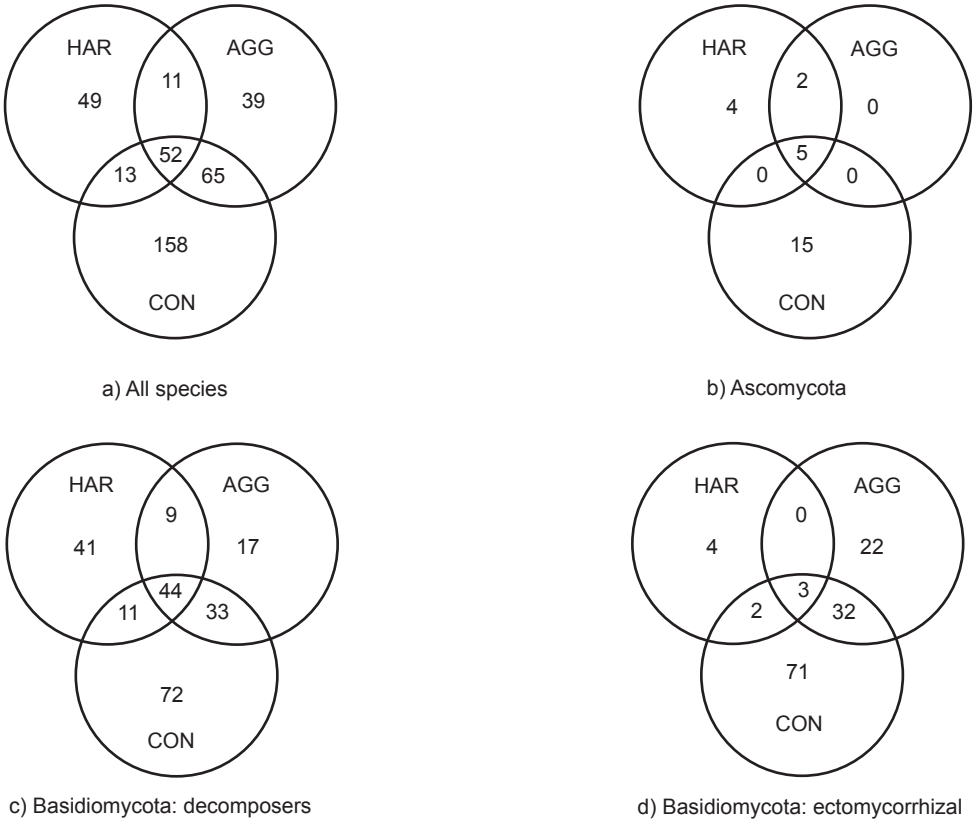

Figure 6. Venn diagrams representing macrofungal species richness in the comparisons among the three sampling units, for the various phylum/life-mode combinations.

features are apparent: the low numbers of basidiomycetous ectomycorrhizal species unique to HAR and its combinations with the other sampling units, and the lower number of species of all three phylum/life mode combinations unique to AGG compared to CON.

Discussion

Species identification

The high proportion of undescribed species identified in this survey (53.7%) is typical of Australian studies, as only a small fraction of Australian macrofungi has been named to species level. We noted in our previous study (Gates *et al.* 2005) that the prevalence of so many undescribed species in this type of study was common, even in countries where the macrofungi are relatively well known (e.g. Straatsma *et al*. 2001). Similarly high proportions of undescribed species have been reported in Tasmanian studies of beetles (Grove *et al.* 2008), while rarity of species is typical in forest studies of lichens (Jarman and Kantvilas 2001). The large number of rarely observed, undescribed species suggests the need for further taxonomic studies of these taxa in forest ecosystems.

Species richness and assemblage composition

The lack of a significant difference in the number of macrofungal species in the aggregates versus the harvested areas at any given visit appears to suggest that the two sampling units are about equally rich in their total macrofungi. However, the species list and ordination analysis show that they differ greatly in their species composition and also in the frequency with which the same species were recorded over successive visits. Many of the species found in HAR had individual fruiting bodies that persisted over successive visits, whereas few such persistent species occurred in AGG. Thus HAR, while totalling fewer species than AGG overall (125 versus 167 species) nevertheless appeared equally rich on a per-visit basis. The species found only in HAR include some that were observed frequently in the regenerating coupe of the CBS silvicultural treatment studied previously (Gates *et al.* 2005), such as *Aleuria aurantia, Byssomerulius corium, Galerina nana, Pycnoporus coccineus, Schizophyllum commune* and *Trametes versicolor*, but other species were observed in the present study that did not occur in the previous study, such as *Coprinellus angulatus, Loreleia marchantiae, Pholiota highlandensis* and *Tephrocybe anthracophila.* The reason for this relates to the shorter time after burning during which the fungal survey was carried out in ARN compared to the CBS study (Ratkowsky and Gates 2009). In general, species found only in HAR are species that tend to be associated either with burnt environments, or are typical of disturbed or drier conditions.

Other tests indicated higher species richness in the mature forest than in either component part of ARN. Of particular importance is the comparison between CON and AGG, as this relates to the question of whether aggregates (AGG) can maintain biodiversity when surrounded by a much larger harvested area (HAR), which is in turn relevant if aggregated retention is to be adopted as a standard silvicultural procedure for managing Tasmanian lowland wet forests. Superficially, the total of 288 fungal species recorded in CON is considerably greater than the 167 species recorded in AGG. A clearer perspective is gained by examining a Venn diagram (see Figure 6). This shows that there is a considerable mycota shared between the two sampling units, comprising 117 species (of which 52 also occurred in HAR). Nevertheless, the 158 species unique to CON is far in excess of the 39 species that occurred only in AGG, suggesting that some mechanism may be operating that is suppressing the full development of the macrofungal species richness in AGG. One factor may be a consequence of the drying effect experienced by aggregates of the size 0.5-0.73 ha, especially when

