The ecology and habitat requirements of saproxylic beetles native to Tasmanian wet eucalypt forests: potential impacts of commercial forestry practices

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A research thesis submitted in fulfilment of the requirements for the degree of Doctor of Philosophy
November 2005

Declaration

I declare that this thesis does not contain any material which has been accepted for a degree or diploma by the University of Tasmania or any other institution. To the best of my knowledge, this thesis contains no material previously published or written by another person except where due acknowledgment is made.

Marie Yee

12th November 2005

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Abstract

Large diameter *Eucalyptus obliqua* decaying logs are characteristic features of wet eucalypt forests in Tasmania. In production coupes, however, rotation lengths of around 80 years will eventually lead to their elimination. This thesis investigates the role of these features as habitat for saproxylic beetles, and thus whether their retention is warranted to maintain biodiversity. Large diameter (>100cm) logs derived from commercially over-mature trees were compared with small diameter (30-60cm) logs derived from trees of an age approaching commercial maturity, in two forest types: mature, unlogged forest; and 20-30 year logged forest that had regenerated after clearfelling.

Two field studies were conducted, in which a highly species rich fauna of 360 saproxylic beetle species (representing 54 families) are first recorded.

The first, destructive sampling study investigated whether small diameter logs follow similar decomposition processes to large diameter logs, and so support similar rot types and beetle assemblages. Eleven rot types were differentiated, each associated with a particular region within the log. Small diameter logs had a relatively high incidence of white rot towards their outer edges, probably originating from fungal colonisation after treefall. Large diameter logs had a higher incidence of brown rot towards their cores, probably originating from internal decay already present in older, living eucalypt trees prior to treefall. Some of the beetle species characteristic of this brown rot are possibly poor dispersers and may be of particular conservation concern in production forests.

The second, log emergence trapping study examined the extent to which beetle assemblages differ between small and large diameter logs, and whether they respond in the same way to forest successional processes induced by stand level disturbance. Distinct suites of species were associated with large diameter logs irrespective of forest type, yet there were no apparent small log specialists. Assemblages differed significantly between the mature and logging regenerated forests; there was also significant variation among sites that could not be attributed to forest type. Small diameter logs in the logging regenerated forest lacked some apparent mature forest specialists that were present in large diameter logs in the same forest type. This research

indicates that large diameter logs have unique habitat qualities for saproxylic beetles, and they are important in providing continuity of habitat for the re-establishment of certain species following stand level disturbances, whether induced by logging or by wildfire.

A precautionary and multi-scaled approach towards dead wood management is advocated, with particular consideration of the temporal scale at which the dynamics of the forests operate. In line with current conservation management strategies employed and explored by Tasmanian forestry, retention of some trees during harvesting to improve stand structure complexity and future dead wood supply is strongly recommended as one means of mitigating potential negative impacts. The planning of tree retention should aim to provide sufficient oldgrowth features, and sufficient quantity and continuity of dead wood types, throughout successive forest regeneration cycles for conservation of dead wood dependent biota. At the landscape scale, managing the production forest matrix as a habitat mosaic through diversifying silvicultural regimes is also recommended.

ACKNOWLEDGMENTS

The study of saproxylic beetles has given me new insights into the way I view the forest, particularly in regards its complexity and the plethora of organisms that weave their way through this matrix. To have had this opportunity, there are many people I would like to acknowledge. First, I would like to thank my two primary supervisors, Dr. Caroline Mohammed (School of Agricultural Science, University of Tasmania (UTAS)) and Dr. Simon Grove (Forestry Tasmania). Simon joined the project mid-way after my industry supervisor, Dr. Rob Taylor left (formerly with Forestry Tasmania) to take up another job in Darwin. I greatly appreciate both Caroline's and Simons's support and guidance during my research, particularly for their contributions during the writing-up phase of the thesis.

This project would not have been possible without the initial project outline, research questions and ideas proposed by Drs. Caroline Mohammed, Rob Taylor, Alastair Richardson (School of Zoology, UTAS), ZiQing Yuan (formerly with Cooperate Research Centre for Sustainable Production Forestry (CRC-SPF)) and Peter McQuillan (School of Geography and Environmental Sciences, UTAS).

Special thanks are due to Sue Baker, for introducing me to the wide world of forest conservation, for her constructive ideas on my project and her willingness to help with almost all aspects of this project. Special thanks are also due to Dr. ZiQing Yuan, whom without his collaboration and field assistance, investigating log decomposition and rotten wood would not have been possible.

I appreciate all those volunteers that provided assistance on field trips, particularly with their help constructing log emergence traps, collecting insect samples and removing these traps from the forest. These include Paul Harrington, Yuzuru Hyatake, Sue Baker, Bill Brown, Dean Vincent and his Green-corp crew, David Kolabinski, Rob Taylor, Stuart with the red beard who I met at Tahune one day, Tracey Barker, Georgie Miller, Yoav Daniel Bar-Ness, Gabriel Warren, Lizz Pietrzykowski and Andrew Muirhead. I also thank Gab for measuring the body lengths of each morphospecies without really understanding why, and Dru Haywood, who volunteered her time to help me sort through samples for beetles.

I am grateful for the taxonomic expertise of the many expert Coleopterists that were keen and willing to help with the identification of beetles. The list includes Mr. Tom Weir at the Australian National Insect Collection (ANIC, Canberra), and Drs. Rolf Oberprieler (ANIC), Richard Leschen (Landcare, New Zealand), Don Chandler (University of New Hampshire, United States), John Lawrence (formerly with ANIC), Peter McQuillan, Adam Slipinski (ANIC) and Chris Reid (Australian Museum, Sydney). I was fortunate to spend a few weeks at ANIC at various times to utilise their insect collection, as well as attend a beetle identification course funded by a Maxwell Jacobs Fund Award, Australian Academy of Science. Special thanks extend to Tom Weir, whom was always willing to help with the identification of the smallest, dullest, brown, pubescent and otherwise non-descript beetle.

I acknowledge the statistical advice and help from Marti J Anderson (University of Auckland, New Zealand), who helped me better understand my experimental design for the application of PERMANOVA. I also appreciate the statistical advice from David Ratkowsky (School of Agricultural Science, UTAS) and Leon Barmuta (School of Zoology, UTAS).

I am deeply indebted to the many people that have read drafts of my thesis chapters and provided constructive input to improving my written English. These have included Caroline Mohammed, Simon Grove, Alastair Richardson, Helen Nahrung, Sarah Richards, Martin Steinbauer, Paul Harrington, Giuliana Deflorio, Ronlyn Duncan, Sue Baker and Hilton Redgrove. Also, many thanks to the staff and students at the CRC-SPF, the many resources and friendships they provided.

Financial support was supplied by a University Strategic scholarship with additional funding from the CRC-SPF top-up scholarship. Project costs were provided by the Australian Research Council, Forestry Tasmania, and Gunns Ltd (then North Forest Products). I am also grateful to the School of Zoology, UTAS for providing conference funding to attend the XXII International Congress of Entomology held in Brisbane, 2004.

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1 INTRODUCTION

1.1 GENERAL INTRODUCTION

Habitat loss and fragmentation have been recognised in Australia, and throughout the world, as the greatest threats facing the conservation of biological diversity (reviewed in Bennett 1999; Burgman & Lindenmayer 1998). The loss, or expected loss of 'oldgrowth structures'; are of increasing concern world-wide in managed forests (Angelstam 1998; Franklin *et al.* 2002; Gibbons & Lindenmayer 2001; Grove 2001; Hammond *et al.* 2004; Lindenmayer & McCarthy 2002; Lindenmayer & Franklin 1997; Maser & Trappe 1984; Siitonen 2001; Spies 1998). Oldgrowth structures are stand structures that comprise commercially over-mature trees, stags (dead trees) and large diameter logs on the forest floor (Lindenmayer *et al.* 2000b). Generally, as a hardwood tree ages, it develops rot holes, rotten heartwood, a hollow interior, dead branches of various sizes, and vast amounts of organic matter in form of leaf litter, fine dead wood, and coarse dead wood (>10cm, also known as coarse woody debris, Lofroth 1998).

Intensively managed forests are typically planned on silviculture regimes that are shorter than the natural disturbance regime (see Attiwill 1994a; Lindenmayer & McCarthy 2002; Spies & Turner 1999). For instance, Australian montane Ash forests are currently planned for 50-80 year rotations by clear-fell harvest (Squire *et al.* 1991), which is considerably shorter than the catastrophic or non-catastrophic wildfires of a 100-350 year return time interval (reviewed in Attiwill 1994b). Thus, a natural forest landscape of stands with high stand-structure complexity (multi-aged stands) that include oldgrowth structures, will shift towards a dominance of even aged younger stands after successive rotations (Grove *et al.* 2002; Lindenmayer *et al.* 2000b; Lindenmayer & Franklin 1997). In the absence of mitigation measures, oldgrowth structures would diminish without replacement. This has been a widespread phenomenon of many intensively managed forests in Northern Europe, where forest management has been extensive and long term (e.g. Esseen *et al.* 1997; Haila *et al.* 1994; Kouki *et al.* 2001; Linder & Ostlund 1998; Syrjänen *et al.* 1994). In Sweden, only 3% of the remaining forests have oldgrowth characteristics (Andersson & Östlund 2004

cited in Bryant *et al.* 1997). A more recent study demonstrated that current densities of old coniferous trees (>159 years) were two thirds lower compared to 80 years ago (Andersson & Östlund 2004).

In parts of Tasmania, lowland wet eucalypt forests are intensively managed largely for eucalypt timber and pulpwood production. These are currently planned for harvest under 80-100 year rotations (Whiteley 1999), harvesting by the standard 'clear-fell, burn and sow' (CBS, Gilbert & Cunningham 1972; Hickey *et al.* 2001) silviculture. Clearfell burn and sow silviculture entails clearing all trees in a single operation, burning the debris left from logging to create a receptive seedbed, and aerial sowing with local eucalypt seed for regeneration (Hickey & Savva 1992). Ecologically, CBS is a preferred harvesting method as it is considered most similar to the natural regeneration system of eucalypt trees after severe wildfires (Forestry Tasmania 2004; Hickey *et al.* 2001). However, after successive rotations under this silviculture regime, a truncated forest age and simplified stand structure is projected, and this combined with extensive wood extraction will drastically reduce dead wood volumes (up to two-fold reduction, Grove *et al.* 2002). Without survivor trees or stags to continually supply dead wood throughout the rotation, dead wood recruitment processes would be disrupted (Grove *et al.* 2002; Meggs 1996). In particular, large diameter logs would diminish and this could have profound consequences on the biodiversity of a group of invertebrates dependent on such logs - saproxylic beetles.

Saproxylic beetles are collectively defined by their dependence on dead wood for some part of their life (Speight 1989). They are a functional and speciose faunal group that typically comprise an important component of the forest's biodiversity (Grove 2002b; Speight 1989), yet have largely been unnoticed in Australia. Saproxylic beetles constitute several trophic levels: species that feed directly on dead and decomposing wood, species feeding on micro-organisms (e.g. fungi and bacteria) that decompose wood, and species that predate or parasitise other saproxylics (Speight 1989). Many such species have key functional roles, particularly in wood decomposition and nutrient cycling processes (Ausmus 1977; Dajoz 2000; Gilbertson 1984; Haack & Slansky Jr 1987; Lawrence 1989). For example, some wood boring beetles are major contributors to wood fragmentation processes (Ausmus 1977; Carpenter *et al.* 1988; Edmonds &

Eglitis 1989; Harmon *et al.* 1986). Other species have intimate associations with wood decay fungi (basidiomycetes) - the primary decomposers of dead wood (Kaarik 1974; Kirk & Cowling 1984; Swift 1977). Some beetle species facilitate the entry, and make conditions favourable for fungi, and fungal growth (Haack & Slansky Jr 1987), while others are important fungal vectors (Fager 1968; Gilbertson 1984; Haack & Slansky Jr 1987; Lawrence 1989). In addition, many species are important food sources for vertebrate species (Gibbons & Lindenmayer 2001; Martikainen *et al.* 1998; Maser & Trappe 1984). It is in Northern Europe and Britain where most attention to this fauna has been given. Anywhere between 700 and 1000+ saproxylic beetle species have been recorded in Germany (Köhler 2000), Norway (Hanssen *et al.* 1997), Sweden (Siitonen 2001), Finland (Siitonen 2001) and Britain (Alexander 2002). Köhler (2000) estimated that up to 56% of beetles in a forest in the Rhineland region of Germany are saproxylic. In Australia however, despite the ecological importance of this fauna, at the start of this project only a few studies had been undertaken; with a single study in Northern Queensland (Grove 2000), and few, mostly preliminary studies in Tasmania (Mesibov 1988; Michaels & Bornemissza 1999; Taylor 1990).

Dead and decomposing wood is a highly heterogenous resource for saproxylic beetle biodiversity (Dajoz 2000; Fager 1968; Graham 1925; Harmon *et al.* 1986; Speight 1989; Wallace 1953). Several studies show that dependent species have preferences for different dead wood types. For example, many species have preferences in relation to the source of dead wood, in terms of the host tree species (Bakke 1999; Irmler *et al.* 1996; Kappes & Topp 2004), tree size or age (Esaki 1996; Hammond *et al.* 2004; Kappes & Topp 2004; Siitonen & Saaristo 2000), or whether it has been derived from the branch, root, stump or trunk of a tree (e.g. Schiegg 2001, 2003; Speight 1989). The position of dead wood, that is whether the tree is standing or fallen (Irmler *et al.* 1996; Jonsell & Weslien 2003; Nilsson & Baranowski 1997), or in the sun or shade (Ahnlund 1996; Jonsell *et al.* 1998; Kappes & Topp 2004; Martikainen 2001; Ranius & Jansson 2000; Sverdrup-Thygeson & Ims 2002) are also influencing factors. Also, the effects of fire on dead wood can be favourable to some species (Wikars 1995, 2002). Moreover, as each piece of dead wood decomposes, the biological, chemical and physical properties of the 'wood' change in terms of decay stage and rot type, forming different microhabitats that support successions of different beetle species (Araya 1993; Ausmus

1977; Dajoz 2000; Gilbertson 1984; Greenslade 1972; Haack & Slansky Jr 1987; Hammond *et al.* 2001; Howden & Vogt 1951; Lawrence 1989; Speight 1989). Imler *et al.* (1996) found significant saproxylic beetle, mycetophilid fly and collembola assemblage differences among logs and stumps of different decay stage and tree species in mixed broadleaved forest in northern Germany. Kaila *et al.* (1994) showed birch trees decayed by different wood decay fungi can also host distinct assemblages.

Dead wood is an extremely dynamic component of the forest ecosystem (Edmonds & Marra 1999; Fridman & Walheim 2000; Grove *et al.* 2002; Ranius *et al.* 2004). For example, in the Douglas fir/western hemlock ecosystem in the Cascades of Oregon and Washington US, large high intensity stand replacing fires naturally kill large trees and produce large amounts of dead wood. This dead wood decomposes, but as the stand develops, new inputs from competition, mortality, insect attack, pathogens and wind tend to increase the biomass of dead wood until the next wildfire, and so the cycle repeats (Edmonds & Marra 1999). Natural beech forests in France exhibit dead wood pulses at high levels about every 200-300 years following the rapid break-up of old-growth stands (Mountford 2002). In general, the levels and types of dead wood within the forest stand are considered a function of tree mortality (which is a function of recruitment rate) and decomposition rate; and tree mortality and the quantity and quality of living trees change as the stand ages (Fridman & Stahl 2001; Ranius *et al.* 2004; van Lear 1993).

In Scandinavian temperate and boreal forests that have had a long history of forest use, one of the major factors correlated with saproxylic beetle species reductions in managed forests has been the reduced and discontinuous supply of dead wood, especially of large diameter logs (Økland *et al.* 1996b; Siitonen 1994a, 2001; Similä *et al.* 2003; Sippola *et al.* 2002; Sverdrup-Thygeson 2001; Väisänen *et al.* 1993). In particular, many rare or threatened species, some of which were once widespread and common, now only subsist as residual populations restricted to the few remaining natural and semi-natural stands with long dead wood continuity (Jonsell & Nordlander 2002; Jonsson *et al.* 2001; Kolström & Lumatjärvi 2000; Martikainen *et al.* 2000; Økland *et al.* 1996b; Siitonen & Saaristo 2000; Sverdrup-Thygeson 2001). In Sweden, of the disproportionately large number (446) of threatened (Swedish National Red-List) saproxylic beetle species, 178

of them are reliant on large diameter logs and a further 233 species utilise them (Jonsell *et al.* 1998).

Dead wood discontinuity can be considered as a form of habitat fragmentation in time. If suitable dead wood types are not made available, either due to timber removal or disruptions to the dead wood recruitment process, then dependent species unable to subsist in alternative habitats are likely to locally diminish (Jonsell & Nordlander 2002; Jonsson *et al.* 2001; Siitonen & Saaristo 2000). The Scandinavian situation serves as an indication of how saproxylic beetle communities in Australian temperate forests, which have had a short history of intensive forest management, may respond to such long term effects. In Tasmania, clearfelling only began in the early 1960s and so regrowth forests are at most midway through their first rotation period. Consequently in these regrowth forests, large diameter logs are still well represented (Meggs 1996; Woldendorp *et al.* 2002a). Thus, there is still time to alter forestry practices to ensure a continuous supply of large diameter logs for conservation if warranted.

To determine whether the long term loss of large diameter logs would be detrimental to saproxylic beetle biodiversity, there is a need to understand their specific ecological role in maintaining this biodiversity. Changes induced by forest management are numerable (reviewed in Siitonen 2001), often confounding and acting cumulatively to increase their impact on saproxylic beetles. For example in Central Europe, not only have large diameter logs diminished as a result of intensive forestry, but most managed forests have as little as 1 - 13m^3ha^{-1} of dead wood, compared to natural dead wood levels of 50-200m^3ha^{-1} (reviewed in Vallauri *et al.* 2002). Such reduced densities of certain dead wood types can result in habitat fragmentation at the local scale (e.g. Edman & Jonsson 2001 - wood decay fungi; Schiegg 2000b - saproxylic beetles). Included in intensive forest practices is fire suppression, and in fire-adapted forests, this has led to a significant reduction of certain microhabitats to certain aspects of the saproxylic fauna (Ahnlund & Lindhe 1992; Esseen *et al.* 1997; Kaila *et al.* 1997; Niemelä 1999). In European boreal forests, many species dependent on the dead wood deciduous aspen trees are threatened due to management favouring commercially valuable coniferous trees (e.g. Kolström & Lumatjärvi 2000; Kouki *et al.* 2001; Siitonen 1994b).

Despite these studies, it is unclear to what extent species declines can be attributed to the loss of large diameter logs, or to the other changes associated with intensive forestry. It remains possible that large diameter logs in wet eucalypt forests may constitute redundant saproxylic beetle habitat types that may be substituted by other dead wood types. For instance, small diameter logs may support equivalent assemblages and richness levels to large diameter logs. Schiegg (2001) demonstrated that branch wood contributed significantly to the conservation potential of saproxylic beetles in managed forests. Determining the specific function of large diameter logs would provide a sound basis in discerning whether special consideration to maintain these features within the landscape is warranted.

1.2 THESIS AIMS AND STRUCTURE

The thesis investigates how clearfell burn and sow harvesting on 90-year rotations impacts on saproxylic beetle biodiversity conservation, particularly focusing on the effect that diminishing availability of large diameter logs will have over the long term. The thesis explores the decomposition processes in large and small diameter logs, to determine to what extent these processes shape log substrate quality and hence habitat occupancy of saproxylic beetles. The ecological role of large diameter logs as habitat for saproxylic beetles is compared with that of small diameter logs derived from trees of an age approaching commercial maturity. The overall study is conducted in mature-unlogged forest and forest regenerating from clear-fell burn and sow silviculture. The findings will be discussed to help determine whether the retention of large diameter logs in Tasmanian wet eucalypt production forest is warranted, and thus, avoid potential detrimental impacts on the saproxylic beetle fauna as is implied from studies across Europe.

The specific objectives of the thesis are:
To document the species composition and describe the biology of saproxylic beetles utilising *Eucalyptus obliqua* in wet eucalypt forests of Southern Tasmania (Chapter 3)

- To compare the substrate quality of logs in relation to decomposition processes and log size in logged and unlogged forests (Chapter 4)
- To investigate associations between saproxylic beetles and the substrate quality of large and small diameter logs (Chapter 5)

- To compare saproxylic beetle populations in large and small diameter logs in unlogged and logging regenerated forests (Chapter 6)
- To discuss the ecological role of large diameter logs for saproxylic biodiversity within a production forest matrix, by reviewing possible impacts of forest management and by making recommendations for future research and management (Chapter 7)

Each chapter has been written in the format of a journal article, or journal articles in development, and therefore some repetition has been unavoidable. The reader is referred to previous chapters for information where appropriate. Study site locations and descriptions, and general sampling methods are given in Chapter 2 (General materials and methods).

2 GENERAL MATERIAL AND METHODS

2.1 STUDY SYSTEM

Tasmania has around 3.1 million hectares of native forests, 31 percent of which is managed for timber production (National Forest Inventory 2003). A large proportion (883 000 hectares) of this is wet eucalypt forest (Forestry Tasmania 1998). Wet eucalypt forests are tall open forests with an overstorey of one or more species of *Eucalyptus* and either an understorey of broad-leaved shrubs and ferns or of rainforest plants (Kirkpatrick *et al.* 1988). These are classified as wet sclerophyll forest and mixed forest respectively. *Eucalyptus obliqua* is the most widespread species of this forest type and trees of this species can reach an age of 400 years, heights of 75 m (Hickey *et al.* 2000), and girths over 2 m in diameter (Alcorn 2001).

Wet eucalypt forests are the intermediate successional stage preceding climax temperate rainforest (Gilbert 1959). Periodic wildfire is the natural disturbance mechanism under which these forests regenerate (Mount 1979). Otherwise, in the absence of fire, the eucalypt component dies out and rainforest persists (Gilbert 1959; Gilbert 1963; Jackson 1968). Natural fire frequency has been estimated to occur at one in every 20-100 years for wet sclerophyll forests, and one in every 100-400 years for mixed forest (Gilbert 1959; Mount 1979). Fires vary in intensity, ranging from high intensity that result in complete stand kill, to low intensity, where survivor trees and multi-aged stands persist. Preliminary survey data from this region show that natural levels of forest floor log volumes are wide ranging, with volume measurements between 203 and 1235 m^3 ha^{-1} (Meggs 1996; Woldendorp *et al.* 2002a)

2.2 STUDY AREA

The study was located in Tasmania's Southern Ranges bioregion (Cofinas & Creighton 2001), and was conducted in State production forest), approximately 60 km south-west of Hobart (43° 04' S, 146° 41' E) (Figure 2.1). Large mountain ranges surround the area: Mount Weld (1338 m) in the north-west, Mount Picton (1327 m) in the south-west, and the Hartz Mountains (1255 m) in the south. Part of the study area falls within the Warra Long Term Ecological Research (LTER) site, an area established, in part, to facilitate

the understanding of ecological processes and the biodiversity functions of Tasmania's wet *E. obliqua* forests (Brown *et al.* 2001). The study area has a temperate maritime climate, with prevailing north-westerly winds. In 2001, mean summer maximum and mean winter minimum temperatures were 30.9 °C and – 0.8°C respectively (Bureau of Meteorology). Annual rainfall averages between 1100 and 1400 mm, generally with winter and spring as the wetter seasons. Jurassic basic igneous rock (dolerite) underlie the area, with some Permian mudstone (Laffan 2001).

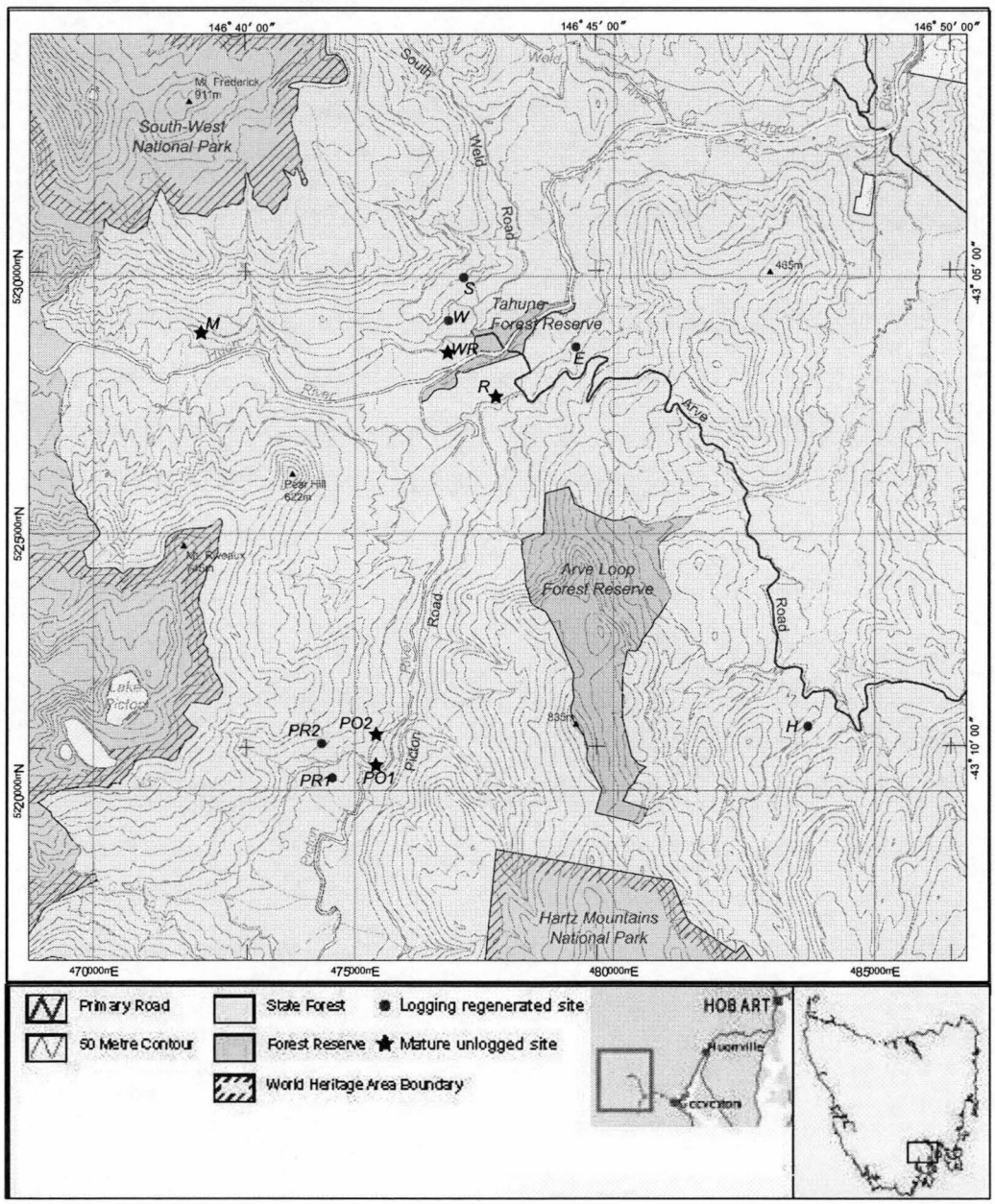

Figure 2.1. Location of the study area in southern Tasmania, showing the 11 study sites, as well as the State forest and Forest reserve boundaries. See Table 2.1 for descriptions of the alphanumeric site codes. Map prepared by Forestry Tasmania.

Recent fire histories of the study area and its surroundings are varied (Figure 2.2). The Warra LTER site had major fires in 1898, 1906, 1916 and 1934 (Alcorn *et al.* 2001), yet none were hot enough to destroy all standing oldgrowth stems (Hickey *et al.* 1999a). Some forest patches had not been burnt since 1850 (Hickey *et al.* 1999a); some areas comprise three different aged cohorts (Alcorn *et al.* 2001; Hickey *et al.* 1999a). To the south, the Picton Valley shares a similar recent fire-history to Warra in that substantial areas of forest regenerated from the 1934 fires, and towards the east, substantial areas within the Arve Valley were more recently burnt in the 1966/67 wild fires.

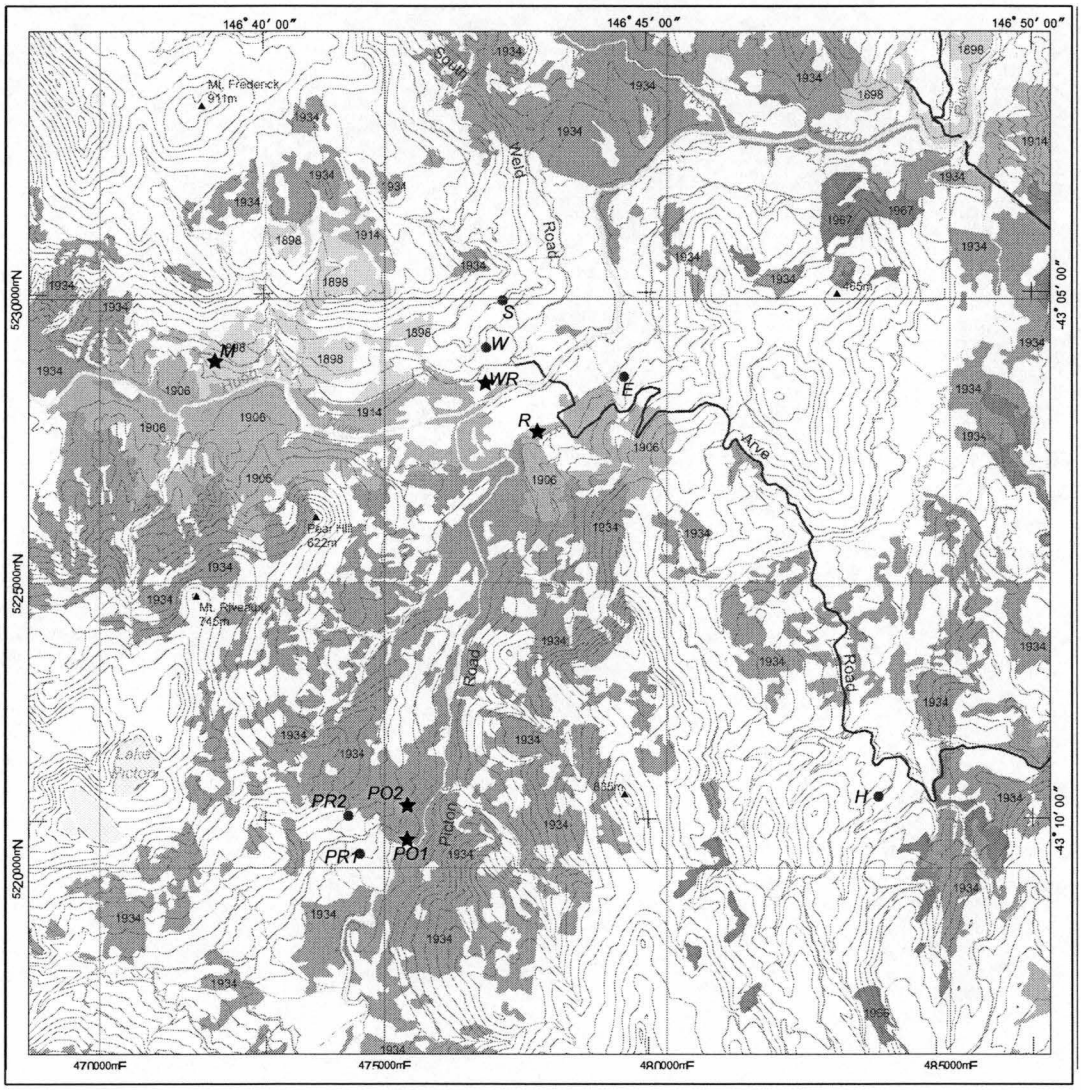

Figure 2.2. Recent wildfire history of forests in the study area and surrounding areas. Year within shaded areas refers to the date of the most recent wildfire. No fire history data were available for unshaded areas. See Table 2.1 for descriptions of the alphanumeric site codes. Map prepared by Forestry Tasmania.

Logging history in the general study area (Figure 2.3) comprises CBS harvested coupes of a young to early medium-aged (~ 30 year old) logging regeneration. Some selective and salvage logging occurred in the study areas prior to 1960 (Alcorn *et al.* 2001).

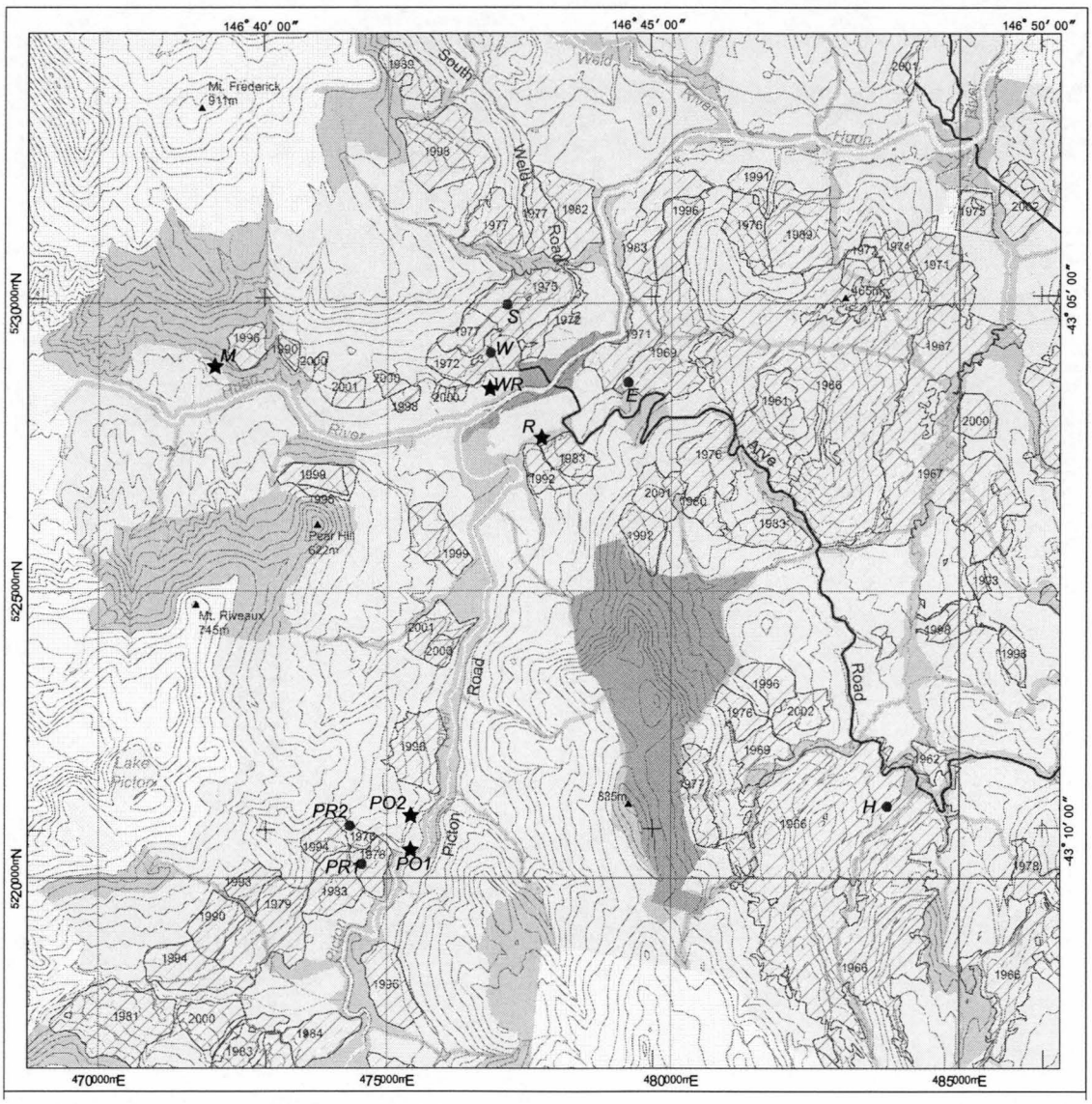

Figure 2.3. Recent logging history of the study area and surrounding areas. Year within the hatched areas refers to the date of forest regeneration. See Table 2.1 for descriptions of the alphanumeric site codes. Map prepared by Forestry Tasmania

The study sites are located in lowland wet eucalypt forests dominated by tall *E. obliqua* trees, and dead and decomposing wood of this species dominate the forest floor structure (Meggs 1996; Woldendorp *et al.* 2002a). Understorey floristics vary within the natural continuum of wet sclerophyll and mixed (rain forest) species, determined, in part, by local fire history and soil fertility (Gilbert 1959; Mount 1979). Descriptions of the vegetation communities are given in Corbett & Balmer (2001) and Neyland (2001).

Two forest type 'treatments' were chosen: mature-unlogged (MU) and logging regenerated (LR) forests. MU forests are unharvested forest with a multi-aged stand of two or more eucalypt cohorts that had regenerated from one or more wildfires. The most recent wildfire has been listed in Table 2.1. LR forests are forest regenerating from single clearfell, burn and sow silviculture (CBS: Gilbert & Cunningham 1972). Since this practice only commenced in the 1960s, the oldest LR forest available were less than 33 years old.

2.3 STUDY SITES

After an extensive search for older aged LR sites and MU within the study area, only five replicates of each treatment that met the requirements were found. Requirements were: dominated by *E. obliqua* trees; understorey composition characteristic of wet sclerophyll forest; and similar elevation, aspect and slope. Of the chosen sites, though, understorey floristics were still variable to some degree - dominant species for each site are listed in Appendix 2.1. Site names and their major attributes are listed in Table 2.1. The two furthest apart sites were within 10 km's of each other and the Huon and Picton rivers separate some sites (see Figure 2.1). Considering the close vicinity among sites, it is presumed that the LR sites prior to harvesting comprised a similar range of forest age classes to that of the MU sites. To trial the sampling methods, an additional LR study site comprising *E. obliqua* and some *E. regnans* trees, situated off Hartz Rd (designated site H), east of the other sites, was selected.

Table 2.1. Site information of the 11 study sites, showing geographic location, recent disturbance history and forest coupe code

	Site code and Access Road	MGA Easting Northing	Latitude x Longitude	Ft Coupe code & pi type	Year of clearfelling	Year of last wildfire
Logging regenerated forest	S South weld Spur 1	477392, 5229974	43 0826 S x 146 7223 E	WR006B1 E(75)NA/1	1975	-
	W Warra Rd	477100, 5229462	43 0872 S x 146 7186 E	WR007C E(72)N/A1	1975	-
	E[1,2] Edwards Rd	479435, 5228956	43.0918 S x 146 7473 E	PC005C E(69)NA/3	1969	-
	PR1 West Picton Rd	474512, 5220182	43.1707 S x 146 6864 E	PC030E E(78)A/1	1978 Burnt 1983	-
	PR2 West Picton Rd	474548, 5220569	43.1672 S x 146 6869 E	PC030D E(76)A/1	1976	-
	H Hartz Rd	483912, 5221382	43 1601 S x 146.8021 E	AR014C E(66)A	1966	-
Mature-unlogged forest	M Manuka Rd	471045, 5228764	43.0933 S x 146 6442 E	- E1dER4dS	-	1906
	WR Manuka Rd	476645, 5228764	43 0935 S x 146.713 E	WR001D E2cER4dS	selectively logged 1983	1914
	R[1] Riveaux Rd	477870, 5227678	43 1033 S x 146 728 E	- E2dER4d.S	-	1906
	P01 West Picton Rd	474547, 5220624	43 1667 S x 146.6869 E	- E2dER2d	-	1934
	P02 West Picton Rd	475526, 5221274	43 1609 S x 146 6989 E	- E2cER4d	-	1934

[1]Sites E, R, and PR1, correspond to sites 9, 11, and 8 in Michaels & McQuillan (1995) respectively, who sampled for ground and litter beetles using pitfall traps.
[2]Mesibov (1988) had also surveyed site E for log dwelling invertebrates.

Within each site, a 50 m x 50 m study plot was established. These dimensions were arbitrary, and were chosen to limit the forest area for searching, but also to ensure the successful finding of suitable logs. Study plot position within a site was in part determined by accessibility to the forest, gentle to moderate slope for working, and similar understorey cover to sites of the same forest type treatment. Study plots were located at least 50 m from the road to minimise likely edge effects (Bennett 1999). All sampling and field measurements were conducted within this study plot.

2.4 ENVIRONMENTAL and STAND STRUCTURAL ATTRIBUTES

Environmental attributes considered to influence saproxylic beetle assemblages were measured at each site. These were chosen based on a significant correlation in past studies. For example, In Finland, species richness was found to correlate with forest stand structure (Rassi *et al.* 1986; 1992), and standing wood volume per hectare (Sverdrup-Thygeson 2001; Grove 2000). In Sweden pasture woodlands, Ranius and Jansson (2000) found the species composition differed depending on degree of the degree of regrowth and sun-exposure.

Attributes measured in this study included canopy openness, altitude, slope, aspect, and dominant understorey plant species. In addition, both dead wood and stand structural attributes were measured for each site. These included volume of dead wood, and dead wood quality – in terms of size range and decay distributions, number of stags, number of survivor trees and stem diameter (dbh) distributions of live eucalypt trees. These data have been used to help interpret and discuss the research results in this thesis. To improve thesis readability, the data, and methods used to collect the data are presented in Appendix 2.1.

2.5 STUDY LOGS

Saproxylic beetles were sampled from *E. obliqua* logs of an intermediate decomposition stage. This stage (also known as decay stage 3) was defined based on the classifications of Lindenmayer *et al.* (1999b) and Meggs (1996) (see Table 2.5). Such logs typically had no bark, soft sapwood, heartwood is solid, but with rotting heartwood in places, and logs still retain their cylindrical log shape. The study logs in LR sites comprised post harvest logging debris, while those in MU sites would have been recruited from natural causes of tree death (Woldendorp *et al.* 2002a). Although it was not possible to determine the date of tree fall for study logs at the MU sites, logs were still considered an appropriate comparison to study logs at the LR sites because they were at the same decompositional stage. Two log size diameter classes were chosen for study: large (>100cm) and small (30-60cm). These size dimensions were based on their representation of a commercially over-mature tree, and a tree approaching commercial maturity respectively. To ensure chosen small diameter logs were not derived from the branch of an over-mature tree, overall log shape and curvature were examined.

2.6 SAPROXYLIC BEETLE SAMPLING METHODS

Saproxylic beetles were sampled using two sampling methods: destructive sampling and emergence trapping. These methods were chosen based on specific research objectives, as explained in the respective chapters. The efficacies of sampling methods were also compared.

2.6.1 Destructive sampling

Destructive sampling involved intensively searching the log and hand collecting for saproxylic beetle inhabitant, as well as surveying the wood rot types. This method has rarely been conducted before, particulary with such large diameter logs. The method was first trialed in a pilot study. The pilot study was conducted at site H, on three large and three small diameter logs, of the same size dimensions specified above. Within each log, a 10-m section of log was destructively sampled using a chainsaw at 1m intervals, for rot types and inhabiting insects. Given the physically demanding nature of this work, the objectives were to determine an effective and physically feasible sampling protocol, while ensuring a reasonable sampling effort of the log's heterogeneity. The variability of insect assemblages and rot type along the log were qualitatively assessed.

Based on results of the pilot study assessment, time constraints, and the trade-off between sampling intensity (number of cross-sections per log) and sample size (number of logs), the destructive sampling programme involved sampling from two 1-m long sections of each log at least 4 m apart (Figure 2.4a). The exact trunk position (e.g. position from tree base) from where the section was sampled could not be determined, especially at the LR site where logs comprised logging residue.

For each 1-m section of log, sampling for saproxylic beetles entailed searching the log surface layer, then peeling away any decomposed litter and former sapwood layer until solid heartwood was reached. Then a 1-m long section was removed with a chainsaw and cut into three parts to allow ease of handling. Each part was cut using an axe and mattock. Around 1 hour was allocated to destructively sample each 1-m log section. Because of the gross differences in volume between log size classes, for large diameter logs only one eighth of each 1-m long section was sampled (Figure 2.4b). Reducing sample volume ensured a more comparable sampling effort between log sizes, made sampling such logs logistically feasible, and still allowed adequate access to the log interior. Log names and diameters of the study logs used for destructive sampling are listed in Table 2.2. Beetle collection was conducted with the aid of a head torch and forceps to search within the log section as it was broken up. A adult and larval beetles were immediately preserved in 80% ethanol. Only subsets of populations were taken

when multiple individuals of the same species were found. Additional samples of larvae with host material were taken for rearing to allow identification and observe life history.

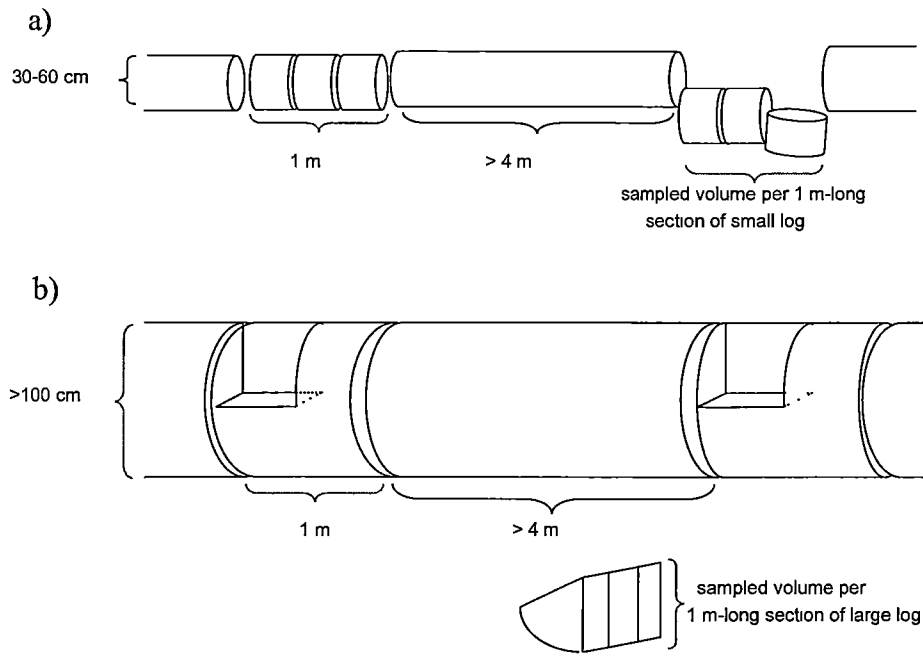

Figure 2.4. Schematic diagram of sampling method used to destructively sample a) small and b) large diameter logs

Table 2.2. Log codes, diameters, and approximate surface area and log volume sampled of the two 1-m log sections used for destructive sampling. Note, only approximately 1/8 of the volume for each 1m long log section belonging to a large log was sampled.

	Site	Large log	Diameter (cm)	Surface area (m^2)	Log volume (m^3)	Small log	Diameter (cm)	Surface area (m^2)	Log volume (m^3)
Logging regenerated forest	E	EDL1	87.5	5.50	0.15	EDS1	42	2 64	0 28
		EDL2	100	6 28	0.20	EDS2	30	1.88	0 14
		EDL3	99	6 22	0.19	EDS3	35	2 20	0 19
	S	SDL1	92	5 78	0.17	SDS1	39	2 45	0 24
		SDL2	95	5.97	0 18	SDS2	55	3 45	0.47
		SDL3	85	5 34	0 14	SDS3	49	3 08	0.38
	PR2	PR2DL1	94	5 90	0.17	PR2DS1	43	2.70	0 29
		PR2DL2	100	6 28	0 20	PR2DS2	52	3.27	0 42
		PR2DL3	95	5.97	0 18	PR2DS3	49	3 08	0 38
	H	HDL1	120	7 54	0 28	HDS1	30	1 88	0 14
		HDL2	105	6.59	0 22	HDS2	36	2 26	0.20
		HDL3	90	5.65	0 16	HDS3	30	1 88	0 14
Mature unlogged forest	M	MDL1	97.5	6 12	0 19	MDS1	32	2 01	0.16
		MDL2	125	7 85	0 31	MDS2	35	2 20	0.19
		MDL3	95	5 97	0 18	MDS3	46	2 89	0.33
	PO1	PO1DL1	100	6 28	0 20	PO1DS1	49	3 08	0.38
		PO1DL2	90	5 65	0 16	PO1DS2	53	3.33	0.44
		PO1DL3	100	6.28	0 20	PO1DS3	50	3 14	0 39
	WR	WRDL1	90	5 65	0 16	WRDS1	43.5	2 73	0.30
		WRDL2	110	6 91	0 24	WRDS2	44	2 76	0 30
		WRDL3	105	6 59	0 22	WRDS3	33	2.07	0 17

2.6.2 Emergence trapping

A modified version of the emergence traps used elsewhere at Warra and described in Bashford *et al.* (2001) was used to sample saproxylic beetles emerging from the study logs. Each trap (Figure 2.5a) consisted of strong netting (<1mm fine mesh to ensure trapping small beetles) encasing the log. Trap length varied anywhere between 2 and 4 metres. Dimensions of individual emergence traps are given in Table 2.3. Netting material was attached to the log using a staple gun and supported above the log by 15 cm long modified wooden stakes (Figure 2.5b). Trap design was tested for durability and sample effectiveness in a pilot study at site H, and had been modified accordingly. Trap design was kept simple so that traps could be assembled by one person. Traps would have had a limited lifetime of perhaps no more than 3 years - sufficient for the purpose of this study.

Similar to Bashford *et al.* (2001), emerging beetles are captured in any of two to three collecting containers: one at the top to catch those that move towards the light (Figure 2.5c), and one to two fixed containers at the base of the trap to catch beetles whose behaviour is to crawl off the log (Figure 2.5d). The top container consisted of an empty PET 2-litre fruit juice bottle connected to a piece of elbow piping, which directed emergent insects from the trap into the container. This top system was kept in place using a support bracket (Figure 2.5c) constructed from pre-cut and pre-drilled wooden stakes held together by flexible wire. Containers were changed more or less monthly during spring-summer, and every second or third month during autumn-winter. Diluted ethylene glycol (50-70%) was used as preserving fluid.

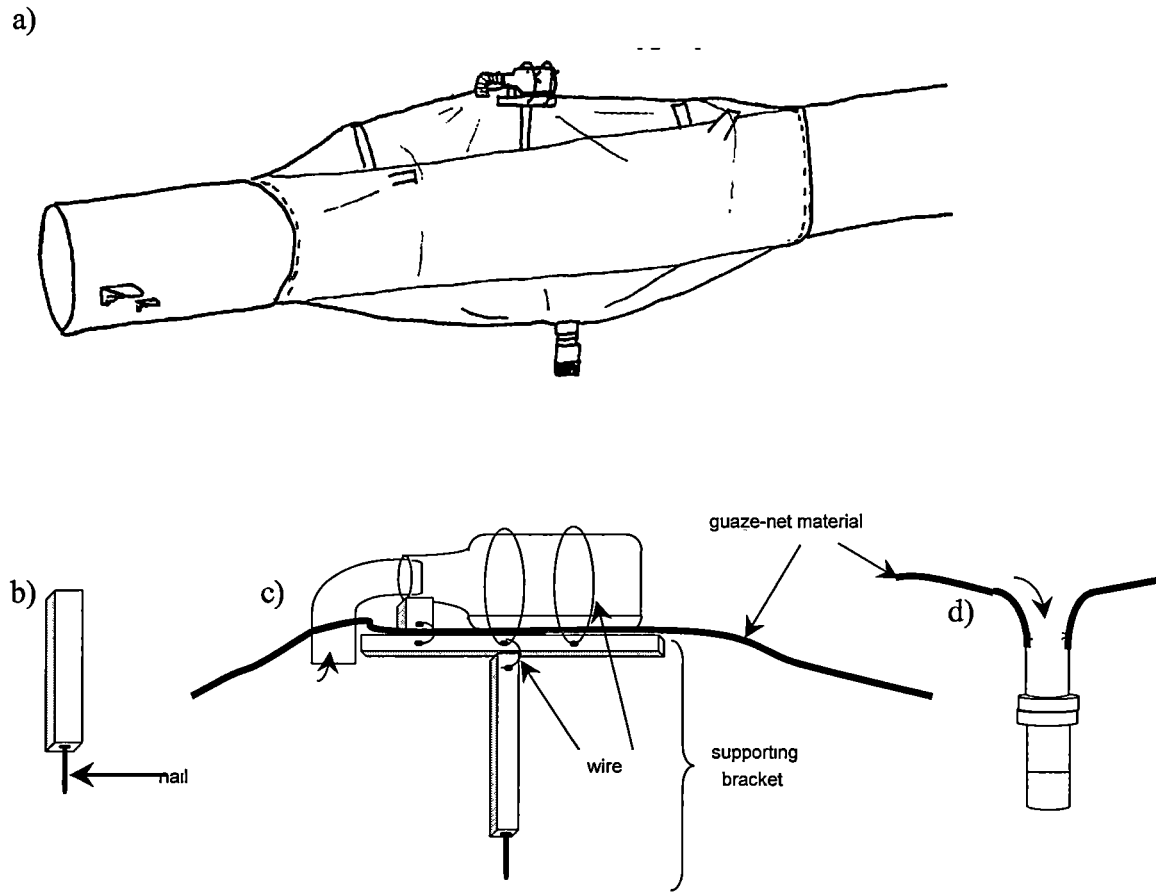

Figure 2.5. Log emergence trap showing the a) overall design, b) wooden stakes used to support material off log, c) top collecting container and support bracket, and d) bottom collecting container

Table 2.3. Log codes, diameters (at trap position), length of each log and approximate surface area and log volume that was sampled for each log emergence trap.

	Site	Large log	Diameter (cm)	Trap length (cm)	Surface area (m^2)	Log volume (m^3)	Small log	Diameter (cm)	Trap length (cm)	Surface area (m^2)	Log volume (m^3)
Logging regenerated forest		ELET1	97	450	13 71	3 32	ESET1	40.5	476	6.05	0.61
	E	ELET2	100	365	11.46	2 87	ESET2	52 5	470	7.75	1.02
		ELET3	133	365	15 24	5 07	ESET3	63	454	8.98	1.41
		WLET1	95	272	8.11	1 93	WSET1	27	271	2 30	0.16
	W	WLET2	102	285	9.13	2.33	WSET2	23	285	2 06	0.12
		WLET3	122	292	11.19	3.41	WSET3	41	296	3 81	0 39
		SLET1	130	368	15 02	4 88	SSET1	24	265	2.00	0 12
	S	SLET2	132	269	11 15	3.68	SSET2	32	278	2 79	0 22
		SLET3	92	263	7 60	1.75	SSET3	26	283	2.31	0 15
		PR1LET1	140	292	12.84	4.49	PR1SET1	64	300	6 03	0 96
	PR1	PR1LET2	125	284	11.15	3.48	PR1SET2	59	178	3 30	0 49
		PR1LET3	120	287	10 81	3.24	PR1SET3	35	287	3.15	0 28
		PR2LET1	100	240	7.54	1.88	PR2SET1	48	155	2.34	0 28
	PR2	PR2LET2	187	252	14 80	6 92	PR2SET2	47	260	3.84	0 45
		PR2LET3	149	278	13 01	4 84	PR2SET3	46 5	159	2 32	0.27
		HLET1	135	289	12 25	4 13	HSET1	45	289	4 08	0.46
	H	HLET2	129	294	11.91	3 84	HSET2	31	346	3 37	0.26
		-	-	-			HSET3	33	313		
Mature-unlogged forest		MLET1	133	285	11.90	3.96	MSET1	34	280	2.99	0.25
	M	MLET2	146	273	12 52	4.57	MSET2	36	275	3 11	0 28
		MLET3	127	267	10 65	3 38	MSET3	42	300	3 96	0 42
		RLET1	100	255	8.01	2.00	RSET1	36	220	2 49	0 22
	R	RLET2	93	280	8 18	1.90	RSET2	33	286	2.96	0 24
		RLET3	85	366	9 77	2 08	RSET3	28	280	2.46	0.17
		WRLET1	115	225	8 12	2 34	WRSET1	35	292	3.21	0 28
	WR	WRLET2	102	267	8 55	2 18	WRSET2	28	267	2.35	0 16
		WRLET3	108	291	9 87	2 66	WRSET3	33	200	2.07	0 17
		PO1LET1	125	290	11.38	3 56	PO1SET1	45	270	3.82	0 43
	PO1	PO1LET2	121	293	11.13	3 37	PO1SET2	64	188	3 78	0 60
		PO1LET3	110	280	9.67	2 66	PO1SET3	44	272	3.76	0 41
		PO2LET1	95	290	8.65	2.05	PO2SET1	42	317	4 18	0 44
	PO2	PO2LET2	90	283	8 00	1.80	PO2SET2	29	265	2.41	0 17
		PO2LET3	93	371	10.83	2.52	PO2SET3	36	288	3 26	0 29

2.7 BEETLE SORTING AND IDENTIFICATION

All beetles were sorted and identified to at least family level and then to morphospecies using the protocols of Oliver & Beattie (1996). Morphospecies were identified to genus or species where feasible, by using various taxonomic keys, consulting with and sending vouchers to the various relevant beetle experts, and comparing vouchers with reference material at the Australian National Insect Collection (ANIC: CSIRO Entomology, Canberra) and Tasmanian Forest Insect Collection (TFIC: Forestry Tasmania, Hobart). Specimens have been lodged at both, but with the primary set of vouchers lodged at the TFIC. The taxonomic experts consulted include Mr Tom Weir

(ANIC - various), Dr Rolf Oberprieler (ANIC-Curculionidae), Dr Simon Grove (TFIC – various), Dr Don Chandler (University of New Hampshire, United States-Pselaphinae), Dr Peter McQuillan (University of Tasmania - various), Dr Richard Leschen (Landcare, New Zealand - various Cucujoidea), and Dr. Chris Reid (Australian Museum, Sydney – Chrysomelidae).

2.8 DATA, EXPERIMENTAL DESIGN AND STATISTICAL ANALYSIS

A summary of the destructive sampling and emergence trapping data used in their respecitve chapters is listed in Table 2.4. While there is some degree of overlap of data among chapters, the aims of the chapter, and hence analysis of the data, differ.

Table 2.4. Summary of the data and type of data used in each chapter

Sampling method	Data type	Chapter 3	Chapter 4	Chapter 5	Chapter 6
DESTRUCTIVE SAMPLING	RW type data (presence/absence)		X	X	
	Beetle data (presence/absence)	X		X	
EMERGENCE TRAPPING	Beetle data (species abundance)	X			X

Different experimental designs and statistical analyses were used for each chapter, and so have been outlined in their respective chapters.

2.9 APPENDICES

Appendix 2.1: Study site environmental and stand structural attributes – methods and data

Site-scale environmental and stand structural variables (Table 2.5) were measured from the four corners of the 50 x 50 m study plot within each site. Data from the four locations were pooled and the mean value calculated for each site. Stand structural variables included counts of total number of live and dead 'oldgrowth' trees occurring in the study plot. The percentage of live *E. obliqua* stems in each of the five diameter (dbh) classes was also calculated. This was based on measuring dbh of 40 trees: ten eucalypt trees occurring nearest to each study plot corner.

Qualitative and quantitative assessments of the dead wood habitat were measured following the line intersect procedure outlined in Waddell (2002). This was considered the most appropriate method for plot level sampling of dead wood at the time of sampling. Three 33 m (total = 99m) line transects were marked out, radiating from the centre of the study plot at bearings of 0, 135, and 225 degrees (Figure 2.6). This configuration, as recommended by Waddell (2002), was chosen to minimise biases associated with forests with highly clumped patches of dead wood, typical of harvested sites (Hess 2001; Marshall *et al.* 2000); and non-randomly orientated logs, such as logs of wind fallen trees after storm events. All logs (>12.5cm) intersecting these lines were measured for diameter (at point of line intersect) and log decomposition stage was also visually assessed, following the classifications of Lindenmayer *et al.* (1999b) and Meggs (1996) (Table 2.6). From this, site dead wood volumes per hectare were calculated (V=pi**/8L(d**): V = volume (m^3/ha), L = length of transect (m), d = log diameter (cm) at the point that intersects the line: Lindenmayer *et al.* 1999b; Ringvall & Stahl 1999; van Wagner 1968). Note, after this sampling was conducted, a study (Woldendorp *et al.* 2002b) reviewing sampling methods for dead wood in Australian forests recommended continuous longer line transects (preferably > 100m) in preference to sampling the same length split into shorter transects, to provide estimates with higher precision. Therefore, although dead wood volume estimates in this study may not accurately reflect absolute stand level volumes, they should still reflect relative differences among study sites. Table 2.7 displays the data for environmental and stand

structure site attributes, and this includes dominant understorey vegetation floristics and dead wood quality and quantity for each site.

Table 2.5. Description of environmental and stand structure variables recorded at study sites.

Variable name	Description of variable
Variables recorded at each corner of the study plot	
Canopy cover (%)	Measured from hemispherical photographs
Aspect	Measured in degrees
Slope	Measured in degrees
Percentage of trees by stem diameter	From 40 trees, number of trees in one or four dbh classes (10-30, 30-60, 60-90, >90cm)
Understorey floristics (%)	% cover of shrubs and non eucalypt trees within 10 m x 10m sub plot
Variables recorded for 50 m x 50 m study plot	
Number of stags	
Number of survivor trees	
Variables recorded along three 33m line transects at bearings 0, 135 and 225 degrees	
Volume of dead wood (ha^{-1})	Calculated volumes of dead wood per hectare using the formula Volume per hectare = pi**/8Ld**, used in Lindenmayer *et al* (1999b). L = length of transect, d = log diameter at point that intersect the line.
Percentage of logs grouped by diameter class and decomposition stage	From all logs intersecting the line, number of logs in one of four diameter classes (10-30, 30-60, 60-90, >90cm), in one of five decomposition stages (see Table 2.5)

Table 2.6. Log decomposition stage (DS) classifications used to assess in this study.

DS	(Meggs 1996)	Lindenmeyer *et al.* (1999)
1	logs that are entire, cylindrical shape, freshly down, few (<5% - imperfections such as splits, holes etc, no fruit bodies, hard sound wood	solid log, bark intack, and log recently fallen
2	presence of fungal fruiting bodies, presence of splits, cracks, wounds, decayed ends showing signs of rot to an overall surface area of no more than 10% may have small amount of bark present, retains much of its original shape	solid log, and no bark
3	Logs beginning to lose 'tree-like' appearance, containing splits, cracks etc, exposing rot to an overall surface area of 11-20% of log surface area. May be moderately soft	some decomostion of log, soft sapwood and solid heartwood
4	losing much of its 'log-like- appearance with often large sections of exterior wood missing Exposed rot to 21-50% of log surface area. May be moderately soft Rotting wood roughly in the shape of a log, often only solid wood present along sides of log, often embedded partly in the soil >50% of surface area consisting of rot Usually soft and wet	isoft sapwood or sapwood not present, soft heartwood, and log 'breaking-up'
5		advanced decompostion of log, soft sapwood and heartwood (if identifiable) log fragmented

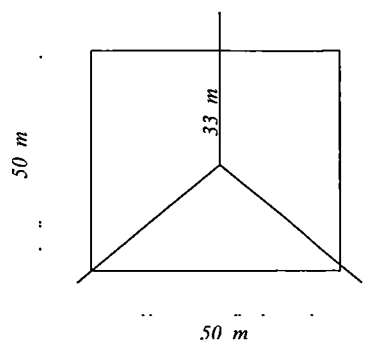

Figure 2.6. a) A schematic of the study plot and line intersect layout used to assess dead wood quality and quantity within the study site

Table 2.7. Environmental and stand structure attributes for each study site.

	Logging regenerated sites					Mature unlogged sites				
Site name	S	W	E	PR1	PR2	M	WR	R	PO1	PO2
Canopy cover (%)± s d	48 1 ± 8.9	59 9 ± 10.3	65.3 ± 6 1	61.4 ± 5.4	49 4 ± 8.7	76 6 ± 4 2	51 8 ± 11 4	82.5 ± 6.5	78 8 ± 7.4	85 9 ± 4 0
Aspect (degrees)	105	137	268	90	180	180	90	230	120	92
Slope (degrees)	3	2	13	22	9	26	5	2 5	6	16
	Percentage of standing trees grouped by dbhob class (cm)									
10-30 cm	83 3	57 5	57.5	92.5	95	7 7	44 7	10 4	66.7	51.3
31-60 cm	16 7	42.5	30	7 5	5	33 3	13.2	62 4	18.2	33.3
61-90 cm	0	0	12 5	0	0	20 5	23 7	11.4	3 0	10.2
>90 cm	0	0	0	0	0	38 5	18.4	15.8	12.1	5 2
Dominant non-eucalypt species	P.ape P asp G gra	G gra P.apt A mel	P ape N.cun D ant	P ape G gra	G gra E.luc P squ	D.ant P.squ P ape	G gra P.ape A big P squ B.rub	L lan G gra	A.big E.luc A.gla P squ	A.big P.ape B.rub
Number of stags	9	6	0	0	1	1	9	3	5	2
Number of survivor trees	0	0	0	0	0	8	7	21	36	18
Dead wood volume ± s d. (m^3ha^{-1})	276.3 ± 30 9	345.5 ± 55.2	372 8 ± 13.7	269 4 ± 52 2	422 1 ± 11 9	234 4 ± 39 5	211 8 ± 22 5	158.2 ± 14.4	218.9 ± 22.0	192 3 ± 16.7
	Percentage of logs grouped by diameter class (cm) and decomposition stage (DS)									
> 90 cm, DS 1	0	0	0	0	0	0	0	0	0	0
> 90 cm, DS 2	0	0	0	0	0	0	0	4.3	0	0
> 90 cm, DS 3	11.8	0	9.5	3 6	6.0	5 6	5 3	4.3	8.0	0
> 90 cm, DS 4	3 9	2 2	4.8	7.1	2.0	0	0	4.3	4.0	5.6
> 90 cm, DS 5	2 0	0	0	3.6	2.0	0	0	8.7	4.0	0
61-90 cm, DS 1	0	0	0	0	0	0	0	0	0	0
61-90 cm, DS 2	0	0	0	0	0	0	0	0	0	0
61-90 cm, DS 3	5.9	6.7	4 8	7.1	6 0	11.1	7 9	0	12.0	11 1
61-90 cm, DS 4	3.9	2.2	2 4	3.6	6 0	5 6	2.6	0	4.0	5.6
61-90 cm, DS 5	0	6.7	2 4	0	0	0	0	0	4 0	0
31-60 cm, DS 1	0	0	0	0	2 0	0	5.3	0	0	0
31-60 cm, DS 2	0	0	0	0	0	0	2.6	4 3	0	11 1
31-60 cm, DS 3	11 8	20	4 8	17 9	34 0	22.2	23.7	4 3	8 0	5 6
31-60 cm, DS 4	7 8	4.4	14.3	7 1	6 0	11 1	5.3	8 7	8.0	11 1
31-60 cm, DS 5	2.0	6.7	2.4	7.1	0	0	5.3	13 0	4 0	11 1
10-30 cm, DS 1	2.0	0	2 4	0	4.0	0	0	0	0	5 6
10-30 cm, DS 2	2 0	6 7	2.4	3 6	0	11.1	0	21 7	8 0	5 6
10-30 cm, DS 3	29 4	26.7	28 6	32 1	24.0	16.7	28.9	13 0	8 0	16 7
10-30 cm, DS 4	17 6	15.6	19 0	7.1	8.0	16.7	5.3	13 0	8 0	11 1
10-30 cm, DS 5	0	2 2	2.4	0	0	0	7.9	0	20	0

Descriptions of log decomposition stage (DS) are described in Table 2.6. Only dead wood pieces greater than 10cm diameter were measured.

Species names of abbreviations are: A.mel - *Acacia melanoxylon;* A.big - *Anodopetalum biglandulosum;* A.gla - *Anopterus glandulosus;* B.rub - *Bauera rubioides;* D.ant - *Dicksonia antarctica,* E.luc - *Eucryphia lucida,* G.gra - *Gahnia grandis,* L.lan - *Leptospermum lanigerum;* N.cun - *Nothofagus cunninghamii;* P.squ - *Phebalium squamosum;* P.asp - *Phyllocladus aspleniifolius;* P.ape - *Pomaderris apetala.*

3 INVENTORY AND BIOLOGY OF SAPROXYLIC BEETLES USING TWO SAMPLING METHODS

ABSTRACT

In many different regions of the world, saproxylic beetles have been recognised as a group at risk from intensive forestry practices. It is unknown whether similar trends are apparent in Australia, as this fauna has largely gone unnoticed. In wet eucalypt forest in southern Tasmania, a total of 104 *Eucalyptus obliqua* logs, at an intermediate decomposition stage, were surveyed for saproxylic beetles using two sampling methods, namely emergence trapping and destructive sampling. Data on biological traits of beetles were compiled and various aspects of the overall assemblage described. The effectiveness of the two sampling methods was compared.

This field study demonstrated that decomposing *Eucalyptus obliqua* logs at an intermediate decomposition stage are an essential habitat for a rich, functionally diverse saproxylic beetle fauna that have a diverse range of life histories, representing 54 families and 360 species. Species included xylophages, mycophages, detritivores and predators. Rotten wood and the log surface/litter layer seemed to be the most species rich microhabitat types. Of the saproxylic beetles collected in this study, about 25% of species seemed to ground dispersers, and over 71 % of all species had a body length less than 4mm.

This study also highlights the taxonomic impediments faced with studying saproxylic beetles as indicated by the many species (58%) not identified to a species name. Because of their relatively cryptic and diverse life histories, sampling this fauna is better achieved using log emergence traps than hand sampling. In spite of intensive sampling, the inventory of saproxylic species in these forests is still far from complete. The species list presented in this study is valuable base-line data for researchers and nature conservations undertaking study of the highly species rich group.

3.1 INTRODUCTION

Systematic surveys of fauna are vital for the assessment of forest biodiversity and risks to this biodiversity, and baseline data from project-based surveys are important contributors to this knowledge (Anon 2001; e.g. Majer *et al.* 2002). Saproxylic beetles comprise a poorly studied, yet speciose functional group of forest organisms in Australia that warrants urgent attention (Grove & Meggs 2003). They are defined by their dependence on dead and decaying wood microhabitats (Speight 1989). Throughout many regions in Europe, saproxylic beetles are now threatened due to the effects of deforestation and long term forest management (e.g. Alexander 2002; Berg *et al.* 1995; Harding & Alexander 1994; Jonsell *et al.* 1998; Kirby & Drake 1993; Martikainen & Kouki 2003; Siitonen 2001; Speight 1989). In Tasmania, around 883 000 hectares of native wet eucalypt forest is available for timber production (National Forest Inventory 2003), though knowledge of the saproxylic beetle fauna in these forests is lacking, with only a few preliminary studies undertaken (Grove & Bashford 2003; Mesibov 1988; Michaels & Bornemissza 1999; Taylor 1990).

The effectiveness of conservation planning will, in part, depend on understanding how species respond to changes resulting from forest practices, and identifying those species most susceptible to such changes (Anon 2001; Burgman & Lindenmayer 1998). Habitat fragmentation (spatial and temporal) brought about by decreased availability of certain dead wood microhabitat types (includes wood decay fungi) is the main threat to saproxylic beetle species conservation, in northern European forests (Økland *et al.* 1996a; Schiegg 2000b; Siitonen *et al.* 2000; Similä *et al.* 2003). On the basis of experimental field studies, several authors suggest that species with certain life history traits are more susceptible to fragmentation effects (Davies *et al.* 2000; Didham *et al.* 1998; Henle *et al.* 2004; Schiegg 2000a). For instance, poor dispersers tend to be more prone to extinction (Jonsson 2003), as are occupants of rare habitat types (e.g. Golden & Crist 1999; Lawton *et al.* 1998), species naturally occurring at low abundances (e.g. Davies *et al.* 2000), predators (e.g. Davies *et al.* 2000; Didham *et al.* 1998; Komonen *et al.* 2000; Schiegg 2000a), and large-bodied species (c.f. Davies *et al.* 2000; Gaston 1996; Henle *et al.* 2004). Moreover, it is often the combination of certain traits that determines a species' susceptibility to fragmentation (Davies *et al.* 2004; Henle *et al.* 2004). For example, low dispersal ability, coupled with poor competitiveness and

prolonged development can limit a species' rate of recovery from periodic disturbance events (Bengtsson 2002; Tscharntke *et al.* 2002; Wood & Pullin 2002). Poor dispersers that are confined to rare and specialised microhabitats are equally limited (e.g. Nilsson & Baranowski 1997; Tscharntke *et al.* 2002). Therefore, such life-history information would be both valuable in interpreting biologically meaningful species responses to forestry-induced changes in the availability of dead wood microhabitats, and in setting priorities for the conservation of target species.

This chapter collates the saproxylic beetle taxonomic data from large (>100cm) and small (30-60cm) diameter *Eucalyptus obliqua* logs of an intermediate decomposition stage, sampled in wet eucalypt forests in Tasmania's southern bioregion. Such data were obtained from two separate studies (see Chapters 5, 6) that used two different sampling methods: emergence trapping and destructive sampling. Various biological traits that were considered important in understanding a species' response to forest practices were recorded. The overall faunal assemblage was described and discussed. In addition, the efficacies of both sampling methods were compared.

3.2 METHODS

3.2.1 Study location

Beetles were collected from wet eucalypt forest, representing 11 study sites (coupes), at three localities in Tasmania's southern forests. Six sites were in and near the Warra Long Term Ecological Research (LTER) site (43°04'S, 146°41'E); four in the Picton Valley, 10 km south of Warra; and one in the Arve Valley, 10 km south-east of Warra LTER site. Descriptions and maps of study sites are provided in Section 2.2. and 2.3. The canopy of all the sites was dominated by *E. obliqua* and logs of this species dominated the dead wood habitat. All study logs were at an intermediate decomposition stage (defined in Section 2.5). Six study sites were in single-aged native forest that had regenerated from 'clearfell, burn and sow' silviculture during the 1960s and 70s. The other five were in multi-aged unlogged forests that had regenerated following wildfires in the early 1900s. Sampled logs were of two diameter classes (>100cm diameter and 30-60cm diameter).

3.2.2 Sampling programme and methods

Two sampling methods were used to collect saproxylic beetles. Destructive sampling involves direct searching, which has advantages in gathering biological information of a species.Emergence trapping, a passive trapping method, collects beetles over a measurable period of time.

Destructive sampling occurred in seven of the 11 sites used in this study (see Section 2.6.1). At each site, six logs were destructively sampled. For all but logs at site H, this occurred between March and June 2001. Sampling at site H was conducted earlier, between February and May 2000 as this was part of a pilot study that trialled destructive sampling methodologies (see Section 2.6.1). In total. 42 logs were destructively sampled.

Emergence trapping occurred at all of the 11 sites. For all but site H, emergence traps were erected on six logs and operated for 18 months from October 2000 to May 2002 (included two summers). At site H, five emergence traps were erected, and these operated for seven months from March to December 2000. Emergence-trap collecting jars were changed at approximately monthly intervals during the spring-summer months and every second or third month during the autumn-winter months. Emergence trap beetle data were derived from 62 log emergence traps, as data from three traps were excluded. These traps were mistakenly erected on non-eucalypt logs, possibly *Phyllocladus asplenifolius* (Podocarpaceae). Data from these logs have been excluded from the final species list.

3.2.2.1 Destructive sampling

Direct searching can vary in sampling intensity, ranging from sieving and beating wood in order to dislodge insects (Martikainen & Kouki 2003), through to bark peeling (Siitonen 1994a) and prising apart logs by hand (Mesibov 1988; Taylor 1990), to destructively sampling an entire log using a chainsaw (Fager 1968). A variation of the latter method was adopted, where two 1-m long sections of log were destructively sampled for beetles (method is detailed in Section 2.6.1). This direct sampling method allowed information to be gained on species' microhabitat type, feeding guild, and an indication of its within-log population density.

3.2.2.2 Emergence trapping

Emergence trapping, is a non-destructive method that samples beetles directly from a particular log. An emergence trap samples a known amount of log over an extended period of time, thus catering for the different seasonal emergence times and development rates of beetles (Hammond 1997; Owen 1992). These traps have also been referred to as photo-eclectors (Rauh & Schmitt 1991), trunk eclectors (Schiegg 2001), and extraction cylinders (Økland 1996a). The traps were constructed from strong netting that encased between 2 and 4 m of log. Trap dimensions are listed in Table 2.3. Collecting jars were positioned at the top and at the base of the trap to catch species that disperse by flying or crawling respectively. Trap design is outlined in Section 2.6.2.

3.2.3 Beetle identifications

All beetles were sorted and identified to at least family level and then to morphospecies (Oliver & Beattie 1996). Morphospecies were identified to a genus or species, where feasible, following the protocol outlined in Section 2.7. Due to the taxonomic difficulties with identifying larvae, only results for adults are presented.

3.2.4 Biological traits of species

The majority of saproxylic beetles from these forests had not previously been studied. Therefore, many sources of information were examined to determine a species' biological traits. This included information from personal observations during direct searching; information from the various beetle experts; and records in the scientific literature, including some which were obscure. The main consulted references were Wilson (1928), Lawrence & Newton (1980), Speight (1989), Leschen (1993), Lawrence & Britton (1994), Lawrence & Milner (1996), Lawrence (1999), and Alexander (2002). As most species found within this study had not been recorded in the scientific literature, and some species were undescribed, information was often inferred from species of the same genera/sub-family/family. Information compiled for each morphospecies included saproxylicity, main microhabitat type, main feeding guild, vagility, body length and maximum emergence density.

3.2.4.1 "Saproxylicity"

A beetle species was considered to be either obligately, facultatively or non-saproxylic. Obligate saproxylics are species dependent on dead wood, or dependent on others that are dead-wood dependent, for some part of their life (namely the larval stage) (Økland 1996a; Speight 1989). Facultative saproxylics breed in dead wood, but can also breed in other detrital based habitats, such as fungi, fallen plant seeds, leaf litter and the soil/fermentation layer. Non–saproxylic species are those that shelter in, but do not breed or feed in, dead wood, such as overwintering chrysomelid leaf beetles (Hammond 1997). Non-saproxylics were excluded from all species tallies.

A conservative approach was used to determine 'saproxylicity'. Saproxylicity was determined, where possible, from personal observation during destructive sampling and rearing, personal communication with the relevant experts, published information on life history of the species/genera or related taxa, and the degree to which particular species have been collected in other habitat types using other collecting methods. The wet forests in which this study was conducted had previous and concurrent research studies on ground and litter beetle fauna, collecting by pitfall trapping (Michaels 1999, Michaels and McQuillan 1995, Baker *et al* 2004), and saproxylic beetles, collecting by hand (Mesibov 1988, Taylor 1990). This allowed the comparison of species collected in this study with those of other studies. For example, for species with little known life history information, if the same species was commonly collected from pitfall traps, it was classed facultative. For species identified only to family level, if the larval habits of the family are dead wood dependent, these species were classed obligate. If a species dependency on dead wood was questionable, but clearly associated with dead wood or detritus, the species was classed facultative.

3.2.4.2 Microhabitat type

Microhabitat is defined as the immediate physical environment in which food is sourced. Because it is largely the larval stage that feeds on dead wood substrates, microhabitat type is effectively the larval microhabitat. Species that potentially occupy more than one microhabitat type were assigned to the suspected main microhabitat type based on the various consulted sources of information. While this was rather subjective,

it was the best possible option given the lack of information for these species, and was similar to the approach described in Grove (2002a). Microhabitats within decomposing *Eucalyptus obliqua* logs were grouped into nine categories: the litter/log surface layer, bark, subcortical layer, solid wood, rotten wood, wet cavities, insect burrows in wood, fungal sporocarp and unknown. Each microhabitat corresponds to a particular region within a log (Figure 3.1).

Litter/ surface layer consists of the thick (usually 0.5 – 2.0 cm) moist layer of leaf litter and mosses that respectively accumulates and grows on the log surface. *Bark* refers to the periderm tissue. This was usually absent from logs at the intermediate stage of decomposition used in this study. The *subcortical layer* refers to the sapwood layer, and is commonly found on the outer surfaces (1-5cm) of the log. This was usually partially decayed, moist, cream-coloured and fibrous. *Solid wood* comprises hard and usually discoloured wood. *Rotten wood* includes any decomposed wood tissue derived from the heartwood. *Wet cavities* are the water and detritus filled cavities and cracks within the log. *Insect burrows* refer to the galleries and tunnels that have been excavated by other insects, in particular by woodborers and termites. *Fungal sporocarp* microhabitat refers to the fruiting bodies of various fungi that occur on the surface of logs.

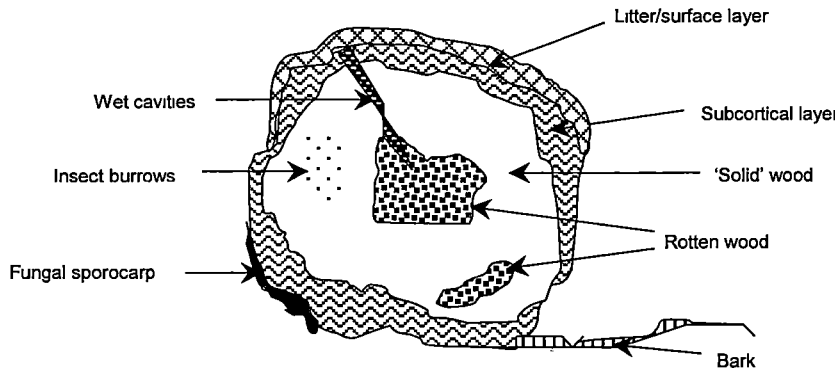

Figure 3.1. Visual representation of the different microhabitat types occurring within *Eucalyptus obliqua* logs at an intermediate stage of decomposition, showing their typical position and relative proportion of area within the cross-section.

3.2.4.3 Feeding guild

Saproxylic beetle larvae have a diverse range of feeding modes and strategies (Dajoz 2000; Lawrence & Britton 1994; Speight 1989). Species were allocated to one of five feeding guilds: xylophagous, predatory, saprophagous, mycophagous or "other". *Xylophagous* includes beetle species that bore into dead wood, feed on solid wood, or feed on decomposing wood tissue. This guild includes all beetles that ingest wood, including those that actually derive nutriment from the microorganisms (fungi and bacteria) involved in wood decomposition. *Predatory* species prey on other beetle larvae, snails, flies, earthworms, termites, springtails, mites and other microarthropods. *Saprophagous* species include scavengers of dead insects and species that feed on detritus, or on the microorganisms associated with the detritus, such as yeasts, bacteria, and slime moulds. Detritus includes any loose-particle substrata of plant or animal tissue that has been broken down by microorganisms (Lawrence & Milner 1996). *Mycophagous* species comprise those that feed on living fungal material (sporocarp, hyphae and spores). Species that did not fit the above categories, such as species that feed on epixylic moss, were termed 'other'.

3.2.4.4 Vagility

Vagility is categorised according to a species' propensity to fly or crawl from the log as adults. Known flightless species (e.g. *Lissotes* spp.: Lucanidae) were categorised as

crawlers; as were species caught exclusively in the lower collecting jars of the emergence trap. However, in order to minimise chance effects the latter criterion only applied to species occurring in more than 5 log emergence traps. For species caught in fewer than 5 traps, or only collected by hand, the presence of fused elytra was used to determine this. All other species not fitting these criteria were categorised as flyers. Species where the allocation to the crawler group remained questionable were also regarded as flyers.

3.2.4.5 Maximum emergence density

Maximum emergence density reflects the potential population density and pattern of colonisation of a species within a log (Simandl 1993). This was only determined for species caught within the emergence traps. Maximum emergence density for a species is defined as its largest number of individuals emerging from any single log during the collecting period.

3.2.4.6 Body Size

Body length was used as an indication of body size. Body length of one individual of each species was measured to the nearest 0.1 mm using a stereomicroscope. Although, the measurement of one individual does not capture the natural variation of body size within a species, the measurement of one individual was deemed sufficient to provide an indication of the species' general body-size range. Range of body lengths of species was described for each feeding guild.

3.2.5 Assemblage structure

Assemblage structure was investigated by tallying the various biological traits (vagility, microhabitat type and body size) of species, and grouping them by their feeding guild. For species collected in emergence traps, the maximum emergence density was described in relation to feeding guild.

3.2.6 Community structure

Community structure refers to the distribution of individuals among species within the community. This is a mathematical description of the data that emphasizes abundance

while utilizing species richness information where species abundance models are used to describe how species 'interact' with each other, partition the available resources and niches. For each emergence trap, the within-log community structure was measured by determining which distribution model (geometric, truncated log-normal, broken-stick and log series model (Magurran 1988) best fitted the species abundance distribution. This was calculated using the computer program, *Species Diversity and Richness* (Henderson & Seaby 1998). This program uses the distribution of the abundance classes and χ^2 goodness of fit tests to test for each of these model distributions.

3.2.7 Comparison of sampling methods

One-way Analysis of Variance (ANOVA) using *SAS ® 8* (Anon 1999) was used to compare sampling methods based on the number of species sampled per log. Chi-square tests were used to test for significant differences in occurrence of common species between sampling methods. Common species were defined as those occurring in over 15 logs from either sampling method combined.

3.3 RESULTS

3.3.1 Taxonomic composition

A total of 360 morphospecies, representing 54 families, were collected (Table 3.1). The Curculionidae and Staphylinidae families were the most species rich, with 56 and 80 species respectively. Many species were apparently undescribed, especially from these main families. A complete list of all species with their associated biological traits is given in Appendix 3.1. At least three species were new to science: *Enhypnon* TFIC 'sp nov' 01 (Zopheridae); *Alloproteinus* 'ANIC Thayer sp nov' 01 (Staphylinidae); *Tyrogetus* 'sp nov' 01 (Staphylinidae: Pselaphinae). Overall, 149 morphospecies could be identified to a known species, a further 114 morphospecies to genus level; and a further 41 and 54 morphospecies to family and sub-family level respectively. Two species remained undetermined to family level, and life history information attributed to these species was unknown.

Table 3.1. Summary of the number of saproxylic beetle families and species sampled from *Eucalyptus obliqua* logs at an intermediate decomposition stage, in wet eucalypt forest in southern Tasmania. Families are listed in taxonomic order.