contrasted with a closed-canopy area of contiguous forest. Although nominally of the same forest type as the mature forest CON, there were discernible differences among the three aggregates of AGG that were studied. Aggregate "W" had the greatest number of species (99), followed by "C" (86), then "E" (68) (data not shown), suggesting a correlation between species richness and the degree of wetness of the individual aggregates, as "W" appeared to be consistently wetter than the other aggregates, having a thick understorey of *Bauera rubioides*. Aggregate "E" was the driest, and also had more encroachment from the regeneration burn than either of the other two aggregates, resulting in patches of *Gahnia grandis*. Aggregate "C" was intermediate in dryness between "W" and "E", with some *Gahnia* present. Amongst the species absent from HAR are some frequently occurring species found both in CON and in AGG, e.g. *Boletellus obscurecoccineus, Lactarius clarkeae, Mycena toyerlaricola, Galerina* 'with sphaeropendunculate cheilocystidia', *Marasmiellus affixus*, and *Cortinarius* 'C62, varnished, golden brown …'. Similarly, other commonly occurring species, e.g. *Stereum ostrea, Cantharellus concinnus, Podoserpula pusio* and *Pholiota squarrosipes*, were abundant in CON but never recorded in AGG. However, no commonly occurring species was found in AGG but not recorded in CON. This suggests that, although the habitat of the aggregates is similar to that of the mature forest, there is an impediment to the full development of their macromycota.

In a study of aggregated retention on Vancouver Island, British Columbia, Jones *et al*. (2008) examined the proportion of living roots and ectomycorrhizal fungal communities in and adjacent to aggregates of coastal hemlock forest 4-6 months after harvest. Their study differed from the present one in two major ways, in that the regeneration was from planted seedlings rather than from natural seed fall, and their aggregates were much smaller than ours, the largest being only 0.13 ha. Nevertheless, they found that soil samples collected at the centres of the aggregated retention patches had similar ectomycorrhizal fungal species richness to their unharvested control plots, suggesting that fungal diversity at the below-ground level tends to be maintained in this silvicultural system, with aggregate size having little effect.

Substrate and main life mode

The present study confirms the finding of our previous study of a CBS plot compared to an unharvested control (Gates *et al.* 2005), that most fungi in these forests are found on soil or wood, with smaller numbers on litter or dung. However, as stated earlier, it is difficult to separate the effects of substrate from those of life mode, as decomposer species predominate on wood, whereas ectomycorrhizal species occur mainly on soil. Thus, the result that species were found on soil more frequently than on wood in AGG and CON, compared to HAR where larger numbers were recorded on both burnt and unburnt wood (Table 2), may have as much to do with life mode as it has to do with substrate. Ectomycorrhizal fungi play a very important role in Australian eucalypt forests, with an involvement in a wide variety of associations (Ashton 1976; Tommerup and Bougher 2000). In the present study, the aggregates and unharvested forest have significantly more ectomycorrhizal components than harvested areas.

The relative paucity of the large ectomycorrhizal species, such as those of the Cortinariaceae and the Tricholomataceae, in HAR is a striking and important difference between the macrofungi of regenerating and mature forest. Work carried out in regenerating eucalypt forest in Victoria suggested that it may take seven years before large numbers of fruiting bodies of ectomycorrhizal species appear in the regeneration (McMullan-Fisher *et al.* 2002). Although decomposer species greatly outnumbered the ectomycorrhizal species amongst the Basidiomycota in HAR, no

Entoloma species were found there, as was only one *Hygrocybe* species (*H. roseoflavida*, two records). This parallels the results of our previous survey (Gates *et al.* 2005), where only four of 14 *Entoloma* species were found in the regeneration along with only one *Hygrocybe* species. These results reflect the relative lack of leaf and small twig litter in the regeneration, both in the previous and the present study. However, the state of regeneration of the HAR part of the ARN coupe in the present study was quite different from that of the CBS coupe studied previously (Gates *et al.* 2005), even though their ages overlapped, and this difference may account for some of the differences in their mycota. At 26 months, the CBS coupe supported flourishing *Eucalyptus obliqua, Pomaderris apetala* and *Acacia verticillata* seedlings forming dense thickets; the new canopy had allowed establishment of a new litter layer, thereby providing some saprophytic fungi with a substrate to colonise. In comparison, HAR at the same age had much sparser regeneration, and no corresponding litter layer, although the nearby aggregates were a continuing source of new litter.

Aggregates 'influencing' the harvest area?

Our study did suggest that some ectomycorrhizal species may be able to colonise harvested forest, perhaps directly from retained forest. This is perhaps circumstantial evidence of the aggregates 'influencing' the macrofungal assemblage composition of the surrounding newly regenerating forest. For instance, in HAR, *Tricholoma* sp. 'red cap, very white gills' was found several times in the harvested area close to the periphery of the aggregate. Members of the genus *Tricholoma* are considered to be late-stage successional ectomycorrhizal fungi. This could suggest that the fruit bodies were still in association with a host tree in the aggregate, the roots of which were still alive and extending into the harvested area. Similarly, *Laccaria* spp. were found on the snig track around aggregate 'E' and where the burn had encroached upon its periphery. Because of the proximity of the fruiting bodies to the aggregate, these too may have still been in association with the living hosts in the aggregate rather than reflecting a new ectomycorrhizal association with a host from inoculum in the soil. However, *Laccaria* spp. can also take on the role of an early coloniser after disturbance, having saprotrophic capabilities (May and Simpson 1997). Studies over much larger periods of time are thus required to determine if and how retained aggregates influence the macromycota of harvested areas.

Conclusions

This study is the second to document the rich macrofungal assemblages of contrasting coupes in the Tasmanian lowland wet eucalypt forests at Warra, following the previous study (Gates *et al.* 2005). The central importance for macrofungi of the substrates soil and wood, on which almost 90% of the species were found in the previous study (Gates *et al.* 2005), has been confirmed by the present study.