Family	No. of species	Family	No. of species	Family	No of species
Carabidae	20	Clerdae	3	Zopheridae	9
Ptiliidae	4	Melyridae	2	Ulodidae	1
Leiodidae	14	Sphindidae	2	Tenebrionidae	10
Scydmaenidae	10	Brachypterdae	1	Prostomidae	2
Staphylinidae	80	Nitidulidae	5	Oedemeridae	2
Lucanidae	6	Phloeostichidae	1	Pyrochroidae	2
Scarabaeidae	3	Silvanidae	3	Salpingidae	1
Clambidae	2	Phalacridae	3	Anthicidae	1
Scirtidae	9	Hobartiidae	1	Aderidae	1
Byrrhidae	7	Cryptophagidae	3	Scraptiidae	2
Eucnemidae	2	Erotylidae	1	Cerambycidae	4
Throscidae	3	Cerylonidae	1	Chrysomelidae	6
Elateridae	14	Coccinellidae	10	Anthribidae	3
Lycidae	7	Corylophidae	8	Belidae	1
Cantharidae	4	Latridiidae	9	Attelabidae	2
Dermestidae	1	Archeocrypticidae	1	Curculionidae	56
Anobiidae	4	Ciidae	1	undetermined adults	2
Lymexylidae	1	Melandryidae	7	TOTAL	360
Trogossitidae	1	Mordellidae	1		

3.3.2 Biological traits and assemblage structure

3.3.2.1 Saproxylicity

Two hundred and two species were considered obligate saproxylics, 158 facultative saproxylics and 16 non-saproxylics (Appendix 3.2). This figure for obligate species is considered conservative as species with a definite but unknown degree of saproxylicity were categorised as facultative.

3.3.2.2 Microhabitat type

Most species were associated with the rotten wood and litter/surface layer of the log microhabitat types (104 and 92 species respectively) (Figure 3.2). The number of species associated with the other microhabitats ranged between 10 and 31 species, and 63 species had an unknown microhabitat association.

3.3.2.3 Feeding guild

The overall fauna was functionally diverse, represented by the four main feeding guilds in relatively even proportions, ranging between 16 and 28% (Figure 3.3). Eleven percent of the fauna had an unknown feeding guild.

3.3.2.4 Vagility

Approximately 25% of the species were considered crawlers. Xylophages and predators comprised a major proportion of these, while almost all mycophages and saprophages where thought to disperse by flying (Figure 3.4).

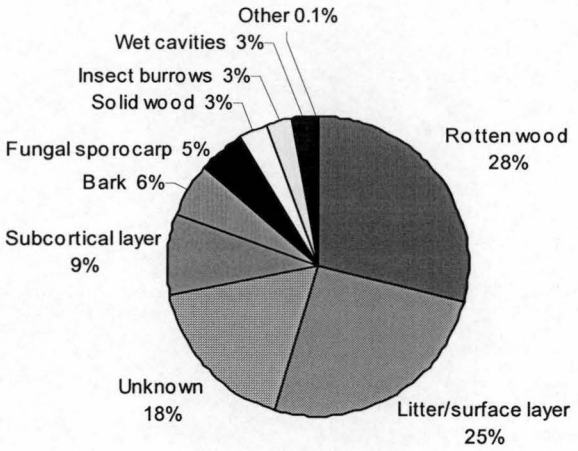

Figure 3.2. Proportions of saproxylic beetle species by microhabitat type, N = 360

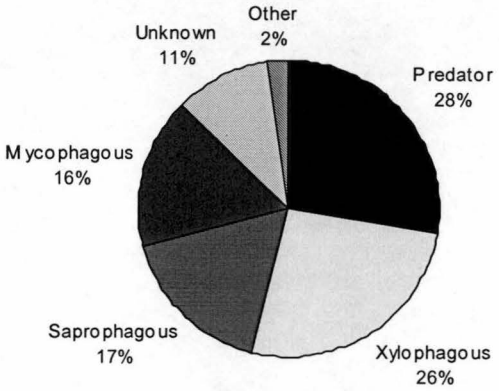

Figure 3.3. Proportions of saproxylic beetle species by feeding guild, N = 360

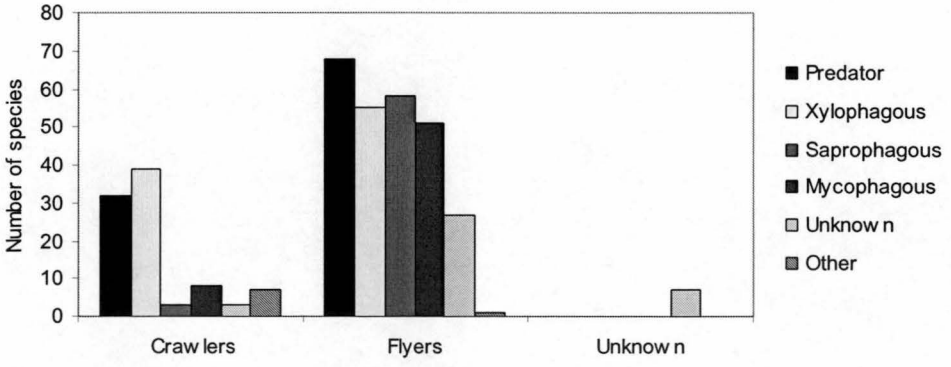

Figure 3.4. Number of saproxylic beetle species by dispersal mode and feeding guild, N = 360

3.3.2.5 Body size

Of all the species, over 71% had a body length less than 4 mm. The range of body lengths varied among feeding guilds (Figure 3.5). Xylophages and predators had a larger range of body lengths, while saprophages and mycophages had a narrower range. Body lengths of xylophages ranged from 1 mm (*Miocallus pygmaeus,* Curculionidae) to 41 mm (*Toxeutes arcuatus,* Cerambycidae), with over 63% of xylophages less than 4 mm. For predators, body length ranged from 0.5 mm (*Protoplectus* 'Tasmania 1', Staphylinidae: Pselaphinae) to 27.5 mm (*Elatichrosis exarata,* Elateridae), with 57% of predators less than 4 mm. In contrast, saprophages body length ranged from 1 to 8.5 mm, with 77% less than 4 mm; and . mycophages body length ranged between 1 and 5.3mm, with over 92% of members less than 4 mm in length - the smallest species being Ptilidae Yee sp 02 (1 mm). Of the saprophages, the smallest members were predominantly from the cucujoid complex of families, mostly latridiids. In the 'unknown' and 'other' feeding guilds, over 73% and 88% of species respectively were less than 4 mm in length.

3.3.2.6 Maximal emergence densities

For the 18-month sampling period, over 80% of the 341 species caught in emergence traps had a maximum emergence density of one or two individuals per trap (Figure 3.6). Of the remainder, 16% of species emerged in densities of 5-20 individuals per trap, and these were mostly xylophages; and 4% of species emerged with a maximum density greater than 20 individuals per trap. Of this 4%, six species emerged in numbers greater than 50 individuals per trap. These included four xylophagous species: *Ancytallia oleariae* (Curculionidae) (99 individuals per trap), *Dohrnia simplex* (Oedemeridae)(80), *Decilaus nigronotatus* (Curculionidae) (70), and *Decilaus* nr *striatus/subfasciatus,* (Curculionidae) (64); and two saprophagous species: *Prionocyphon?* TFIC sp 01, (Scirtidae) (109) *Cryptamorpha* TFIC sp 01 (Silvanidae) (55). Data for the maximum emergence densities for all species collected from emergence traps are presented in Appendix 3.1.

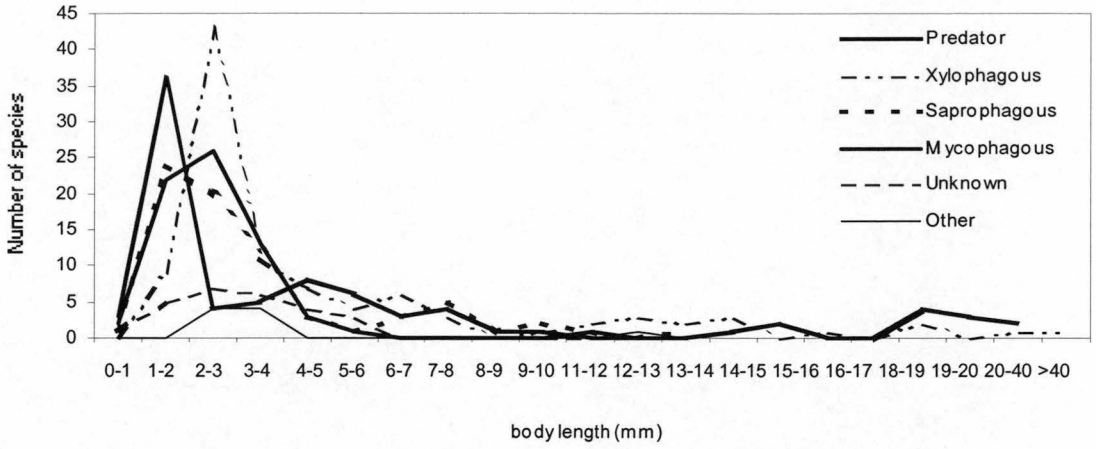

Figure 3.5. Ranges of body lengths of saproxylic beetle species within the main feeding guilds

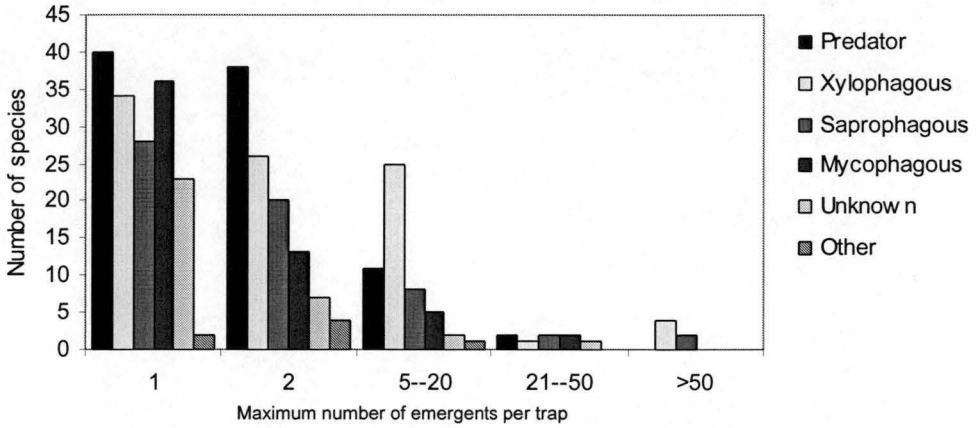

Figure 3.6. Number of saproxylic beetle species grouped by their maximum emergence density and feeding guild, N=341

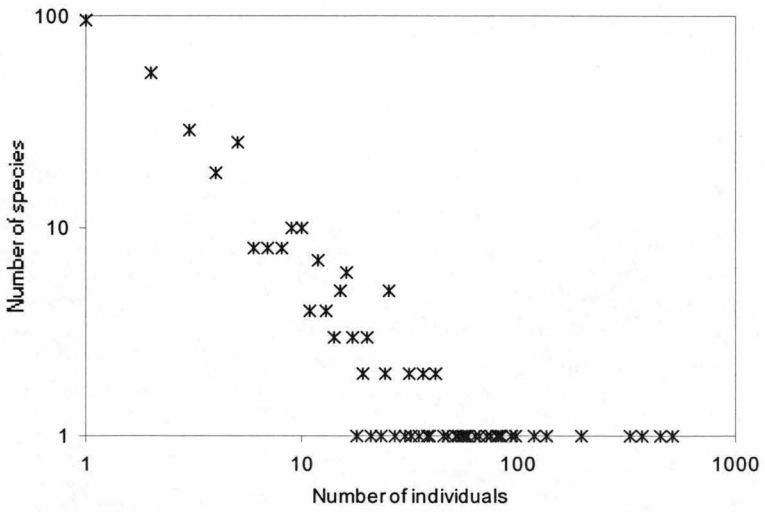

Figure 3.7. Rank abundance plot of saproxylic beetle species from all 62 emergence traps combined, N = 341 species. Both axes are logarithmic.

3.3.3 Community structure

Of the 341 species pooled across emergence traps, 103 were found within only one log, and of this number, 96 were singletons. Species abundance data showed that 266 species were represented by 1 to 5 individuals, 105 species were represented by 5 to 50 individuals, 15 species represented by 50 to 100 individuals, while eight species occurred in their hundreds (Figure 3.7). For individual traps, the majority of species-abundance distributions resembled a truncated log-normal species abundance distribution (Table 3.2) (Magurran 1988).

3.3.4 Comparison of sampling methods

In total, three times more species (341 species) were collected from the emergence trap program than by destructive sampling (94 species). Per log, emergence traps caught a significantly higher number of species than did destructive sampling ($p < 0.001$, $F_{1, 103} = 43.98$). The lowest and highest number of species per emergence trap was 9 and 78 respectively, with an average of 26 (S.D. ± 11). For destructive sampling, this ranged from 2 to 28, with an average of 11 (S.D. ± 6) species per log. While it is acknowledged that emergence traps sampled a greater surface area and volume of habitat than destructive sampling (compare Table 2.3 with Table 2.2), the question was to compare the effectiveness of sampling method by sample unit, with the number of logs being the 'cost' of sampling. This interpretation was taken because it is the sample unit (number of logs) that is the limiting factor in such biodiversity studies on saproxylic insects, rather than the amount of log sampled.

Seventy-nine species were common to both methods. In other words, only 15 of the 360 morphospecies were absent from emergence traps while 272 were absent from destructive sampling samples. Of the 39 frequently collected species (occurring in over 15 logs), three species were sampled significantly more by destructive sampling, while 29 species were sampled significantly more by emergence trapping (Table 3.3). For each species, its log occurrence by sampling method is given in Appendix 3.1.

Table 3.2. Tests of the frequency distribution data for saproxylic beetles from each log emergence trap against the four common species distribution models. (See Section 3.2.6 for details).

	Geometric	Brokenstick	Log normal	Log series
ELET1			1	
ELET2	1			
ELET3			1	
ESET1			1	
ESET2			1	
ESET3			1	1
HLET1			1	1
HLET2			1	
HSET1			1	1
HSET2	1	1	1	1
HSET3	1		1	
MLET1			1	
MLET2			1	
MLET3	1		1	1
MSET1	1	1		1
MSET2	1		1	1
MSET3	1	1	1	1
PO1LET1	1	1	1	1
PO1LET2	1		1	1
PO1LET3			1	
PO1SET1	1		1	1
PO1SET2	1	1	1	1
PO1SET3	1	1	1	1
PO2LET1	1		1	1
PO2LET2			1	
PO2LET3			1	1
PO2SET1	1		1	1
PO2SET2	1	1	1	1
PO2SET3	1	1	1	1
PR1LET1	1	1	1	1
PR1LET2	1	1	1	1
PR1LET3	1	1	1	1
PR1SET1				1
PR1SET2	1	1	1	1
PR1SET3	1	1	1	1
PR2LET1	1		1	1
PR2LET2	1	1	1	1
PR2LET3			1	
PR2SET1			1	
PR2SET2	1	1	1	1
PR2SET3	1	1	1	1
RLET1	1		1	1
RLET2			1	1
RLET3			1	
RSET1	1	1	1	1
RSET2	1	1	1	1
RSET3			1	
SLET1			1	1
SLET2	1		1	1
SLET3	1	1	1	1
SSET1			1	1
SSET2			1	1
SSET3			1	1
WLET1			1	1
WLET2	1	1	1	1
WLET3	1		1	1
WRLET2			1	
WRLET3			1	1
WRSET1			1	
WRSET2			1	
WRSET3	1	1	1	1
WSET3	1	1	1	1

Table 3.3. The 39 most frequently collected saproxylic beetle species (occurring in over 15 logs). Numbers represent the number of occupied logs as detected by Emergence Trapping (62 logs were sampled by this method) and Destructive Sampling (42 logs were sampled by this method. Species that differed significantly in their occurrence according to chi-square tests are annotated with a < or >. Species are listed in taxonomic order.

Family	Species binomial	ET	DS	TOTAL	
Carabidae	*Stichonotus leai*	14	7	21	ET < DS
Carabidae	*Sloaneana tasmaniae*	13	3	16	ET < DS
Carabidae	*Trechimorphus diemenensis*	24	7	31	ET < DS
Staphylinidae	*Aleocharinae TFIC sp 13*	20	8	28	ET < DS
Staphylinidae	*Aleocharinae TFIC sp 34*	11	10	21	
Lucanidae	*Syndesus cornutus*	10	9	19	
Lucanidae	*Lissotes cancroides*	21	27	48	
Lucanidae	*Lissotes subcaeruleus*	21	6	27	ET < DS
Scirtidae	*Prionocyphon? TFIC sp 01*	25	1	26	ET < DS
Scirtidae	*Pseudomicrocara atkinsoni?*	16	5	21	ET < DS
Throscidae	*Aulonothroscus elongatus*	21	0	21	ET < DS
Elateridae	*Parablax ooliekirra*	23	0	23	ET < DS
Elateridae	*Denticollinae TFIC sp 01*	14	5	19	ET < DS
Cantharidae	*Heteromastix TFIC sp 01*	25	0	25	ET < DS
Sphindidae	*Aspidiphorus humeralis*	20	0	20	ET < DS
Silvanidae	*Cryptamorpha TFIC sp 01*	29	1	30	ET < DS
Silvanidae	*Cryptamorpha victoriae?*	14	1	15	ET < DS
Cerylonidae	*Philothermus tasmanicus*	6	10	16	
Corylophidae	*Holopsis TFIC sp 01*	39	1	40	ET < DS
Latridiidae	*Aridius nodifer*	23	0	23	ET < DS
Melandryidae	*Orchesia alphabetica*	29	0	29	ET < DS
Zopheridae	*Pycnomerus TFIC sp 02*	6	21	27	DS > ET
Zopheridae	*Enhypnon tuberculatus*	37	1	38	ET < DS
Tenebrionidae	*Brycopia picta*	11	15	26	
Tenebrionidae	*Coripera deplanata*	11	25	36	DS > ET
Prostomidae	*Prostomis atkinsoni*	12	25	37	DS > ET
Oedemeridae	*Dohrnia simplex*	26	9	35	ET < DS
Curculionidae	*Ancyttalia olearíae*	28	0	28	ET < DS
Curculionidae	*Ancyttalia tarsalis*	32	0	32	ET < DS
Curculionidae	*Decilaus albonotatus*	16	0	16	ET < DS
Curculionidae	*Decilaus lateralis*	25	1	26	ET < DS
Curculionidae	*Decilaus nigronotatus*	43	0	43	ET < DS
Curculionidae	*Decilaus nr striatus/subfasciatus*	41	3	44	ET < DS
Curculionidae	*Exithius capucinus*	18	0	18	ET < DS
Curculionidae	*Miocallus pygmaeus*	15	0	15	ET < DS
Curculionidae	*Roptoperus tasmaniensis*	22	0	22	ET < DS
Curculionidae	*Dryophthorus TFIC sp 01*	3	16	19	DS > ET
Curculionidae	*Exeiratus TFIC sp 01*	14	9	23	
Curculionidae	*Mandalotus muscivorus*	23	0	23	ET < DS

3.4 DISCUSSION

3.4.1 Richness and diversity of saproxylic beetles

This baseline survey clearly demonstrates that the species richness and functional diversity of saproxylic beetles in just a small area within Tasmania's southern wet *E. obliqua* forest is high. Of the total 360 saproxylic beetle species collated from 103 logs of an intermediate decomposition stage within a 10km^2 study area of the southern ranges bioregion, some species were new to science (e.g. *Enhypnon* TFIC 'sp nov' 01: Zopheridae; *Alloproteinus* 'ANIC Thayer sp nov' 01: Staphylinidae; *Tyrogetus* 'sp nov' 01: Pselaphinae, Staphylinidae) and for others, this was their first record of occurrence in this bioregion, and/or state (e.g. *Chalcoplectus depressus*: Pselaphinae, Staphylinidae, only known from Victoria and ACT, Chandler pers. comm.). Furthermore, many species are yet to be described (e.g. *Dryophthorus TFIC sp 01, Dryophthorus TFIC sp 02:* Curculionidae; *Staphylinidae ANIC 88088; Enischnelater TFIC sp 01: Elateridae; and* several members of the Pselaphinae subfamily).

This study presents a ten-fold increase in the number of records on earlier preliminary studies that sampled beetle by hand-collecting (Mesibov 1988; Taylor 1990). This is probably due to more efficient or extensive sampling over a larger number of sites. This study sampled 11 forest coupes, compared to just two in the earlier studies. In this study, an entire log section, from log surface to log interior was destructively sampled, instead of just sampling log areas accessible by a crowbar. Emergence traps (not used in previous Tasmanian studies) were also more likely to be more proficient in sampling saproxylic beetles. This is further discussed in section 3.4.4.

The species richness in this Tasmanian forest area is high relative to several northern temperate and boreal forests, which, in comparison to this present study, have been surveyed more extensively and over a longer period of time. For example, a total of 335 species were collected from a Norwegian spruce and deciduous forest reserve over six years using three trapping methods (Bakke 1999). In old-growth spruce forests in Northern Finland, 270 saproxylic beetle species were collected by bark peeling and window traps, which are traps considered more efficient than emergence traps (Grove 2000). Also, a three-year study in aspen dominated forest in Canada using rearing and window traps collected 257 species (Hammond 1997).

Saproxylic beetles for the Tasmanian forests are likely to increase substantially with further survey. The sampling regime in this present study was limited to one decompositional stage (intermediate) of one host species (*Eucalyptus obliqua*) of two log diameter size classes. It has been speculated that for *E. obliqua* logs the period from tree fall through different stages of log decomposition to complete mineralisation is over 100 years (Grove *et al.* 2002; Mackensen *et al.* 2003) – an average of 92 years for other eucalypt species). It is likely that the various decomposition stages and successions would support distinct assemblages, as has been reported for other tree species (Ausmus 1977; Dajoz 2000; Greenslade 1972; Howden & Vogt 1951; Speight 1989). Among the beetles emerging from *E. obliqua* logs during the first stage of decomposition (a one year period following felling) in another recent study at Warra (Grove & Bashford 2003), 66 species are different from those found in the present study in the intermediate stage of decomposition. The number of species associated with this early decomposition stage is increasing with the continuation of emergence trapping (Grove and Bashford, pers. comm.)

Different tree species may also host specific saproxylic beetle assemblages. Marked differences between the beetle assemblages of hardwood and softwood logs have been clearly shown in several Northern European forests (Bakke 1999; Irmler *et al.* 1996). Preliminary data collected from the three non-eucalypt logs in this study also indicates that a similar phenomenon of host specificity could operate in Tasmanian wet eucalypt forest and is a factor which will also augment saproxylic beetle richness and diversity (data unpublished). Moreover in this study, it was logistically impossible to specifically sample the log-soil interface using either sampling method, and so potential epigean and edaphic (Lawrence & Britton 1994) saproxylic beetles may have been missed which could considerably add to overall saproxylic beetle species richness.

3.4.2 Assemblage structure of saproxylic beetles

The high level of within log species richness reflects the multitude and heterogeneity of microhabitats that can occur within a log (Simandl 1993; Speight 1989). In this study, a single trap covering 2.67m length of a 1 m diameter log hosted 79 saproxylic beetle species (61 species were obligate). As a log decomposes, it undergoes a succession of

ecological processes. With each process the woody material is altered in certain ways to create a substrate that hosts a specific assemblage of interacting, colonising and emigrating species (Harmon *et al.* 1986). The overall truncated log-normal species abundance distribution of logs supports the idea of the existence of this type of community structure, which can be interpreted as niches being partitioned successively (Magurran 1988).

Dead wood is an important resource for detrital based faunal communities. For many species, the habitat specificity for dead wood is unknown, yet it is likely that some species, especially mycophages, also breed in other detrital based habitats, such as twigs, fungal sporocarps, slime moulds, leaf litter and the soil/fermentation layer (Lawrence 1989; Lawrence & Britton 1994; Lawrence & Milner 1996). Irmler *et al.* (1996) compared the species assemblages in dead wood with those in neighbouring leaf litter in a German beech/alder forest and showed that assemblage overlap between these two habitat types increases as log decomposition proceeds – especially for predators and mycophages. In the present study, less than 60% of species could be considered obligately saproxylic. While this figure may vary due to misclassification of individual species saproxylicity, it is unlikely this figure would change dramatically. Pitfall traps that had operated within and near the study area (S. Baker unpublished data, Michaels 1999) collected species common to those deemed saproxylic in this study. The degree of overlap between habitat types remains unknown, as while pitfall traps generally sample ground dwelling or litter dwelling beetles (e.g. Michaels & McQuillan 1995), they have the potential to sample flightless obligately saproxylic species dispersing between logs (e.g. Michaels & Bornemissza 1999). In any case, the rich beetle fauna associated with dead wood illustrates its important value as food, habitat or shelter for detrital based communities (Taylor 1990). More detrital habitat in these forests is available as dead wood than as leaf litter (e.g. 1089 t/ha to 22.2 t/ha respectively Turnbull & Madden 1986).

3.4.3 Some relationships between the biological attributes of saproxylic beetles

The relationship between body size and feeding guild supports the theories that body size and feeding guild are interrelated (reviewed in Henle *et al.* 2004). For example, the

wide range of predator body sizes can be generally explained by the diversity in prey size, ranging from mites (prey for scydmaenid and pselaphine beetles), larval cerambycids (prey for specialised elaterids) to snails (prey for large generalist carabids). The large proportion of small sized mycophages (92% of species were less than 4 mm) can be explained by an adaptation to feeding on small food sources, such as fungal spores and hyphae, as well as the requirement to move between the crevices, fungal pores, and insect tunnels to access this substratum (Lawrence 1989; Lawrence & Milner 1996). In contrast, xylophages had a large range in body sizes. This may be due partly to being less constrained by their surroundings, as their microhabitat (woody material) is their food source, and they create their own tunnels to move through.

The interaction between the dispersal mode and feeding guild of species in this study can be explained by the relationship between species' vagility and the spatial and temporal dynamics of its food or habitat resource (Southwood 1977). For mycophages and saprophages, the dominance of flight behaviour within these guilds may relate to the relatively ephemeral nature of their food, such as fungi and detritus respectively. The variation in dispersal mode within the xylophagous guild can be explained partly by species having adapted to woody habitats of varying stability, ranging from the short-lived bark and solid wood habitats to the more long lived rotten wood microhabitats (Jonsell 1999). For predators, their high variation in dispersal mode may relate to the availability and dispersal capability of their prey. Generalist predators, such as carabid beetles, pselaphine and scydmaenid beetles tend to feed on prey that is relatively ubiquitous and flightless, such as snails and worms, mites and collembola respectively. The flighted predators, such as the elaterid and clerid beetles, usually prey on organisms that are generally flighted, such as wood boring beetles (Lawrence & Britton 1994). Bakke (1999) also noted that certain predatory cantharid beetles had similar flight behaviours to their prey (saproxylic flies). More specific predator – prey relationship have been described in Kappes & Topp (2004), who observed a positive correlation between predatory staphylinid and xylophagous scolytid beetle emergence from dead wood in Germany.

3.4.4 Advantages and disadvantages of sampling methods

As different methods often sample different components of the saproxylic beetle fauna (Bakke 1999; Økland 1996a; Siitonen 1994a) it has been suggested that by using a combination of methods, a more complete inventory can be obtained (Grove 2000; Hammond 1997), especially of rare species (Martikainen & Kouki 2003). However, results of this study suggest that as a sole sampling method, emergence traps would be adequate for comprehensively sampling the saproxylic beetles within a log. Of course, this is on the proviso that life-history information, such as microhabitat type and saproxylicity, gained from personal observations during destructive sampling is not considered necessary to the particular research being undertaken. In this study, emergence trapping collected over three times more species compared to the destructive sampling method and more than twice as many species per log. More importantly, the overlap between emergence traps and destructive sampling was good i.e. emergence traps shared a high proportion (84%) of those species that were collected by destructive sampling.

The effectiveness of log emergence traps can be explained by their ability to collect continuously over the different seasons. Such traps are also efficient in sampling very small beetles (71% of species collected in this study were less than 4 mm in body length). With direct searching the probability of collecting a particular species or adequately sampling its population size is negatively correlated with a species' body size (Martikainen & Kouki 2003). Log emergence traps provide a more logistically feasible and environmentally friendly sampling method. Direct searching destroys the habitat, especially if chainsaws are used. Also, it is quite laborious, time consuming and costly. Furthermore, destructive sampling is relatively subjective and open to operator error when compared to emergence trapping methods (this study, Bakke 1999; Siitonen 1994a). As saproxylic beetles are generally inherently cryptic, very small, and well hidden within their substrates, or highly vagile (mobile), finding and collecting these species is difficult. Moreover, destructive sampling is to some extent limited to sampling beetles that are present as adults at the time of sampling, and so this method may miss those species that occur in their larval form at the time of sampling or miss those only present within the log as a larva (e.g. *Dohrnia simplex,* Oedemeridae).

Certain species were commonly detected by destructive sampling but were either absent from or less frequently collected by emergence traps. One explanation could be that emergence traps alter the microclimate and such modified conditions hinder beetle development, although there are no data to support this hypothesis. A more likely explanation for this discrepancy between the two sampling methods is that the emergence trapping period was not sufficient to collect species with either prolonged development (e.g. *Toxeutes arcuatus* and *Enneaphyllus aeneipennis*) or with lower dispersal rates. Field and laboratory observations suggest that some xylophagous feeders on rotten wood, such as *Dryophthorus* TFIC sp 01, *Pycnomerus* TFIC sp 02 and *Prostomis atkinsoni,* may undergo consecutive generations within a log before dispersal, and so may be under represented in emergence traps for this reason. Therefore, provided emergence traps are left on a log for a sufficient period of time, it is suggested that they seem adequate to survey the saproxylic fauna of individual logs greater than 30cm diameter.

While emergence traps are not destructive of the habitat, there is one consideration needed when using emergence to long term monitoring. In principle, emergence traps make colonisation of the wood covered by the trap impossible. This will eventually lead to decreases in catches and prevent natural succession in the logs unless the trap is removed during periods or moved along the length of the log. Such has been the strategy adopted by Grove and Bashford (2003) for monitoring the succession of saproxylic insects from a decomposing log.

Specially designed flight intercept traps, such as trunk window traps (Kaila 1993), or standard free-hanging window traps (Økland 1996a) have been widely adopted in northern Europe and can be very effective in sampling saproxylic beetles (Bakke 1999; Økland 1996a). Similar conclusions have also been made from studies on tropical saproxylic beetles in North Queensland (Grove 2000). However, these trap types catch all flying insects, not just saproxylic species, and are more appropriate for sampling species at a stand-level scale (see Økland 1996a). Therefore, these traps were not appropriate for initial surveys of this fauna. For future studies though, the effectiveness and simplicity of window traps could contribute greatly to the study of saproxylic beetles in Tasmanian wet eucalypt forests, particularly if specific species or groups of

species are targeted. However, as up to 25% of saproxylic beetle species collected in this study seemed to disperse by crawling, sampling programs should consider the inclusion of other trapping methods that would sample species dispersing along the forest floor (e.g. pitfall traps, Michaels & Bornemissza 1999).

Few studies have used the data from the various trapping methods to deduce information of a species life history, though Hammond (1997) considered that the biological information derived from different trapping methods was quite different. This study demonstrates that for emergence traps, provided sample size is sufficient and they are monitored regularly, they can provide a novel approach for gaining information about a species' dispersal mode (this study, Grove & Bashford 2003), emergence times and behaviour. Examination of when a species is caught and in what quantities it is caught may be indicative of its pattern of colonisation and population density. For example, the xylophagous *Dohrnia simplex* consistently had relatively high emergence densities per trap. Conspecifics aggregating during oviposition or reproductive females having large batches of eggs are some explanations for these observed emergence densities. Meanwhile, species that had emerged as singletons may possess some level of rarity or potentially have a lower population density relative to the more abundant species. Although much speculation is involved in interpreting emergence densities and behaviour, this type of data does provide a quick and easy method for gaining an indication of species biological and behavioural traits. This is particularly valuable in situations such as these where very little is known of the biology of this highly species rich fauna.

3.5 CONCLUSIONS

This study clearly shows that emergence traps are a suitable and efficient single method for sampling saproxylic beetles within an individual log provided that traps remain in position over a period that is of sufficient duration to permit the emergence of species with long generation times or low dispersal rates.

The saproxylic beetle species records in this study are a significant increase on previous records (Mesibov 1988; Taylor 1990), and the checklist provided by this study is an

important contribution to the knowledge of saproxylic beetles from the wet eucalypt forests in southern Tasmania. This list is very much a work-in-progress, and as with other provisional annotated checklists (e.g. Alexander 2002), the data is by no means definitive, especially since over half of all species could not be identified beyond genus level. The biology of many of these species remain unknown or the biological information derived for these species was inferred from the various sources of information and so requires further investigation. However, the information on saproxylic beetles presented here is a hitherto unavailable starting point for researchers and nature conservationists undertaking study of this highly species rich group. Most importantly the records from this study serve as a baseline reference taken prior to any long term changes in saproxylic beetle richness and diversity which may result from the current intensive forestry practices in wet eucalypt forests of southern Tasmania.

3.6 APPENDICES

Appendix 3.1. List of 360 saproxylic beetles with biological traits, collected from *Eucalyptus obliqua* logs at an intermediate decomposition stage in wet eucalypt forest in southern Tasmania, using two trapping methods: emergence trapping (ET) and destructive sampling (DS). The number of logs in which species were present is also listed under trapping method. Abbreviations of the biological traits are OBL = obligate saproxylic, FAC = facultative saproxylic, UNK = unknown, CRAW = crawler, FLY = flyer, LT/SF = litter/surface layer, SUBC = subcortical layer, SOLID = solid wood, ROTT = rotten wood, WET = wet cavities, BURR = insect burrows, FUNGI = fungal sporocarp, XYLO = xylophagous, PRED = predator, SAPRO = saprophagous, MYCO = mycophagous. Species are listed in taxonomic order.

Fam-sub code	Family-subfamily	Species binomial	DS	ET	maximum emergence density	sapro-xylicity	dispersal mode	microhabitat type	feeding guild	body length (mm)
0017-00	Carabidae	*Carabidae YEE sp 21*	0	1	1	FAC	UNK	UNK	UNK	UNK
0017-09	Carabidae-Migadopinae	*Stichonotus leai*	7	14	9	FAC	CRAW	LT/SF	PRED	6
0017-12	Carabidae-Trechinae	*Sloaneana tasmaniae*	3	13	9	OBL	FLY	LT/SF	PRED	4.5
0017-12	Carabidae-Trechinae	*Tasmanotrechus leai*	0	1	1	FAC	CRAW	LT/SF	PRED	5 1
0017-12	Carabidae-Trechinae	*Trechimorphus diemenensis*	7	24	7	OBL	FLY	LT/SF	PRED	4 9
0017-17	Carabidae-Broscinae	*Chylnus ater*	0	10	8	OBL	CRAW	ROTT	PRED	18
0017-17	Carabidae-Broscinae	*Percosoma carenoides*	0	3	1	FAC	CRAW	LT/SF	PRED	23
0017-17	Carabidae-Broscinae	*Promecoderus tasmanicus*	6	7	2	OBL	CRAW	SUBC	PRED	9
0017-18	Carabidae-Callistinae	*Lestignathus sp nr foveatus*	1	0		FAC	FLY	SUBC	PRED	6
0017-19	Carabidae-Lebiinae	*Agonocheila curtula*	1	0		FAC	FLY	LT/SF	PRED	4.3
0017-20	Carabidae-Pentagonicinae	*Pentagonica vittipennis*	0	1	1	FAC	FLY	LT/SF	PRED	3 5
0017-20	Carabidae-Pentagonicinae	*Scopodes intermedius?*	4	4	2	FAC	FLY	LT/SF	PRED	4.2
0017-21	Carabidae-Psydrinae	*Amblytelus longipennis*	0	1	1	FAC	FLY	LT/SF	PRED	6.7
0017-21	Carabidae-Psydrinae	*Amblytelus placidus*	0	2	1	OBL	FLY	ROTT	PRED	4 1
0017-21	Carabidae-Psydrinae	*Amblytelus TFIC sp 01*	2	4	2	FAC	FLY	SUBC	PRED	6.8
0017-21	Carabidae-Psydrinae	*Theprisa convexa*	2	1	2	FAC	CRAW	LT/SF	PRED	6
0017-22	Carabidae-Pterostichinae	*Notonomus politulus*	2	6	2	OBL	CRAW	LT/SF	PRED	15
0017-22	Carabidae-Pterostichinae	*Rhabdotus reflexus*	2	4	1	FAC	CRAW	SUBC	PRED	18
0017-26	Carabidae-Zolinae	*Percodermus niger*	0	2	1	FAC	CRAW	LT/SF	PRED	4 4
0017-26	Carabidae-Zolinae	*Pterocyrtus tasmanicus*	2	10	30	OBL	CRAW	ROTT	PRED	4.7
0023-00	Ptiliidae	*Ptiliidae TFIC sp 01*	0	10	2	FAC	FLY	UNK	UNK	0 7
0023-00	Ptiliidae	*Ptiliidae TFIC sp 03*	0	3	2	FAC	FLY	FUNGI	MYCO	1 1
0023-00	Ptiliidae	*Ptiliidae TFIC sp 04*	2	9	1	FAC	FLY	LT/SF	MYCO	1
0023-00	Ptiliidae	*Ptiliidae YEE sp 02*	0	2	1	FAC	FLY	FUNGI	MYCO	1
0025-00	Leiodidae	*Leiodidae TFIC sp 02*	0	2	1	FAC	CRAW	LT/SF	SAPRO	1 6
0025-01	Leiodidae-Camiarinae	*Agyrtodes tasmanicus*	0	1	2	FAC	FLY	LT/SF	SAPRO	1.9
0025-01	Leiodidae-Camiarinae	*Myrmicholeva ligulata*	0	3	5	OBL	CRAW	BARK	SAPRO	4 2
0025-01	Leiodidae-Camiarinae	*Neopeltops TFIC sp 01*	0	4	21	FAC	FLY	LT/SF	SAPRO	2.9

Fam-sub code	Family-subfamily	Species binomial	DS	ET	maximum emergence density	sapro-xylicity	dispersal mode	microhabitat type	feeding guild	body length (mm)
0025-03	Leiodidae-Leiodinae	*Sogdini 'ANIC gen B' TFIC sp 01*	0	2	1	FAC	FLY	LT/SF	SAPRO	3
0025-05	Leiodidae-Cholevinae	*Austronemadus TFIC sp 01*	0	6	3	FAC	FLY	LT/SF	SAPRO	2
0025-05	Leiodidae-Cholevinae	*Austronemadus TFIC sp 03*	0	5	4	OBL	CRAW	ROTT	SAPRO	3.8
0025-05	Leiodidae-Cholevinae	*Nargomorphus jeanneli*	1	2	1	FAC	FLY	LT/SF	SAPRO	1 7
0025-05	Leiodidae-Cholevinae	*Nargomorphus TFIC sp 01*	0	5	1	FAC	FLY	LT/SF	SAPRO	3
0025-05	Leiodidae-Cholevinae	*Nargomorphus TFIC sp 02*	1	1	2	FAC	FLY	LT/SF	SAPRO	2.5
0025-05	Leiodidae-Cholevinae	*Nargomorphus TFIC sp 03*	0	1	1	FAC	FLY	LT/SF	SAPRO	UNK
0025-05	Leiodidae-Cholevinae	*Nargomorphus TFIC sp 04*	0	1	1	FAC	FLY	LT/SF	SAPRO	2
0025-05	Leiodidae-Cholevinae	*Nargomorphus TFIC sp 05*	0	2	1	FAC	FLY	FUNGI	MYCO	2 4
0025-05	Leiodidae-Cholevinae	*Paragyrtodes percalceatus*	0	6	3	OBL	FLY	BARK	SAPRO	2 1
0026-00	Scydmaenidae	*Scydmaenidae TFIC sp 03*	0	2	1	FAC	CRAW	LT/SF	PRED	1 7
0026-00	Scydmaenidae	*Scydmaenidae TFIC sp 04*	1	6	2	FAC	CRAW	ROTT	PRED	1.3
0026-00	Scydmaenidae	*Scydmaenidae TFIC sp 05*	0	4	2	FAC	CRAW	LT/SF	PRED	1 2
0026-00	Scydmaenidae	*Scydmaenidae TFIC sp 06*	0	4	2	FAC	CRAW	LT/SF	PRED	1 3
0026-00	Scydmaenidae	*Scydmaenidae TFIC sp 07*	0	4	3	FAC	CRAW	LT/SF	PRED	1
0026-00	Scydmaenidae	*Scydmaenidae TFIC sp 08*	1	1	1	FAC	CRAW	LT/SF	PRED	1 1
0026-00	Scydmaenidae	*Scydmaenidae TFIC sp 09*	0	2	1	FAC	CRAW	LT/SF	PRED	1 5
0026-00	Scydmaenidae	*Scydmaenidae TFIC sp 10*	1	5	8	FAC	CRAW	ROTT	PRED	1 2
0026-00	Scydmaenidae	*Scydmaenidae TFIC sp 11*	0	5	1	FAC	CRAW	LT/SF	PRED	1 5
0026-00	Scydmaenidae	*Scydmaenidae YEE sp X*	0	4	2	FAC	FLY	LT/SF	PRED	
0028-00	Staphylinidae	*Staphylinidae ANIC 88.0088*	3	8	3	OBL	CRAW	SUBC	PRED	7 5
0028-00	Staphylinidae	*Staphylinidae YEE sp 02*	2	3	1	OBL	FLY	ROTT	MYCO	3
0028-00	Staphylinidae	*Staphylinidae YEE sp 63*	0	3	1	FAC	FLY	UNK	UNK	
0028-00	Staphylinidae	*Staphylinidae YEE sp 64*	0	1	1	FAC	FLY	UNK	UNK	1.4
0028-00	Staphylinidae	*Staphylinidae YEE sp X*	0	1	1	FAC	FLY	UNK	UNK	
0028-03	Staphylinidae-Omaliinae	*Ischnoderma parallelus*	0	2	1	FAC	FLY	BARK	SAPRO	1.8
0028-03	Staphylinidae-Omaliinae	*Metacorneolabium darlingtoni*	0	2	2	FAC	FLY	UNK	PRED	1.2
0028-05	Staphylinidae-Proteininae	*Alloproteinus 'ANIC Thayer sp nov'*	0	1	15	OBL	FLY	BURR	UNK	1 6
0028-05	Staphylinidae-Proteininae	*Anepius koebelei*	0	1	1	FAC	FLY	UNK	UNK	2 5
0028-10	Staphylinidae-Pselaphinae	*Anabaxis CHANDLER 'Type 1'*	0	4	4	FAC	FLY	SOLID	PRED	1.8
0028-10	Staphylinidae-Pselaphinae	*Aulaxus CHANDLER 'Tasmania 1'*	0	2	2	FAC	FLY	UNK	PRED	1.3
0028-10	Staphylinidae-Pselaphinae	*Chalcoplectus depressus*	0	2	2	OBL	FLY	SUBC	PRED	2.8
0028-10	Staphylinidae-Pselaphinae	*Chichester CHANDLER 'Tasmania 1'*	0	8	2	FAC	FLY	UNK	PRED	1 3