With respect to the question of whether aggregated retention can become an efficacious replacement for CBS as a silvicultural system, it appears from the present study that ectomycorrhizal species, which are widely acknowledged to be vital in the maintenance of forest health, are preserved in the aggregates, although their diversity, as measured by species number, is less than that in the mature forest. The lower diversity is probably a result of the combined effect of aggregate size, their propensity towards drying out due to the more open environment and, in some cases, singeing or scorching at the edges of the aggregates that occurred during the regeneration burn. With the passage of time and further maturation of the regenerating site, the macrofungal species richness of the aggregates could increase

to approach that of the mature forest. In the meantime, the aggregates may continue to influence macrofungal assemblage composition in the young regeneration as this matures, although it is unclear whether the level of influence would be sufficient to alter its successional trajectory from that experienced by regeneration following CBS. The tentative conclusion is thus that ARN appears to be a promising silvicultural system if the preservation of macrofungal biodiversity is an important consideration.

Acknowledgement

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Appendix 1. Fungal species found in the ARN coupe (HAR, harvested area, and AGG, retained aggregates) and the control coupe CON. Species are listed in alphabetical order.
Number of records refers to the number of visits (maximum possible = 35 per sample unit) in which the species was recorded: HAR = harvested areas, AGG = aggregates, CON = control.
Substrate observed for species in this study: LB = litter, burnt; LUB = litter, unburnt; NS = non-specific; SB = soil, burnt; SUB = soil, unburnt; WB = wood, burnt; WUB = wood, unburnt
Phylum/Life mode derived from prior knowledge: A=Ascomycota; BD = Basidiomycota/Decomposer (incl. saprophytes and parasites); BM = Basidiomycota/Ectomycorrhizal

Species binomial	**Number of records**			**Substrate**	**Phylum/ Life mode**
	HAR	AGG	CON		
Aleuria aurantia (Fr.) Fuckel	10	0	0	SB & SUB	A
Amanita 'A122, grey brown scab, white annulus, small spores'	0	0	1	SUB	BM
Amanita 'A123, grey brown, glabrous'	0	1	2	SUB	BM
Amanita 'A126, brown, applanate, lubricous, no annulus'	0	2	1	SUB	BM
Amanita 'A139, dry, white with some ochraceous tinges'	0	0	1	SUB	BM
Amanita 'dark brown with grey universal veil remnants'	0	0	1	SUB	BM
Amanita 'grey with white scales & stipe, no volva'	0	1	1	SUB	BM
Amanita 'grey-brown, no annulus'	1	0	0	SUB	BM
Amanita ananiceps (Berk.) Sacc.	0	0	1	SUB	BM
Amanita effusa (Kalchbr.) D.A. Reid	0	0	1	SUB	BM
Amanita ochrophylla (Cooke & Massee) Cleland	0	0	1	SUB	BM
Amanita ochrophylloides D.A. Reid	0	0	2	SUB	BM
Amanita pagetodes D.A. Reid	0	0	1	SUB	BM
Amanita peltigera D. A. Reid	0	4	1	SUB	BM
Amanita punctata (Cleland & Cheel) D.A. Reid	0	1	0	SUB	BM
*Arcangeliel*a sp.	0	1	2	SUB	BM
Armillaria hinnulea Kile & Watling	0	1	1	WUB	BD
Armillaria novaezelandiae (G. Stev.) Herink	1	1	6	WUB	BD
Ascocoryne sarcoides (Jacq.) J.W. Groves & D.E. Wilson	3	3	18	WB & WUB	A
Ascomycete 'brown buttons, gelatinous disc'	1	0	0	LUB	A
Ascomycete 'small buff gelatinous disc on cut wood face'	0	0	1	WUB	A
Ascomycete 'white disc bruising orange'	0	0	5	WUB	A
Auriscalpium 'warrensis'	0	3	5	SUB	BD
Australoporus tasmanicus (Berk.) P.K. Buchanan & Ryvarden	0	0	1	WUB	BD
Bisporella 'green-yellow'	2	1	7	WUB	A
Bisporella citrina (Batsch ex Fr.) Korf & S.E. Carp.	0	0	7	WUB	A
Bisporella sulfurina (Quél.) S.E. Carp.	0	0	2	WUB	A
Bolete 'B174, pink cap and stipe, yellow tubes'	0	0	3	SUB	BM
Bolete 'green-pink, with bright yellow tubes and pores'	0	0	1	SUB	BM
Boletellus obscurecoccineus (Höhn.) Singer	0	13	12	SUB	BM
Boletus 'rosy brown'	0	0	4	SUB	BM
Boletus 'Stephens'	0	1	0	SUB	BM
Boletus 'wedgensis'	0	1	2	SUB	BM
Boletus 'yellow and pink, blueing'	0	0	1	SUB	BM
Bovista brunnea Berk.	1	1	1	SB	BD
Byssomerulius corium (Pers. : Fr.) Parmasto	11	0	0	WUB	BD
Callistosporium 'maroon on wood'	0	0	1	WUB	BD
Calocera 'spathulate'	1	1	3	WUB	BD
Calocera guepinioides Berk.	7	6	14	WB & WUB	BD
Campanella olivaceonigra (E. Horak) T.W. May & A.E. Wood	0	0	1	WUB	BD
Cantharellus concinnus Berk.	0	0	13	SUB	BD
Ceriporiopsis subvermispora (Pilát) Gilb. & Ryvarden	0	0	1	WUB	BD

Appendix 1. Continued.

Species binomial	Number of records			Substrate	Phylum/ Life mode
	HAR	AGG	CON		
Cheilymenia coprinaria (Cooke) Boud.	1	1	0	Dung	A
Cheimonophyllum candidissimum (Berk. & M.A. Curtis) Singer	0	0	1	WUB	BD
Chlorociboria aeruginascens (Nyl.) Kanouse	0	0	2	WUB	A
Chondrostereum purpureum (Pers.) Pouzar	0	0	4	WUB	BD
Clavaria amoena Zoll. & Moritzi	0	0	2	SUB	BD
Clavaria zollingeri Lév.	0	0	1	SUB	BD
Clavariaceae sp. 'yellow'	0	1	0	SUB	BD
Clavicorona piperata (Kauffman) Leathers & A.H. Sm.	0	4	4	WUB	BD
Clavulina rugosa (Bull. : Fr.) J. Schröt.	0	0	1	SUB	BM?
Clitocybe 'with white bloom'	0	1	1	SUB	BD
Clitocybe semiocculta Cleland	0	0	1	WUB	BD
Clitocybula 'Notley yellow'	1	2	7	LUB	BD
Clitocybula 'streaky grey-brown'	0	0	3	WUB	BD
Clitopilus prunulus (Scop.) P. Kumm.	0	0	2	SUB	BM
Collybia 'brown with pruinose stipe'	0	0	2	WUB	BD
Collybia 'dry red'	0	0	1	SUB	BD
Collybia 'eucalyptorum on soil'	0	7	0	SUB	BD
Collybia 'pink furry'	2	0	0	WUB	BD
Collybia eucalyptorum Cleland	4	12	21	WB & WUB	BD
Coltricia 'brownish orange'	0	0	1	SUB	BD
Coprinus 'furry'	0	1	0	WUB	BD
Coprinus 'on wallaby dung'	0	0	1	Dung	BD
Coprinellus angulatus (Peck) Redhead, Vilgalys & Moncalvo	11	0	0	SB	BD
Coprinellus disseminatus (Pers.) J.E. Lange	3	0	0	WB	BD
Corticioid 'yellowy brown'	1	0	0	WUB	BD
Corticioid 'grey bloom'	0	1	0	WUB	BD
Corticioid 'peach polypore'	0	1	0	WUB	BD
Corticioid 'creamish'	0	1	0	WUB	BD
Corticioid 'pale tan'	1	0	0	WUB	BD
Corticioid 'buff'	1	0	0	WUB	BD
Corticioid 'white, no obvious hymenium'	0	0	1	WUB	BD
Corticioid 'greenish yellow'	0	0	1	WUB	BD
Corticioid 'white, powdery'	0	0	1	WUB	BD
Corticioid 'grey'	0	0	1	WUB	BD
Corticioid 'yellow cobwebs'	0	0	1	WUB	BD
Corticioid 'grey, powdery'	0	0	1	WUB	BD
Corticioid 'white, bruising ochre'	0	0	1	WUB	BD
Corticioid 'olivaceous/khaki'	0	0	1	WUB	BD
Cortinarius 'brown acuti'	0	2	0	SUB	BM
Cortinarius 'brown umbonate, long white stipe'	0	2	0	SUB	BM
Cortinarius 'C100, golden brown with uplifted undulating margin'	1	0	0	SUB	BM
Cortinarius 'C101, violet-brown, hygrophanous, becoming light ochre at centre'	0	0	1	SUB	BM
Cortinarius 'C106, golden-brown, dry, small umbo'	0	1	0	SUB	BM
Cortinarius 'C166, medium brown, frosty patches'	0	0	1	SUB	BM
Cortinarius 'C167, v. dark orangy brown, drying orangy buff'	0	0	1	SUB	BM

Appendix 1. Continued.

Species binomial	Number of records			Substrate	Phylum/ Life mode
	HAR	AGG	CON		
Cortinarius 'C168, violet brown with appendiculate margin'	0	0	1	SUB	BM
Cortinarius 'C169, orangy brown, drying bright orange'	0	0	1	SUB	BM
Cortinarius 'C170, orangy brown, small pointed umbo'	0	0	1	SUB	BM
Cortinarius 'C29, buttery ochre, viscid'	0	2	0	SUB	BM
Cortinarius 'C31, squamulose, tawny brown, lubricous'	0	0	4	SUB	BM
Cortinarius 'C34, brown-ochre centre with white frosting, white stipe'	0	1	1	SUB	BM
Cortinarius 'C36, small, sharp umbo'	0	0	2	SUB	BM
Cortinarius 'C38, C71, burnt yellow-ochre and pink-buff, bruising'	0	1	1	SUB	BM
Cortinarius 'C39, ochre-brown with lilac margin'	0	0	1	SUB	BM
Cortinarius 'C40, lilac with inner stipe pink, odour spicy, Phlegmacium'	0	0	1	SUB	BM
Cortinarius 'C41, stunted, brown with white hoary covering in youth'	0	0	1	SUB	BM
Cortinarius 'C42, lilac-brown with big spores, Myxacium'	0	0	1	SUB	BM
Cortinarius 'C43, rozites'	0	1	7	SUB	BM
Cortinarius 'C44, orange'	0	0	3	SUB	BM
Cortinarius 'C45, dry lilac-brown, dry'	0	0	1	SUB	BM
Cortinarius 'C46, furry'	0	2	4	SUB	BM
Cortinarius 'C48, lilac and brown, Phlegmacium'	0	7	5	SUB	BM
Cortinarius 'C49, glutinous, estriate, dark chestnut brown, then golden brown'	0	0	1	SUB	BM
Cortinarius 'C52, small, white becoming rosy pink and yellow'	0	0	1	SUB	BM
Cortinarius 'C57, caramel brown'	0	3	0	SUB	BM
Cortinarius 'C58, dark violet, Phlegmacium'	0	0	1	SUB	BM
Cortinarius 'C61, brown with yellow gills'	0	1	0	SUB	BM
Cortinarius 'C62, varnished, golden brown with sharp reddish umbo'	0	5	9	SUB	BM
Cortinarius 'C63, small green'	0	1	1	SUB	BM
Cortinarius 'C64, rindlike orangy disc, remainder soft violet-brown'	0	1	1	SUB	BM
Cortinarius 'C65, orangy brown throughout'	0	0	1	SUB	BM
Cortinarius 'C68, small, orangy brown, iodine odour'	0	0	1	SUB	BM
Cortinarius 'C75, medium brown with violet hues'	0	1	0	SUB	BM
Cortinarius 'C79, pale violet at margin, becoming ochre towards centre'	0	0	1	SUB	BM
Cortinarius 'C82, v. pale buff with ochre and rose-pink hues'	0	0	1	SUB	BM
Cortinarius 'C83, pale violet with ochre-brown centre, Myxacium'	0	0	1	SUB	BM
Cortinarius 'C91, lilac-brown, radially rugulose'	0	1	1	SUB	BM
Cortinarius 'C97, pallid buff, wide marginal zone'	0	0	1	SUB	BM
Cortinarius 'caramel brown, Myxacium'	0	0	1	SUB	BM
Cortinarius 'golden brown'	1	0	1	SUB	BM
Cortinarius 'green gills'	0	1	0	SUB	BM
Cortinarius 'large, reddish orange'	0	0	1	SUB	BM
Cortinarius 'lilac and cream'	0	0	1	SUB	BM
Cortinarius 'lilac Myxacium'	0	0	4	SUB	BM
Cortinarius 'lilac, with large spores, Phlegmacium'	0	0	1	SUB	BM
Cortinarius 'lubricous brown cap, white stipe'	1	0	0	SUB	BM
Cortinarius 'Phlegmacium, pale buff'	0	1	0	SUB	BM