Fam-sub code	Family-subfamily	Species binomial	DS	ET	maximum emergence density	sapro-xylicity	dispersal mode	microhabitat type	feeding guild	body length (mm)
0028-10	Staphylinidae-Pselaphinae	*Chichester CHANDLER 'Tasmania 2'*	0	1	1	FAC	FLY	UNK	PRED	1 3
0028-10	Staphylinidae-Pselaphinae	*Deroplectus excisus*	0	1	1	FAC	FLY	UNK	PRED	1 6
0028-10	Staphylinidae-Pselaphinae	*Eupinella dentiventris*	0	4	2	FAC	CRAW	UNK	PRED	1.1
0028-10	Staphylinidae-Pselaphinae	*Eupinella tarsalis*	0	1	2	FAC	FLY	UNK	PRED	1 6
0028-10	Staphylinidae-Pselaphinae	*Eupines CHANDLER 'Tasmania 1'*	0	2	2	FAC	FLY	UNK	PRED	1.2
0028-10	Staphylinidae-Pselaphinae	*Euplectops CHANDLER 'Tasmania 1'*	0	3	1	FAC	FLY	UNK	PRED	1 2
0028-10	Staphylinidae-Pselaphinae	*Gerallus CHANDLER 'Tasmania 1'*	0	1	1	OBL	CRAW	SUBC	PRED	1.8
0028-10	Staphylinidae-Pselaphinae	*Logasa CHANDLER 'Tasmania 1'*	0	2	1	FAC	FLY	UNK	PRED	1 4
0028-10	Staphylinidae-Pselaphinae	*Macroplectus CHANDLER 'Type 1'*	4	0		OBL	CRAW	ROTT	PRED	1 9
0028-10	Staphylinidae-Pselaphinae	*Macroplectus quadratipennis*	0	1	1	FAC	FLY	SUBC	PRED	1 2
0028-10	Staphylinidae-Pselaphinae	*Macroplectus tasmaniae*	1	4	2	FAC	CRAW	UNK	PRED	1 6
0028-10	Staphylinidae-Pselaphinae	*Palimbolus victoriae*	0	7	3	OBL	CRAW	SUBC	PRED	1 1
0028-10	Staphylinidae-Pselaphinae	*Paraplectus CHANDLER 'Tasmania 1'*	0	4	5	FAC	CRAW	UNK	PRED	1 2
0028-10	Staphylinidae-Pselaphinae	*Plectusodes CHANDLER 'Tasmania 1'*	0	2	1	FAC	FLY	UNK	PRED	1 3
0028-10	Staphylinidae-Pselaphinae	*Protoplectus CHANDLER 'Tasmania 1'*	0	2	1	FAC	FLY	UNK	PRED	0 8
0028-10	Staphylinidae-Pselaphinae	*Pselaphaulax CHANDLER 'Tasmania 1'*	0	5	2	OBL	CRAW	SUBC	PRED	2
0028-10	Staphylinidae-Pselaphinae	*Rybaxis CHANDLER 'Tasmania 1'*	0	1	2	FAC	FLY	UNK	PRED	1 6
0028-10	Staphylinidae-Pselaphinae	*Rybaxis parvidens*	0	8	11	FAC	CRAW	UNK	PRED	2 2
0028-10	Staphylinidae-Pselaphinae	*Rybaxis variabilis*	0	6	13	FAC	CRAW	UNK	PRED	1 9
0028-10	Staphylinidae-Pselaphinae	*Sagola CHANDLER 'Tasmania 1'*	0	1	0	FAC	FLY	UNK	PRED	1 8
0028-10	Staphylinidae-Pselaphinae	*Sagola CHANDLER 'Tasmania 2'*	0	8	5	FAC	FLY	UNK	PRED	1.8
0028-10	Staphylinidae-Pselaphinae	*Sagola rugicornis*	0	7	2	FAC	FLY	UNK	PRED	2.1
0028-10	Staphylinidae-Pselaphinae	*Startes CHANDLER 'Tasmania 1'*	2	11	7	OBL	FLY	ROTT	PRED	1.4
0028-10	Staphylinidae-Pselaphinae	*Tasmanityrus newtoni*	1	2	1	OBL	FLY	SUBC	PRED	1 8
0028-10	Staphylinidae-Pselaphinae	*Tyrogetus CHANDLER 'Tasmania 1'*	0	1	2	OBL	FLY	SUBC	PRED	1 7
0028-10	Staphylinidae-Pselaphinae	*Washpool CHANDLER 'Tasmania 1'*	0	9	3	OBL	CRAW	UNK	PRED	1 5
0028-13	Staphylinidae-Tachyporinae	*Ischnosoma TFIC sp 01*	0	2	1	FAC	FLY	UNK	UNK	3 5
0028-13	Staphylinidae-Tachyporinae	*Sepedophilus TFIC sp 01*	2	9	4	OBL	FLY	SUBC	MYCO	3.9
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 01*	0	5	9	FAC	FLY	UNK	UNK	UNK
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 02*	0	1	1	FAC	FLY	UNK	UNK	3 9
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 04*	0	3	1	FAC	FLY	UNK	UNK	3
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 10*	0	6	1	FAC	FLY	UNK	UNK	2.4
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 13*	8	20	19	FAC	FLY	UNK	UNK	UNK

Fam-sub code	Family-subfamily	Species binomial	DS	ET	maximum emergence density	sapro-xylicity	dispersal mode	microhabitat type	feeding guild	body length (mm)
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 14*	0	12	43	FAC	FLY	UNK	UNK	1.5
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 15*	0	4	1	FAC	CRAW	UNK	UNK	4.3
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 16*	0	1	1	FAC	FLY	UNK	UNK	4 1
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 25*	2	0		OBL	FLY	ROTT	MYCO	2.2
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 26*	0	6	2	FAC	FLY	UNK	UNK	1.6
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 27*	1	0		FAC	FLY	ROTT	MYCO	2.3
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 28*	1	0		FAC	FLY	LT/SF	MYCO	2.6
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 29*	0	7	2	FAC	CRAW	UNK	UNK	3.1
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 30*	0	1	1	FAC	FLY	UNK	UNK	3
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 32*	0	1	1	FAC	FLY	UNK	UNK	3 7
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 33*	0	2	1	FAC	FLY	UNK	UNK	3 5
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 34*	10	11	3	OBL	CRAW	ROTT	MYCO	1 5
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 35*	0	2	1	FAC	FLY	UNK	UNK	2 8
0028-16	Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 36*	0	1	3	FAC	FLY	UNK	UNK	0
0028-16	Staphylinidae-Aleocharinae	*Falagria TFIC sp 04*	0	2	1	FAC	CRAW	UNK	UNK	2.3
0028-19	Staphylinidae-Scaphidiinae	*Baeocera TFIC sp 01*	0	6	8	FAC	FLY	FUNGI	MYCO	1 5
0028-19	Staphylinidae-Scaphidiinae	*Scaphidium alpicolum*	0	1	1	OBL	FLY	UNK	UNK	5.2
0028-19	Staphylinidae-Scaphidiinae	*Scaphidium YEE sp 01*	1	0		OBL	FLY	UNK	UNK	5 2
0028-19	Staphylinidae-Scaphidiinae	*Scaphisoma indutum*	0	4	2	FAC	FLY	FUNGI	MYCO	2
0028-19	Staphylinidae-Scaphidiinae	*Scaphisoma TFIC sp 01*	0	2	1	FAC	FLY	FUNGI	MYCO	2.5
0028-22	Staphylinidae-Oxytelinae	*Anotylus TFIC sp 03*	0	6	4	FAC	FLY	BARK	SAPRO	4
0028-22	Staphylinidae-Oxytelinae	*Anotylus TFIC sp 04*	0	3	2	FAC	FLY	BARK	SAPRO	3.3
0028-22	Staphylinidae-Oxytelinae	*Anotylus YEE sp 21*	0	1	1	FAC	FLY	BARK	MYCO	
0028-22	Staphylinidae-Oxytelinae	*Homalotrichus TFIC sp 01*	0	1	1	FAC	FLY	UNK	UNK	5
0028-30	Staphylinidae-Paederinae	*Hyperomma bryophilum*	1	5	1	FAC	UNK	UNK	UNK	UNK
0028-30	Staphylinidae-Paederinae	*Macrodicax TFIC sp 01*	0	1	1	OBL	UNK	UNK	UNK	UNK
0028-30	Staphylinidae-Paederinae	*Paederinae TFIC sp 03*	2	0		OBL	CRAW	BURR	PRED	5
0028-30	Staphylinidae-Paederinae	*Paederinae TFIC sp 04*	0	1	1	FAC	FLY	UNK	UNK	2.5
0028-30	Staphylinidae-Paederinae	*Paederinae TFIC sp 05*	0	1	1	OBL	FLY	BURR	MYCO	1 4
0028-31	Staphylinidae-Staphylininae	*Philonthus TFIC sp 01*	0	1	1	FAC	FLY	UNK	PRED	8
0028-31	Staphylinidae-Staphylininae	*Quedius TFIC sp 04*	1	4	2	OBL	FLY	LT/SF	PRED	7.5
0028-31	Staphylinidae-Staphylininae	*Staphylininae TFIC sp 03*	3	0	2	OBL	CRAW	BURR	PRED	6 2
0028-31	Staphylinidae-Staphylininae	*Staphylininae TFIC sp 08*	0	2	1	FAC	FLY	UNK	UNK	4 5

Fam-sub code	Family-subfamily	Species binomial	DS	ET	maximum emergence density	sapro-xylicity	dispersal mode	microhabitat type	feeding guild	body length (mm)
0028-31	Staphylinidae-Staphylininae	*Staphylininae TFIC sp 10*	0	4	1	FAC	FLY	UNK	PRED	5
0029-00	Lucanidae-Syndesinae	*Syndesus cornutus*	9	10	7	OBL	FLY	ROTT	XYLO	12
0029-06	Lucanidae-Lucaninae	*Lissotes cancroides*	27	21	14	OBL	CRAW	SUBC	XYLO	12 5
0029-06	Lucanidae-Lucaninae	*Lissotes curvicornis*	2	6	5	OBL	CRAW	SUBC	XYLO	14
0029-06	Lucanidae-Lucaninae	*Lissotes menalcas*	0	1	2	OBL	CRAW	ROTT	XYLO	16
0029-06	Lucanidae-Lucaninae	*Lissotes rodwayi*	0	2	1	OBL	CRAW	ROTT	XYLO	13 5
0029-06	Lucanidae-Lucaninae	*Lissotes subcaeruleus*	6	21	17	OBL	CRAW	ROTT	XYLO	13 5
0040-01	Scarabaeidae-Aphodiinae	*Saprus griffithi*	0	1	1	OBL	FLY	SOLID	XYLO	3.1
0040-10	Scarabaeidae-Melolonthinae	*Phyllochlaenia TFIC sp 01*	3	3	2	OBL	FLY	SUBC	XYLO	10
0040-10	Scarabaeidae-Melolonthinae	*Telura vitticollis*	2	2	2	OBL	FLY	ROTT	XYLO	12
0043-03	Clambidae-Clambinae	*Clambus bornemisszai*	0	8	5	FAC	FLY	LT/SF	SAPRO	1
0043-03	Clambidae-Clambinae	*Sphaerothorax tasmani*	0	4	1	FAC	FLY	LT/SF	SAPRO	1 3
0044-00	Scirtidae	*Heterocyphon australis?*	0	1	1	OBL	FLY	WET	SAPRO	6 8
0044-00	Scirtidae	*Prionocyphon? TFIC sp 01*	1	25	109	OBL	FLY	WET	SAPRO	2
0044-00	Scirtidae	*Pseudomicrocara atkinsoni?*	5	16	9	OBL	FLY	WET	SAPRO	6 3
0044-00	Scirtidae	*Pseudomicrocara TFIC sp 01*	0	5	2	OBL	FLY	WET	SAPRO	7.9
0044-00	Scirtidae	*Pseudomicrocara TFIC sp 02*	0	3	2	OBL	FLY	WET	SAPRO	3
0044-00	Scirtidae	*Scirtidae YEE sp 07*	0	1	1	OBL	FLY	WET	SAPRO	2.8
0044-00	Scirtidae	*Scirtidae YEE sp 11*	0	2	35	OBL	FLY	WET	SAPRO	3.2
0044-00	Scirtidae	*Scirtidae YEE sp 14*	0	4	4	OBL	FLY	WET	SAPRO	2.5
0044-00	Scirtidae	*Scirtidae YEE sp 15*	0	2	1	OBL	FLY	WET	SAPRO	2.2
0048-00	Byrrhidae-Syncalyptinae	*Microchaetes bryophilus*	0	5	4	FAC	CRAW	LT/SF	OTHER	2.8
0048-00	Byrrhidae-Syncalyptinae	*Microchaetes hystricosus*	0	14	4	FAC	CRAW	LT/SF	OTHER	2.5
0048-00	Byrrhidae-Syncalyptinae	*Microchaetes scoparius*	0	2	1	FAC	CRAW	LT/SF	OTHER	2 3
0048-01	Byrrhidae-Byrrhinae	*Pedilophorus griffithi*	8	4	3	FAC	CRAW	LT/SF	OTHER	3 8
0048-01	Byrrhidae-Byrrhinae	*Pedilophorus multicolor*	0	3	6	FAC	CRAW	LT/SF	OTHER	3
0048-01	Byrrhidae-Byrrhinae	*Pedilophorus nr ANIC sp 04*	0	3	2	FAC	CRAW	LT/SF	OTHER	3.4
0048-01	Byrrhidae-Byrrhinae	*Pedilophorus nr ANIC sp 88 0313*	1	0		FAC	CRAW	LT/SF	OTHER	3 4
0063-00	Eucnemidae	*Aderus acaciae*	0	2	1	OBL	FLY	ROTT	SAPRO	1.7
0063-00	Eucnemidae	*Neocharis tasmanicus*	1	1	1	OBL	FLY	BARK	SAPRO	
0064-00	Throscidae	*Aulonothroscus elongatus*	0	21	23	OBL	FLY	ROTT	MYCO	3 5
0064-00	Throscidae	*Aulonothroscus YEE sp 02*	0	2	2	OBL	FLY	ROTT	MYCO	3 5
0064-00	Throscidae	*Aulonothroscus YEE sp 03*	0	1	1	OBL	FLY	ROTT	MYCO	3.5

Fam-sub code	Family-subfamily	Species binomial	DS	ET	maximum emergence density	sapro-xylicity	dispersal mode	microhabitat type	feeding guild	body length (mm)
0065-00	Elateridae	*Elateridae TFIC sp 18*	0	1	1	OBL	FLY	BARK	PRED	5 6
0065-00	Elateridae	*Elateridae TFIC sp 22*	0	2	2	OBL	FLY	BARK	PRED	5 6
0065-00	Elateridae	*Elateridae YEE sp 06*	1	0	1	OBL		SUBC	PRED	
0065-06	Elateridae-Pityobiinae	*Parablax ooliekirra*	0	23	4	OBL	FLY	BURR	PRED	13 2
0065-06	Elateridae-Pityobiinae	*Tasmanelater pelionensis*	1	0		OBL	FLY	SUBC	PRED	
0065-08	Elateridae-Agrypninae	*Agrypnus TFIC sp 01*	1	6	3	OBL	FLY	BARK	PRED	8
0065-08	Elateridae-Agrypninae	*Conoderus australasiae*	0	3	1	OBL	FLY	BARK	PRED	18.8
0065-09	Elateridae-Denticollinae	*Denticollinae TFIC sp 01*	5	14	3	OBL	FLY	BARK	PRED	17 5
0065-09	Elateridae-Denticollinae	*Denticollinae TFIC sp 16*	2	1	2	OBL	FLY	BARK	PRED	10
0065-09	Elateridae-Denticollinae	*Elatichrosis exarata*	1	1	1	OBL	FLY	BARK	PRED	27 5
0065-09	Elateridae-Denticollinae	*Elatichrosis trisulcata*	0	1	1	OBL	FLY	BARK	PRED	19
0065-09	Elateridae-Denticollinae	*Enischnelater specularis*	0	4	1	OBL	FLY	BARK	PRED	18 5
0065-09	Elateridae-Denticollinae	*Enischnelater TFIC sp 01*	4	2	1	OBL	FLY	UNK	PRED	
0065-12	Elateridae-Elaterinae	*Augenotus quadriguttatus*	1	0		OBL	FLY	BURR	PRED	
0069-00	Lycidae	*Lycidae TFIC sp 01*	0	4	0	OBL	FLY	ROTT	PRED	
0069-00	Lycidae-Calochrominae	*Calochromus scutellaris*	0	1	2	OBL	FLY	ROTT	PRED	7.1
0069-00	Lycidae-Metriorrhynchinae	*Metriorhynchus ?erythropterus*	0	4	3	OBL	FLY	ROTT	PRED	9.5
0069-00	Lycidae-Metriorrhynchinae	*Metriorrhynchus rhipidius*	0	3	1	OBL	FLY	ROTT	PRED	13
0069-00	Lycidae-Metriorrhynchinae	*Metriorrhynchus TFIC sp 01*	0	2	1	OBL	FLY	ROTT	PRED	10 6
0069-00	Lycidae-Metriorrhynchinae	*Metriorrhynchus TFIC sp 02*	0	1	1	OBL	FLY	ROTT	PRED	10
0069-00	Lycidae-Metriorrhynchinae	*Metriorrhynchus TFIC sp 03*	0	7	1	OBL	FLY	ROTT	PRED	7.5
0074-01	Cantharidae-Cantharinae	*Heteromastix nigripes*	0	8	22	OBL	FLY	LT/SF	PRED	3.7
0074-01	Cantharidae-Cantharinae	*Heteromastix TFIC sp 01*	0	25	12	OBL	FLY	LT/SF	PRED	3 9
0074-01	Cantharidae-Cantharinae	*Heteromastix TFIC sp 02*	0	1	1	OBL	FLY	LT/SF	PRED	3 4
0074-01	Cantharidae-Cantharinae	*Heteromastix TFIC sp 03*	0	1	1	OBL	FLY	LT/SF	PRED	3.4
0079-00	Dermestidae-Megatominae	*Orphinus TFIC sp 01*	0	1	1	FAC	FLY	UNK	SAPRO	
0082-00	Anobiidae-Xyletininae	*Lasioderma sericorne*	0	5	2	OBL	FLY	SOLID	XYLO	
0082-02	Anobiidae-Ptininae	*Ptinus exulans*	0	1	1	OBL	FLY	SOLID	SAPRO	3
0082-05	Anobiidae-Anobiinae	*Hadrobregmus areolicollis*	0	5	1	OBL	FLY	SOLID	XYLO	5.8
0082-09	Anobiidae-Dorcatominae	*Dorcatoma TFIC sp 01*	0	1	1	OBL	FLY	SOLID	XYLO	
0083-02	Lymexylidae-Lymexylinae	*Australymexylon australe*	0	2	1	OBL	FLY	SOLID	XYLO	10.1
0084-04	Trogossitidae-Rentoniinae	*Rentoninae TFIC sp 01*	0	7	2	FAC	FLY	LT/SF	PRED	1.2
0086-00	Cleridae	*Cleridae YEE sp 02*	0	1	1	OBL	FLY	BURR	PRED	6

Fam-sub code	Family-subfamily	Species binomial	DS	ET	maximum emergence density	sapro-xylicity	dispersal mode	microhabitat type	feeding guild	body length (mm)
0086-01	Cleridae-Phyllobaeninae	*Lemidia subaenea*	0	8	3	OBL	FLY	BURR	PRED	6.7
0086-01	Cleridae-Phyllobaeninae	*Lemidia YEE sp 02*	1	1	1	OBL	FLY	BURR	PRED	
0090-04	Melyridae-Dasytinae	*Dasytes TFIC sp 01*	0	4	1	OBL	FLY	ROTT	PRED	2.6
0090-04	Melyridae-Dasytinae	*Dasytes? TFIC sp 03*	0	1	1	OBL	FLY	ROTT	PRED	4.7
0092-00	Sphindidae-Sphindinae	*Aspidiphorus humeralis*	0	20	18	FAC	FLY	LT/SF	SAPRO	1.4
0092-00	Sphindidae-Sphindinae	*Notosphindus slateri*	0	1	1	FAC	FLY	LT/SF	SAPRO	2
0093-00	Brachypteridae	*Notobrachypterus TFIC sp 01*	0	4	2	FAC	FLY	FUNGI	MYCO	2 4
0094-04	Nitidulidae-Nitidulinae	*Epuraea victoriensis*	0	12	2	OBL	FLY	BARK	SAPRO	2 4
0094-04	Nitidulidae-Nitidulinae	*Thalycrodes cylindricum*	0	6	1	FAC	CRAW	FUNGI	MYCO	2.8
0094-04	Nitidulidae-Nitidulinae	*Thalycrodes pulchrum*	0	8	2	FAC	FLY	FUNGI	MYCO	2 2
0094-06	Nitidulidae-Cryptarchinae	*Amlearcha obscurior?*	0	2	1	FAC	FLY	FUNGI	MYCO	2.3
0094-06	Nitidulidae-Cryptarchinae	*Cryptarcha laevigata*	1	0		FAC	FLY	BARK	SAPRO	6
0099-00	Phloeostichidae-Hymaeinae	*Hymaea succinifera*	0	1	1	OBL	FLY	BARK	SAPRO	3 5
0100-01	Silvanidae-Brontinae	*Cryptamorpha optata*	0	1	1	OBL	FLY	LT/SF	SAPRO	3.4
0100-01	Silvanidae-Brontinae	*Cryptamorpha TFIC sp 01*	1	29	55	OBL	FLY	LT/SF	SAPRO	2 7
0100-01	Silvanidae-Brontinae	*Cryptamorpha victoriae?*	1	14	3	OBL	FLY	LT/SF	SAPRO	3
0105-00	Phalacridae-Phalacrinae	*Litochrus ?alternans*	0	6	1	FAC	FLY	FUNGI	MYCO	1 9
0105-00	Phalacridae-Phalacrinae	*Parasemus TFIC sp 01*	0	1	1	FAC	FLY	FUNGI	MYCO	1 4
0105-00	Phalacridae	*Phalacridae TFIC sp 01*	0	1	1	FAC	FLY	FUNGI	MYCO	2 8
0106-00	Hobartiidae	*Hobartius eucalypti*	0	4	2	FAC	FLY	FUNGI	MYCO	2.2
0108-00	Cryptophagidae	*Cryptophagidae TFIC sp 01*	0	3	1	FAC	FLY	LT/SF	MYCO	2.6
0108-02	Cryptophagidae-Cryptophaginae	*Cryptophagus sp nr gibbipennis*	1	4	1	FAC	FLY	LT/SF	MYCO	2
0108-02	Cryptophagidae-Cryptophaginae	*Cryptophagus tasmanicus*	1	3	1	FAC	FLY	LT/SF	MYCO	2 4
0111-01	Erotylidae-Dacninae	*Thallis compta*	0	1	1	OBL	FLY	FUNGI	MYCO	4 5
0115-05	Cerylonidae-Ceryloninae	*Philothermus tasmanicus*	10	6	3	OBL	CRAW	ROTT	MYCO	2
0119-02	Coccinellidae-Coccidulinae	*Rhyzobius alphabeticus*	0	1	1	FAC	FLY	LT/SF	MYCO	2
0119-02	Coccinellidae-Coccidulinae	*Rhyzobius TFIC sp 05*	0	5	3	FAC	FLY	LT/SF	MYCO	2.2
0119-02	Coccinellidae-Coccidulinae	*Rhyzobius TFIC sp 14*	0	4	1	FAC	FLY	LT/SF	MYCO	3.8
0119-02	Coccinellidae-Coccidulinae	*Rhyzobius TFIC sp 15*	0	14	16	FAC	FLY	LT/SF	MYCO	2.2
0119-02	Coccinellidae-Coccidulinae	*Rhyzobius TFIC sp 16*	0	4	2	FAC	FLY	LT/SF	MYCO	2 2
0119-02	Coccinellidae-Coccidulinae	*Rhyzobius TFIC sp 17*	0	1	1	FAC	FLY	LT/SF	MYCO	3
0119-02	Coccinellidae-Coccidulinae	*Rhyzobius TFIC sp 18*	0	1	1	FAC	FLY	LT/SF	MYCO	2 5
0119-02	Coccinellidae-Coccidulinae	*Rhyzobius TFIC sp 19*	0	1	1	FAC	FLY	LT/SF	MYCO	1 8

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0119-02	Coccinellidae-Coccidulinae	*Rhyzobius TFIC sp 20*	0	2	1	FAC	FLY	LT/SF	MYCO	2.2
0119-02	Coccinellidae-Coccidulinae	*Rhyzobius TFIC sp 21*	0	1	1	FAC	FLY	LT/SF	MYCO	3 1
0120-02	Corylophidae-Corylophinae	*Corylophodes YEE sp 03*	0	2	13	OBL	CRAW	ROTT	MYCO	2 3
0120-02	Corylophidae-Corylophinae	*Holopsis TFIC sp 01*	1	39	10	OBL	CRAW	ROTT	MYCO	1.8
0120-02	Corylophidae-Corylophinae	*Holopsis TFIC sp 02*	0	1	1	FAC	FLY	LT/SF	MYCO	1 7
0120-02	Corylophidae-Corylophinae	*Holopsis TFIC sp 04*	0	2	1	OBL	FLY	ROTT	MYCO	1.3
0120-03	Corylophidae-Sericoderinae	*Sericoderus TFIC sp 02*	0	3	1	FAC	FLY	LT/SF	MYCO	1.4
0120-03	Corylophidae-Sericoderinae	*Sericoderus TFIC sp 03*	0	1	1	FAC	FLY	LT/SF	MYCO	1 2
0120-03	Corylophidae-Sericoderinae	*Sericoderus TFIC sp 05*	1	7	1	OBL	FLY	LT/SF	MYCO	1.3
0120-03	Corylophidae-Sericoderinae	*Sericoderus TFIC sp 07*	0	1	1	FAC	FLY	LT/SF	MYCO	1.1
0121-01	Latridiidae-Latridiinae	*Adistenia watsoni*	0	1	1	FAC	FLY	LT/SF	SAPRO	1.4
0121-01	Latridiidae-Latridiinae	*Aridius costatus*	0	3	2	FAC	FLY	LT/SF	SAPRO	1.7
0121-01	Latridiidae-Latridiinae	*Aridius nodifer*	0	23	9	FAC	FLY	LT/SF	SAPRO	1.6
0121-01	Latridiidae-Latridiinae	*Cartodere TFIC sp 01*	0	2	3	FAC	FLY	LT/SF	SAPRO	1.8
0121-01	Latridiidae-Latridiinae	*Enicmus TFIC sp 01*	0	2	1	FAC	FLY	LT/SF	SAPRO	1 7
0121-01	Latridiidae-Latridiinae	*Enicmus TFIC sp 02*	0	1	1	FAC	FLY	LT/SF	SAPRO	1 3
0121-02	Latridiidae-Corticariinae	*Bicava verrucifera*	0	1	1	FAC	FLY	LT/SF	SAPRO	1 8
0121-02	Latridiidae-Corticariinae	*Corticaria TFIC sp 02*	0	2	1	OBL	FLY	SUBC	SAPRO	1.3
0121-02	Latridiidae-Corticariinae	*Cortinicara TFIC sp 02*	0	14	5	OBL	FLY	SUBC	SAPRO	1 3
0123-00	Archeocrypticidae	*Enneboeus ovalis*	0	1	2	FAC	UNK	UNK	UNK	UNK
0125-02	Ciidae-Ciinae	*Cis cervus?*	0	1	1	FAC	FLY	FUNGI	MYCO	1 1
0127-00	Melandryidae	*Melandryidae TFIC sp 04*	0	10	6	OBL	FLY	LT/SF	MYCO	2 6
0127-00	Melandryidae-Melandryinae	*Mystes YEE sp 01*	3	1	1	OBL	FLY	SOLID	MYCO	
0127-00	Melandryidae-Melandryinae	*Orchesia TFIC sp 02*	0	5	1	OBL	FLY	LT/SF	MYCO	3 2
0127-03	Melandryidae-Melandryinae	*Orchesia ?australina*	0	3	2	OBL	CRAW	LT/SF	MYCO	3 4
0127-03	Melandryidae-Melandryinae	*Orchesia alphabetica*	0	29	26	OBL	CRAW	LT/SF	MYCO	3.4
0127-03	Melandryidae-Melandryinae	*Orchesia eucalypti?*	0	1	1	OBL	FLY	LT/SF	MYCO	
0127-03	Melandryidae-Melandryinae	*Orchesia TFIC sp 01*	0	7	4	OBL	CRAW	LT/SF	MYCO	3.3
0128-00	Mordellidae	*Mordellidae TFIC sp 03*	0	1	1	FAC	FLY	FUNGI	MYCO	3
0132-00	Zopheridae	*Colydiinae? YEE sp 01*	1	0		OBL	FLY	BURR	PRED	
0132-00	Zopheridae incertae sedis	*Docalis funerosus*	1	1	2	OBL	FLY	ROTT	XYLO	4
0132-00	Zopheridae incertae sedis	*Latometus differens*	0	5	9	OBL	FLY	ROTT	XYLO	2.7
0132-00	Zopheridae	*Penthelispa fuliginosa*	1	1	3	OBL	CRAW	ROTT	XYLO	3.7

Fam-sub code	Family-subfamily	Species binomial	DS	ET	maximum emergence density	sapro-xylicity	dispersal mode	microhabitat type	feeding guild	body length (mm)
0132-03	Zopheridae-Pycnomerinae	*Pycnomerus TFIC sp 02*	21	6	5	OBL	FLY	ROTT	XYLO	3 3
0132-04	Zopheridae-Colydiinae	*Coconissus gibbicollis*	0	4	2	FAC	FLY	LT/SF	SAPRO	1 3
0132-04	Zopheridae-Colydiinae	*Enhypnon TFIC 'sp nov' 01*	0	3	3	OBL	CRAW	ROTT	XYLO	3.6
0132-04	Zopheridae-Colydiinae	*Enhypnon tuberculatus*	1	37	16	OBL	CRAW	ROTT	XYLO	2 7
0132-04	Zopheridae-Colydiinae	*Enhypnon YEE sp 01*	0	5	1	OBL	CRAW	ROTT	XYLO	2.5
0133-00	Ulodidae	*Ganyme sapphira*	0	1	1	OBL	FLY	FUNGI	MYCO	5.3
0137-01	Tenebrionidae-Lagriinae	*Adelium abbreviatum*	3	9	4	OBL	CRAW	ROTT	XYLO	10.4
0137-01	Tenebrionidae-Lagriinae	*Adelium YEE sp 07*	5	0		OBL	CRAW	ROTT	XYLO	
0137-01	Tenebrionidae-Lagriinae	*Brycopia coelioides*	3	7	4	OBL	CRAW	ROTT	XYLO	5 9
0137-01	Tenebrionidae-Lagriinae	*Brycopia hexagona*	1	3	1	OBL	CRAW	ROTT	XYLO	6 4
0137-01	Tenebrionidae-Lagriinae	*Brycopia picta*	15	11	3	OBL	CRAW	ROTT	XYLO	4.8
0137-01	Tenebrionidae-Lagriinae	*Conpera deplanata*	25	11	3	OBL	CRAW	SUBC	XYLO	13
0137-01	Tenebrionidae-Lagriinae	*Diemenoma commoda*	0	3	1	OBL	CRAW	ROTT	XYLO	6 7
0137-03	Tenebrionidae-Zolodininae	*Tanylypa morio*	1	0		OBL	CRAW	SUBC	XYLO	13
0137-06	Tenebrionidae-Alleculinae	*Atoichus tasmanicus*	0	2	2	OBL	FLY	ROTT	SAPRO	5 2
0137-06	Tenebrionidae-Alleculinae	*Nypsius aeneopiceus*	0	1	5	OBL	FLY	ROTT	SAPRO	7 9
0138-00	Prostomidae	*Dryocora cephalotes*	4	0		OBL	FLY	ROTT	XYLO	4 2
0138-00	Prostomidae	*Prostomis atkinsoni*	25	12	5	OBL	FLY	ROTT	XYLO	7
0140-00	Oedemeridae	*Dohrnia miranda*	0	5	5	OBL	FLY	ROTT	XYLO	7.9
0140-00	Oedemeridae	*Dohrnia simplex*	9	26	80	OBL	FLY	ROTT	XYLO	6.1
0147-00	Pyrochroidae-Pilipalpinae	*Binburrum ruficollis*	0	1	1	OBL	FLY	SUBC	SAPRO	4.3
0147-02	Pyrochroidae-Pilipalpinae	*Binburrum concavifrons*	0	1	2	OBL	FLY	SUBC	PRED	5 3
0148-00	Salpingidae	*Orphanotrophium frigidum*	0	1	1	OBL	FLY	BARK	PRED	2
0149-00	Anthicidae-Tomoderinae	*Tomoderus TFIC sp 01*	0	2	1	FAC	FLY	LT/SF	SAPRO	3
0150-00	Aderidae	*Aderidae TFIC sp 03*	0	2	4	OBL	FLY	ROTT	SAPRO	2 1
0151-01	Scraptiidae-Scraptiinae	*Scraptia laticollis*	0	4	2	OBL	FLY	SUBC	SAPRO	2 6
0151-01	Scraptiidae-Scraptiinae	*Scraptia TFIC sp 01*	0	9	6	OBL	FLY	SUBC	SAPRO	3 6
0152-07	Cerambycidae-Prioninae	*Enneaphyllus aeneipennis*	9	4	2	OBL	FLY	ROTT	XYLO	27
0152-07	Cerambycidae-Prioninae	*Toxeutes arcuatus*	10	3	1	OBL	FLY	ROTT	XYLO	41
0152-12	Cerambycidae-Cerambycinae	*Mecynopus cothurnatus*	0	4	2	OBL	FLY	SOLID	XYLO	11.1
0152-13	Cerambycidae-Lamiinae	*Dorcadida TFIC sp 01*	0	2	1	OBL	CRAW	BARK	XYLO	17 5
0155-09	Chrysomelidae-Cryptocephalinae	*Aporocera lagopus*	0	3	1	FAC	FLY	LT/SF	SAPRO	4
0155-09	Chrysomelidae-Cryptocephalinae	*Aporocera viridipennis*	0	1	1	FAC	FLY	LT/SF	OTHER	3 2

Fam-sub code	Family-subfamily	Species binomial	DS	ET	maximum emergence density	sapro-xylicity	dispersal mode	microhabitat type	feeding guild	body length (mm)
0155-09	Chrysomelidae-Cryptocephalinae	*Aporocera viridis*	1	10	2	FAC	FLY	LT/SF	SAPRO	7 3
0155-09	Chrysomelidae-Cryptocephalinae	*Cryptocephalinae TFIC sp 01*	0	1	1	FAC	FLY	LT/SF	SAPRO	8 5
0155-09	Chrysomelidae-Cryptocephalinae	*Cryptocephalinae TFIC sp 02*	0	6	2	FAC	FLY	LT/SF	SAPRO	2.2
0155-09	Chrysomelidae-Cryptocephalinae	*Cryptocephalinae TFIC sp 06*	0	1	1	FAC	FLY	LT/SF	SAPRO	6.4
0157-00	Anthribidae	*Anthribidae TFIC sp 02*	0	4	6	OBL	FLY	ROTT	XYLO	1 2
0157-00	Anthribidae	*Anthribidae TFIC sp 03*	0	1	0	OBL	FLY	ROTT	XYLO	2.7
0157-03	Anthribidae-Choraginae	*Xynotropis micans*	0	14	2	OBL	FLY	ROTT	XYLO	1.9
0158-00	Belidae-Belinae	*Sphinctobelus sp nr pyriatrus*	0	1	1	OBL	FLY	ROTT	XYLO	8
0159-00	Attelabidae-Rhynchitinae	*Auletobius melanocephalus*	0	8	8	FAC	FLY	UNK	XYLO	1.3
0159-00	Attelabidae-Rhynchitinae	*Auletobius suturalis/varicollis?*	0	3	1	OBL	FLY	ROTT	XYLO	2.3
0163-00	Curculionidae	*Curculionidae TFIC sp 10*	0	3	2	OBL	FLY	ROTT	XYLO	2.5
0163-00	Curculionidae	*Curculionidae YEE sp 31*	0	1	1	OBL	CRAW	ROTT	XYLO	
0163-00	Curculionidae	*Curculionidae YEE sp 49*	3	0	1	OBL	FLY	ROTT	XYLO	
0163-00	Curculionidae	*Curculionidae YEE sp 60*	0	1	1	OBL	FLY	ROTT	XYLO	2.2
0163-00	Curculionidae-Scolytinae	*Acacicis abundans?*	0	1	2	OBL	FLY	SUBC	XYLO	3
0163-00	Curculionidae-Curculioninae	*Emplesis TFIC sp 01*	0	3	1	OBL	FLY	ROTT	XYLO	2 7
0163-02	Curculionidae-Curculioninae	*Ancyttalia oleariae*	0	28	99	OBL	FLY	ROTT	XYLO	4.2
0163-02	Curculionidae-Curculioninae	*Ancyttalia tarsalis*	0	32	11	OBL	FLY	SOLID	XYLO	2 2
0163-02	Curculionidae-Curculioninae	*Elleschus wellingtoniensis?*	0	8	3	OBL	FLY	SUBC	XYLO	1 9
0163-02	Curculionidae-Curculioninae	*Eugnomini TFIC sp 08*	0	1	1	OBL	FLY	ROTT	XYLO	2.5
0163-02	Curculionidae-Curculioninae	*Eugnomini TFIC sp 09*	0	1	1	OBL	FLY	ROTT	XYLO	2.4
0163-02	Curculionidae-Curculioninae	*Eugnomini TFIC sp 16*	0	3	1	OBL	FLY	ROTT	XYLO	2.2
0163-03	Curculionidae-Cryptorhynchinae	*Cryptorhynchinae TFIC sp 10*	0	1	1	OBL	FLY	ROTT	XYLO	2 3
0163-03	Curculionidae-Cryptorhynchinae	*Cryptorhynchinae TFIC sp 11*	0	2	1	OBL	CRAW	ROTT	XYLO	2.3
0163-03	Curculionidae-Cryptorhynchinae	*Cryptorhynchinae TFIC sp 17*	0	2	1	OBL	CRAW	ROTT	XYLO	2.7
0163-03	Curculionidae-Cryptorhynchinae	*Cryptorhynchinae TFIC sp 20*	0	2	1	OBL	CRAW	ROTT	XYLO	2 2
0163-03	Curculionidae-Cryptorhynchinae	*Cryptorhynchinae TFIC sp 21*	0	1	1	OBL	FLY	ROTT	XYLO	2 5
0163-03	Curculionidae-Cryptorhynchinae	*Cryptorhynchinae TFIC sp 23*	0	1	1	OBL	FLY	ROTT	XYLO	2 3
0163-03	Curculionidae-Cryptorhynchinae	*Cryptorhynchinae TFIC sp 28*	0	8	2	OBL	CRAW	ROTT	XYLO	3
0163-03	Curculionidae-Cryptorhynchinae	*Cryptorhynchinae TFIC sp 29*	0	1	1	OBL	CRAW	ROTT	XYLO	2 4
0163-03	Curculionidae-Cryptorhynchinae	*Cryptorhynchinae TFIC sp 30*	0	2	1	OBL	CRAW	ROTT	XYLO	3 6
0163-03	Curculionidae-Cryptorhynchinae	*Cryptorhynchinae TFIC sp 31*	0	10	2	OBL	CRAW	ROTT	XYLO	1.8
0163-03	Curculionidae-Cryptorhynchinae	*Decilaus albonotatus*	0	16	12	OBL	FLY	ROTT	XYLO	2.9

Fam-sub code	Family-subfamily	Species binomial	DS	ET	maximum emergence density	sapro-xylicity	dispersal mode	microhabitat type	feeding guild	body length (mm)
0163-03	Curculionidae-Cryptorhynchinae	*Decilaus lateralis*	1	25	13	OBL	CRAW	SUBC	XYLO	3 3
0163-03	Curculionidae-Cryptorhynchinae	*Decilaus nigronotatus*	0	43	70	OBL	CRAW	ROTT	XYLO	2.1
0163-03	Curculionidae-Cryptorhynchinae	*Decilaus nr striatus/subfasciatus*	3	41	64	OBL	CRAW	LT/SF	XYLO	2 4
0163-03	Curculionidae-Cryptorhynchinae	*Decilaus TFIC sp 02*	0	7	5	OBL	FLY	ROTT	XYLO	2.7
0163-03	Curculionidae-Cryptorhynchinae	*Exithius capucinus*	0	18	5	OBL	FLY	ROTT	XYLO	5.7
0163-03	Curculionidae-Cryptorhynchinae	*Exithius loculiferus*	0	3	7	OBL	FLY	ROTT	XYLO	4 8
0163-03	Curculionidae-Cryptorhynchinae	*Miocallus pygmaeus*	0	15	7	FAC	FLY	ROTT	XYLO	1.1
0163-03	Curculionidae-Cryptorhynchinae	*Poropterus alboscutellaris*	0	2	2	OBL	FLY	ROTT	XYLO	10
0163-03	Curculionidae-Cryptorhynchinae	*Poropterus antiquus*	1	3	1	OBL	CRAW	SUBC	XYLO	11.5
0163-03	Curculionidae-Cryptorhynchinae	*Poropterus TFIC sp 05*	0	4	3	OBL	FLY	ROTT	XYLO	4 5
0163-03	Curculionidae-Cryptorhynchinae	*Roptoperus tasmaniensis*	0	22	16	OBL	CRAW	ROTT	XYLO	4
0163-03	Curculionidae-Cryptorhynchinae	*Tyrtaeosus ustulatus*	1	3	8	OBL	FLY	ROTT	XYLO	5
0163-04	Curculionidae-Dryophthorinae	*Dryophthorus TFIC sp 02*	2	5	9	OBL	CRAW	ROTT	XYLO	4
0163-04	Curculionidae-Dryophthorinae	*Dryophthorus TFIC sp 01*	16	3	31	OBL	CRAW	ROTT	XYLO	3.3
0163-05	Curculionidae-Molytinae	*Dinichus terreus*	4	10	7	OBL	CRAW	ROTT	XYLO	10 2
0163-05	Curculionidae-Molytinae	*Exeiratus TFIC sp 01*	9	14	3	OBL	CRAW	ROTT	XYLO	2 5
0163-06	Curculionidae-Cossoninae	*Cossoninae TFIC sp 06*	1	2	6	OBL	FLY	ROTT	XYLO	2 2
0163-06	Curculionidae-Cossoninae	*Cossonus simsoni*	11	1	1	OBL	CRAW	ROTT	XYLO	5 2
0163-06	Curculionidae-Cossoninae	*Pentarthrum TFIC sp 01*	2	2	1	OBL	UNK	UNK	UNK	UNK
0163-06	Curculionidae-Cossoninae	*Pentarthrum TFIC sp 02*	0	1	1	OBL	FLY	ROTT	XYLO	3
0163-08	Curculionidae-Platypodinae	*Platypus subgranosus*	0	12	16	OBL	FLY	SOLID	XYLO	4 1
0163-09	Curculionidae-Entiminae	*Mandalotus arciferus*	0	3	1	FAC	CRAW	OTHER	XYLO	4 3
0163-09	Curculionidae-Entiminae	*Mandalotus muscivorus*	0	23	10	OBL	CRAW	ROTT	XYLO	3 4
0163-09	Curculionidae-Entiminae	*Mandalotus sp nr vacillans*	0	2	2	OBL	FLY	ROTT	XYLO	6.3
0163-09	Curculionidae-Entiminae	*Merimnetes TFIC sp 04*	0	1	1	OBL	FLY	ROTT	XYLO	2 3
0163-09	Curculionidae-Entiminae	*Prostomus murinus*	0	1	1	OBL				
0163-17	Curculionidae-Tychiinae	*Tychiinae TFIC sp 05*	0	7	2	OBL	FLY	ROTT	XYLO	2.3
0163-17	Curculionidae-Tychiinae	*Tychiinae TFIC sp 06*	0	12	3	OBL	FLY	ROTT	XYLO	2 7
0163-17	Curculionidae-Tychiinae	*Tychiinae TFIC sp 08*	0	10	2	OBL	FLY			
0163-17	Curculionidae-Tychiinae	*Tychiinae TFIC sp 16*	0	1	1	OBL	FLY	ROTT	XYLO	2.4
0163-17	Curculionidae-Tychiinae	*Tychiinae TFIC sp 22*	0	12	3	OBL	FLY			
0163-17	Curculionidae-Tychiinae	*Tychiinae TFIC sp 26*	0	2	2	OBL	FLY	SUBC	XYLO	1 4
0163-17	Curculionidae-Tychiinae	*Tychiinae TFIC sp 27*	0	2	1	OBL	FLY	ROTT	XYLO	1 9
0200-00	Coleoptera adults	*Coleoptera unknown YEE sp 05*	0	1	2	FAC	UNK	UNK	UNK	
0200-00	Coleoptera adults	*Coleoptera unknown YEE sp 13*	0	3	2	FAC	UNK	UNK	UNK	

Appendix 3.2. List of non-saproxylic beetles that were collected during the survey on *Eucalyptus obliqua* logs at an intermediate decomposition stage in wet eucalypt forest in southern Tasmania, using two trapping methods: emergence trapping (ET) and destructive sampling (DS) to collect saproxylic beetles.