Appendix 1. Continued.

Species binomial	Number of records			Substrate	Phylum/ Life mode
	HAR	AGG	CON		
Cortinarius 'rusty'	0	1	0	SUB	BM
Cortinarius 'tawny with bitter gluten, Phlegmacium'	0	1	1	SUB	BM
Cortinarius 'white, bruising orange'	0	0	2	SUB	BM
Cortinarius 'yellow ochre with yellow stipe trama'	0	1	3	SUB	BM
Cortinarius abnormis Watling & T.W. May	0	0	1	SUB	BM
Cortinarius fuscoumbonatus Gasparini	0	0	1	SUB	BM
Cortinarius rotundisporus Cleland & Cheel	0	3	2	SUB	BM
Cortinarius sinapicolor Cleland	0	0	3	SUB	BM
Cotylidia undulata (Fr.) Karst.	1	0	0	SB	BD
Crepidotus applanatus (Pers.) P. Kumm.	1	0	0	WUB	BD
Crepidotus stromaticus (Cooke & Massee) Sacc.	0	4	0	WUB	BD
Crepidotus variabilis (Pers. : Fr.) P. Kumm.	2	4	4	LUB & WB	BD
Cystolepiota 'pinkish buff, stipe vinaceous or reddish brown'	1	0	0	LB	BD
Cystolepiota 'white'	0	0	1	SUB	BD
Dentipellis leptodon (Mont.) Maas Geest.	0	0	1	SUB	BD
Dermocybe 'brown with greenish apex to stipe'	0	0	1	SUB	BM
Dermocybe 'brown with orange UV remnants over stipe'	0	1	0	SUB	BM
Dermocybe 'C84, dirty brown'	0	0	2	SUB	BM
Dermocybe 'conical brown'	0	0	1	SUB	BM
Dermocybe 'dark'	0	0	1	SUB	BM
Dermocybe 'olivaceous'	0	1	0	SUB	BM
Dermocybe 'reddish brown'	0	1	0	SUB	BM
Dermocybe 'reddish with black centre to cap'	0	0	1	SUB	BM
Dermocybe 'yellowy brown'	1	1	3	SUB	BM
Dermocybe clelandii (A.H.Sm.) Grgur.	0	1	4	SUB	BM
Dermocybe kula Grgur.	0	1	3	SUB	BM
Discinella terrestris (Berk. & Broome) R.W.G. Dennis	2	6	18	SB & SUB	A
Entoloma 'black, bitter disappearing'	0	1	0	SUB	BD
Entoloma 'brown, bitter disappearing'	0	0	1	SUB	BD
Entoloma 'cystidiosum'	0	0	2	SUB	BD
Entoloma 'inflated pileipellis hyphae'	0	0	1	SUB	BD
Entoloma 'Marriotts Marvel'	0	2	2	SUB	BD
Entoloma 'medium isopentagonal spores'	0	6	3	SUB	BD
Entoloma 'shapeless spores'	0	1	0	SUB	BD
Entoloma aff. *nitidum* Quél.	0	0	1	SUB	BD
Entoloma austroprunicolor G. Gates & Noordel.	0	4	6	SUB	BD
Entoloma austrorhodocalyx G. Gates & Noordel.	0	2	1	SUB	BD
Entoloma camarophyllus G. Gates & Noordel.	0	0	3	SUB	BD
Entoloma coeruleogracilis G.Gates & Noordel.	0	1	4	SUB	BD
Entoloma panniculum (Berk.) Sacc.	0	0	1	SUB	BD
Entoloma procerum G. Stev.	0	1	0	SUB	BD
Entoloma readiae G. Stev.	0	2	3	SUB	BD
Entoloma rodwayi (Massee) E. Horak	0	1	1	SUB	BD
Entoloma viridomarginatum (Cleland) E. Horak	0	0	1	SUB	BD
Exidia 'grey'	1	0	0	WUB	BD
Fistulina hepatica (Schaeff. : Fr.) Fr.	2	0	0	WB	BD
Flammulina velutipes (Curtis : Fr.) Singer	0	0	5	WUB	BD
Galerina 'large reddish brown'	0	0	3	SUB	BD

Appendix 1. Continued.

Species binomial	Number of records			Substrate	Phylum/ Life mode
	HAR	AGG	CON		
Galerina 'long spores'	0	0	1	SUB	BD
Galerina 'ochre-brown, pellucid, in moss'	0	0	1	Moss	BD
Galerina 'pimply'	0	2	6	SUB + LUB	BD
Galerina 'with sphaeropedunculate cheilocystidia'	0	7	11	SUB + LUB	BD
Galerina hypnorum (Schrank : Fr.) Kühner	0	1	6	Moss	BD
Galerina nana (Petri) Kühner	20	0	0	SB & SUB	BD
Galerina patagonica Singer	3	0	1	WUB	BD
Gerronema 'pink-buff'	1	0	0	SB	BD
Gloeoporus taxicola (Pers. : Fr.) Gilb. & Ryvarden	1	0	0	WB	BD
Gymnopilus allantopus (Berk.) Pegler	9	8	10	LUB, WB & WUB	BD
Gymnopilus ferruginosus B.J. Rees	5	2	2	WB & WUB	BD
Gymnopilus tyallus Grgur.	7	7	5	WB & WUB	BD
Gymnopus 'brown frilly'	6	7	5	NS	BD
Gymnopus 'hygrophanous reddish brown'	7	3	0	NS	BD
Hebeloma 'small'	0	0	1	SUB	BM
Hemimycena 'pseudocrispula'	0	0	1	LUB	BD
Hemimycena lactea (Pers. : Fr.) Singer	0	0	2	LUB	BD
Heterotextus peziziformis (Berk.) Lloyd	6	6	4	LB,WB & WUB	BD
Hohenbuehelia 'brown or yellowy tan, with farinaceous odour'	1	3	5	WB	BD
Hydnoplicata convoluta (McAlpine) Trappe & Claridge	0	0	1	SUB	A
Hydnum repandum L. : Fr.	0	0	3	SUB	BM
Hygrocybe graminicolor (E. Horak) T.W. May & A.E. Wood	0	5	1	SUB	BD
Hygrocybe roseoflavida A.M. Young & A.K. Mills	2	3	5	LB & SUB	BD
Hymenochaete cruenta (Pers. : Fr.) Donk	0	2	5	WUB	BD
Hymenoscyphus pezizoideus (Cooke & W. Phillips) Gamundí	0	0	1	WUB	A
Hypholoma brunneum (Massee) D.A. Reid	7	2	7	LB & WUB	BD
Hypholoma fasciculare (Huds. : Fr.) P. Kumm.	2	1	4	WB & WUB	BD
Hypocrea aff. *sulphurea* (Schwein.) Sacc.	0	0	1	WUB	A
Hypocrea rufa (Pers.:Fr.) Fries	0	0	2	WUB	A
Hypoxylon aff. *placentiforme* Berk. & M. A. Curtis	0	0	1	WUB	A
Inocybe 'blonde with smooth spores'	0	1	1	SUB	BM
Inocybe 'blue-green base to stipe'	0	0	1	SUB	BM
Inocybe 'brown, shaggy'	0	0	3	SUB	BM
Inocybe 'I112, brown-ochre squamulose, spores smooth'	0	0	1	SUB	BM
Inocybe 'large, smooth spores, smooth cheilocystidia'	0	1	0	SUB	BM
Inocybe 'lilac-pink stipe'	0	0	1	SUB	BM
Inocybe cystidiocatenata Grgur.	0	0	1	SUB	BM
Laccaria spp.	12	13	10	SB & SUB	BM
Laccocephalum sclerotinium (Rodway) Núñez & Ryvarden	2	0	0	SB	BD
Lactarius clarkeae Cleland	0	8	16	SUB	BM
Lactarius eucalypti O.K. Mill. & R.N. Hilton	0	1	12	SUB	BM
Lactarius stenophyllus Berk.	0	2	3	SUB	BM
Laetiporus portentosus (Berk.) Rajchenb.	6	1	0	WB	BD
Leccinum 'chocolate chip'	0	0	2	SUB	BM
Lentinellus pulvinulus (Berk.) Pegler	0	0	1	WUB	BD
Lepiota 'brown scaly centre'	0	1	0	SUB	BD

Appendix 1. Continued.

Species binomial	Number of records			Substrate	Phylum/ Life mode
	HAR	AGG	CON		
Loreleia marchantiae (Singer & Clémençon) Redhead, Moncalvo, Vilgalys & Lutzoni	23	0	0	SB	BD
Lycoperdon perlatum Pers. : Pers.	0	0	1	SUB	BD
Lycoperdon pyriforme Schaeff. : Pers.	0	0	1	WUB	BD
Marasmiellus 'apricot'	0	1	1	LUB	BD
Marasmiellus 'cream, no odour'	0	1	0	LUB	BD
Marasmiellus 'earth odour'	1	0	1	LUB	BD
Marasmiellus 'small, white, subdecurrent gills'	0	0	1	WUB	BD
Marasmiellus affixus (Berk.) Singer	0	5	11	WUB	BD
Marasmius 'angina'	0	0	6	LUB	BD
Marasmius 'horsehair stipe, nutmeg'	0	0	1	LUB	BD
Marasmius 'pink-brown or cream cap, close gills, horsehair stipe, no odour'	0	3	2	LUB	BD
Marasmius 'reddish brown'	0	1	0	LUB	BD
Marasmius 'soft pink'	0	0	1	LUB	BD
Marasmius 'white, close gills'	0	2	1	LUB	BD
Marasmius crinisequi F. Muell.	0	2	1	LUB	BD
Melanophyllum haematospermum (Bull. : Fr.) Kreisel	1	0	0	SB	BD
Melanotus hepatochrous (Berk.) Singer	23	4	0	WB & WUB	BD
Mesophellia glauca (Cooke & Massee) D. A. Reid	0	0	1	SUB	BM
Mollisia cinerea (Batsch) P. Karst.	0	0	4	WUB	A
*Mucronella pendul*a (Massee) R.H. Petersen	0	1	3	WUB	BD
Mycena 'brown striate with bleach odour'	1	0	0	SB	BD
Mycena 'brown striate, becoming sulcate'	12	0	0	NS	BD
Mycena 'brown'	1	0	0	WUB	BD
Mycena 'grey rubbery'	0	2	0	WUB	BD
Mycena 'grey'	1	0	0	LUB	BD
Mycena 'grey-brown cap, white decurrent gills, glutinous stipe'	1	3	5	LUB	BD
Mycena 'M142, brown conical, on wood'	0	0	1	WUB	BD
Mycena 'M143, dark brown, pellucid, v.sulcate when dry'	2	0	0	SB	BD
Mycena 'M147, dark brown disc, caespitose on wood'	0	2	0	WUB	BD
Mycena 'M156, black & grey'	0	0	1	WUB	BD
Mycena 'M157, pink or greyish rose with bleach odour'	1	0	0	LB	BD
Mycena 'M158, dark grey-brown, pellucid, caespitose on wood'	1	0	0	WUB	BD
Mycena 'pink or brown on soil with bleach odour & long slender stipe'	0	1	1	SUB	BD
Mycena 'pink-yellow with iodine odour'	0	2	1	LUB	BD
Mycena 'small grey bonnets'	2	0	1	WUB	BD
Mycena 'small, brown, decurrent gills with red margins'	0	0	2	WUB	BD
Mycena 'small, greyish'	1	0	0	SB	BD
Mycena 'small, pink, fragile, bleach odour'	0	0	1	LUB	BD
Mycena 'small, white, on twigs, with adnexed, distant gills'	0	0	2	WUB	BD
Mycena 'very black, estriate with grey gills'	0	0	1	SUB	BD
Mycena 'white, fragile, on litter, no odour'	0	0	1	LUB	BD
Mycena 'yellowy/yellow-ochre with earth odour'	0	1	1	LUB	BD
Mycena albidocapillaris Grgur. & T.W. May	1	4	6	WUB	BD
Mycena albidofusca Cleland	1	5	7	LUB & SUB	BD
Mycena austrofilopes Grgur. & A.A. Holland	0	0	2	LUB	BD