Fam-sub code	Family-subfamily	Species binomial	number of DS logs	number of ET logs	Dispersal mode	body length (mm)
0040-10	Scarabaeidae-Melolonthinae	*Heteronyx pilosellus*	2	9	FLYER	13
0040-10	Scarabaeidae-Melolonthinae	*Phyllochlaenia villosus*	2	1	FLYER	8
0155-00	Chrysomelidae	*Chrysomelidae 'gen nov Reid' TFIC sp 01*	0	1	FLYER	3 3
0155-06	Chrysomelidae-Chrysomelinae	*Chrysophtharta bimaculata*	14	37	FLYER	8.9
0155-06	Chrysomelidae-Chrysomelinae	*Chrysophtharta lignea*	1	0	FLYER	9 7
0155-06	Chrysomelidae-Chrysomelinae	*Paropsis rubidipes*	0	1	FLYER	10.8
0155-06	Chrysomelidae-Chrysomelinae	*Trachymela rugosa*	2	1	FLYER	
0155-07	Chrysomelidae-Galerucinae	*Arsipoda erichsoni*	0	6	FLYER	4 1
0155-07	Chrysomelidae-Galerucinae	*Galerucinae REID 'gen nov 01'*	0	1	FLYER	9 7
0155-07	Chrysomelidae-Galerucinae	*Microdonacia incurva*	0	3	FLYER	2 8
0155-07	Chrysomelidae-Galerucinae	*Microdonacia truganina*	0	2	FLYER	2.7
0155-07	Chrysomelidae-Galerucinae	*Monolepta TFIC sp 01*	1	5	FLYER	8.9
0155-07	Chrysomelidae-Galerucinae	*Monolepta TFIC sp 02*	0	0	FLYER	3 3
0155-09	Chrysomelidae-Cryptocephalinae	*Cryptocephalinae TFIC sp 24*	0	2	FLYER	3
0155-09	Chrysomelidae-Cryptocephalinae	*Platycolaspis pubescens*	0	3	FLYER	
0160-06	Brentidae-Apioninae	*Apion tasmanicum?*	0	13	FLYER	1 1
0155-09	Chrysomelidae-Cryptocephalinae	*Cadmus strigillatus*	0	1	FLYER	4 5

4 ROTTEN WOOD TYPES AND DECOMPOSITION PROCESSES IN DECOMPOSING LOGS

ABSTRACT

Decomposition processes in dead wood are important ecological processes in forest ecosystems. Through destructively sampling *Eucalyptus obliqua* logs of an intermediate decomposition stage, 11 Rotten Wood (RW) types were differentiated, based largely on the rot colour, texture, hardness, and region within the log. Each RW type presumably represents a different stage or path of succession of decomposition processes. Assemblages of RW types were compared between large (>100cm) and small (30-60cm) diameter logs and from logs that occurred in sites of mature unlogged and logged wet eucalypt forests. The effects of forest type and site were also investigated.

Significant differences were found in the type and spatial arrangement of rotten wood for all treatments. Large diameter logs had a higher frequency of discoloured but solid wood, and brown rotted wood within the log centre. Small diameter logs had more white rot on the outer regions of the log. These distinctive patterns of rot suggest that logs of different size follow different decomposition paths or processes. One explanation for this may lie in the history of the living tree before it becomes a log. Older trees have a higher susceptibility to internal decay than younger trees. The brown rot within the inner heartwood of logs may constitute a later successional stage of this internal decay. The white rot in the outer log regions is probably associated with decomposition that takes place after tree-fall. The findings show that rot patterns in large diameter logs generally differ to those in small diameter logs, and that there is also an indication that, whatever the log size, rot patterns within logs could potentially vary in relation to forest age and logging history.

4.1 INTRODUCTION

The decomposition of dead wood is an important ecological process in forest ecosystems (Carpenter *et al.* 1988; Harmon *et al.* 1986; Kaarik 1974; Kirk & Cowling 1984; Mackensen & Bauhus 1999; Swift 1977). Not only is it vital in nutrient cycling – converting the nutrients bound within wood into more mineralised, and thus available forms to be incorporated in the growing phases of forest vegetation; but this process also support major components of the forest's biodiversity (Elton 1966; Fager 1968; Maser & Trappe 1984). Dead and decomposed wood supports a high diversity of organisms that are involved in its decomposition, especially bacteria (Clausen 1996), fungi (Rayner & Boddy 1988; Swift 1977), and invertebrates (Ausmus 1977; Haack & Slansky Jr 1987; Lawrence 1989; Swift 1977). Decomposing wood also provides habitat and shelter for a wide range of other biota, such as symbiotic bacteria, non-wood decay fungi, epixylic bryophytes (Andersson & Hytteborn 1991; Turner 2003), and saproxylic invertebrates and insectivorous vertebrates that are dependent on these decomposer organisms for food and shelter (Franklin *et al.* 1987; Gibbons & Lindenmayer 2001; Maser & Trappe 1984; McComb & Lindenmayer 1999).

In Tasmanian wet eucalypt forests, the types of decomposition processes in fallen trees within intensively managed forests may change as successive harvesting is expected to truncate forest successional age, and hence alter forest conditions (Hickey 1994), change dead wood dynamics (Grove *et al.* 2002), and disrupt the natural dead wood recruitment processes (Grove *et al.* 2002). For instance, a forest landscape of stands with high stand structural complexity, including oldgrowth elements will shift towards a dominance of even aged stands of younger, mostly eucalypt trees after successive 90 year clearfelling harvesting operations (Attiwill 1994b; Lindenmayer & McCarthy 2002; Lindenmayer & Franklin 1997). One expected change will be the diminution of large diameter logs in managed forests, as the presence of ecologically mature *Eucalyptus* trees will not be perpetuated under such rotation lengths. It is unknown how this affects decomposing wood types in the long term, however various overseas studies have documented that wood decay fungal successions differ in relation to log size (Bader *et al.* 1995; Heilmann-Clausen & Christensen 2004; Renvall 1995). Sippola & Renvall (1999) reported that some fungal species in dead wood derived from mature-oldgrowth *Pinus* trees in Finnish boreal forests seemed unable to colonise the dead

wood derived from logging waste. Moreover, it is often reported that large diameter logs can have different temperature and moisture dynamics (reviewed in Harmon *et al.* 1986), which are factors that influence the community development of decomposer organisms (Mackensen & Bauhus 1999; Rayner & Boddy 1988). In Australia however, no studies aside from that of (Meggs 1996) have investigated whether the types of decomposition processes would differ within decomposing logs of different size diameters or within managed and unmanaged forests.

Describing and categorising wood decomposing on the forest floor can be difficult, as it passes through a wide continuum between solid wood and material comprising humus that becomes incorporated into the soil. Typically, wood decay fungi have been considered the main decay-causing organisms, and they can be broadly categorised as acting as brown or white rot fungi (Kaarik 1974; Rayner & Boddy 1988). This categorisation is largely based on the enzymatic strategies deployed in breaking down wood at the cellular level, such that wood is chemically and structurally degraded in a specific way, thus resulting in a characteristic brown or white rot (Kaarik 1974). However, wood decomposing on the forest floor is usually the product of various processes (Mackensen & Bauhus 1999), that is, it is not exclusively the product of actions from wood decay fungi. Rather, these can include the decomposition actions by faunal communities, including wood comminution by xylophagous arthropods, especially wood-boring beetles and termites (Ausmus 1977; Carpenter *et al.* 1988; Greenslade 1972). Other processes may include mechanical breakage, physical weathering and leaching (Mackensen & Bauhus 1999); or the biochemical breakdown of wood cells by ascomycete fungi and bacteria (Carpenter *et al.* 1988; Harmon *et al.* 1986; Kaarik 1974; Kirk & Cowling 1984; Mackensen & Bauhus 1999; Sollins *et al.* 1987; Swift 1977). Thus, the term "Rotten Wood type" (RW type), instead of rot type, is herein used to refer to decomposing wood - to collectively reflect the succession of decomposition processes, including those mediated by faunal activities.

Investigating the variability of decomposition processes among different logs may benefit from a multivariate approach to data analysis. This is because an individual log on the forest floor typically undergoes a series of different physical, chemical and biochemical processes throughout its decomposition (e.g. Brown *et al.* 1996; Harmon *et al.* 1986). For example, multiple variables that could be used to describe to a log's

decomposition state include presence of bark, cracks, decay and overall log shape, (e.g. Lindenmayer *et al.* 1999b). Generally, a log is invaded by a succession of microorganisms and invertebrates, attacking it at different positions of the log. Therefore, at any one point in time, a log can exhibit many spatially separated rot types of varying stages of decomposition. Each rot type may not only be the result of decomposer organisms observed at the time of study, but rather the product of past processes, and the activities of preceding decomposers (e.g. Boddy 2001; Niemelä *et al.* 1995; Sippola & Renvall 1999). Therefore, the difference in rot type assemblages could be used the determine the different decomposition processes among logs.

Studies that have investigated wood decomposition in *Eucalyptus* have mostly focussed on fungal-mediated decomposition within living trees (reviewed in Kile & Johnson 2000; e.g. Parkin 1942; Refshuage 1938; Tamblyn 1937; Wardlaw 1996, 2002; White & Kile 1993; Wilkes 1982; Wilkes 1985a), and have often taken a wood production rather than ecological perspective. In terms of decomposing wood on the forest floor, two preliminary studies have characterised the rot types of eucalypt logs within Tasmania (Meggs 1996; Mesibov 1988). The rot classification developed by these systems were markedly different. Mesibov (1988) used five broad categories to describe the decomposing wood based on structural properties, and did not consider decay type. By contrast, Meggs (1996) outlined twice as many rotten wood type categories, using a larger number of descriptors (colour, structure, texture and presence of fungal hyphae), however, in the field, this classification was somewhat ambiguous and difficult to apply objectively (pers. obs). Therefore, a classification, that built on these past studies, of rotten wood types occurring in decomposing *Eucalyptus obliqua* logs was first objective of this study. This will then be used to objectively describe and document the rotten wood types in logs, in order to compare the decomposition processes among different logs.

The aim of this study was to compare the types of decomposition processes of large and small diameter logs, as indicated by the different rotten wood types within logs. The specific objectives were to:

1) Develop a user friendly, objective and repeatable classification system for the Rotten Wood (RW) types based on the rotten wood of *Eucalyptus obliqua* logs at an intermediate stage of decomposition stage;
2) Compare the richness and frequency of individual RW types between log size classes;
3) Compare the assemblages of RW types according to log size, forest type and site.

4.2 METHODS

4.2.1 Study location and experimental design

Research was conducted at seven study sites in wet eucalypt production forests in southern Tasmania. Four (designated as study sites H, E, S, PR2) were 20-30 yr CBS logging regeneration of one harvesting event; and the other three (designated as M, WR and PO1) were in mature unlogged forest. Study site locations and descriptions are detailed in Section 2.2 and 2.3. Within each study site, three pairs of large diameter (>100 cm) and small diameter (30-60 cm) *Eucalyptus obliqua* logs of an intermediate decomposition stage (defined in Section 2.5) were sampled. The study logs in the logging regeneration had essentially derived from logging residue left after harvesting, while logs in the mature unlogged forests had naturally recruited through windfalls. Names and diameters of the study logs are listed in Table 2.2.

4.2.2 Sampling method

Two 1m-long sections, at least 4 metres apart, were dissected from the log (Figure 4.1). The position of dissection was partly determined by safety and accessibility to the log, due to slope instability, and obstructions such as thick undergrowth and other fallen logs, though where possible, the position corresponded to the basal and mid regions of the log (fallen tree). A 5cm wide disc was taken from each end of a 1m-long section. Each disc was photographed, and the rot patterns were described and drawn (Figure 4.2a,b). For each 1m-long section, samples of the different types of rotten wood (between 250 to 1500ml) were placed in an airtight bag, and taken for more detailed laboratory descriptions and chemical analysis. These samples of rotten wood were labelled corresponding to the map drawn of each disc. Two other components of this study were conducted in parallel; collection of saproxylic beetles (Chapter 5), and isolation of basidiomycete fungi (Z.Q. Yuan unpublished data) from these samples.

4.2.3 Developing a RW type classification

The classification of rotten wood into distinct types was carried out in three steps.
1) All the rotten wood samples collected were sorted into Preliminary Rotten Wood (PRW) types using several descriptors. These included rot colour, texture, presence of features such as discoloured markings or fungal tissue (hyphae or mycelium), and wood wetness. Colour was taken as an indication of the predominant fungal decay type (white or brown rot) at the time of sampling. The texture of the wood was described as blocky, crumbly, stringy or fibrous. The PRW types are listed in Appendix 4.1.

2) The PRW types were then reduced to the final Rotten Wood (RW) types by grouping together PRW types that were assessed as variants or different decomposition stages of the same rot type. Two sources of information were used to match PRW types:

- Fungal isolations from rotten wood samples (Z.Q. Yuan unpublished data). PRW types that had the same dominant fungal species were considered to be the same rotten wood type (Appendix 4.1).
- A cluster analysis of similarity (using a Bray Curtis distance measure and UPGMA sorting strategy in *PC-ORD,* (McCune & Mefford 1999) based on how consistently PRW types were observed in proximity to each other within the same log section (Appendix 4.2).

3) Each RW type was designated into one of five regions of the log cross-section: the surface, outer heartwood, inner heartwood, heartwood (both inner and outer) and localised pockets of rot within the heartwood region where the pocket boundaries are well defined (Figure 4.3). This was visually assessed and was based on the main and most common log region of where it had occurred

4.2.4 Chemical measurements of RW types

Preliminary chemical analyses of selected RW types were undertaken. These included measurements of moisture content, total carbon and nitrogen. However, due to money constraints for chemical analyses, only a limited number of rotten wood samples could be measured. Therefore, due to low sample size, data from the chemical and moisture analyses were not analysed statistically. To improve thesis readability, the data, and methods used to measure wood chemical content are presented in Appendix 4.5.

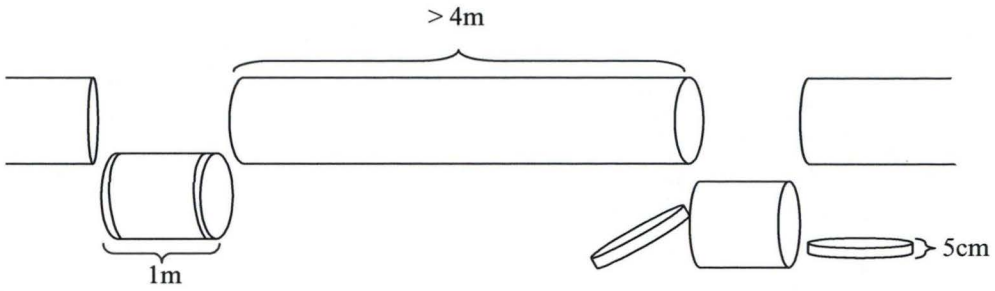


Figure 4.1. Method for sampling rotten wood from two 1m log-sections per fallen log in the mid and basal log , taking 5cm-wide discs from either side of each section.

a)

b)

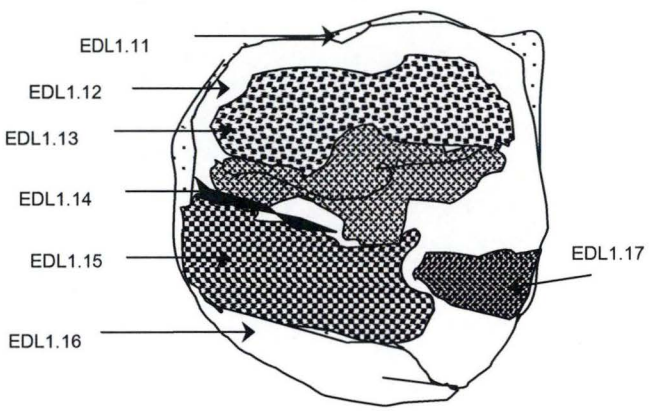


Figure 4.2. An example of a) a photograph taken for each cross-section disc and b) the corresponding map drawn showing the rotten wood patterns and unique codes assigned for each sample of rotten wood

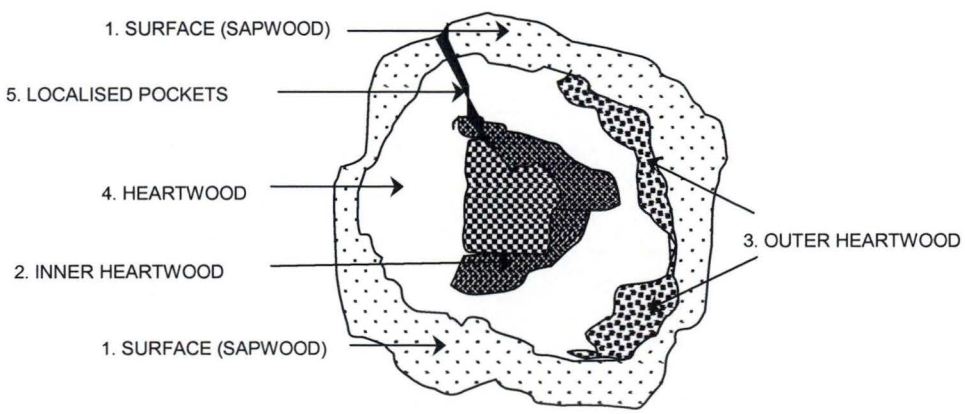


Figure 4.3. Stylised *Eucalyptus obliqua* log cross-section showing the five main regions where rotten wood occurred. Regions are called 'RW region' (see Section 4.2.3, step 3 for explanation).

4.2.5 Rotten wood data and statistical analyses

Data comprised the presence and absence of RW types within each log, pooled from the two 1m-long sections. Analysis of Variance (ANOVA) was used to test the difference in the number of RW types per log between log size classes. The frequency of individual RW types between large and small diameter logs were also compared using Chi-square analysis.

Principle Components Analysis (PCA) was used to explore the variation among logs based on the similarity of RW type assemblage, in order to find possible differences relating to the treatments of log size, forest type and site. RW assemblage is based on the different RW types within a log, pooled from the two log discs. PCA displays the similarity of logs in multidimensional space using a smaller number of synthetic variables. These synthetic variables, represented as principle components axes, each explain a unique proportion of variation of the original data. To determine which RW types contribute most to any variation, RW type vectors were overlaid onto the ordination as a joint plot. The PCA was based on a covariance/variance matrix, using a Sorensen (Bray-Curtis) distance measure, and was conducted in PC-ORD (McCune & Mefford 1999).

Multi-Response Permutation Procedures (MRPPs) were then applied to statistically test for RW assemblage differences among the treatments (log size, forest type and site). MRPP in PC-ORD is a non-parametric method that uses permutation procedures to test the hypothesis of no difference between two or more *a priori* groups based on multi-variate data. This method provides a test statistic, T, which describes the separation between groups: the more negative the T, the stronger the separation. It also provides a p-value, which determines whether the observed difference is greater than expected by chance. As recommended by the program, the method was run on the Euclidean distance measure and used the natural group weighting of n/sum (n).

4.3 RESULTS

4.3.1 RW types categorised from decomposing *E. obliqua* logs

The rotten wood from decomposing *E. obliqua* logs were classified into 11 RW types, which are summarised in Table 4.1. A matrix of characters for each RW type is listed in Appendix 4.3, with a detailed description given in Appendix 4.4. A series of photographs is also provided to illustrate the characteristic features of each RW type, and to display the colour and texture variations of RW types that varied in relation to their decomposition state (Appendix 4.4). Upon visual assessment, RW types could be associated to one of the five designated regions of the log cross-section.).

Table 4.1. Classification of 11 Rotten Wood types, listed in order by RW region, from *Eucalyptus obliqua* logs in wet eucalypt forests in southern Tasmania.

Rotten wood type	Suspected main decomposition agent	Apparent decay type	RW REGION
Fibrous surface rot	Fungi	Unknown	Surface (sapwood)
White jelly surface rot	Fungi	Unknown	Surface (sapwood)
White pocket rot	Fungi	White	Outer heartwood
White stringy rot *	Fungi	White	Outer heartwood
Yellow dry slatey rot	Fungi	Unknown	Outer heartwood
Brown cubic friable rot	Fungi	Brown	Outer heartwood
Discoloured wood	Unknown	N/A	Heartwood
Wet cracks	Mechanical and other	N/A	Localised
Brown blocky crumbly rot	Fungi	Brown	Inner heartwood
Red brown blocky fibrous rot	Fungi	Brown	Inner heartwood
Brown mudgut rot	Insects, fungi and other	Brown	Inner heartwood

Incipient decomposition stage of this rotten wood type appears as dark crimson discoloured wood

4.3.2 Comparison of RW type richness and occurrence between log size classes

Large diameter logs had a significantly higher number of RW types per log than small ones (ANOVA: $F_{2,41} = 4.51$, $p = 0.04$), averaging five (s.e. =1.4) and four (s.e. = 1.5) RW types, respectively.

While it is acknowledged that a greater wood volume is sampled from a large diameter log versus a small diameter log, comparing the number of RW types was still considered valid. This is because RW type presence/absence and richness was determined using the log cross-section. The presence of a RW type represents the

presence of a rot/decay columns and pockets. It is unlikely RW type data would change if equal wood volumes of large and small diameter logs were compared by taking thinner and thicker log cross-sections respectively.

The relative frequency of RW types significantly differed between log sizes (χ^2_{10} = 28.7, p = 0.001). The three inner heartwood and discoloured wood RW types were significantly more frequent in large diameter logs, while white stringy rot was exclusive to small diameter logs (Figure 4.4). White pocket rot and yellow slatey rot occurred in twice as many small diameter logs than in large diameter logs, however the lack of statistical significance is probably due to low sample size. In general, most large diameter logs (90%) had at least one inner heartwood RW type, where as only 33% of small diameter logs had an inner heartwood RW type. By contrast, most small diameter logs (90%) had at least one outer heartwood RW type compared to 33% of large diameter logs.

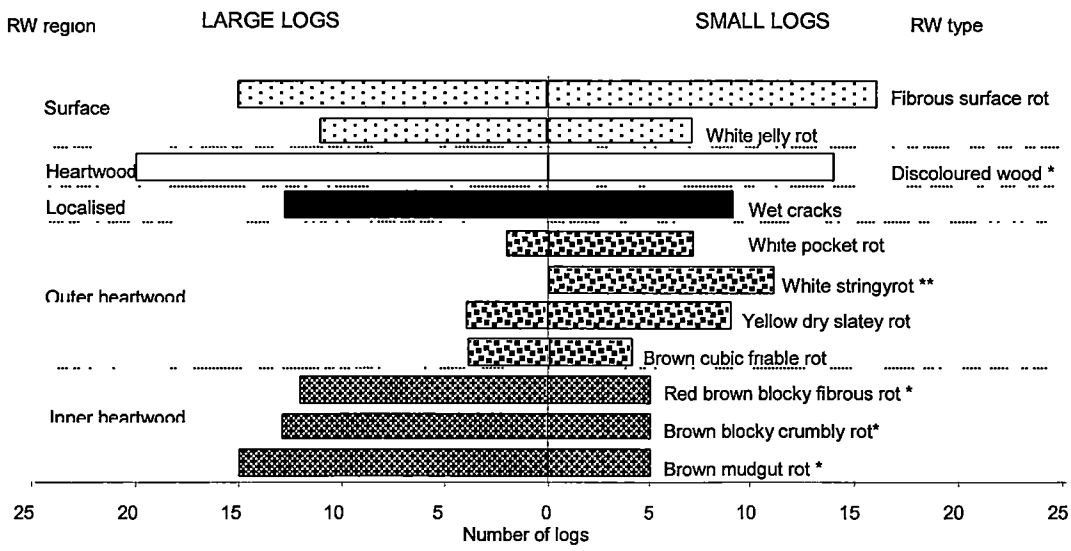


Figure 4.4. Frequency of RW types found in 21 large (left) and 21 small (right) *Eucalyptus obliqua* logs at an intermediate decomposition stage. RW types are grouped by RW region. RW types which differed significantly in occurrence ($p \leq 0.01$, Chi-square analysis) between the two log size-classes are denoted by *, while those exclusive to a particular log size-class are denoted by **.

4.3.3 Comparison of RW assemblages among log sizes, forest types and sites

4.3.3.1 Log size

The first three axes of the PCA on RW assemblages explain 51% of the variation of the original data set (Figures 4.5a,b). Axis 1 explains 24.2% of the variation among logs (Figure 4.5a), and most large and small diameter logs are separate along this axis. Correlating with Axis 1 in the direction of the cluster of large diameter logs are the three brown inner heartwood RW types and wet cracks. The difference in RW assemblages between log size is significant ($T = -8.22$, $p = 0.000003$).

Five small diameter logs (HSD1, SDS1, PO1DS1, PR2DS1, and PR2DS3) had more similar RW assemblages to that of large diameter logs, four of which were in logging regenerated forests. A closer inspection of these five logs show that they possess at least one brown inner heartwood RW type.

4.3.3.2 Forest type

The RW assemblages of logs in logging regenerated forest differed significantly from those in mature unlogged forest ($T = -3.08$, $p = 0.01$).

Furthermore, there seems to be a log-size/forest-type interaction, as there is almost no overlap between large diameter logs in logging regenerated forests and small diameter logs in the mature-unlogged forests (Figure 4.5a). When each log-size/forest-type combination is analysed as an independent treatment, the difference in RW assemblages amongst them was highly significant ($T = -6.92$, $p = 0.0000001$).

4.3.3.3 Site effects

Logs within the same site are more similar to each other than to logs of other sites (shown in PCA axes 2 and 3, Figure 4.5b), and this variation among sites is significant ($T = -2.77$, $p = 0.007$).

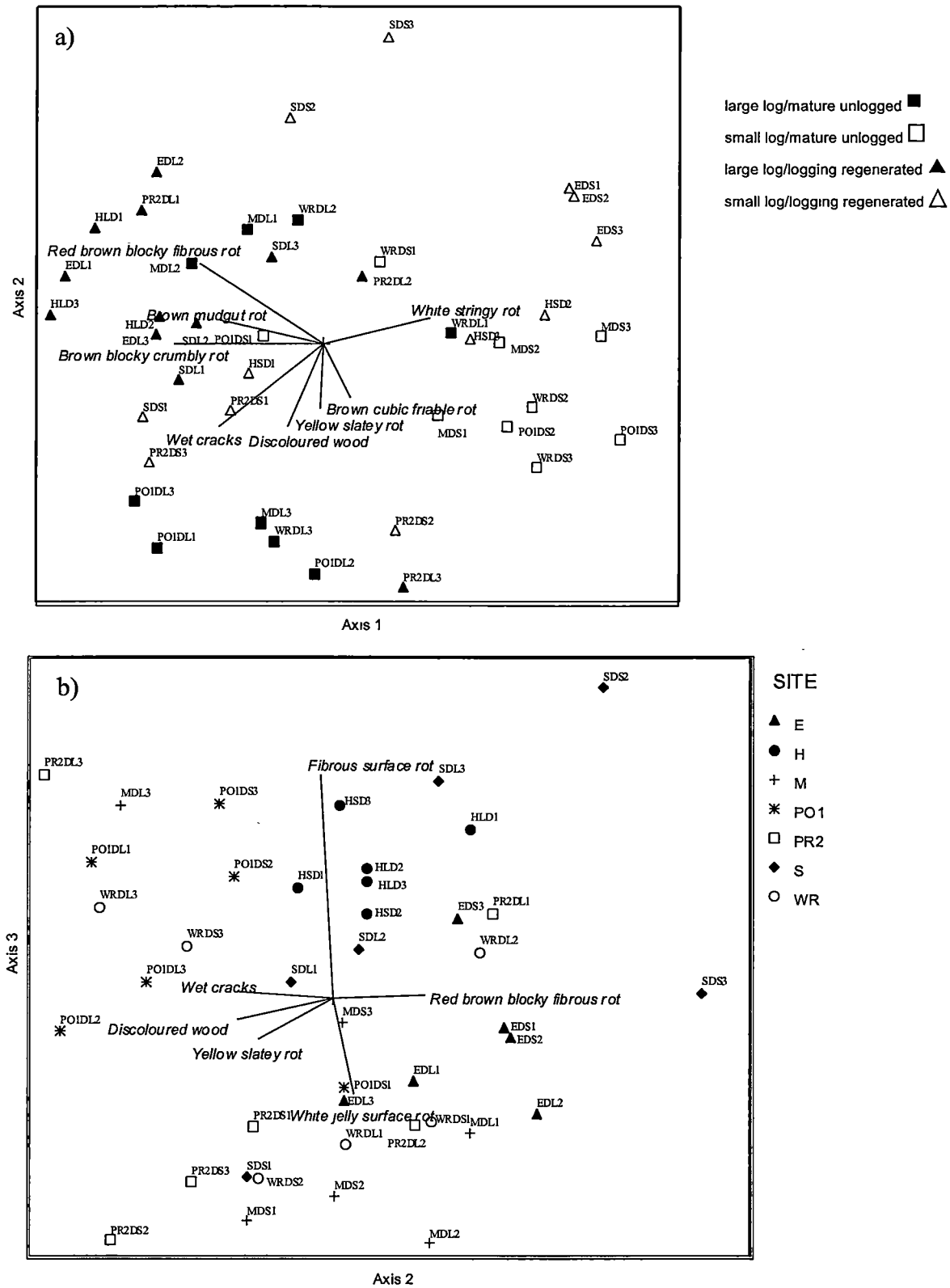


Figure 4.5. Principlal components analysis ordination of 42 *E. obliqua* logs based on 11 RW types, showing axes a) 1 and 2, with log size-forest type overlaid, and b) 2 and 3, with site locations overlaid. RW type vectors are overlaid as a joint plot. Vector scaling 100%. Only vectors with r^2 value > 0.2 are shown. Site codes H, E, S, PR2, M, WR and PO1 correspond to the location map in Section 2.1. Alphanumeric log codes refer to logs listed in Table 2.2. A total of 51 % of variation was explained in the first three axes (24.2, 14.0 and 12.9% respectively).

4.4 DISCUSSION

4.4.1 Rotten wood classification system

The RW classification provides an important tool with which to objectively and repeatably classify rotten wood that results from various decomposition processes. In this study of *E. obliqua* logs at an intermediate stage of decomposition, a total of 11 distinct RW types were classified, each potentially representing a different array of physical, chemical and biological properties. The RW classification system improves upon past classifications (Meggs 1996; Mesibov 1988) of rot types in *E. obliqua* logs. While there is a certain degree of comparability to these previous studies (see Table 4.2 and Table 4.3), an important feature of this new system is the use of information relating to the region and patterns of rot within the log, which can indicate how a particular rot type and log decomposition process has originated and how it develops. The classification also benefits by the inclusion of additional categories (e.g. 'discoloured wood' and decomposed wood apparently created by mechanical fractures – 'wet cracks'). It should be noted that this classification is a work-in-progress, as there are more different RW types present in logs at a earlier or later decomposition stage, and logs occurring in different site locations (pers. obs.).

4.4.2 Factors affecting the different decomposition processes in decomposing logs

Decomposition processes are extremely complex (Rayner & Boddy 1988), there are a number of interrelated factors that may be influencing underlying rotten wood types and heterogeneity in decomposing logs on the forest floor. This includes the environmental forest conditions; the log microclimate (e.g. moisture, temperate) within the forest (Boddy 1999; Rayner & Boddy 1988); wood quality (e.g. presence of fungitoxic extractives, Rayner & Boddy 1988); the species pool of decomposer organisms within these forests (Willig & Schlechte 1995); the effect of fire (Wikars 2002) and the condition of the living wood prior to tree fall (Boddy 2001; Rayner & Boddy 1988). In this study, aspects of the rotten wood type assemblages varied significantly among logs, in relation the log size, forest type and site.

Table 4.2. Classification of 11 Rotten Wood types from this study, compared with classifications from other studies in Tasmanian wet eucalypt forests. Rotten wood types in the same row are thought to be the same.

This study, *E. obliqua*	Meggs (1996), *Eucalyptus* spp.	Mesibov (1988), various
Fibrous surface rot (SF)	Soft yellow fibrous rot	
White jelly surface rot (SF)	Other (includes blue stain fungi and wet, jelly-like rot)	
White pocket rot (OH)		Skeletal rot
White stringy rot (OH)		Spongy/fibrous rot
Yellow dry slatey rot (OH)		
Brown cubic friable rot (OH)		
Discoloured wood (H)		
Wet cracks (L)		
Brown blocky crumbly rot (IH)	Orange/red/brown crumbly rot	Friable/crumbly rot
Red brown blocky fibrous rot (IH)	Red blocky rot	Blocky rot
	Red blocky rot with white fungal hyphae	
Brown mudgut rot (IH)	Orange/ red clayey rot	Mudgut rot

Table 4.3. Classification of 11 rotten wood types from this study, compared with fungal derived decay classifications from other studies. Rotten wood types in the same row are thought to be the same.

This study *E. obliqua*	Refshuage (1938) *E. regnans*	Tamblyn (1937) *E. marginata*	Parkin (1942) *E. regnans*	Kile & Johnson (2000) *Eucalyptus* spp.	Wardlaw (2002) *Eucalyptus* spp
Fibrous surface rot			Yellowish stringy rot		
White jelly surface rot					
White pocket rot	Small white pocket rot	White pocket rot	White pocket rot		
	Small brown pocket rot				
	Brown stain associated with small white pocket rot				
White stringy rot	White spongy rot			White pocket rot	
	Large white pocket rot of white stringy type				
Yellow dry slatey rot					
Brown cubic friable rot					
Discoloured wood					
Wet cracks					
Brown blocky crumbly rot	Brown cubical rot	Brown trunk rot	Brown cubical rot		Butt rot
Red brown blocky fibrous rot			Yellow brown spongy rot		
Brown mud gut rot (IH)					

4.4.3 The effect of log size

This survey provides quantitative data to show that *Eucalyptus obliqua* logs of the different classes studied do not follow the same sequence of decomposition events. This is demonstrated by;

- the higher incidence of brown rot types in large diameter logs, and of white rot types in small diameter logs
- a localisation of brown rot types common to large diameter logs in the central part of a log, and
- a marked association of the white rot types characteristic of small diameter logs with the outer log regions.

Patterns in the types of rot have been previously reported as differing between large and small diameter logs (e.g. Araya 1993; Edmonds & Marra 1999), however, the specific underlying mechanisms that determine these differences have been less understood. In this study, several trends relating to the age of the living tree may explain the differences in RW types between large and small diameter logs. Older (large diameter) living eucalypt trees are more susceptible to heartrot, which can originate from infection courts such as those caused by fire damage or by the breakage of large branches (Greaves *et al.* 1965; Perry 1985; Tamblyn 1937; Wardlaw 2002; Wilkes 1985a). The brown rotten wood frequently observed in the centre of *E. obliqua* large diameter logs would then be related to heartrot in the living tree, either by continued decomposition in the log by the same fungus as in the living tree (e.g.Tamblyn 1937), or as a the result of succession of certain processes and organisms (Boddy 2001; Niemelä *et al.* 1995; Rayner & Boddy 1988; Renvall 1995) where the original heartrot fungus is displaced (e.g. Tamblyn 1937). This follows similar ideas of a recent study by Heilmann-Clausen & Christensen (2004). They compared the decay fungi of small and large diameter logs in Danish beech and hypothesised that the infection history in the living tree is crucial for the establishment of specialist heartrot agents in the decomposing log.

Unfortunately, there are few data on differences in successional processes between, or the identity of decomposer organisms in, standing and fallen *E. obliqua* trees. In conjunction with this study, fungal isolations were obtained from rotten wood types (ZQ Yuan unpublished data). However, isolations were usually not successful from

advanced stages of rot, and of the successes, the majority were difficult to identify to a taxonomically known fungus (ZQ Yuan unpublished data). Generally, the identification of fungal isolates in culture based on morphological characters is an extremely specialist task, and even if cultures can be identified to a morphospecies, matching them to cultures from known fungal fruit bodies is still required. Only recently have molecular methods been used to assist in the identification of fungi, where the molecular profile of an unknown isolate is matched to that of a known fungus (ZQ Yuan, unpublished data, Glen *et al.* 2001),). Yet the effectiveness of this tool is limited by the size of the library of known fungal molecular profiles to which to refer. Often the fungi of the innermost heartrot decay do not regularly produce perennial fruit bodies, and even if fruit bodies are seen on the log (mostly resupinate), much of the wood decay fungal flora is undescribed in Australia (May & Simpson 1997). Moreover, recent preliminary work shows that isolating the fungi that cause the rotten wood, from rotten wood, may not be possible as at this stage of wood decomposition as the decay causing fungi are likely to have "gone" (Hopkins, A. pers. comm.)

Younger (small diameter) trees are less likely to have heartrot, as such trees have higher sapwood to heartwood ratios than older trees (Florence 1996), and sapwood is integral in excreting antibiotic compounds that inhibit and thus restrict microbial decay (Wilkes 1985b). Thus, it is probable that decomposition in the small diameter logs had started following the tree fall event. In small diameter logs, the majority of rotten wood was concentrated on the outer log regions, which is a type of decay pattern more typical after tree death (Boddy 2001). While small diameter logs have a higher incidence of white rot in the log outer regions, the lack of these RW types in large diameter logs may be may be due to wood chemistry. In old trees, the outer heartwood is rich in complex polyphenols (fungi toxic compounds known as extractives), and so this area is highly durable and decay resistant (Rudman 1963, 1965). The preponderance of discoloured but solid heartwood observed in the outer regions of the large diameter logs in this study supports this explanation.

Although inner heartwood RW types were less common in small diameter logs, they did occur in five logs. These RW types may have been present prior to tree death, as relatively young trees (~30 cm diameter) with many dead branches can be susceptible to

heartrot. However the rot in these young living trees is typically associated with white rot fungi (Wardlaw 1997). Another, but not mutually exclusive explanation, relates to the metabolic actions induced by wood borers. Wardlaw (1994) reported that the activities of stem boring larvae, especially hepialid moths and cerambycid beetles are a common source of decay column initiation in young eucalypt trees in wet eucalypt forests. In the present study, found associated with the inner heartwood rot of these small diameter logs were either live large prionine cerambycid larvae, or remains of their mandibles – which they shed with each moult, and extensive amounts of frass material and comminuted wood. It is likely that in downed logs, the feeding activities of such larvae facilitate certain successional processes, or at least enhance decomposition, as found for wood borers in dead wood hosts elsewhere (Ausmus 1977; Carpenter *et al.* 1988; Edmonds & Eglitis 1989; Fager 1968; Swift 1977).

4.4.4 The effect of silvicultural practices, forest age, and site factors

There was some indication that RW types differed between logs in logging regenerated forest and logs in mature-unlogged forests. There appeared to be a higher frequency of large diameter logs with 'red brown blocky fibrous rot' in the logging regenerated forest, and a slightly higher incidence of small diameter logs with white stringy rot in mature unlogged forests. While the difference between forest types was not as conclusive as that between log sizes, it is a point still worthy of discussion.

Mature unlogged and logging regenerated forests are of different forest ages, and so it is unclear as to whether variation in RW assemblages would relate to the different forest age and succession, or different log types between CBS forests and mature-unlogged forests. Logs in logging regenerated forests are typically derived from felled trees left after the harvest, are burnt, and begin decomposition in the absence of a forest canopy. While, logs in the mature unlogged forests are recruited to the forest floor via natural causes, such as tree fall from wind, rot, and/or breakage from falling neighbouring trees (Woldendorp *et al.* 2002a). Logs presumably undergo decomposition under a relatively established forest with a closed canopy. To confidently attribute any observed RW type differences between forest types to a specific factor requires knowledge of the decomposer organisms involved in RW type formation.

Based on studies elsewhere, some implications relating to the effects of CBS silviculture can be suggested. Logs burnt after a silvicultural regeneration burn, and left to decompose under a open canopy are likely to undergo distinct fungal successions compared to logs that are naturally recruited to closed forest conditions. This is because the substrate quality of logs and the pool of decomposers within the forest/site would differ. Generally, logs that decompose in an open environment are more prone to desiccation, and exposed to high levels of insolation, and greater fluctuations in temperature (Boddy 1983), and these factors can determine the types of decomposer microorganisms available for wood decomposition (Harmon *et al.* 1986; Rayner & Boddy 1988). Moreover, burnt wood is likely to influence fungal successional processes (e.g. Wikars 2002), 2001). In Victoria, Parkin's (1942) survey after the 1938 forest fires observed a higher incidence of white stringy rot on burnt *Eucalyptus regnans* F. Muell branches than unburnt ones. Various studies in Europe have shown that wood decay fungal assemblages can differ between disturbed and undisturbed forests (Pugh & Boddy 1988): UK), and between burnt and unburnt forests (Penttilä & Kotiranta 2001): Sweden). Recent study in Tasmania showed that macrofungal communities differ between mature and younger logging regenerated wet eucalypt forest (Packham *et al.* 2002).

Logs left after forest harvesting are selectively left based on their economic importance, often based on decay severity, and this has the potential to inadvertently influence decomposition processes within the stand. In the present study, one of the most likely explanations for the higher prevalence of large diameter logs with 'red brown blocky fibrous rot' in logging regenerated forest is that past management history may have selected for these logs to be left after harvest. During the 1960's and 70's, when these forests were felled, only high-grade sawlogs were taken, leaving on any logs that showed signs of rot. Of the five small diameter logs that had this rot, four were located in logging regenerated forest. In the mature unlogged forests, the decomposing logs would have been recruited to the forest floor through natural causes, often from a range of processes including wind, rot, and/or breakage from falling neighbouring trees (see Woldendorp *et al.* 2002a). The greater range of RW types among these logs in the mature unlogged forests further support this interpretation. As harvesting practices since the 1980's utilise logs with heartrot for pulpwood and to a less extent fuelwood (Grove

& Meggs 2003), these higher levels of red brown blocky fibrous rot may not be apparent in more recently felled forests.

Another outcome of this study is the variation of RW types among sites, where logs of the same site had similar RW types to each other. Historical effects of past wild-fire events that consequently determine the succession processes of the forest offers another explanation for the significant assemblage variation among sites. Fire history within the study area is highly variable (see Section 2.2). Moreover, it seems that site-factors not only affect vascular plants (Corbett & Balmer 2001), litter beetles (Baker *et al.* 2004) and saproxylic beetle species (see Section 6.3.2), but also the decomposition processes of wood. Recent stem decay surveys conducted within the same forest locality also found wood decay fungi were site-affected (Wardlaw, T., pers.comm.). It is unknown how these communities relate, or whether the ecological processes that have determined this variability for rotten wood are the same processes that determined the variation for these other communities. Further investigation on the types of decomposer organisms involved in the formation of RW types that are site-affected would be needed to determine the nature of this relationship.