Appendix 1. Continued.

Species binomial	Number of records			Substrate	Phylum/ Life mode
	HAR	AGG	CON		
Mycena austrororida Singer	1	0	4	WUB	BD
Mycena carmeliana Grgur.	2	3	6	WUB	BD
Mycena cystidiosa (G. Stev.) E. Horak	6	12	15	LUB, SB & SUB	BD
Mycena epipterygia (Scop. : Fr.) Gray	2	6	8	LUB	BD
Mycena interrupta (Berk.) Sacc.	0	5	9	WUB	BD
Mycena kurramulla Grgur.	5	5	11	LB, LUB, WB & WUB	BD
Mycena lividorubra Segedin	0	4	4	SUB	BD
Mycena maldea Grgur.	0	0	1	WUB	BD
Mycena mulawaestris Grgur.	3	4	8	LUB, WB & WUB	BD
Mycena nargan Grgur.	2	3	5	WUB	BD
Mycena sanguinolenta (Alb. & Schwein. : Fr.) P. Kumm.	9	5	3	LB, LUB, SB & SUB	BD
Mycena subgalericulata Cleland	0	2	7	WUB	BD
Mycena toyerlaricola Grgur.	0	8	11	SUB	BD
Mycena vinacea Cleland	1	3	2	SUB	BD
Mycena viscidocruenta Cleland	1	4	8	LUB	BD
Nectria cinnabarina (Tode) Fr.	0	0	4	WUB	A
Nothojafnea cryptotricha M.A. Rifai	1	0	0	SB	A
Nothojafnea thaxteri (Cash) Gamundí	3	0	0	SB	A
Oudemansiella 'burnt'	8	0	0	SB & SUB	BD
Oudemansiella 'gelatinous white on wood'	0	0	3	WUB	BD
Panellus ligulatus E. Horak	0	0	2	WUB	BD
Panellus longinquus (Berk.) Singer	4	3	2	WB & WUB	BD
Panellus stipticus (Bull. : Fr.) P. Karst.	6	1	13	WB & WUB	BD
Perenniporia cf. *medulla-panis* (Jacq. : Fr.) Donk	0	0	1	WUB	BD
Peziza repanda M.A. Rifai	3	3	0	SB	A
Phaeocollybia tasmanica B.J. Rees & A.E. Wood	0	0	4	SUB	BM?
Phanerochaete filamentosa (Berk. & M.A. Curtis) Burds.	1	0	2	WUB	BD
Phellodon 'brown'	0	0	4	SUB	BM
Phellodon niger (Fr. : Fr.) P. Karst.	0	1	14	SUB	BM
Phlebia cf. *deflectens* (P. Karst.) Ryvarden	0	0	1	WUB	BD
Pholiota highlandensis (Peck) Smith & Hesler	18	0	0	SB	BD
Pholiota multicingulata E. Horak	1	0	1	WUB	BD
Pholiota squarrosipes Cleland	0	0	11	SUB	BD
Pholiota viscofumosa Y.S. Chang & A.K. Mills	0	0	4	SUB	BD
Pholiotina 'small, with evanescent annulus'	1	0	0	SUB	BD
Phylloporus aff. *rhodoxanthus* (Schwein. : Fr.) Bres.	0	0	1	SUB	BM
Pluteus 'brown velvet cap, pink stipe and gills'	9	0	1	WB & WUB	BD
Pluteus aff. *lutescens* (Fr.) Bres.	1	0	0	WB	BD
Pluteus atromarginatus (Konrad) Kühner	6	1	4	WB & WUB	BD
Pluteus cervinus (Schaeff.) P. Kumm.	2	3	3	LB & WUB	BD
Podoserpula pusio (Berk.) D.A. Reid	0	0	13	SUB	BD
Polypore 'ochre with white growing edge'	0	1	0	WUB	BD
Polypore 'overlapping segments, dry, smooth, ridged, violet-brown'	0	0	1	WUB	BD

Appendix 1. Continued.