4.5 CONCLUSIONS

The RW classification is a useful tool for categorising the different substrate qualities of wood that arise from the various decomposition processes. Application of the RW classification system to the collection of rot type data and the analysis of these data provides insights into the complexity of decomposition processes within *Eucalyptus obliqua* fallen logs. Each RW type may also represent a specific habitat type for saproxylic beetles.

These study demonstrates that decomposition processes in large diameter logs differ to small diameter logs. However, without knowing the history of wood decomposition within a tree prior to or post tree fall, nor the identity or ecology of the decomposer organisms involved, determining the underlying mechanisms that shape these rot patterns is speculative. Current research projects are seeking to answer some of these questions (Hopkins *et al.* 2003). This type of knowledge would be valuable for

determining how to manage for changes in the substrate quality of logs that result from the various effects of intensive forestry.

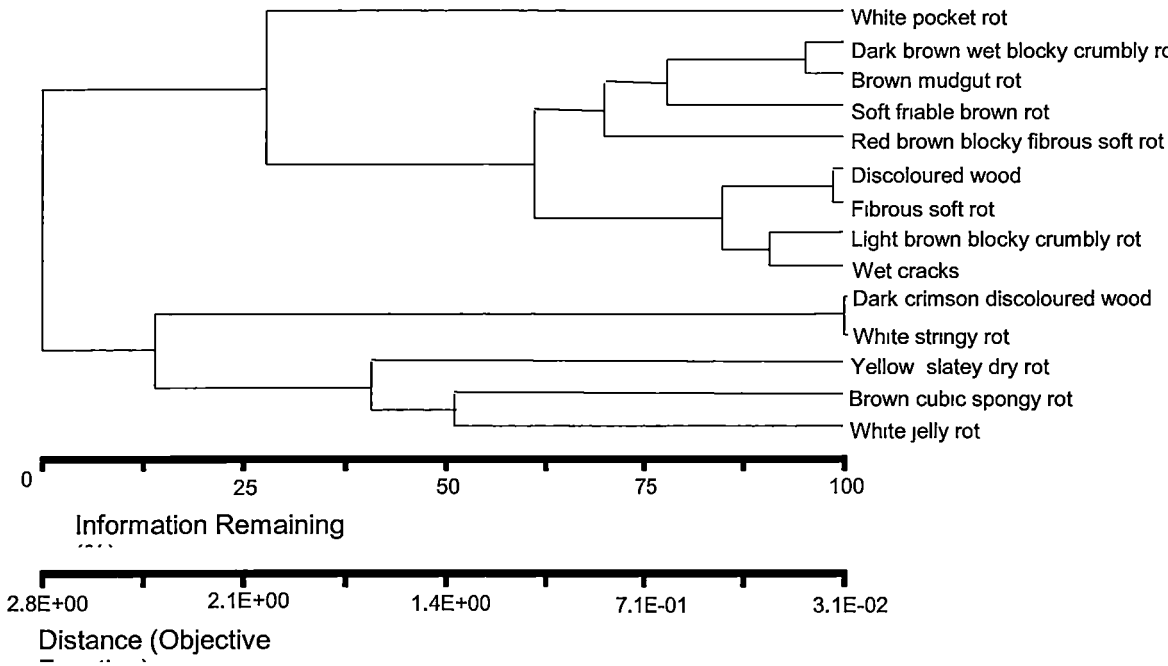
Intensive forest management practices has the potential to alter log decomposition processes within managed forests compared to unmanaged forests. As discussed, this may occur by reducing the availability of large diameter logs, reducing the likelihood of fallen trees undergoing decomposition under closed (mature) forest conditions, or through selectively leaving logs based on their decay. There is a dearth of information on the effects of fire, forest disturbance and forest successional processes on log decomposition processes. It is clear, however, that research in this area of better understanding the ecology of wood decomposing communities (insect and fungal succession) warrants further attention.

4.6 APPENDICES

Appendix 4.1. Reducing the number of PRW types to RW types, as highlighted by }. This was based on evidence from preliminary fungal data from Z.Q. Yuan (unpublished). RW region: SF = surface, OH = outer heartwood, H = heartwood, L = localised, IH = inner

PRW TYPES	RW REGION	RW TYPES
White jelly rot	SF	White jelly rot
Fibrous soft rot	SF	Fibrous soft rot
White pocket rot	OH	White pocket rot
White stringy rot	OH/H	White stringy rot
Dark crimson discoloured wood	OH/H	
Yellow slatey dry rot	OH	Yellow slatey dry rot
Soft friable brown rot	OH	Brown cubic friable rot
Brown cubic spongy rot	OH	
Discoloured wood	H	Discoloured wood
Wet cracks	L	Wet cracks
Dark brown wet blocky crumbly rot	IH	Brown blocky crumbly rot
Light brown blocky crumbly rot	IH	
Red brown blocky fibrous rot	IH	Red brown blocky fibrous rot
Brown mudgut rot	IH	Brown mudgut rot

Appendix 4.2. UPGMA cluster analysis of PRW types within individual log sections, using a Bray Curtis distance measure.



Appendix 4.3. Matrix of characters of the 11 RW types. RW region: SF = surface, OH = outer heartwood, H = heartwood, L = localised, IH = inner heartwood. RW types have been abbreviated as WJR – white jelly rot, FSR – fibrous surface rot, WPR –white pocket rot, WSR – white stringy rot, BCR = brown cubic friable rot, YSR – yellow slatey rot, DW – discoloured wood, WC –wet cracks, RBR – red brown blocky fibrous rot, BBR – brown blocky crumbly rot, and BMR – brown mudgut rot.

	RW REGION	SF	SF	OH	OH	OH	OH	H	L	IH	IH	IH
	RW TYPE	WJR	FSR	WPR	WSR	YSR	BCR	DW	WC	BBR	RBR	BMR
Texture	BLOCKY/CUBIC	×	×	×	×	×	✓	×	×	✓	✓	✓
	CRUMBLY	×	×	×	×	×	✓	×	×	✓	×	×
	STRINGY/FIBROUS	✓	✓	×	✓	×	×	×	×	×	✓	×
	HARD	×	×	✓	✓	✓	×	✓	×	×	✓	×
	SOFT/SPONGY	✓	✓	✓	✓	×	✓	×	×	×	✓	✓
	BRITTLE	×	×	×	×	✓	×	×	×	✓	×	×
Colour	LIGHT BROWN	×	✓	×	×	✓	✓	✓	×	✓	×	×
	DARK BROWN	×	×	×	✓	×	✓	×	✓	✓	×	✓
	RED BROWN	×	×	×	×	×	✓	×	×	×	✓	✓
	BLACK	×	×	×	×	×	×	×	✓	×	×	×
	WHITE	✓	✓	✓	✓	✓	×	✓	×	×	×	×
	YELLOW	✓	✓	✓	×	✓	×	✓	×	×	×	×
	CRIMSON	×	×	×	✓	×	×	×	×	×	×	×
Wetness	WET WOOD	✓	✓	×	×	×	×	×	✓	×	×	✓
	DRY WOOD	×	✓	×	×	×	✓	×	×	✓	×	×
Features	MYCELIUM	✓	×	✓	×	×	×	×	×	✓	×	×
	POCKETS	✓	×	✓	×	×	×	×	×	×	×	×

Appendix 4.4. Detailed descriptions of the 11 RW types categorised from the rotten wood of *Eucalyptus obliqua* decomposing logs in wet eucalypt forest in Southern Tasmania

The rotten wood from decomposing *E. obliqua* logs was classified into 11 RW types, which are summarised in Table 4.1. A matrix of characters for each RW type is listed in Appendix 4.3. A series of photographs is also provided to illustrate the characteristic features of each RW type, and to display the colour and texture variations of RW types that varied in relation to their decomposition state. Upon visual assessment, RW types were strongly linked to one of the five designated regions of the log cross-section. Two RW types, fibrous surface rot and white jelly rot, were generally restricted to the top 1-5cm of the log surface. It is unlikely that this layer equates to bark, as this would have either completely disintegrated in logs at an intermediate stage of decomposition (Mackensen & Bauhus 1999); or for logs within the logged forest, it would have burnt away in the pre-sow burn (Slijepcevic 2001). This surface region most likely represents the original sapwood, especially as there was usually an abrupt change underneath this layer to harder more solid wood of heartwood appearance.

Four RW types were characteristically found in the outer heartwood of the log. These RW types are designated white stringy rot, white pocket rot, yellow dry slatey rot and brown cubic friable rot. The two white RW types are characterised by a typical and distinct 'white' rot appearance. The observed patterns of the two white rots indicate that decomposition is proceeding in a radial direction from the outer to the inner regions of the log (see Plates 4.3c-f, 4.4g, 4.5, 4.6d).

The innermost regions (inner heartwood) of the log were characterised by three RW types with a brown appearance; brown blocky crumbly rot, red brown blocky fibrous rot and brown mudgut rot. Decomposition associated with these RW types appeared to have originated central to the log and to extend outwards in an axial and radial direction (see Plates 4.9c, 4.9g, 4.11d).

Within many logs, substantial areas of wood were discoloured but still solid and hard. This type of wood is classed as discoloured wood. Cracks and fractures present in discoloured wood are called wet cracks.

Surface RW types

WHITE JELLY ROT

'White jelly surface rot' occupies the top 1 – 4 cm of the log surface layer. It is characterised by large (> 50 mm) irregular pockets filled with white, soft, very wet, gelatinous material (Plates 4.1a-c). The pockets can also be dehydrated (Plate 4.1c), which probably represents a later decay stage. A distinguishing feature of this rotten wood type includes black 'zone' lines, which demarcate the pockets (Plates 4.1a-c). Another feature is the presence of rhizomorphs, varying in colour from brownish red to black. *Ceratocystis moniliformopsis* sp nov. was also isolated from this RW type (Yuan & Mohammed 2002). *Armillaria* sp.is also considered associated with this RW type (Wardlaw, T. pers. comm.). This RW type can progress into the heartwood, as indicated by white lattice-like markings (Plate 4.1c), which further progresses into jelly pockets separated by areas of intact wood.

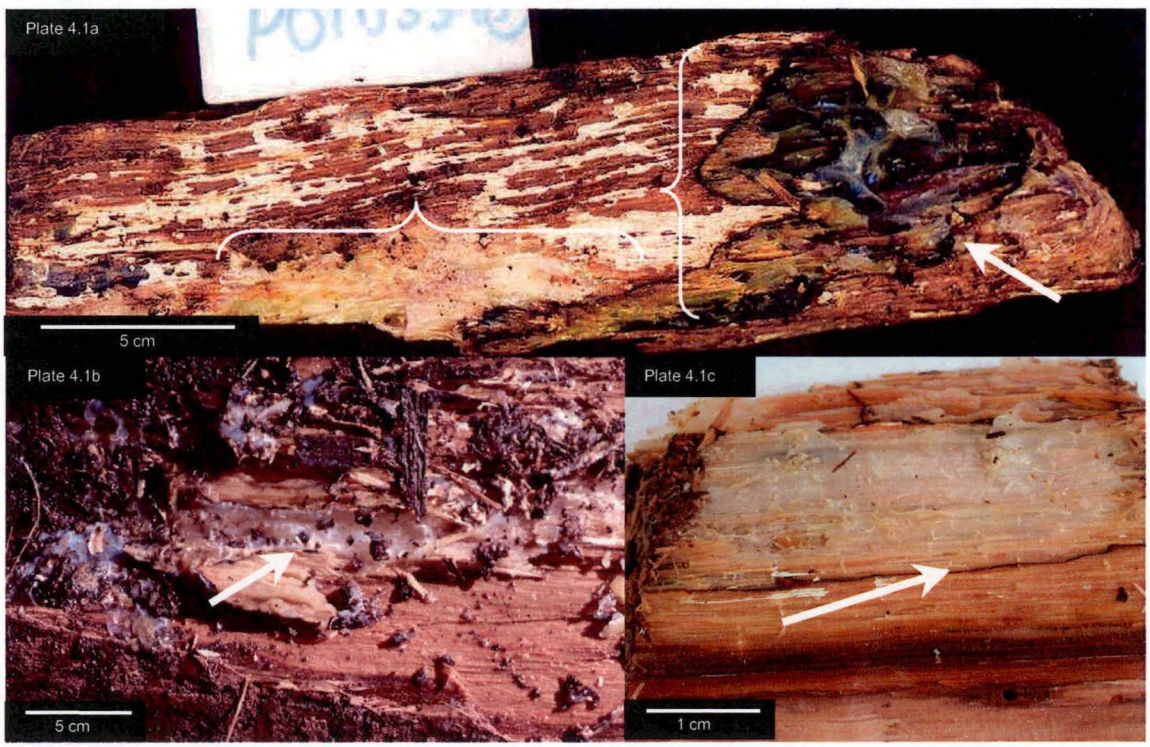


Plate 4.1. White jelly surface rot, showing a) large dehydrated gelatinous pocket with black zone lines demarcating the pocket, b) gelatinous pocket on log surface, and c) a close-up view, of pocket and black zone line. Arrows highlight the black zone lines.

FIBROUS SURFACE ROT

'Fibrous surface rot' can occupy the top 1 – 5 cm of the log surface layer. It has a soft stringy texture, with the colour ranging from grey, white to a deep straw, and sometimes brown (Plates 4.2a-e). The rotted wood seems to consist of numerous minute irregular pockets with soft bleached fibres speckled throughout it (Plates 4.2c-d). In comparison to the 'white jelly surface rot', 'white fibrous surface rot' has no black zone lines or rhizomorphs. This rot type appeared on occasion to extend into the outer heartwood – often yellow in colour.

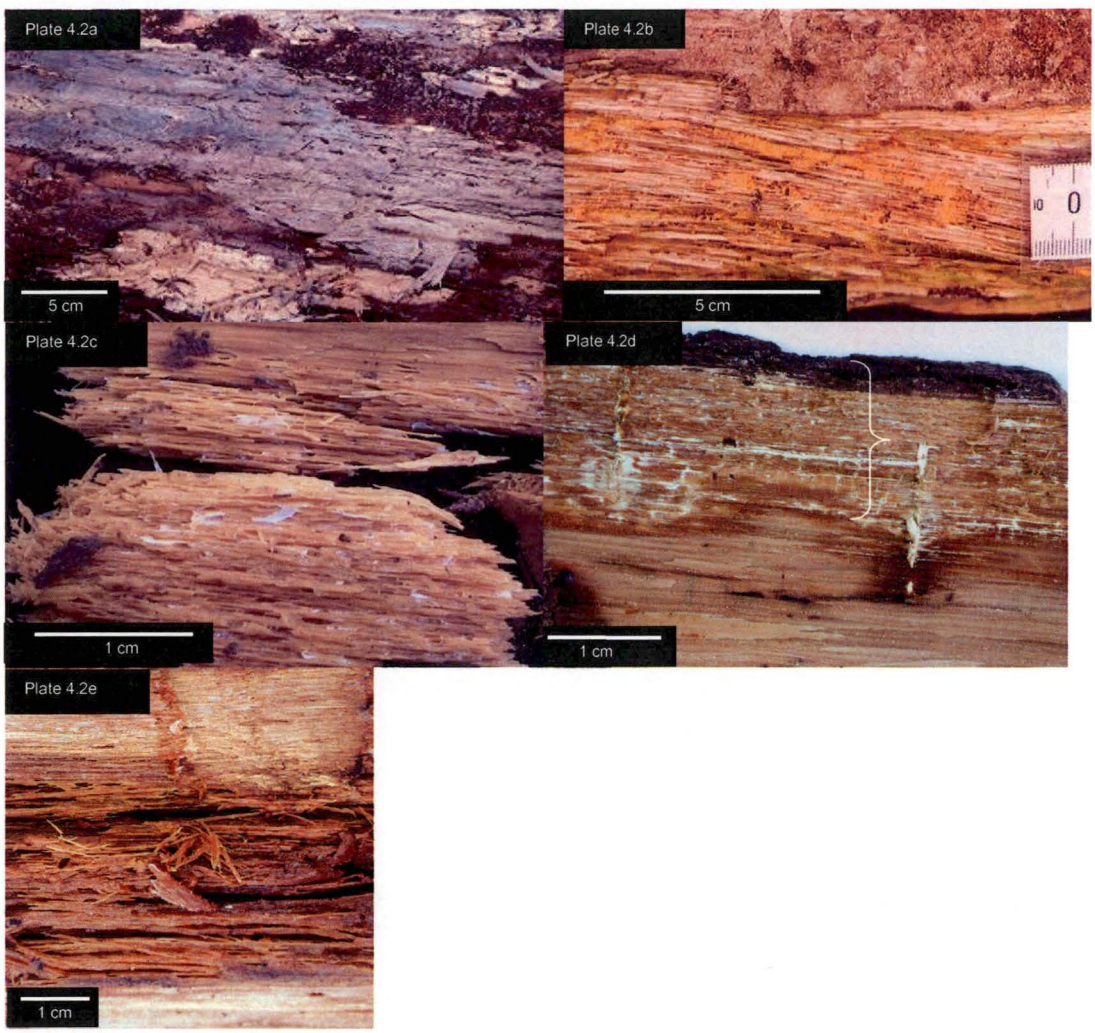


Plate 4.2. Fibrous surface rot on log surface, showing variations in colour a) grey to white to b) straw-yellow; and a close-up view of the c) speckled pattern of bleached white fibres. d) A close-up view of an earlier stage of this rotten wood type as it spreads from the log surface into the solid heartwood, and e) a later stage of this rotten wood type.

Outer Heartwood RW types

WHITE STRINGY ROT

'White stringy rot' is composed of continuous long spongey wool-like bleached-white fibres (Plate 4.3a). Crimson to dark brown coloured solid wood was always found adjacent to this rotten wood type (Plates 4.3b-f), and it seemed to be the incipient stage. The white fibres appear to spread into this crimson discoloured solid wood (Plate 4.3b-d). The same fungal species was isolated from both white stringy and discoloured solid wood forms (Z.Q. Yuan unpublished data). The location of this RW type was often found associated with the outer heartwood, and sometimes in contact with the log surface. Though columns of this RW type can be seen within the inner heartwood.

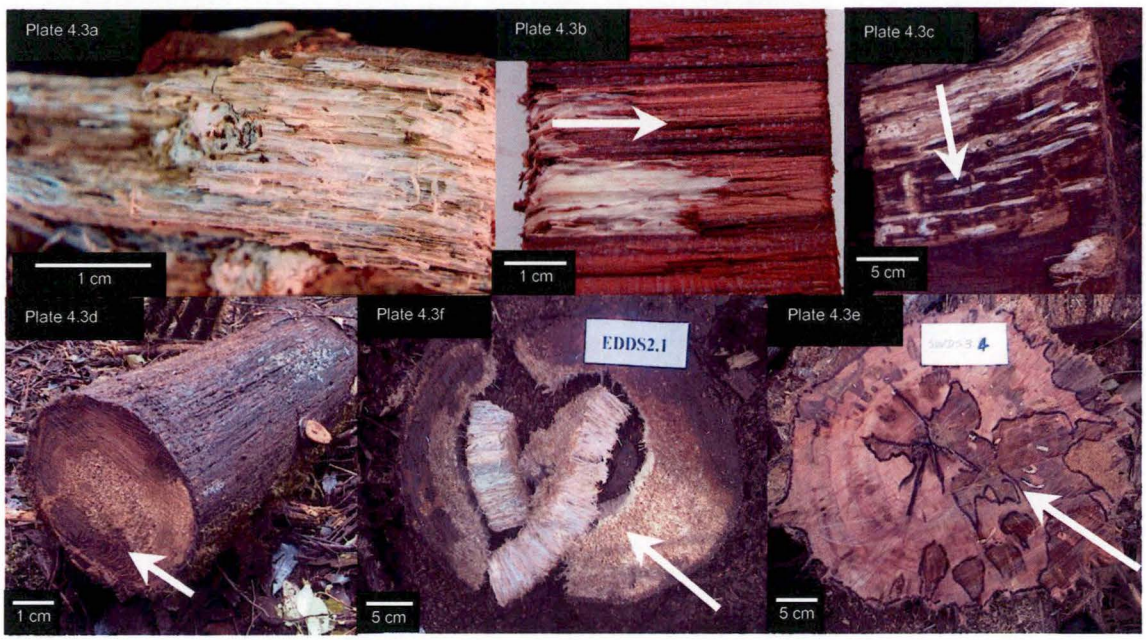


Plate 4.3. White stringy rot, showing a) a close-up view of the white long spongy wool-like fibres that spread b) axially and c) radially in the log. A view showing e) this rot type spreading into the log centre with f) dark brown discoloured heartwood or g) crimson discoloured solid wood adjacent to this rot type. Arrows show the direction in which the decomposition is spreading.

WHITE POCKET ROT

'White pocket rot' is characterised by 5 – 20 mm regular round to elliptical pockets (Plate 4.4a-f). These pockets are (1) filled with white spongy gelatinous material and appear white (Plate 4.4b,c) (2) are empty (Plate 4.4d) (3) are lined with white or yellow mycelium (Plate 4.4e). Pockets are separated by thin areas of seemingly intact wood. This rotten wood type mostly occurred on the outer regions of the log (Plate 4.4f,g).

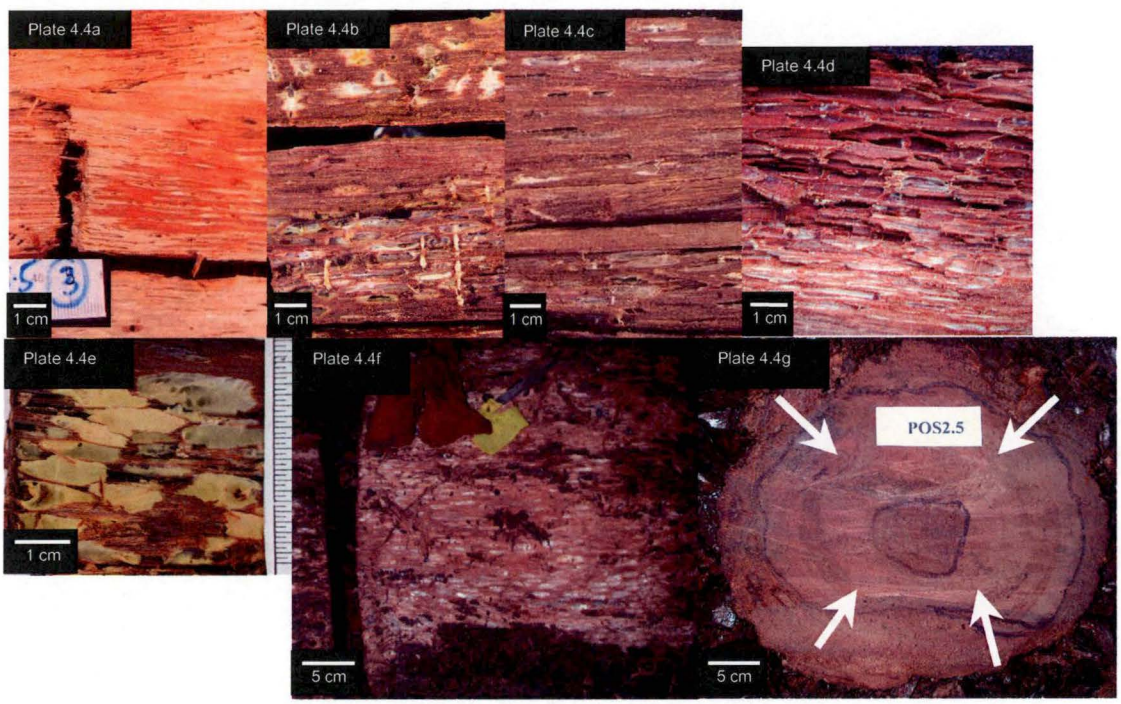


Plate 4.4. White pocket rot, showing a close-up view of a) elliptical pockets beginning to form b) round pockets and c) elliptical pockets filled with white gelatinous material, d) empty pockets and e) pockets lined with yellow mycelium. A view showing f) the rot pockets just beneath the log surface and g) the decomposition spreading from the log surface towards the centre, highlighted by arrows. In (g) the decomposed wood patterns are marked with a black outline

BROWN CUBIC FRIABLE ROT

'Brown cubic friable rot' is orange-brown coloured rotten wood that can be easily broken into 2cm wide cubes, and is easily crumbled to a friable mass in the hand. It was mostly found in patches on the undersides of logs (Plate 4.5).

Plate 4.5. Brown cubic friable rot spreading out from the underside of the log. The decomposed wood patterns are marked with a black outline.

YELLOW DRY SLATEY ROT

'Yellow dry slatey rot' is characterised by wood that superficially appears intact, but is dry, lightweight, brittle, and inclined to break along the growth rings (Plates 4.6a-d). The grain of the wood often has sheen like appearance. This is a rather homogenous RW type that occurs in the outer heartwood and greater heartwood regions.

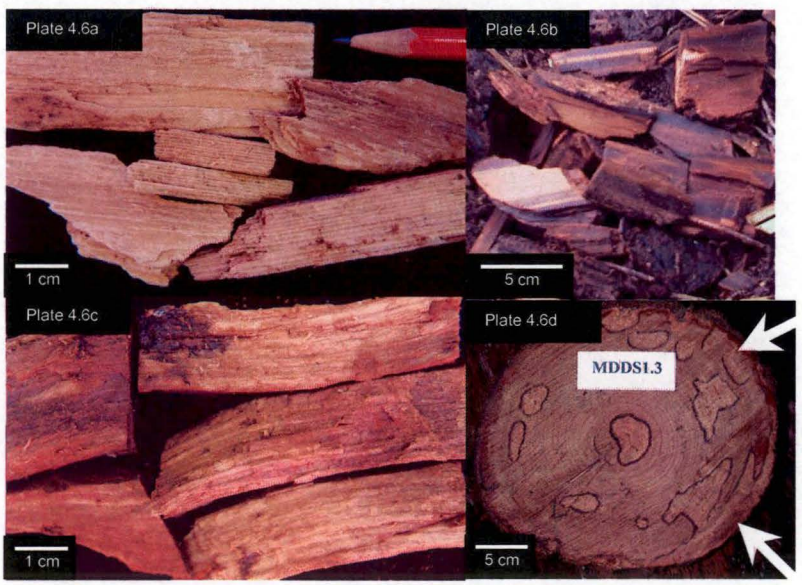


Plate 4.6. Yellow dry slatey rot, showing the a-c) brittle texture of the wood, where it breaks along the growth rings, and d) pattern of decomposition spreading out from the log surface. The decomposed wood patterns are marked with a black outline.

Heartwood RW type

DISCOLOURED WOOD

'Discoloured wood' comprises any wood that has been slightly discoloured, but still has the apparent physical structure of sound wood. Discolouration can vary from light pink, to yellow, or brown. The wood can have a grainy appearance (Plate 4.7a-c). Often present are insect pinhole borer galleries (2 – 3 mm wide), which are sometimes outlined by a black discolouration (Plate 4.7a). This possibly results from the mutualistic association between platypodid beetles and ambrosia fungi (Kile et al. 1991). Discoloured wood can occur throughout the outer and inner heartwood regions.

Plate 4.7. Discoloured wood, showing the a) black stained pinhole borer holes, and the variation in wood colour variation from yellow, to b) light brown and c) darker brown

Localised RW type

WET CRACKS

'Wet cracks' are defined as the wet cracks, splits or fractures within the log (Plate 4.8a,b), and these can occur along the wood grain or along the rays (Plate 4.8c,d). These cracks are probably caused by mechanical processes, such as internal stresses arising from the weight of the log. 'Wet cracks' have a thin film of moisture and detritus that lines the crack, which is dark brown to black in colour (Plate 4.8a,b).

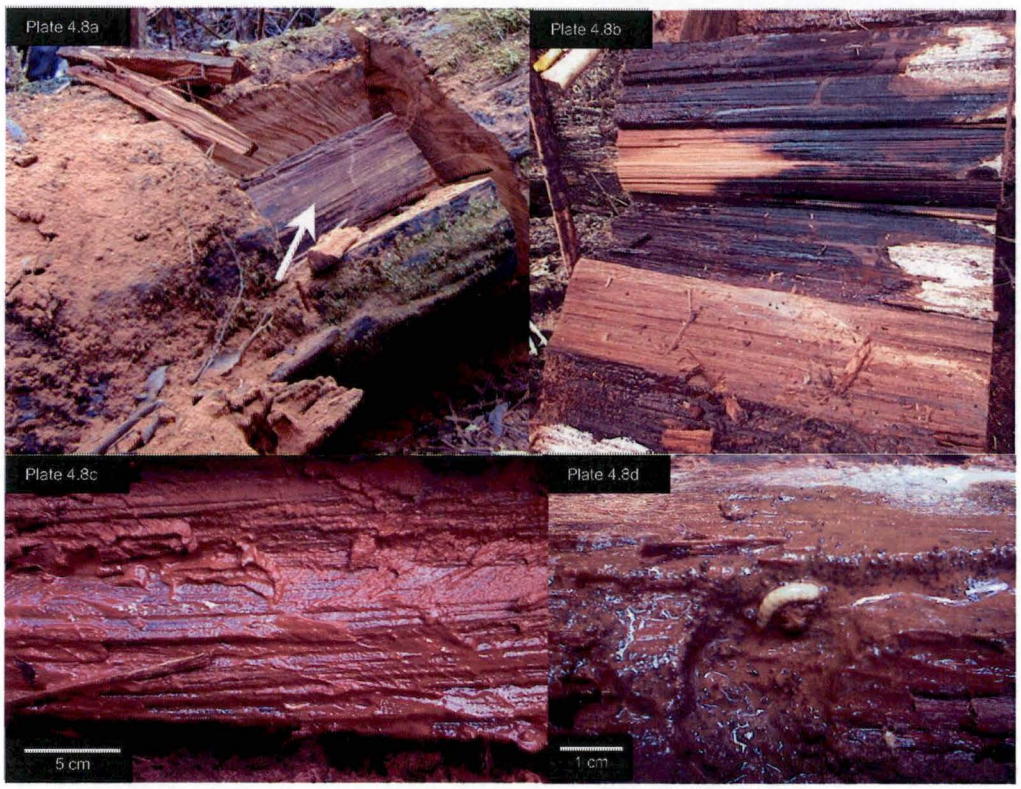


Plate 4.8. Wet cracks, showing a) the large fracture within the log, that sometimes has b) black discolouration. A close-up view of the wet cracks showing c) and d) wet detritus and muddy material that line the cracks.

Inner Heartwood type

BROWN BLOCKY CRUMBLY ROT

'Brown blocky crumbly rot' is characterised by wood that breaks off in regular blocks and can be crumbled by hand to a powder. This rotten wood type ranges between dry light brown blocky wood (Plate 4.9a) to a dark brown blocky wood (Plate 4.9b). Distinguishing features include either sheets of mycelium resembling a chamois-like texture (Plates 4.9c-d), or thick cheese-like sclerotia often found growing along the cracks, progressing along the rays (Plates 4.9e-f). This is possibly in response to the fungus moving along the path of least resistance and its exposure to oxygen (Mohammed, C. pers. comm.).

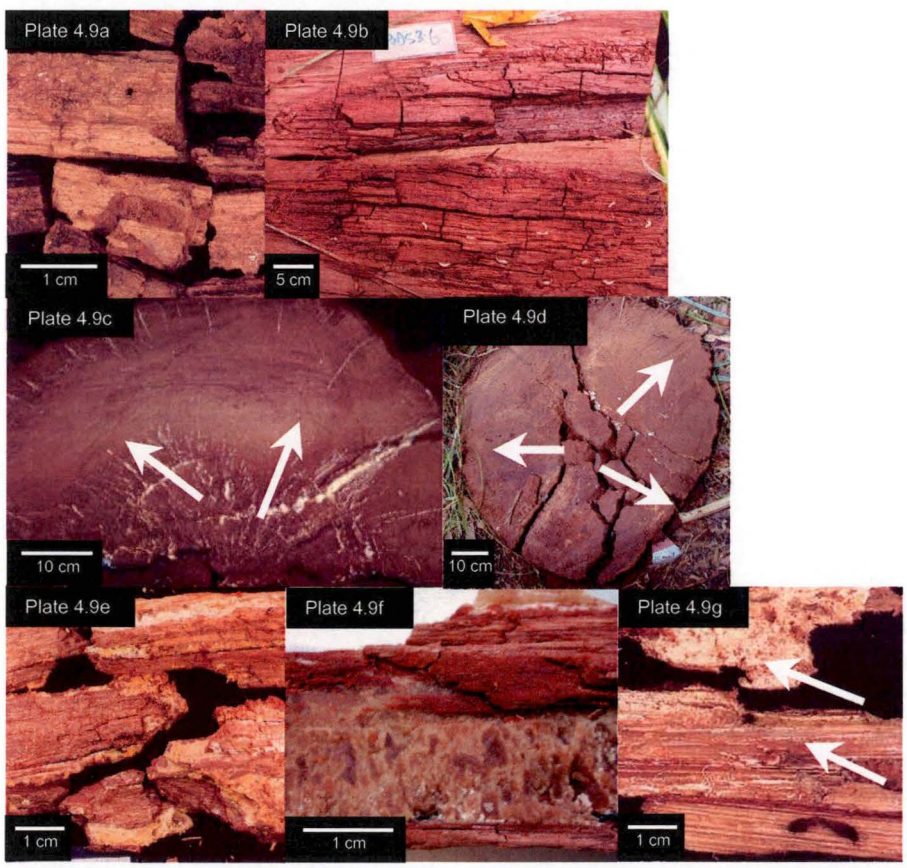


Plate 4.9. Brown blocky crumbly rot, showing a) the dry light brown blocks to b) wet dark brown blocks. A view shows c) the spread of decomposition from the log centre, with d) white mycelium growing along the rays. A close-up view shows the e) thick sheets of mycelium, f) thick cheese-like sclerotia and g) white threads found within bore hole along the rotted wood grain.

The latter fungal organ is known as 'poor man's bread'. Another feature is the presence of holes (<0.5mm diameter holes along the wood grain, which give the wood a speckled appearance when the wood is broken across the grain. These holes are filled with white

threads of an unknown substance (Plate 4.9d). These holes are possibly fungal derived 'bore' holes (Schwarze et al. 2000). This RW type occurs throughout the greater heartwood region, and but more decomposed wood occured in the central area of the log.

RED-BROWN-BLOCKY FIBROUS ROT

'Red-brown blocky fibrous rot' has a distinctive red-brown colour. It is different from the 'brown blocky crumbly rot' in that it breaks into irregular blocks, and maintains a soft fibrous, often relatively moist, texture rather than a crumbly, brittle one (Plate 4.10a-c). In less decomposed wood, the wood is hard yet the intact wood fibres can be teased apart (Plates 4.10d-e). In more decomposed wood, the fibres are more moist and soft, giving the wood a spongy texture. This rotten wood type was mostly found in the central area of the log, but it also occurred in localised patches, and occasionally in areas adjacent to the 'brown blocky crumbly rot' (Plate 10f).

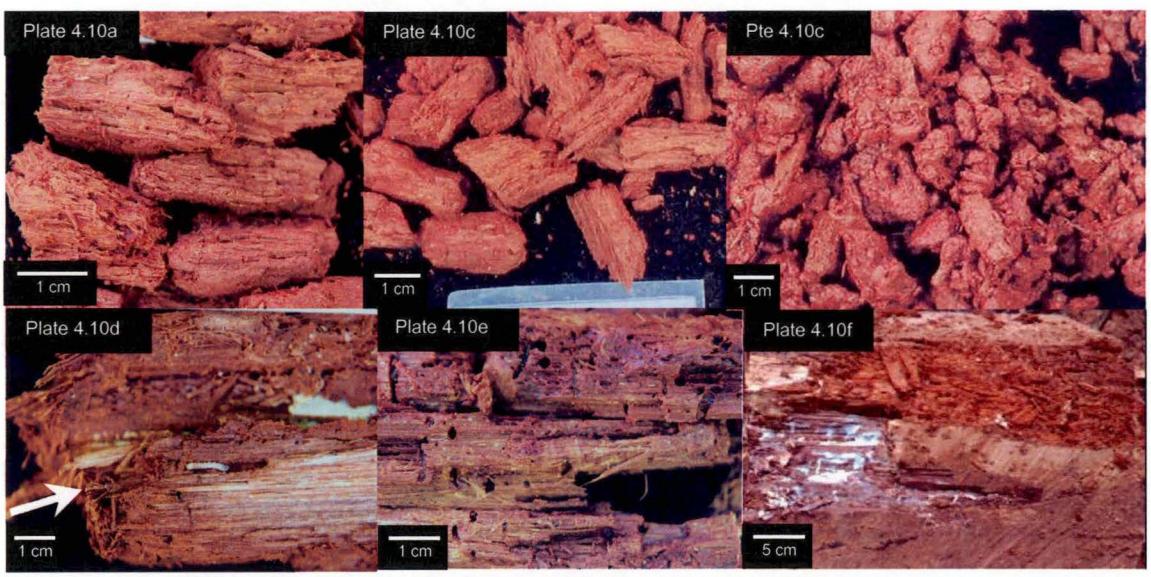


Plate 4.10. Red brown blocky fibrous rot, showing a close-up view of a) the soft fibrous irregular blocks to b) a more decomposed state, progressing to a c) wetter and mud-like texture. A close-up view d) of this rot at an early stage of decomposition, where e) wood fibres can be teased from the more intact wood. A view of f) red brown blocky fibrous rot found adjacent to brown blocky crumbly rot

BROWN MUDGUT ROT

'Brown mudgut rot' has a characteristic wet mud- to clay-like consistency, which appears devoid of any recognisable wood fibres (Plate 4.11a-c). This rotten wood type mostly occurred in the internal heartwood of logs (Plate 4.11d), sometimes associated with a hollow. But, it was also found in localised patches in the outer heartwood. 'Brown mudgut rot' was often found adjacent to the 'red brown blocky fibrous rot', possibly indicating some kind of association or succession.

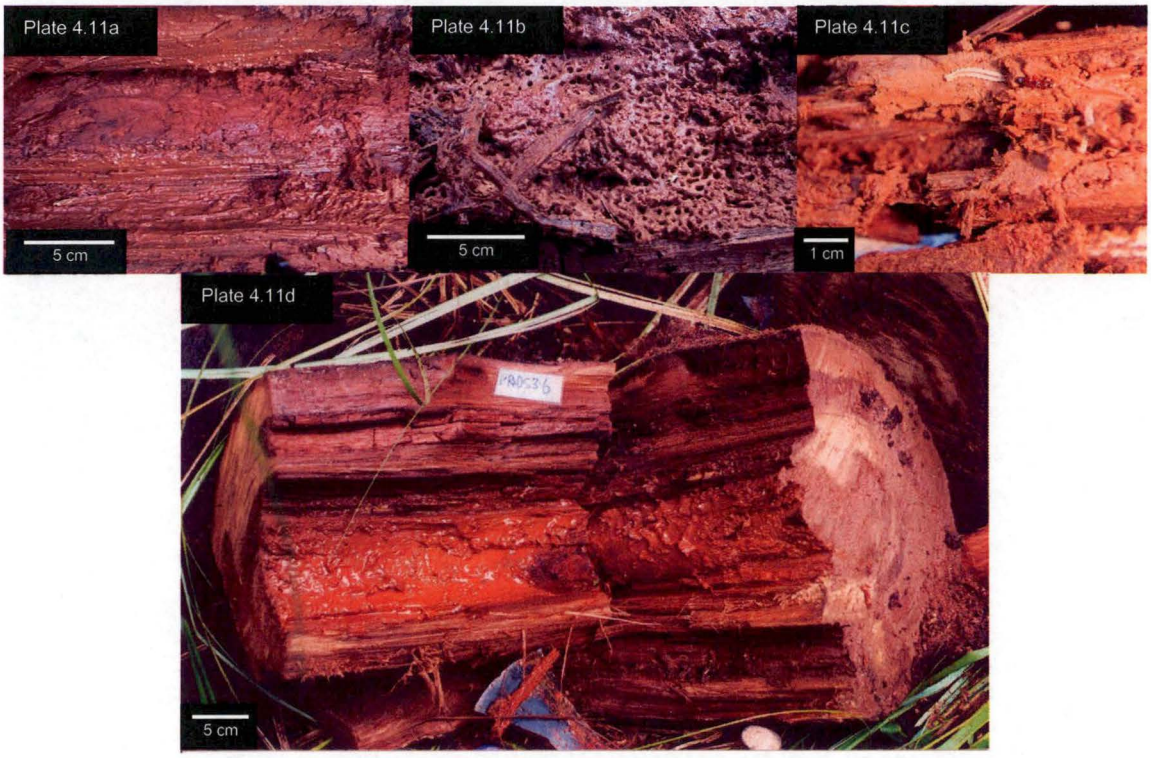


Plate 4.11. Brown mudgut rot, showing close-up views of a) red-brown wet detrital material, ranging from b) mud-like to c) clay-like consistency. A view shows d) brown mud gut rot within the log centre.

Appendix 4.5. Methods for chemical analyses,

Moisture content measurements of rotten wood samples were calculated by dividing the difference in original wet weight and dry weight, over original wet weight. Dry weight was measured after oven drying samples at ~80° C to a constant weight. For carbon and nitrogen, over 10 g of the oven-dried samples used for moisture content analyses were ground to a fine powder using a wood grinder (Thomas Wiley Laboratory Mill, Model 4). Nutrient analyses involved measuring percent N and percent C. Dried wood samples were sent away to the Plantation Research Centre at CSIRO-Forestry and Forest Products in Mount Gambier, South Australia. Samples were analysed using the Dumas technique, using a Leco CNS2000.

Dumas technique is as follows: for each sample, 0.200 g of wood is combusted in pure O_2. The combustion gases are collected and entrained into helium gas. All N by-products are passed through a copper catalyst column to convert them all to N_2. This is then quantified using a thermal conductivity cell. For carbon concentrations, the dry combustion gasses are passed through an Infra-red cell to measure the amount of CO_2. For these analyses, calibration was done with high purity EDTA of varying masses to validate the regression.

Appendix 4.6. Moisture and chemical data for rotten wood types of *Eucalyptus obliqua* logs at an intermediate decomposition stage. NM = number of wood samples used for moisture measurements. NC = number of wood samples used for C and N measurements.

ROTTEN WOOD TYPES	% Moisture content (mean ± SD)	NM	% Carbon (mean ± SD)	% Nitrogen (mean ± SD)	C/N ratio (mean ± SD)	NC
White jelly rot	57.31 ± 10.03	31	55.15	0.0580	950.7	1
Fibrous soft rot	58.99 ± 14.26	43	49.41	0.1143	432.4	1
White pocket rot	56.77 ± 14.13	14	50.39 ± 2.78	0 1057 ± 0.0411		8
White stringy rot	52 97 ± 9.31	31	47.65 ± 0 17	0 1373 ± 0.0052	347 ± 12	2
Yellow slatey dry rot	44 46 ± 13 23	26	47.16 ± 0.72	0.0318 ± 0.0104	1591 ± 455	4
Brown cubic friable rot	64 89 ± 13 80	22	52.50 ± 1.98	0.1059 ± 0.0233	520 ± 130	12
Discoloured wood	51 54 ± 9 40	122	50.06 ± 3 30	0 1032 ± 0.0625	595 ± 273	3
Wet cracks						
Brown blocky crumbly rot	61.73 ± 13.40	51	50 09 ± 2.44	0 0829 ± 0.0553	777 ± 321	14
Red brown blocky fibrous rot	61.06 ± 8 26	47	48.34 ± 1.60	0 0825 ± 0.0517	800 ± 499	29
Brown mudgut rot	77.09 ± 8 53	38	51.72 ± 1.91	0.1208 ± 0.0598	538 ± 263	28

5 ROT TYPE HABITAT REQUIREMENTS OF SAPROXYLIC BEETES: THE EFFECT OF LOG SIZE

ABSTRACT

Studies frequently show that large diameter logs generally host saproxylic beetle assemblages different to that of small diameter logs. In a study in Tasmanian wet eucalypt forest, two size-classes of *Eucalyptus obliqua* logs (>100cm and 30-60cm diameter) were destructively sampled to assess their beetle fauna and the associations of this fauna with decomposing wood. Ninety species were collected as adults from 42 logs; at least 19 species were also collected as larvae. The two log size-classes differed in beetle assemblage composition. These differences could be explained by the observation that certain beetle species were associated with specific successional phases of decomposing wood (rotten wood types). Those that were preferentially found in brown rotted heartwood, which was common in large diameter logs, were rare or absent in small diameter logs. This rotten wood type seems to be a relatively stable microhabitat and accordingly, the four most strongly associated species (in the genera *Cossonus, Dryophthorus, Prostomis* and *Pycnomerus*) seem likely to have low dispersal ability. Although relatively common in this habitat, each belongs to a genus whose European counterparts have undergone drastic range reductions. Our research highlights the importance of a degree of landscape level planning in Tasmanian forestry which would maintain sufficient large diameter logs in the landscape over the long term.

5.1 INTRODUCTION

Saproxylic beetle assemblages have been studied in many forest ecosystems, including the boreal forests of Scandinavia (reviewed in Siitonen 2001) and Canada (Hammond *et al.* 2004), the temperate forests of Germany (Kleinevoss *et al.* 1996), and the Douglas fir forests of the Northwest U.S. (Edmonds & Marra 1999; Maser & Trappe 1984). These studies demonstrate that large diameter logs host specific saproxylic beetle assemblages that are different from those found in smaller sized logs. The ecological processes that shape these assemblages and create the differences between large and small diameter logs are not well understood. One possibility is that differences in the decomposition pathways in large and small diameter logs, resulting in differences in rotten wood types that potentially represent different microhabitats, may influence the saproxylic beetles assemblages within those logs.

Rotten wood is defined here as wood that has undergone some degree of decomposition. Decomposition results from either one or a combination of biotic and abiotic agents (Harmon *et al.* 1986). These include mechanical, physical-chemical processes, and the physical and metabolic actions of various organisms (Kaarik 1974; Kirk & Cowling 1984; Swift 1977). They include bacteria (Clausen 1996), xylophagous arthropods (Carpenter *et al.* 1988; Edmonds & Eglitis 1989), basidiomycete and ascomycete fungi, and micro-arthropods (Ausmus 1977; Seastedt 1984; Sollins *et al.* 1987; Swift 1977). Depending on the types of processes and organisms, the physical, chemical and biological wood properties change in a specific way (Rayner & Boddy). This gives rise to a specific rotten wood type that can be described by its wood microstructure and chemistry, relative density, moisture content and nutrient levels (Ausmus 1977; Christensen 1984; Harmon *et al.* 1986; Swift & Boddy 1984). To illustrate, brown rotted wood arises when 'brown-rot' fungi selectively remove cellulose and hemicellulose from the wood, leaving a residue of slightly modified lignin. By contrast, 'white-rot' fungi utilise all components of the wood cells, removing lignin, cellulose and hemicellulose and leaving the wood bleached, with a spongy, stringy or laminated structure (Kaarik 1974).

Investigations of the rotten wood types within decomposing *Eucalyptus obliqua* logs clearly established that large (>100 cm diameter) and small (30-60 cm diameter) logs at

an intermediate decomposition stage differ in both type and spatial arrangement of rotten wood (Chapter 4). Eleven distinct rotten wood types have been classified within these logs. Although little is known of the actual decomposition processes or of the organisms involved, each type may results from a specific decomposition pathway and potentially provides a unique microhabitat for saproxylic beetles. Large diameter logs have a higher frequency of brown rotted heartwood occurring within the log centre. In small diameter logs, white rotten wood commonly occurs in the outer regions of the log. The presence of the different types of rotten wood demonstrates differing decay processes occurring in each size class of log. In large diameter logs internal decay probably established when the tree was alive, as heartrot is frequent in large old trees. Younger (smaller diameter) trees are less likely to give rise to logs with pre-existing heart rot, but such logs were more frequently rotted in their outer regions.

Many saproxylic beetles are specially adapted to and intimately associated with the microhabitats and microclimates that occur in rotten wood (Dajoz 2000, Gilbertson 1984, Haack & Slansky, 1987; Lawrence 1989, Speight, 1989). For instance, in Japan the lucanids *Ceruchus lignarius* and *Aesalus asiaticus* occur more frequently in wood decomposed by brown rot fungi, whilst *Platycerus acuticollis* prefers wood decomposed by soft rot fungi (Araya 1993). Some beetle species rely on the actions of certain wood decay fungi to process and precondition the wood. Fungi can provide metabolic water and vitamins necessary for insect development, and they can produce enzymes for cellulose digestion that can be ingested and then taken up by insects living within the wood. Fungi can detoxify wood that contains toxic or repellent allelochemicals, or decompose the wood to a softer and more chewable resource that can be more readily assimilated (Hanula 1996; Swift & Boddy 1984).

Saproxylic beetles may also be indirectly associated with one or more rot types through their dependence on organisms that are more intimately associated with a specific type of rot (Dajoz 2000; Speight 1989). For example, some elaterid beetles specifically prey on tipulid flies that only live in the moist wood invaded by white rot fungi (Dajoz 2000). The European *Elater ferrugineus* (Elateridae) is a predator of scarabaeid beetles that occurs in the red rotted wood of old trees (Svensson *et al.* 2004).

This study investigates the saproxylic beetle assemblages found in large and small diameter logs in the wet eucalypt forest of Tasmania, with the aim to determine whether the differences observed in the beetle assemblages between two log diameter classes could be explained by associations between beetle species and rotten wood types specific to a log size class.

5.2 METHODS

5.2.1 Study location and experimental design

Research was conducted at seven study sites in wet eucalypt production forests in southern Tasmania. Four (designated as study sites H, E, S, PR2) were 20-30 yr CBS logging regeneration of one harvesting event and the other (designated as M, WR and PO1) were in mature unlogged forest. The influence of forest type on saproxylic beetles was not analysed in this study, but is reported in Chapter 6. Study site locations and descriptions are described in Section 2.2 and 2.3. Within each study site, three pairs of large diameter (>100 cm) and small diameter (30-60 cm) *Eucalyptus obliqua* logs of an intermediate decomposition stage (defined in Section 2.5) were destructively sampled. Names and diameters of the study logs are listed in Table 2.2.

5.2.2 Sampling method

Two 1 m sections were destructively sampled from each log, with one to two hours being spent sampling each log section. Destructive sampling involves intensively searching and hand collecting adult and larval saproxylic beetles inhabiting a log, as well as surveying the rotten wood types within the log. The method for collecting, sampling, and identifying beetles is described in Section 2.6.1. This included collecting additional samples of larvae with host material for rearing to adulthood, to allow identification and to observe life history.

The rot types present within each section were categorised into one of 11 previously characterised Rotten Wood (RW) types. See Table 4.1 for a summary RW types, and see Appendix 4.4 for detailed descriptions of each type. The classification system for RW types of *Eucalyptus obliqua* logs had been developed alongside this study (see Section 4.3.2), on the basis of colour, texture, hardness and 'RW region'. RW region to some extent indicates where decomposition may have started, for example, within the

log or on the log surface. This was based on the consistent spatial association of a rot type with one of five regions within the log cross-section, and the direction from which the decomposition appeared to be spreading. The five regions specified were surface (sapwood), outer heartwood, inner heartwood, localised pockets from which the decay did not appear to spread, and throughout the heartwood (see Figure 4.3). Colour was taken as indicative of the predominant type of fungal decay in process at the time of sampling: a 'white' or a 'brown' rot.

5.2.3 Statistical analyses

5.2.3.1 Data and general statistical technique

Presence-absence data were used instead of abundance because it was considered more relevant for determining a species' association with RW type. Sampling absolute numbers of beetles within 1m long sections of solid to rotten wood was well beyond the scope of the study. More importantly, using presence/absence data reduced the influence a species' breeding strategy and aggregative behaviour can have on the result. For example, species such as *Prostomis atkinsoni* have a gregarious/colonial life history with populations of over 20 individuals within a handful or rot, while elaterids are solitary. The presence of either species equally indicates a positive association with a unit RW type within a log.

Although the amount of wood sampled varied between logs, beetle presence/absence data were not standardised by the amount of rot area or volume sampled as 1) it was considered that the confounding issues with sampling effort would be less important than if abundance data were used, 2) other than rarefaction techniques, which compares number of species standardized by sampling effort, methods to compare species assemblages standardised by sampling effort were unknown, and 3) because the volume of wood sampled for large diameter logs was limited to $1/8^{th}$ of the 1m long log section, the volume of wood sampled from large diameter logs did not grossly differ to that of small diameter logs (see Table 2.2.)

Many larvae could not be identified even to family level, were seldom encountered, yet may be the larval stage of some sampled adult beetle species. Therefore, species occurring only as larvae were documented separately and excluded from statistical

analyses. Larval elaterids and scirtids were the exception. They were included because for these families, only larvae inhabit the log so there was no risk of double-counting. Furthermore, elaterids and scirtids are a common and important component of the saproxylic community, and are relatively easy to identify to family and morphospecies.

Two multivariate statistical methods were used, Non-metric Multidimensional Scaling (NMS) and Multi-Response Permutation Procedures (MRPP). NMS is a non-parametric ordination technique that relates the similarity of entities (e.g. logs or rotten wood samples), based on ranked distances, in multidimensional space (McCune & Grace 2002). NMS was performed using a Sorensen (Bray-Curtis) distance measure, in *PC-ORD* (McCune & Mefford 1999), choosing the 'slow and thorough autopilot' mode. MRPP in *PC-ORD* is a non-parametric method that uses permutation procedures for testing the hypothesis of no difference between two or more *a priori* groups based on multi-species data. This method provides a test statistic, T, which describes the separation between groups: the more negative the T, the stronger the separation. It also provides a p-value, which evaluates whether the observed difference is greater than expected by chance. As recommended in the program, the method was run on an Euclidean distance measure and used the natural group weighting of n/sum (n).

5.2.3.2 Comparison of beetles between log diameter classes

The frequency of occurrence of individual beetle species was compared between large and small diameter logs, using Chi-square analyses. Data comprised the presence-absence of a species within a log, pooled from all RW types from both log sections. Only common species (occurring in more than 25% logs) were analysed. Beetle assemblages in large and small diameter logs were graphically compared using NMS. Beetle species occurrences and RW type vectors were overlaid onto the ordination as a joint plot. RW type data comprised the presence-absence of RW types within a log, pooled from the two 1 m-long sections. MRPP were used to test for differences in beetle assemblage composition between log size-classes.

5.2.3.3 Beetle species incidence, richness and diversity associated with RW types

Beetle species incidence was defined as the proportion of units or rotten wood/log sampled in which a saproxylic beetle was found. This analysis highlights the habitat suitability of RW types standardised by number of RW units sampled.

Species richness was defined as the total number of new saproxylic beetle species associated with a RW type. A one-way ANOVA was used to investigate differences in species richness among RW types, and a follow-up multiple comparison test (Ryan-Einot-Gabriel-Welsch Multiple Range Test: REGW test) was used to determine the nature of these differences. Data comprised number of species per RW type per log (i.e. pooled from both 1-m log sections). Data were first tested for homoscedascity and normality, and subsequently log-transformed to meet the assumptions of the ANOVA. Units of rotten wood with zero beetles were omitted from this analysis. I excluded RW types per log with zero beetles as beetle absence may have been a reflection of other factors such as proximity off the ground, rather than the RW type within the log *per se*.

Species diversity was defined as the mean number of species within a unit of RW type/log.

5.2.3.4 Beetle associations with RW types/regions

Individual beetle species and assemblages were investigated for their association with RW types. Data comprised the presence-absence of species within a RW type, pooled from both log sections. Since many species were absent from over 20% of RW types per log, many standard statistical analyses, such as Chi-square analysis, would not have been reliable. Therefore interpretation of this aspect is limited to a discussion of observed trends on larval feeding and on species associations with rotten wood. NMS was used to determine whether RW types were characterised by similar beetle assemblages. MRPP were used to test whether the assemblages within rotten wood differed significantly among RW types. As RW region was found to be an important difference between large and small diameter logs, species associations with RW region were also examined by overlaying RW region onto the ordination plot instead of RW

type, and by testing group differences using MRPP. Beetle species vectors were also overlaid on the ordination plot as a joint plot.

5.3 RESULTS

In total, 94 species of adult beetles from 23 families were collected (Appendix 5.1). The most species-rich families were Staphylinidae (16 species), Curculionidae (12 species) and Carabidae (12 species). At least 19 of these species were also collected as larvae (Appendix 1), their identities being confirmed following successful larval rearing. Only 14 species occurred in over 25% of logs, and all of these were collected in both life stages, except Aleocharinae TFIC sp 34 (Staphylinidae) and *Exeiratus* TFIC sp 01 (Curculionidae), which were only collected as adults. In total, 27 morphospecies were collected as larvae only (Appendix 5.2). Some of these may have represented the larval stages of species also collected as adults. However, those larvae identified as species in the families Lycidae, Cantharidae, Cleridae and Melandryidae were not represented in the collection as adults. However, many of these larvae were only represented as singletons.

5.3.1 Comparison of beetles between log diameter classes

Sixty-three species of adult beetles were collected from large diameter logs and 65 from small diameter logs, with 38 species common to both. Of the 14 species that occurred in over 25% of logs, *Cossonus simsoni* (Curculionidae) occurred only in large diameter logs, and *Pycnomerus* TFIC sp 02 (Zopheridae) and *Coripera deplanata* (Tenebrionidae) were significantly more frequent in large diameter logs than in small ones ($p = 0.013$ and 0.0278 respectively) (Figure 5.1). Meanwhile, *Enneaphyllus aeneipennis* (Cerambycidae) only occurred in small diameter logs.

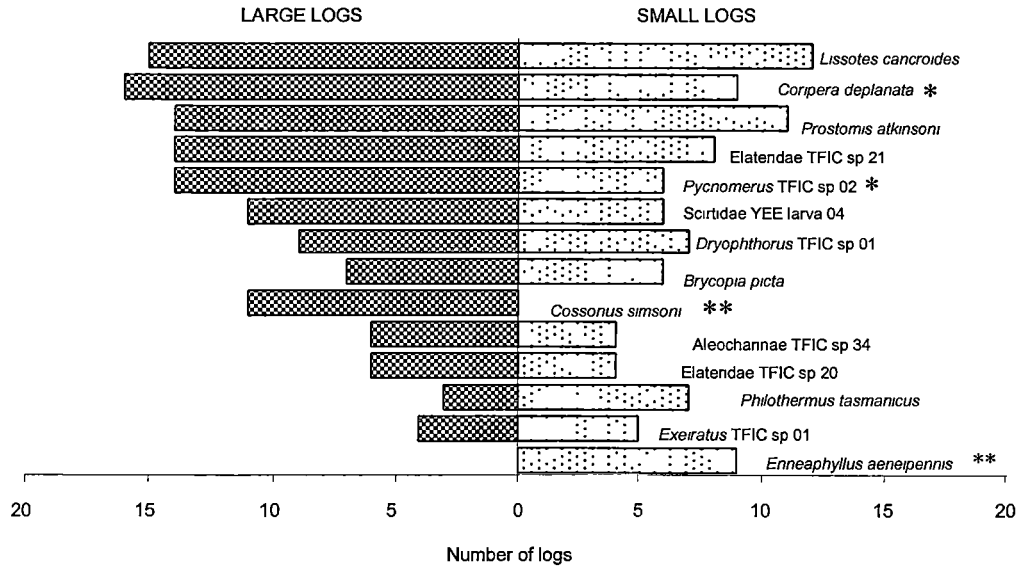


Figure 5.1. Frequency of common (> 25% of logs) saproxylic beetles found in 21 large (left) and 21 small (right) *Eucalyptus obliqua* logs at an intermediate decomposition stage. Species whose occurrences differed significantly ($p<0.05$) between the two log size-classes are denoted by *, while those exclusive to a particular log size-class are denoted by **

Results from the NMS (Figure 5.2a,b) and MRPP together showed that large and small diameter logs differed significantly in their beetle assemblages (Figure 5.2b, separation along Axis 3; $p = 0.001$, $T = -4.5$). Ten small diameter logs were clearly different from the cluster of large diameter logs. Overlaying the beetle species onto the ordination plot revealed that *Enneaphyllus aeneipennis* had a strong influence on this pattern, correlating with Axis 3 ($r^2 = 0.65$). Several species correlated in the opposite direction: *Prostomis atkinsoni* (Prostomidae) ($r^2 = 0.31$), Elateridae TFIC sp 21(Elateridae) ($r^2 = 0.24$), *Dryophthorus* TFIC sp 01 (Curculionidae) ($r^2 = 0.25$), *Pycnomerus* TFIC sp 02 (Zopheridae) ($r^2 = 0.20$) and Scirtidae YEE sp 04 (Scirtidae) ($r^2 = 0.23$). Two RW types, 'brown mudgut rot' and 'wet cracks', which are both wet RW types, also correlated with this axis ($r^2 = 0.24$ and .20 respectively).

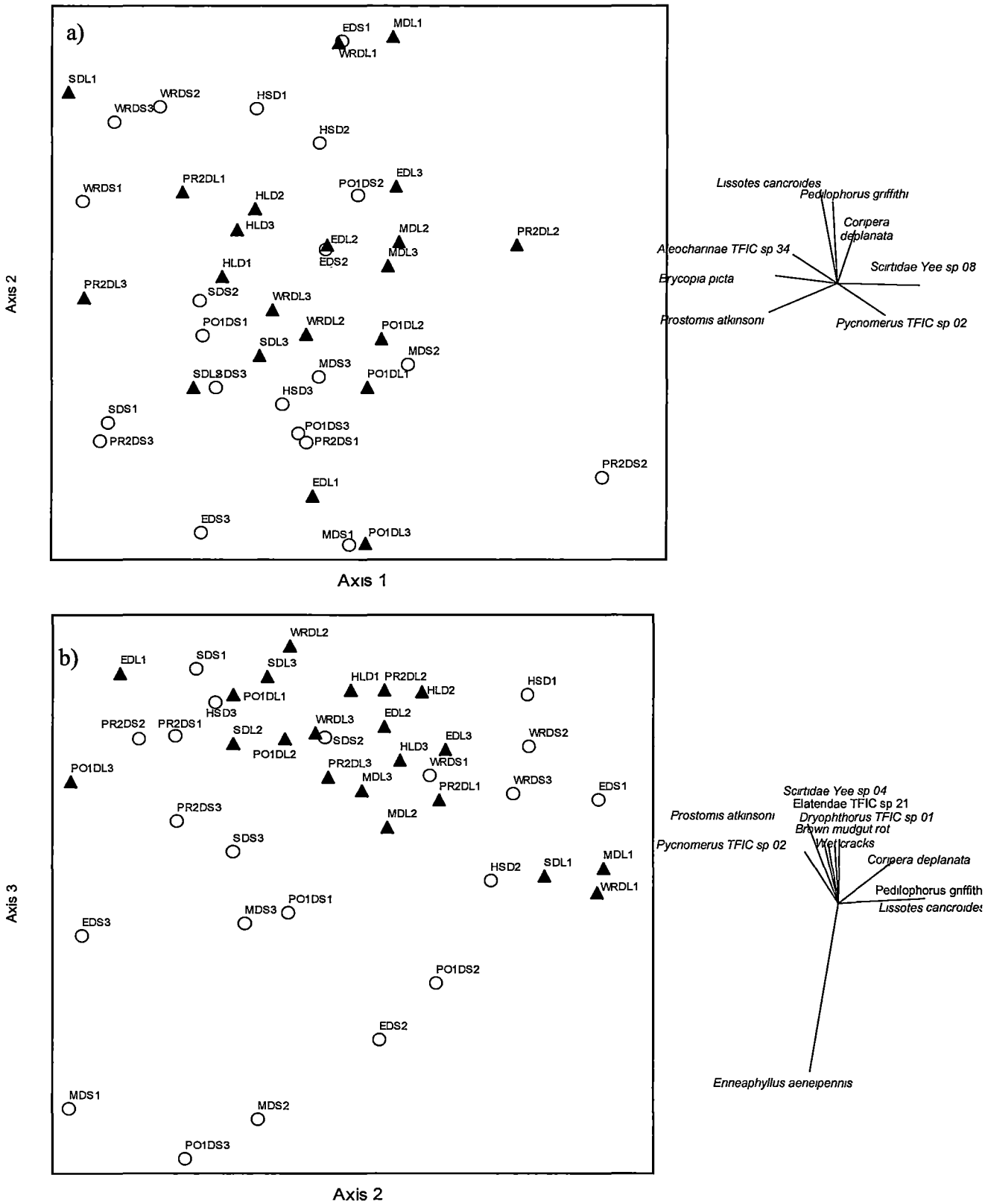


Figure 5.2. NMS ordination showing saproxylic beetle assemblages from 21 large (▲) and 21 small (O) *Eucalyptus obliqua* logs. (a) axes 1 and 2; (b) axes 2 and 3. Based on presence-absence data for saproxylic beetle species pooled from two 1m long sections per log (single occurrences were excluded). Alphanumeric codes are log names. Vectors based on beetle species occurrence and rotten wood type (refer to Table 4.1) are overlaid as a joint plot; for greater clarity, these are displayed adjacent to the ordination. Stress = 0.18, p = 0.0196. Vector scaling 100%. Only vectors with r^2 >0.2 are shown

5.3.2 Incidence, species richness and diversity of saproxylic beetles within RW types

The 'brown' inner-heartwood RW types (red-brown blocky fibrous and brown mudgut rot) and surface/sapwood-fibrous soft rot had a high incidence of beetles (Figure 5.3). Saproxylic beetles were found in atleast 80% of the rotten wood units/log of fibrous surface rot and brown mudgut rot sampled. Furthermore, both fibrous surface rot and brown mudgut rot were the most species rich, with almost 50 and 40 species respectively associated with these RW types (Figure 5.4). Of the logs that beetles had colonised, brown mudgut rot had the highest diversity of beetles, with an average of 6 to 7 species per log (Figure 5.5; $F_{10,104} = 2.06$, $p = 0.03$).

By contrast, only 40% at most of the white jelly rot, wet cracks, white pocket rot, white stringy rot and brown blocky rot units of rotten wood/log sampled had a saproxylic beetle. The yellow slatey dry rot was the least favourable microhabitat types, having the lowest incidence of beetles, with only two individuals collected from this RW type.

5.3.3 Beetle associations with RW types and regions

The relative frequencies of individual species differed among RW types. No species was restricted to a single RW type but some were more common for either a RW region or for an amalgamation of RW types into decay type (white or brown) (Table 5.1). For example, the xylophagous species *Dohrnia simplex* (Oedemeridae), *Dryophthorus* TFIC sp 01, *Prostomis atkinsoni, Cossonus simsoni* and *Pycnomerus* TFIC sp 02 were more common in the brown rotten heartwood (inner) types, whilst *Enneaphyllus aeneipennis* exclusively occurred in the white outer heartwood RW types. Two further xylophagous species *Coripera deplanata* and *Lissotes cancroides* (Lucanidae) were more common in the surface (sapwood) rotten wood than in other log regions, but their occurrence also extended into the brown rotted heartwood (inner). The saprophagous species Scirtidae YEE sp 04 (Scirtidae) was more common in the very wet RW types ('wet cracks' and 'brown mudgut rot'). The xylophagous *Syndesus cornutus* (Lucanidae) was exclusive found in brown rot, where many larvae were found feeding within brown rotted wood that was either cubic or crumbly, and occurring in either inner or outer heartwood.

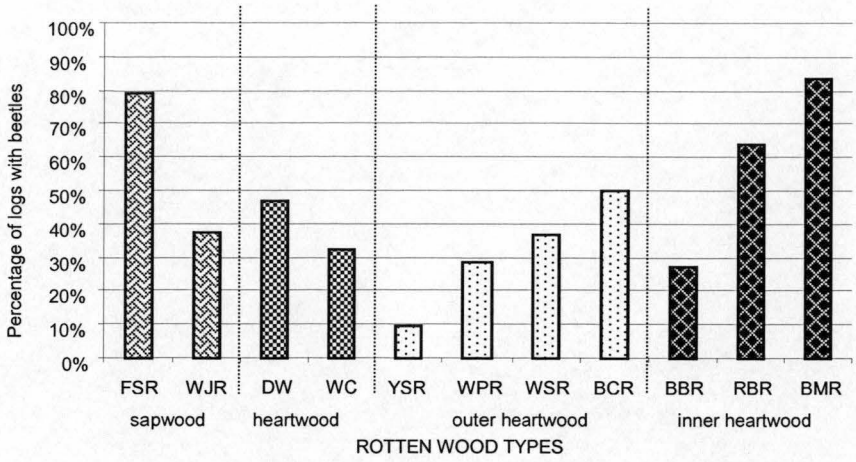


Figure 5.3. Proportion of RW types with saproxylic beetles present. Data uses presence/absence of beetles within RW type, pooled from two 1-m log sections per log. RW types are abbreviated as WJR – white jelly surface rot, FSR – fibrous surface rot, YDR – yellow dry slatey rot, WPR – white pocket rot, WSR – white stringy rot, BSR – brown spongy cubic rot, BDW – brown discoloured wood, RBR – red brown soft blocky fibrous rot, BBR- brown blocky crumbly rot, BMR – brown mudgut rot, and WC – wet cracks

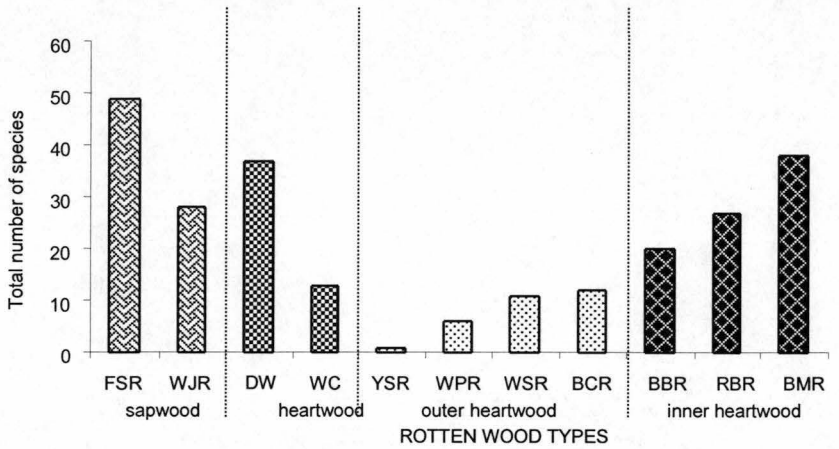


Figure 5.4. Total number of saproxylic beetle species found in each RW type, pooled across all logs. Rotten wood type abbreviations are the same as in Figure 5.3.

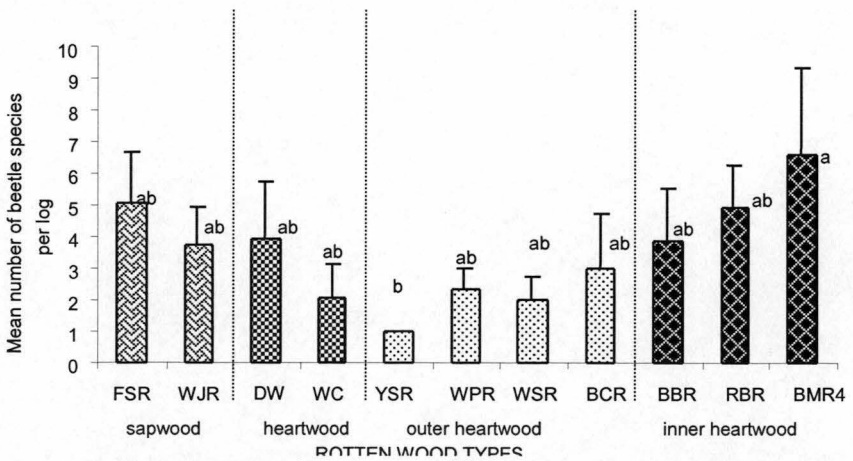


Figure 5.5. Mean number (95% confidence intervals) saproxylic beetle species within each RW type, per log. Data uses number of beetle species pooled from two 1-m log sections. Mean numbers with the same letter are not significantly different ($p > 0.05$). Units of rotten wood with zero beetles were omitted. RW type abbreviations are same as in Figure 5.3.

Table 5.1. Species associated with Rotten Wood (RW) type, grouped by RW region and by apparent decay type. RW region is abbreviated as SF (SP) – surface (sapwood), OH – outer heartwood, IH – inner heartwood, H-heartwood, L- localised. RW types are abbreviated as WJR – white jelly surface rot, FSR – fibrous surface rot, YDR – yellow dry slatey rot, WPR – white pocket rot, WSR – white stringy rot, BSR – brown spongy cubic rot, BDW – brown discoloured wood, RBR – red brown soft blocky fibrous rot, BBR- brown blocky crumbly rot, BMR – brown mudgut rot, and WC – wet cracks. The apparent decay type is abbreviated as Wh– white rot, and Br– brown rot. Number within a cell represents the number of logs in which a species occurred. Grey cells highlight more than two occurrences. Species are listed in decreasing order of most to least frequency. Species with fewer than four occurrences were excluded.

RW REGION	SF (SP)		OH				H	IH			L	
RW TYPE	WJR	FSR	YDR	WPR	WSR	BSR	BDW	RBR	BBR	BMR	WC	Total
APPARENT DECAY TYPE	-	-	-	Wh	Wh	Br	Br	Br	Br	Br	-	
Lissotes cancroides	8	14	2	1	2	1	6			3		37
Prostomis atkinsoni	1	2			2	2	5	6	5	11	2	36
Coripera deplanata	7	16		1		1	3	1		4		33
Elateridae TFIC sp 21	5	9				2	4	3	2	4		29
Dryophthorus TFIC sp 01	2	5			1		1	8	1	7		25
Pycnomerus TFIC sp 02		2				1	6	6	2	7		24
Cossonus simsoni	1	4		1		1	4	7		4		22
Scirtidae YEE sp 04		1			1		2	1	2	7	9	22
Diemenoma TFIC sp 01		3			1	1	3	4	3	2		17
Aleocharinae TFIC sp 34	3	4				1	2		1	1		12
Enneaphyllus aeneipennis		2		2	5		2			1		12
Dorhnia simplex	1						1	4	2	3		11
Exeiratus TFIC sp 01		2		1	2			3		3		11
Aleocharinae TFIC sp 13	1	2					2	1	1	3		10
Elateridae TFIC sp 20	2	7								1		10
Philothermus tasmanicus	1	1			1		2			3	2	10
Syndesus cornutus	1					3	1	3		1		9
Pedilophorus griffithi		7								1		8
Promecoderus tasmanicus	1	6					1					8
Trechimorphus diemenensis		1				1	2	2		2		8
Adelium abbreviatum	2	4					1					7
Stichonotus leai	2	4			1							7
Denticollinae TFIC sp 01	1							1		3	1	6
Elateridae TFIC sp 23	2	1					2	1				6
Dryocora cephalotes							1	1	1	2		5
Elateridae TFIC sp 19							1	2		2		5
Lissotes subcaeruleus	2						1			2		5
Macroplectus CHANDLER 'Type 1'		1					1		1	1	1	5
Scirtidae YEE sp 02										4	1	5
Scirtidae YEE sp 08							1			2	2	5
Scopodes intermedius	1	3					1					5
Sloaneana tasmaniae	1	2					1	1				5
Staphylinidae ANIC 88-0088	1	2					1	1				5
Toxeutes arcuatus						1	1	1		2		5
Curculionidae YEE sp 49							3			1		4
Dinichus terreus		3		1								4
Staphylininae TFIC sp 03	1	1					2					4

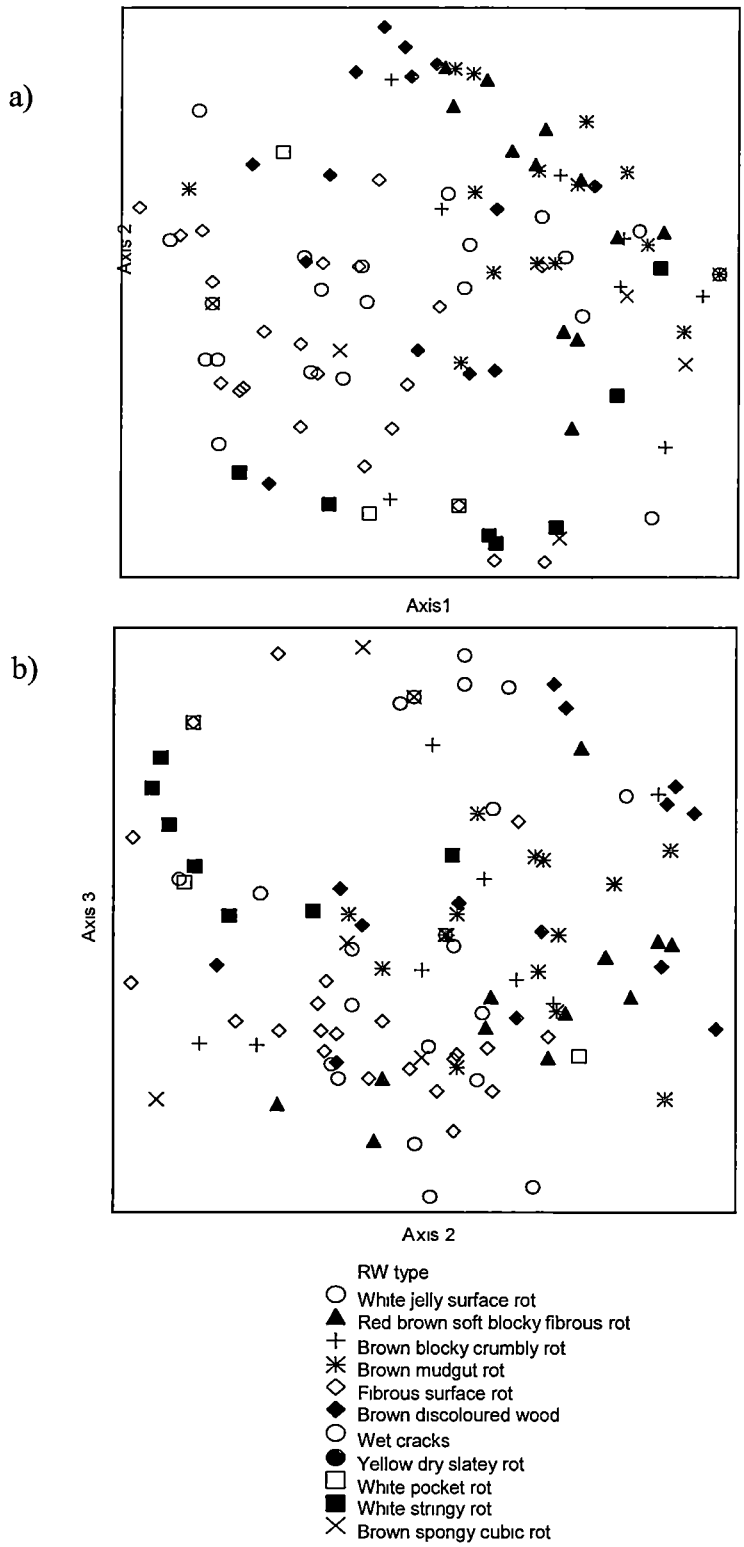


Figure 5.6. NMS ordination of saproxylic beetle assemblages from 119 samples of rotten wood from 42 *Eucalyptus obliqua* logs, with rotten wood type (symbols) overlaid. (a) axes 1 and 2; (b) axes 2 and 3. Based on presence-absence data of 42 beetle species within a rotten wood type pooled from two 1 m-long sections per log (doubletons excluded). Stress = 0.23, p = 0.0196. Samples of rotten wood with no beetles were omitted.

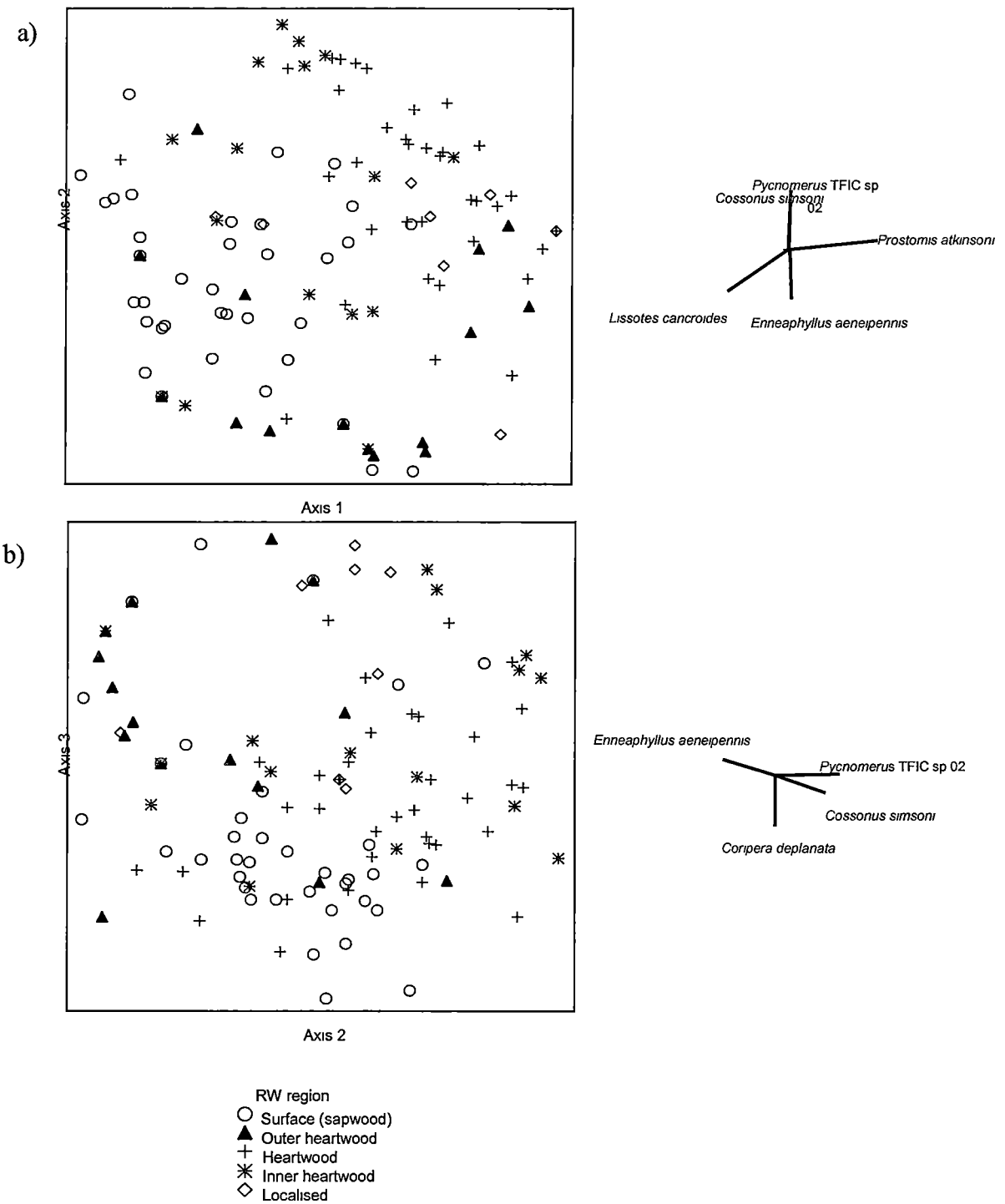


Figure 5.7. Same ordination as in Figure 5.6, but with rotten wood region (symbols) overlaid. (a) axes 1 and 2; (b) axes 2 and 3. Vectors are defined by beetle species occurrence data; for greater clarity, these are displayed adjacent to the ordination. Vector scaling 100%. Only vectors with $r^2 > 0.2$ are shown.

Except for the distinct patterns evident for two single RW types ('brown mudgut rot' and 'fibrous surface rot'), there were no discrete clusters of the same RW type evident in ordination plots based on beetle assemblages (Figure 5.6a,b). That is, no single RW

type had a distinct beetle assemblage. Despite this apparent lack of difference among single RW types, MRPP suggested that there were highly significant differences ($p < 0.000001$, $T = -11.4$). The ordination was re-examined by overlaying the RW region on the ordination instead of RW type, and this showed that some RW regions formed more distinct clusters (Figure 5.7a,b), particularly in terms an distinct suite of beetles associated with the surface/sapwood RW types (Figure 5.7b). This difference among RW regions was significant ($p < 0.000001$, $T = -17.6$). Species that correlated with the ordination included those that showed an association when examining individual species (Table 2): *Prostomis atkinsoni* and *Pycnomerus* TFIC sp 02 were associated with the brown rotten heartwood (inner) types, *Lissotes cancroides* and *Coripera deplanata* with the surface (sapwood) RW types, and *Enneaphyllus aeneipennis* with the white rotten heartwood types.

5.4 DISCUSSION

The results of this study support the hypothesis that for some species, differences in saproxylic beetle occurrence between large and small diameter logs can in part be explained by the discrete decompositional processes undergone in logs of the two size classes, as reflected in the region or type of rotten wood. For example, brown rotten heartwood occurs more frequently in large diameter logs (Chapter 4), and this study has described an association of two beetle species (*Cossonus simsoni* and *Pycnomerus* TFIC sp 02) with brown rotten heartwood. This argument was also supported by other related observations. Some members of the family Scirtidae apparently prefer large diameter logs (this study, Chapter 6, and Grove & Bashford 2003). These beetles appear to be associated with the wetter RW types, such as 'wet cracks' and 'brown mudgut rot', which were more frequent in large diameter logs (Chapter 4). Their association can be explained by their requirement for wet habitats, as larval scirtids have retained an ancestral respiratory system adapted for living in saturated environments and mouthparts designed for filtering wet detritus (Lawrence & Britton 1994). Meanwhile, the white rotten heartwood types are more frequent in small diameter logs than in large diameter logs (Chapter 4).

In this study, one beetle species (*Enneaphyllus aeneipennis*) was restricted to this particular white rot type, and was only detected in small diameter logs. It is therefore

reasonable to imply that one explanation for a species greater occurrence in large diameter logs (in this study) is due to the presence of certain RW types not commonly found in small diameter logs.

Log size preferences and rotten wood type associations could only be demonstrated for common species, as these species occurred in sufficient numbers for statistical analysis. In theory, rarity can be positively related to habitat specificity (Rabinowitz 1981), so the many less common species in this study could also have a preference for log size and/or rotten wood type. Additional sampling would be needed to gain an adequate understanding of the habitat preferences of naturally rare species.