Species binomial	Number of records			Substrate	Phylum/ Life mode
	HAR	AGG	CON		
Polyporus gayanus Lév.	1	0	0	WUB	BD
Polyporus melanopus (Sw. : Fr.) Fr.	7	12	22	WB & WUB	BD
Polyporus nigrocristatus E. Horak & Ryvarden	0	0	5	WUB	BD
Postia caesia (Schrad. : Fr.) P. Karst.	0	2	7	WUB	BD
Postia pelliculosa (Berk.) Rajchenb.	5	1	5	WB & WUB	BD
Protoglossum 'pale violet, glutinous, small white stipe'	0	0	1	SUB	BM
Psathyrella 'conical, squamulose, spores long & narrow'	4	0	0	SB	BD
Psathyrella 'dark brown, hygrophanous, spores 7 x 3.5 um'	7	1	0	SB & SUB	BD
Psathyrella 'pellucid, with pink cheilo- & pleurocystidia'	7	0	0	SB & SUB	BD
Psathyrella 'pseudoechinata'	1	0	0	WUB	BD
Psathyrella 'with large cheilo- and pleurocystidia'	2	0	0	SB	BD
Psathyrella 'with small cheilocystidia'	2	0	0	SB & WB	BD
Psathyrella echinata (Cleland) Grgur.	4	3	0	WB & WUB	BD
Pseudobaeospora 'bloomers'	1	2	2	LB	BD
Psilocybe 'in moss'	1	0	0	SB	BD
Psilocybe 'small, grey, on dung'	3	0	1	Dung	BD
Psilocybe aff. *coprophila* (Bull.) P. Kumm.	0	1	1	Dung	BD
Psilocybe brunneoalbescens Y.S. Chang & A.K. Mills	4	0	4	WB & WUB	BD
Psilocybe fascicularis (Huds.) Kühner var. *armeniaca* Y.S. Chang & A.K. Mills	1	3	5	WB	BD
Psilocybe formosa Y.S. Chang & A.K. Mills	8	5	9	NS	BD
Pulveroboletus ravenelii (Berk. & Curt.) Murrill	0	4	6	SUB	BM
Pycnoporus coccineus (Fr.) Bondartsev & Singer	21	0	0	WB & WUB	BD
Ramaria 'brownish pink'	0	0	3	SUB	BM
Ramaria 'lilac with picric acid yellow stains'	0	2	0	SUB	BM
Ramaria 'orange'	1	0	0	SUB	BM
Ramaria lorithamnus (Berk.) R.H. Petersen	2	0	1	SUB	BM
Ramaria ochraceosalmonicolor (Cleland) Corner	0	0	1	SUB	BM
Resupinatus aff. *applicatus* (Batsch) Gray	0	0	1	WUB	BD
Rhodocollybia butyracea (Bull. : Fr.) Lennox	6	13	5	SB & SUB	BD
Rozites armeniacovelata Bougher, Fuhrer & E. Horak	0	1	0	SUB	BM
Russula 'faded pink'	0	0	1	SUB	BM
Russula 'grey yellow'	0	1	0	SUB	BM
Russula 'greyish'	0	1	0	SUB	BM
Russula 'pink cap, pink stipe, cream or white gills'	0	0	5	SUB	BM
Russula 'purple-yellow'	0	3	2	SUB	BM
Russula 'red cap, yellowy stipe and gills'	0	1	0	SUB	BM
Russula lenkunya Grgur.	0	0	3	SUB	BM
Russula marangania Grgur.	0	2	1	SUB	BM
Russula persanguinea Cleland	0	1	4	SUB	BM
Ryvardenia campyla (Berk.) Rajchenb.	0	2	11	WUB	BD
Ryvardenia cretacea (Lloyd) Rajchenb.	0	1	0	SUB	BD
Schizophyllum commune Fr. : Fr.	10	0	0	WB & WUB	BD
Scutellinia margaritacea (Berk. ex Cooke) O. Kuntze	8	13	1	SB & SUB	A
Scutellinia scutellata (L.) Lambotte	18	2	1	NS	A
Scytinostroma 'FF54, with gloeocystidia and dextrinoid skeletal hyphae'	0	0	1	WUB	BD
Sirobasidium brefeldianum Møller	0	0	5	WUB	BD

Appendix 1. Continued.

Species binomial	Number of records			Substrate	Phylum/ Life mode
	HAR	AGG	CON		
Skeletocutis nivea (Jungh.) Jean Keller	0	0	2	WUB	BD
Steccherinum 'peach'	0	0	1	WUB	BD
Steccherinum 'white'	0	0	1	WUB	BD
Stereum hirsutum (Willd. : Fr.) Pers.	13	15	20	WB & WUB	BD
Stereum illudens Berk.	14	9	2	WB & WUB	BD
Stereum ochraceoflavum (Schwein.) Sacc.	4	5	0	WB & WUB	BD
Stereum ostrea (Blume & Nees : Fr.) Fr.	0	0	16	WUB	BD
Stereum rugosum Pers.	2	2	0	WB & WUB	BD
Stropharia aff. *semiglobata* (Batsch : Fr.) Quél.	2	1	1	Dung	BD
Stropharia coronilla (Bull.) Fr.	1	0	0	WB	BD
Tephrocybe 'grey-brown'	1	2	7	SB	BD
Tephrocybe anthracophila (Lasch) P.D. Orton	14	0	0	SB	BD
Tomentella 'FF27, olivaceous, matted, tomentose, furry'	0	0	2	WUB	BD
Trametes hirsuta (Wulfen : Fr.) Lloyd	1	0	1	WUB	BD
Trametes versicolor (L. : Fr.) Lloyd	14	0	1	WB & WUB	BD
Tremella 'yellow becoming white'	1	1	0	WUB	BD
Tremella fimbriata Pers. : Fr.	1	1	2	WUB	BD
Tremella fuciformis Berk.	8	9	6	WB & WUB	BD
Tremella mesenterica Retz. : Fr.	2	4	0	WUB	BD
Tricholoma 'grey, with odour'	0	0	2	SUB	BM
Tricholoma 'large pink or pink-buff'	2	1	1	SB & SUB	BM
Tricholoma 'red-brown cap with mottled gills'	0	1	0	SUB	BM
Tricholoma 'red cap with very white gills'	0	5	1	SUB	BM
Tricholomopsis rutilans (Schaeff.: Fr.) Singer	0	0	1	WUB	BD
Tubaria rufofulva (Cleland) D.A. Reid & E. Horak	0	1	1	WUB	BD
Vibrissea dura G. Beaton & G. Weste	0	0	2	WUB	A
Xerocomus subtomentosus (L. : Fr.) Quél.	0	0	1	SUB	BM
Xylaria castorea Berk.	0	0	1	WUB	A
Xylaria hypoxylon (L.) Grev.	0	0	2	WUB	A
Zelleromyces sp.	0	1	1	SUB	BM