There may have been factors other than the types of rotten wood to which species may be responding. For example, the xylophagous *Coripera deplanata* was more frequent in large diameter logs, yet showed an association for the surface (sapwood) rotten wood that is common to both log sizes. It may have preferred large diameter logs because the sapwood layer is thicker on large diameter logs than on small logs (Brack *et al.* 1985). This is the case for the northern European sapwood feeding *Pytho kolwensis* (Pythidae) which, in a Finnish study, preferred large spruce logs over small logs for this reason (Siitonen & Saaristo 2000). Another interpretation is that *Coripera deplanata* seems to have relatively broad larval habitat associations, also occurring in the brown rotted heartwood (inner) common in large diameter logs (this study, S. Grove unpublished data). Additional sampling might reveal a better understanding of the mechanisms underlying its apparent preference for large diameter logs.

In spite of the limitations of the present study, the results show that a high incidence, richness and diversity of species are associated with 'brown' rot (especially brown mudgut rot), and there is greater occurrence of certain beetle species in brown rot. Collectively these results suggest that brown rot is an important habitat feature of large *Eucalyptus obliqua* logs. Its value could lie in its relative stability as a habitat. Habitat stability is defined as how favourable it remains for a population over a continuous period of time (Southwood 1977). In general, large diameter logs of the dimensions studied here are considered to offer more stable habitats for saproxylic beetles than smaller sized logs (Grove & Meggs 2003). This is because they tend to have lower

decay rates (Harmon *et al.* 1986; Mackensen *et al.* 2003; Stone *et al.* 1998) and so persist longer in the landscape; maintain more optimal moisture levels (Amaranthus *et al.* 1989) that allow buffering against the effects of desiccation and temperature extremes; and thus provide potential refuges during disturbance events, such as wildfire (Meggs and Taylor 1999, Michaels & Bornemissza 1999). In the present study, brown rotted heartwood had probably originated in the living tree, entering through infection courts such as those caused by fire damage or breakage of large branches (Greaves *et al.* 1965; Perry 1985; Tamblyn 1937; Wardlaw 2002; Wilkes 1985a). Therefore as a habitat, it might begin to sustain an assemblage of beetles from the time of tree-fall or even beforehand. The rotten wood in small diameter logs, on the other hand, almost certainly owed its origin to fungal and microbial colonisation since the tree-fall event.

The apparent poor dispersal potential of species associated with the brown rotted heartwood also supports the notion that this rot type is a relatively stable habitat for saproxylic beetles. Theoretically, species dependent on stable habitats would require lower dispersal abilities, while those in less predictable habitats would require higher ones (Southwood 1977). In this study, *Cossonus simsoni, Prostomis atkinsoni, Dryophthorus* TFIC sp 01 and *Pycnomerus* TFIC sp 02, which were more common in the brown rotted heartwood, each have life history characteristics that appear to fit this pattern. They are small xylophagous species, often found living in aggregates, have a seemingly sedentary behaviour and/or were flightless, or a combination of these (pers. obs). All except *Prostomis atkinsoni* are flightless, and flightlessness is one outcome of habitat stability (Lattin & Moldenke 1990; Stevens 1997). *Prostomis atkinsoni, Dryophthorus* TFIC sp 01 and *Pycnomerus* TFIC sp 02 seem capable of undergoing successive generations within the same log without emerging, and this interpretation is supported for *Prostomis atkinsoni* by a recent study that found genetically similar individuals at very fine spatial scales (Watson 2003). Adults and larvae of *Prostomis atkinsoni, Dryophthorus* TFIC sp 01 and *Pycnomerus* TFIC sp 02 subsisted in the original host wood material for over 25 months under laboratory conditions, with both life stages persisting. Furthermore, these three species were collected from partially decomposed to well-rotted inner heartwood, thus showing their capacity to feed on a broad range of decomposed wood stages; and in the laboratory they seemed to re-ingest previously consumed wood.

In Northern Europe, the declines in saproxylic beetles that have resulted from centuries of timber harvesting and recent intensive forest management (Grove 2002b) provide examples of what may occur in Australian production forests if similar management trajectories were followed. Remarkably, each of the four species more common to the brown rotted heartwood (*Dryophthorus* TFIC sp 01, *Prostomis atkinsoni, Cossonus simsoni,* and *Pycnomerus* TFIC sp 02) belongs to a genus whose European representatives have already experienced drastic declines, with some regional extinctions. And yet, in this Australian (Tasmanian) study, they were among the most common species collected. Moreover, some of the European species appear to have similar rotten wood type preferences to those in this study.

For example, *Dryophthorus corticalis*, which lives in the red heartwood rot of old standing and fallen oak (*Quercus* sp) trees, is threatened in Great Britain (Hyman & Parsons 1992), Germany (Bense 2002), and the Czech Republic (Strejcek 1996). *Prostomis mandibularis,* which occurs in the red-brown muddy rot of decomposing oak logs (personal observation), is extinct in the UK (Boswijk & Whitehouse 2002) and threatened with extinction in parts of Germany (Bense 2002). A number of species from the genus *Cossonus* are threatened in several European countries: *Cossonus linearis* in central Europe (Harde 1984) and the Czech Republic (Strejcek 1996); *C. cylindricus* in Finland (Martikainen 2001); and *C. parallelepipedus* in the Czech Republic (Strejcek 1996) and Germany (Bense 2002). *Pycnomerus terebrans,* which occurs in the red rotten wood of old hardwood trees, has also become extinct in Britain (Buckland and Dinnin 1993), and is close to extinction in parts of Germany (Wenzel 2002). Considering the similarities found in this study with those of Northern European examples, it seems likely that developing an understanding of the dispersal ecology of these species will provide valuable information as to how to manage large diameter logs over appropriate spatial and temporal scales, to ensure that such major declines and extinctions can be avoided in Tasmania and elsewhere.

Growing evidence in Europe suggests that certain old trees with already present heartrot decay have high conservation importance for saproxylic beetle biodiversity (Dudley & Vallauri 2004; Key & Ball 1993; Nilsson & Baranowski 1997; Nilsson *et al.* 2002; Ranius 2002; Vallauri *et al.* 2002). In Australia, the importance of old trees for

conservation has been recognised for conservation of arboreal vertebrates that depend on heartrot decay process in mature eucalypt trees to create tree-hollow habitats (reviewed in Gibbons & Lindenmayer 2001). However, the importance of such decay processes for invertebrate biodiversity conservation is less understood. This study suggests that decay processes not only have implications for fauna dependent on standing living or dead trees, but also for saproxylic beetle assemblages dependent on logs on the forest floor. It was suggested that the internal heartrot decay processes prevalent in large diameter *E. obliqua* logs related to the infection history and age of the living tree (Chapter 4, sensu (Heilmann-Clausen & Christensen 2004) - Danish beech). Current research projects are investigating this issue (Yuan, Z.Q. unpublished data, Harrison *et al.* 2003; Hopkins *et al.* 2003). Note though, the potential impact this decay could have on sustainable wood yields from decay spreading into the neighbouring regenerating trees also warrants investigation.

5.5 CONCLUSION

In conclusion, large *Eucalyptus obliqua* logs in Tasmanian wet eucalypt forests host a distinct suite of beetle species found less common in small diameter logs, and one explanation for this is the greater prevalence of brown rotten heartwood (inner) types within large diameter logs. This rotten wood type probably originated in the standing tree, though the specific decomposer organisms or processes involved in its development are unknown. It seems that this rotten wood type is a relatively stable microhabitat, and species associated with it appear to have lower dispersal potential. Considering these species belong to genera whose European representatives have undergone serious declines, it seems they also could be susceptible to the long-term effects of intensive forest management and fragmentation. Determining how far these species disperse, whether they colonise the living tree, at which stage they colonise the fallen log, and for how long they remain within the log, will provide valuable information as to how to manage for large diameter logs over appropriate spatial and temporal scales. Current research projects are seeking to answer some of these questions (Harrison *et al.* 2003; Watson 2003; Nash 2004). A caveat to this study is that the conclusions have mostly been drawn from the commonly collected species, and so conservation issues relating to naturally rare species still need to be addressed.

5.6 APPENDICES

Appendix 5.1. Taxonomic list of adult beetles hand collected from 42 *Eucalyptus obliqua* logs. * refers to species that were also collected in larval form.

Family-Subfamily	Species
Carabidae-Migadopinae	*Stichonotus leai Sloane, 1910*
Carabidae-Trechinae	*Sloaneana tasmaniae (Sloane, 1915)*
Carabidae-Trechinae	*Trechimorphus diemenensis (Bates, 1878)*
Carabidae-Broscinae	**Promecoderus tasmanicus Castelnau, 1867*
Carabidae-Callistinae	*Lestignathus sp nr foveatus Sloane, 1920*
Carabidae-Lebiinae	*Agonocheila curtula (Erichson, 1842)*
Carabidae-Pentagonicinae	*Scopodes intermedius Blackburn, 1894?*
Carabidae-Psydrinae	*Amblytelus TFIC sp 01*
Carabidae-Psydrinae	*Theprisa convexa (Sloane, 1920)*
Carabidae-Pterostichinae	*Notonomus politulus (Chaudoir, 1865)*
Carabidae-Pterostichinae	*Rhabdotus reflexus (Chaudoir, 1865)*
Carabidae-Zolinae	*Pterocyrtus tasmanicus Castelnau, 1867*
Ptiliidae	*Ptiliidae TFIC sp 04*
Leiodidae-Cholevinae	*Nargomorphus jeanneli Szymczakowski, 1963*
Leiodidae-Cholevinae	*Nargomorphus TFIC sp 02*
Scydmaenidae	*Scydmaenidae TFIC sp 04*
Scydmaenidae	*Scydmaenidae TFIC sp 08*
Scydmaenidae	*Scydmaenidae TFIC sp 10*
Staphylinidae	*Staphylinidae ANIC 88-0088*
Staphylinidae-Pselaphinae	*Macroplectus CHANDLER 'Type 1'*
Staphylinidae-Pselaphinae	*Macroplectus tasmaniae Raffray*
Staphylinidae-Pselaphinae	*Startes CHANDLER 'Tasmania 1'*
Staphylinidae-Pselaphinae	*Tasmanityrus newtoni Chandler, 1987*
Staphylinidae-Tachyporinae	*Sepedophilus TFIC sp 01*
Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 13*
Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 25*
Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 27*
Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 28*
Staphylinidae-Aleocharinae	*Aleocharinae TFIC sp 34*
Staphylinidae-Scaphidiinae	*Scaphidium YEE sp 01*
Staphylinidae-Paederinae	*Hyperomma bryophilum Lea, 1923*
Staphylinidae-Paederinae	*Paederinae TFIC sp 03*
Staphylinidae-Staphylininae	*Quedius TFIC sp 04*
Staphylinidae-Staphylininae	*Staphylininae TFIC sp 03*
Lucanidae-Syndesinae	**Syndesus cornutus (Fabricius, 1801)*
Lucanidae-Lucaninae	**Lissotes cancroides (Fabricius, 1787)*
Lucanidae-Lucaninae	**Lissotes curvicornis (Boisduval, 1835)*
Lucanidae-Lucaninae	*Lissotes subcaeruleus Bomans, 1986*
Scarabaeidae-Melolonthinae	*Heteronyx pilosellus Blanchard, 1850*
Scarabaeidae-Melolonthinae	**Phyllochlaenia TFIC sp 01*
Scarabaeidae-Melolonthinae	*Phyllochlaenia villosus (Le Guillou, 1844)*
Scarabaeidae-Melolonthinae	*Telura vitticollis Erichson, 1842*
Scirtidae	*Prionocyphon? TFIC sp 01*
Scirtidae	*Pseudomicrocara atkinsoni (Waterhouse, 1877)?*

Family-Subfamily	*Species*
Byrrhidae-Byrrhinae	*Pedilophorus griffithi* Lea, 1907
Byrrhidae-Byrrhinae	*Pedilophorus* nr ANIC sp 88-0313
Eucnemidae	*Neocharis tasmanicus* Muona, 1987
Elateridae-Pityobiinae	*Tasmanelater pelionensis* Calder, 1996
Elateridae-Agrypninae	*Agrypnus TFIC sp 01*
Elateridae-Denticollinae	*Denticollinae TFIC sp 01*
Elateridae-Denticollinae	*Denticollinae TFIC sp 16*
Elateridae-Denticollinae	*Elatichrosis exarata* (Candeze, 1863)
Elateridae-Denticollinae	*Enischnelater TFIC sp 01*
Elateridae-Elaterinae	*Augenotus quadriguttatus* (Erichson, 1842)
Cleridae-Phyllobaenlinae	*Lemidia YEE sp 02*
Nitidulidae-Cryptarchinae	*Cryptarcha laevigata*
Silvanidae-Brontinae	*Cryptamorpha TFIC sp 01*
Silvanidae-Brontinae	*Cryptamorpha victoriae* Blackburn?
Cryptophagidae-Cryptophaginae	*Cryptophagus tasmanicus* Blackburn, 1907
Cryptophagidae-Cryptophaginae	*Cryptophagus sp nr gibbipennis* Blackburn, 1892
Cerylonidae-Cerylonlnae	**Philothermus tasmanicus* Slipinski, 1988
Corylophidae-Corylophinae	**Holopsis TFIC sp 01*
Corylophidae-Sericoderinae	*Sericoderus TFIC sp 05*
Zopheridae-Zopherinae	*Docalis funerosus* (Hope, 1845)
Zopheridae-Pycnomerinae	*Penthelispa fuliginosa* Erichson, 1842
Zopheridae-Pycnomerinae	**Pycnomerus TFIC sp 02*
Zopheridae-Colydiinae	*Enhypnon tuberculatus*
Tenebrionidae-Lagriinae	**Adelium abbreviatum* Boisduval, 1835
Tenebrionidae-Lagriinae	*Brycopia coelioides* (Pascoe, 1870)
Tenebrionidae-Lagriinae	*Brycopia hexagona* Carter, 1920
Tenebrionidae-Lagriinae	**Brycopia picta* (Pascoe, 1869)
Tenebrionidae-Lagriinae	**Coripera deplanata* (Boisduval, 1835)
Tenebrionidae-Zolodininae	**Tanylypa morio* Pascoe, 1869
Prostomidae	**Dryocora cephalotes* (Waterhouse)
Prostomidae	**Prostomis atkinsoni* Waterhouse, 1877
Oedemeridae	**Dohrnia simplex* Champion
Cerambycidae-Prioninae	**Enneaphyllus aeneipennis* Waterhouse, 1877
Cerambycidae-Prioninae	**Toxeutes arcuatus* (Fabricius, 1787)
Curculionidae	*Curculionidae* YEE sp 49
Curculionidae-Cryptorhynchinae	*Decilaus lateralis* Lea, 1913
Curculionidae-Cryptorhynchinae	*Decilaus nr striatus/subfasciatus*
Curculionidae-Cryptorhynchinae	*Poropterus antiquus* Boheman
Curculionidae-Cryptorhynchinae	*Tyrtaeosus ustulatus* Pascoe
Curculionidae-Dryophthorinae	*Dryophthorus 'corticalis'*
Curculionidae-Dryophthorinae	**Dryophthorus TFIC sp 01*
Curculionidae-Molytinae	**Dinichus terreus* Pascoe, 1887
Curculionidae-Molytinae	*Exeiratus TFIC sp 01*
Curculionidae-Cossoninae	*Cossoninae TFIC sp 06*
Curculionidae-Cossoninae	**Cossonus simsoni* Lea, 1910
Curculionidae-Cossoninae	*Pentarthrum TFIC sp 01*

Appendix 5.2. Taxonomic list of larvae hand collected from 42 *Eucalyptus obliqua* logs.

Family	Larval morphospecies code· *Genus*
Carabidae	CARLAR15
Carabidae	CARLAR8
Staphylinidae	LAR5; Scaphidium sp
Scirtidae	Scirtidae YEE sp 04
Scirtidae	Scirtidae YEE sp 08
Byrrhidae	LAR29
Eucnemidae	EUCNEM2
Elateridae	Elateridae TFIC sp 23
Elateridae	Elateridae TFIC sp 19
Elateridae	Elateridae TFIC sp 20
Elateridae	Elateridae TFIC sp 21
Elateridae	Elateridae YEE sp 06
Elateridae	LAR33
Elateridae	ELAT1
Lycidae	LYCIDLAR1
Cantharidae	LAR11
Cantharidae	LAR3
Cleridae	CLER2. *Lemidia* sp
Melandryidae	LYMEX1: *Mystes* sp
Tenebrionidae	LAR10
Tenebrionidae	LAR16
Tenebrionidae	TENLAR1
Indet	LAR30
Indet	CURLAR2
Indet.	CARLAR9
Indet.	STAPHLAR1
Indet	STAPHLAR7

6 EFFECTS OF CLEARFELL HARVESTING ON SAPROXYLIC BEETLES: EVALUATING THE IMPORTANCE OF LARGE DIAMETER LOGS

6.1 INTRODUCTION

Conservationists and forest managers increasingly accept that silviculture regimes more closely resembling natural disturbance regimes and promoting structural complexity are more likely to ensure that biodiversity is maintained (Angelstam 1998; Angelstam *et al.* 1997; Bengtsson *et al.* 2000; Bergeron *et al.* 2002; Franklin *et al.* 2002; Haila *et al.* 1994; Hansen *et al.* 1991; Hunter 1993; Lindenmayer 1995; Niemelä 1999; Seymour *et al.* 2002; Spies & Turner 1999). This is based on the rationale that because forests ecosystems have partly evolved in relation to stochastic disturbance events that drive the regeneration and succession of the forest, then the forest biota are more likely to be resilient to and recover from silvicultural practices that emulate the conditions of a naturally disturbed forest (Attiwill 1994a; Haila 1994; Hunter 1993; Niemelä 1999).

6.1.1 How the effects of clearfelling on log recruitment processes leads to the loss of large diameter logs in managed forests

In Tasmania, the common harvesting regime for lowland wet eucalypt production forests is standard clearfell burn and sow silviculture (CBS) on 80-100 rotations (Hickey *et al.* 2001; Whiteley 1999). This involves clearing all trees within a set area (generally around 50-100ha, Forest Practices Board 2000) in a single operation, burning the logging debris to create a receptive seedbed, then aerially sowing eucalypt seed from local sources for natural regeneration (Hickey & Savva 1992). This has been a preferred harvesting method as it is considered to be most similar to the natural regeneration system of eucalypt trees after severe wildfire (Ashton 1982; Forestry Tasmania 2004; Hickey *et al.* 2001; Jackson 1968; Mount 1979). However, after successive harvests by clearfelling, an altered and simplified forest structure of even-aged younger trees is projected (Lindenmayer & McCarthy 2002; Lindenmayer *et al.* 2000b). From this, dead wood composition and dynamics could become drastically altered (Grove *et al.* 2002). In particular, no new recruitment of large diameter logs (derived from mature trees) will

be apparent, and future inputs will comprise an increased proportion of small diameter logs (derived from commercially mature trees) (Grove *et al.* 2002). How such long term predicted changes affect the conservation of saproxylic beetles (dead wood dependent, Speight 1989), is an important issue in the implementation of ecologically sustainable forestry (National Forest Policy Statement Commonwealth of Australia 1992; Grove & Meggs 2003; Meggs 1996; Taylor & Savva 1988).

6.1.2 Why researchers conclude that large diameter logs are important for dead wood dependent communities

In order to determine whether the loss of large diameter logs would be detrimental to maintaining saproxylic beetle biodiversity requires understanding the specific ecological role of these structures (Hammond *et al.* 2004). Several authors demonstrate that large diameter logs host higher numbers of species than other dead wood types, and these species are often specialist taxa (Kolström & Lumatjärvi 2000). Thus, large diameter log abundance would significantly contribute to stand-level species richness. Kleinevoss *et al.* (1996) and Kappes & Topp (2004) in broadleaved German forests showed that saproxylic beetle species richness positively correlates with log diameter. This pattern is repeated for mycetophilid flies emerging from spruce logs in Norway (Økland 1996b), wood-decay fungi on spruce logs in Finland (Renvall 1995), and bryophytes on beech and spruce logs in Sweden (Andersson & Hytteborn 1991). More recent studies show, however, that validity of this diameter relationship can depend on how adequately sampling effort is considered, because log surface area and volume are inherently functions of log diameter (e.g. Grove & Bashford 2003 - beetles; Heilmann-Clausen & Christensen 2004 - wood decay fungi; Kruys *et al.* 1999 - various cryptogams; Schiegg 2001). Also, this pattern may only be reflected be a feature of certain tree species For example, saproxylic beetle species richness correlated with log diameter for beech dead wood and less so for oak (Kappes & Topp 2004). Perhaps logs of different decay stages also illicit different patterns (Grove & Bashford 2003; Irmler *et al.* 1996). Grove & Bashford (2003) preliminary analysis of large and small diameter *Eucalyptus obliqua* logs at Warra in the first year following felling explained that the number of species emerging could easily be due to log volume differences.

Various other studies indicate that large diameter logs support unique saproxylic beetle assemblages (e.g. Kappes & Topp 2004; Kleinevoss *et al.* 1996). Thus, the loss of such features would be detrimental for these habitat specialists. For instance, some authors suggest that the increased surface area of phloem associated with larger diameter logs provide greater chance of survival for larvae of certain saproxylic bark beetle species (e.g. Esaki 1996; Haack & Slansky Jr 1987; Hughes & Hughes 1982; Siitonen & Saaristo 2000). In Japan, Araya (1993; Araya 1994) showed that the occurrences of soft rot and brown rot vary in relation to log size, and certain lucanid beetles species exhibit a rot type, and thus a log size, preference. Large diameter logs can also have lower decay rates (Harmon *et al.* 1986), and some authors suggest this may provide a more stable microclimate for species confined to such stable conditions (Grove *et al.* 2002; Väisänen *et al.* 1993).

6.1.3 Shortfalls of previous approaches to understanding the importance of large diameter logs

Most studies implicating the conservation importance of large diameter logs, though, are retrospective in that they have occurred in forest regions where the availability of large diameter logs has already drastically reduced. Such has been seen in the United Kingdom (Alexander 2002; Hammond & Harding 1991; Kirby & Drake 1993), central Europe (e.g. Kappes & Topp 2004; reviewed in Vallauri *et al.* 2002) and northern Europe (reviewed in Siitonen 2001). Moreover, most of these studies are based on correlative assumptions, showing that the abundance of large diameter logs, or their reduced and discontinuous availability correlates with lower saproxylic beetle species richness and fewer rare or threatened species (Kolström & Lumatjärvi 2000; Økland *et al.* 1996b; Siitonen 1994a; Siitonen *et al.* 2000; Siitonen *et al.* 2001; Siitonen & Saaristo 2000; Similä *et al.* 2003; Väisänen *et al.* 1993). Thus, the specific factors driving species decline are not yet fully understood. This is because, often in these regions, the reduced availabilities of decomposing large diameter logs, is repeatedly confounded by factors relating to the 'managed' forest condition, such as younger forest age, significantly lower dead wood volumes and lower diversity of dead wood types (e.g. Kruys *et al.* 1999; Martikainen *et al.* 2000; Siitonen *et al.* 2000; Sverdrup-Thygeson 2002; Väisänen *et al.* 1993). As an example, the threatened bark beetle *Pytho kolwensis* in Finland was considered restricted to oldgrowth forests because of the microclimate or

host-tree quality of such sites (Saalas 1923; Burakowski, 1962 cited in Siitonen & Saaristo 2000). However, recent studies demonstrated that because of its poor dispersal ability, its current distribution was due to its dependence on a long-term continuous availability of suitable host trees - which in Sweden and much of Europe, dead wood continuity is now only apparent in unmanaged oldgrowth forests.

6.1.4 How the present study seeks to circumvent some of these shortfalls

The present study investigates how currently planned 90 year CBS rotations affect saproxylic beetle biodiversity, with particular consideration to the effect diminishing availabilities of large diameter logs have on biodiversity over the long term. In Tasmania, clearfelling began in the early 1960s, and so large diameter logs are still well represented in these forests (Meggs 1996; Woldendorp *et al.* 2002a). This provides a valuable opportunity to investigate their habitat value prior to any long-term effects of forest management. That is, the present study is not retrospective. To avoid the confounding "sampling effort" issue associated with sampling logs of different sizes, saproxylic beetle species richness was standardised by sampling effort (amount of dead sampled), and by the number of individuals collected.

As wet eucalypt forests are naturally dynamic systems, the "ideal" experimental design for assessing the effects of CBS harvesting on biodiversity conservation unconfounded by forest succession and age would be to compare logging regeneration with similar aged wildfire regenerated forest (e.g. Baker *et al.* 2004; Ough 2001; Turner 2003). This is because comparing unlogged forests with typically younger logged forests confounds the effects of logging and different forest succession and ages (Attiwill 1994b; e.g. Chandler 1987; Hickey 1994; Taylor 1990). At this stage in Tasmanian forestry the only available logging regenerated forests are at most midway through their first rotation period. With this in consideration, research findings of this study are discussed in relation to forest succession and age; and in relation to the effects of CBS harvesting.

This study aims to:

- Compare the saproxylic beetle species richness, diversity and assemblage composition of large diameter (>100cm) with small diameter (30-60cm) logs,

comparing between naturally disturbed mature forests and forest regenerating from CBS silviculture

- Identify habitat specialists of either log size or forest type combination
- Discuss the effects of clearfell logging on saproxylic beetle populations
- Discuss the specific ecological role of large diameter logs, compared to small diameter logs, in maintaining saproxylic beetle biodiversity

6.2 METHODS

6.2.1 Study location, experimental design and sampling method

Research was conducted at ten study sites in wet eucalypt production forests in Southern Tasmania (see Section 2.2 and Section 2.3 for site locations and descriptions). Study sites are all within 10kms of each other. The study area and its environs experienced several major, but patchy, wildfires in the early 1900's (Alcorn *et al.* 2001; Hickey *et al.* 1999b), see Section 2.2.for the recent fire history of study sites). Five sites (designated as sites E, S, W, PR1, PR2) were 20-30 yr logged forest coupes regenerating from clearfell burn and sow (CBS) silviculture (logging regenerated forest). The other five sites (designated as sites WR, M, R, PO1, PO2) were in mature unlogged forest. Environmental and stand structure attributes for each study site have been presented in Table 2.6.

Saproxylic beetle populations were sampled using log emergence traps (ET) (see Section 2.6.2 for trap design), with traps operating for 18 months between October 2000 – May 2002 (includes two summers). At each site, three large (>100cm) and three small (30-60cm) diameter *Eucalyptus obliqua* logs at an intermediate decomposition stage (defined in Section 2.5) were sampled. Alphanumeric names for logs used in this study are listed in Table 2.3. All beetles, including adults and larvae, were determined to species (or morphospecies) level following the protocol outlined in Section 2.7. Due to the taxonomic difficulties with identifying larvae to known species, only results for saproxylic adult beetles are presented here. Saproxylic beetles presented in this study include both obligate and facultative species, as defined in Section 3.2.4.1.

6.2.2 Data

Data from four logs were excluded from analyses. A large tree fell on log WRLET1 after the first summer collecting period, and logs with traps WSET1, WSET2 and SSET1 were later identified as belonging to *Phyllocladus asplenifolius* (Podocarpaceae: celery top pine) rather than *E. obliqua*. This respective resulted in 14 and 15 large and small diameter logs in mature unlogged forest, and 15 and 12 large and small diameter logs in logging regenerated forest. Unless specified otherwise, data for all statistical analyses comprised species abundance data for each trap pooled across the sampling period.

6.2.3 Comparing species richness

Traps on large diameter logs inherently sample a greater surface area and volume than traps on small diameter logs (see Table 2.3 for trap size dimensions). To consider whether different sampling efforts between log sizes confound trap catches, different approaches were used to standardise species richness of log samples.

6.2.3.1 Standardising trap samples by sampled log volume and surface area

In the first approach, an approach to data analysis similar to that of Schiegg (2001; Schiegg 2003) was followed. This involved standardising samples (i.e. the proportion of the log within the trap) based on either sampled surface area or sampled volume, depending of which variable best correlated with species number. Regression analyses were first conducted to investigate the relationship between species number and sampled log volume; and sampled surface area. However, unlike Schiegg (2001; Schiegg 2003), large and small diameter logs were analysed separately in order to exclude the potential 'log size' effect.

For small diameter logs, the number of species collected per log sample was positively correlated with sampled surface area ($r^2 = 0.36$, $p = 0.001$, Figure 6.1a) and sampled volume ($r^2 = 0.20$, $p = 0.02$, Figure 6.1b). Such correlations were discernible, but were not significant for large diameter logs (surface area: $r^2 = 0.06$, $p = 0.21$; volume: $r^2 = 0.02$, $p = 0.52$). As sampled surface area for small diameter logs showed a stronger correlation with species richness than did volume, species richness was standardised on the basis of surface area.

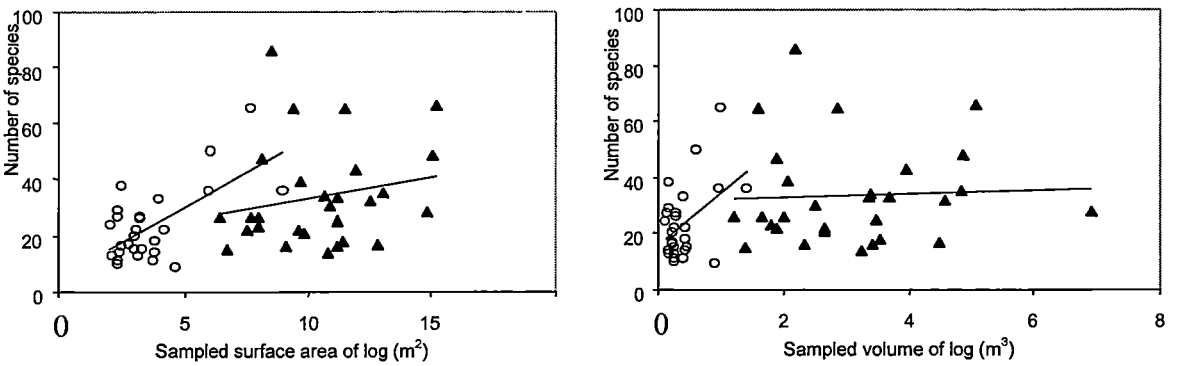


Figure 6.1 Scatterplot and regression lines of number of saproxylic beetle species collected per large (▲) or small (O) diameter log by the (a) surface area and (b) volume of log sampled. Figures show that species number in small diameter logs is more strongly correlated with sampling effort than that of large diameter logs, and this correlation is stronger for surface area than for log volume.

On average, a trap on a large diameter logs sampled just over two times more surface area (7.89 $m^2 \pm 2.2$) than a trap on a small diameter log (3.64 $m^2 \pm 0.99$). Therefore, to compare the species richness of small diameter logs of similar sampled surface area with that of large diameter logs, two small diameter logs (irrespective of forest type) were randomly selected from the 27 small diameter logs and the number of species from both logs calculated. This was repeated until pairs of all small diameter logs were selected, and their species number calculated – resulting in 13 adjusted small diameter log species richness measures. This was again repeated until 29 adjusted small diameter log species richness measures were derived. Species richness between large and small diameter logs (adjusted) were then compared using a one-way analysis of variance (ANOVA).

6.2.3.2 Comparing trap samples by equal log volumes and surface areas

Species accumulation plots for small and large diameter logs grouped by forest type (log size/ forest type 'treatment') were calculated. This involved randomly selecting logs by treatment, and plotting the cumulative number of different species against cumulative sampled volume and cumulative sampled surface area. This involved assigning a random number to logs by treatment, placing these logs in ascending order, then plotting the cumulative number of new species against cumulative sampled volume, and cumulative sampled surface area.

6.2.3.3 Comparing trap samples by equal number of individuals

Rarefaction curves (Krebs 1989; Simberloff 1972, 1978) were used to compare species richness among the log size/forest type treatments. This method calculates an estimated species richness for any given sampling effort, or number of individuals collected, thereby allowing comparisons of species richness between the different treatments of similar sample size. This study standardises the species richness by number of individuals collected. This is done by repeatedly taking sub-samples of a certain size (by number of individuals) from the original catch. From this, average number of species for the different sub-samples can be obtained. Sub-samples were taken at intervals of 20 individuals. Three rarefaction curves by treatment were calculated: including all saproxylic beetles, obligate species only, and facultative species only. Rarefaction estimates were calculated using Internet-based software provided by Brzustowski (2002), and curves were plotted using Microsoft EXCEL (Microsoft Corporation 1997).

6.2.4 Comparing species diversity

Species diversity is a measure of the richness, commonness and rarity of species within a community. However, most diversity indices are highly sensitive to different sample sizes (Magurran 1988). Therefore, rank abundance diagrams, which illustrate the species-abundance distributions of a community, were used to visually compare the numerical dominance of species from logs grouped by treatment. Data were pooled across traps by treatment. Diagrams were generated using Microsoft EXCEL.

6.2.5 Comparing species assemblages

6.2.5.1 Unconstrained ordination

Non-metric multidimensional scaling (NMS: Minchin 1987), an unconstrained non-parametric ordination technique, was used to investigate the variation of beetle assemblages among logs. This involves ordinating the relative similarities of logs in multi-dimensional space. Logs were ranked in similarity based on their beetle assemblages using the Sorensen (Bray-Curtis) distance measure. Species abundance data were $\log_{10}(x + 1)$ transformed to reduce the influence of abundant species relative to the less abundant ones (Magurran 1988). Species abundance vectors were overlaid

onto the ordination as a joint plot to determine which species were influencing the variation in beetle assemblages. NMS ordination was conducted in PC-ORD version 4 (McCune & Mefford 1999), choosing the 'slow and thorough' auto pilot mode. For each log, their log size/forest type treatment is overlaid on the ordination to visually detect any species assemblage patterns among the treatments. As singletons contribute little to assessing the similarity of beetle assemblages among logs, singletons were excluded from all multivariate analyses.

A semi-parametric analysis of variance (PERMANOVA: Anderson 2004b), previously named NP-MANOVA (Anderson 2001) is a newly developed procedure that tests the hypothesis of no difference between two or more groups of entities (e.g. logs), based on multi-species data. PERMANOVA was used to test the significance of observed (unconstrained) variation in beetle assemblages among the effects of forest type, of log size, and of site. The interactions between forest type and log size, and between site and log size were also tested. This used a two-factorial model (forest type and log size) with a nested hierarchical factor – log size is a crossed fixed factor (Table 6.1).

PERMANOVA follows a similar approach to parametric ANOVA, in that the total and within group variation of logs are calculated. From this, among group variation can be derived ($SS_A = SS_T - SS_W$), thus providing the components for F-ratios (MS_A/MS_W). For PERMANOVA, this variation is based on the relative similarity of logs defined by their beetle assemblages. Logs were ranked in similarity using the Bray-Curtis distance measure. As there is no multivariate F-statistic distribution to assess significance levels, a permutation test based on randomisation procedures is used to create a frequency distribution of F-values, and the observed F-ratio is tested for significance against this distribution. For this 4999 unrestricted randomised permutations were used. PERMANOVA procedures were performed using computer programs provided on the Internet by the author, Anderson (2004b). See both McArdle & Anderson (2001) and Anderson (2001) for a more complete description of the method.

Table 6.1. Two-factorial PERMANOVA model used for this experimental design.

Source	Degrees of Freedom	Construction of F ratio
Forest-type = F	2 – 1 = 1	$MS_F/MS_{St(F)}$
Sites (Forest-type) =St(F)	(5-1) x 2 = 8	$MS_{St(F)}/MS_{Res}$
Log size = L	2 – 1 = 1	$MS_L/MS_{St(F)*L}$
F x L	1	MS_{St*L}/MS_{Res}
St(F)xL	8	$MS_{St(F)*L}/MS_{Res}$
Residual	20x(3-1) = 40 (36*)	

* Modified residual degrees of freedom because data from four logs were excluded from analyses.

6.2.5.2 Constrained ordination

Canonical analysis of principal coordinates (CAP: Anderson & Willis 2003), a constrained ordination technique, was used to specifically investigate assemblage structure correlated with treatment effects. Using a similar statistical approach to Willis & Anderson (2003), two canonical analyses were conducted: one to investigate the effect of forest type, and the other to investigate the effect of log size. To test the statistical significance of these correlations, the results were tested using 9999 unrestricted random permutations of the raw data. As both log size and forest type treatments are binary (that is large versus small; and mature unlogged versus logging regenerated), CAP ordination results in a single canonical discriminant axis for each treatment. Thus, similar to Willis & Anderson (2003), the resultant canonical axes scores (position of logs - multivariate points on the two canonical axes) were plotted against each other. Species abundance vectors that correlated ($|r| > 0.35$) with the canonical discriminant axes of forest type and log size from CAP, were presented in a joint plot (as used in Willis & Anderson 2003). This indicates which species were influencing the constrained variation in beetle assemblages. CAP procedures were performed using a computer program that was provided on the Internet by Anderson (2004a).

6.2.6 Investigating habitat preferences of individual species

For determining the habitat preference for species, parametric ANOVA could not be used as data for the majority of species were zero-inflated, thus violating the assumption of normally distributed residuals (Sokal & Rohlf 1995). Instead, indicator species analysis (Dufrêne & Legendre 1997) was used to investigate individual species associations with the log size/forest type treatments. Indicator species analysis calculates a value that reflects a species' indication for a particular group, measured by

its concentration of abundance and faithfulness of occurrence to that group (McCune & Mefford 1999). Indicator values are then tested for significance using randomisation (Monte Carlo) procedures. A cut-off value of IndVal ≥ 25, p <=0.05 was used. Indicator species analysis however can only test one level of treatment at a time. Therefore, to cope with the hierarchical study design, a similar approach to Warncke (1988), cited in McCune & Grace (2002) was used. Five separate analyses were performed: one to determine species indicative of a forest type, irrespective of log size; one for a log size, irrespective of forest type; two to determine species indicative of log size within each forest type, that only included data of that forest type; and one to determine species indicative of site (irrespective of forest type or log size). For the latter analysis, a more conservative cut-off value of IndVal ≥ 40, p <= 0.01 was used. Untransformed species abundance data were used.

6.3 RESULTS

6.3.1 Description of Fauna

A total of 341 species of saproxylic beetles (6423 individuals) were collected as adults and 95 of these were singletons. The fauna comprised 51 families; Curculionidae and Staphylinidae were the most abundant and species rich families trapped. See Appendix 3.1 for a complete list of species. This also lists their biological traits, including apparent vagility, feeding guild and degree of dead wood dependence (obligate or facultative).

Thirty-nine species occurred in over 15% of logs sampled, with species varying in occurrence and abundance among the log size/forest type treatments (Table 6.2). Of these, four species: *Chylnus ater* (Carabidae), Tychiinae TFIC sp 06 (Curculionidae), Tychiinae TFIC sp 08 (Curculionidae) and *Ancyttalia tarsalis* (Curculionidae) were absent from small diameter logs in the logging regenerated forest, and one species - *Exeiratus* TFIC sp 01 (Curculionidae) was absent from small diameter logs in mature unlogged forest. Four species: *Decilaus nigronotatus* (Curculionidae), *Decilaus nr striatus/subfasciatus* (Curculionidae), *Enhypnon tuberculatus* (Zopheridae), *and Holopsis* TFIC sp 01 (Corylophidae) occurred on over 50% of logs, and these were relatively evenly distributed in occurrence and abundance among treatments. Not all frequent species occurred in high abundances. For example, *Xynotropis micans* (Anthribidae), *Denticollinae* TFIC sp 01 (Elateridae), *Epurea victoriensis* (Nitidulidae), *Aleocharinae TFIC sp 34* (Staphylinidae), *Cortinicara* TFIC sp 02 (Latridiidae) and *Cryptorhynchinae TFIC 13* (Curculionidae) were represented by just one or two individuals per log.

Table 6.2. List of frequently occurring species (present in >10 logs) that had emerged from large and small diameter logs in mature unlogged (MU) and clearfell sow and burn logging regenerated (LR) wet eucalypt forest. Number within cells represents: *No. of occurrences (Total no. individuals) in treatment.* Species in bold were considered to locally disperse by crawling. Cells shaded represent more than 5 log occurrences per log size/forest type treatment

Log type		Large logs		Small logs		
Forest type		MU	LR	MU	LR	TOTAL
SPECIES NAME	FAMILY					
Xynotropis micans	Anthribidae	3 (3)	4 (8)	4 (5)	3 (3)	14 (19)
Microchaetes hystricosus	Byrrhidae	3 (3)	6 (10)	2 (4)	3 (8)	14 (25)
Heteromastix TFIC sp 01	Cantharidae	8 (18)	6 (22)	5 (6)	3 (4)	22 (50)
Chylnus ater	Carabidae	6 (25)	2 (2)	2 (2)	--	10 (29)
Stichonotus leai	Carabidae	4 (8)	4 (10)	1 (1)	5 (18)	14 (37)
Trechimorphus diemenensis	Carabidae	6 (19)	8 (27)	3 (3)	5 (9)	22 (58)
Rhyzobius TFIC sp 15	Coccinellidae	3 (3)	1 (16)	7 (7)	2 (4)	13 (30)
Holopsis TFIC sp 01	Corylophidae	9 (29)	6 (20)	10 (31)	9 (15)	34 (95)
Ancyttalia tarsalis	Curculionidae	11 (56)	6 (18)	12 (25)	--	29 (99)
Cryptorhynchinae TFIC sp 31	Curculionidae	3 (3)	3 (4)	2 (2)	2 (3)	10 (12
Decilaus albonotatus	Curculionidae	4 (6)	5 (16)	4 (4)	3 (4)	16 (30)
Decilaus lateralis	Curculionidae	6 (29)	8 (40)	3 (7)	7(24)	24 (100)
Decilaus nigronotatus	Curculionidae	9 (76)	10 (305)	8 (78)	9 (149)	36 (608)
Decilaus nr striatus/subfasciatus	Curculionidae	12 (129)	11 (150)	7 (60)	9 (201)	39 (540)
Exeiratus TFIC sp 01	Curculionidae	3 (3)	3 (5)	--	8 (9)	14 (17)
Exithius capucinus	Curculionidae	4 (14)	2 (2)	6 (12)	3 (5)	15 (33)
Mandalotus muscivorus	Curculionidae	2 (2)	7 (21)	1 (1)	7 (20)	17 (44)
Miocallus pygmaeus	Curculionidae	7 (18)	1 (1)	4 (4)	2 (3)	14 (26)
Roptoperus tasmaniensis	Curculionidae	5 (10)	6 (37)	6 (12)	8 (19)	13 (25)
Tychiinae TFIC sp 06	Curculionidae	6 (8)	2 (4)	2 (2)	--	10 (14)
Tychiinae TFIC sp 08	Curculionidae	7 (8)	2 (2)	1 (1)	--	10 (11)
Denticollinae TFIC sp 01	Elateridae	4 (9)	5 (10)	4 (4)	1 (1)	14 (24)
Aridius nodifer	Latridiidae	4 (5)	5 (15)	4 (6)	6 (10)	19 (36)
Cortinicara TFIC sp 02	Latridiidae	4 (5)	4 (9)	2 (2)	4 (4)	14 (20)
Lissotes cancroides	Lucanidae	4 (22)	6 (16)	5 (6)	4 (6)	19 (50)
Orchesia alphabetica	Melandryidae	5 (47)	11 (66)	4 (9)	3 (8)	23 (130)
Epuraea victoriensis	Nitidulidae	1 (1)	5 (6)	2 (2)	4 (4)	12 (13)
Dohrnia simplex	Oedemeridae	11 (133)	5 (26)	3 (5)	5 (28)	24 (192)
Platypus subgranosus	Platypodidae	3 (22)	6 (29)	1 (2)	2 (2)	12 (63)
Prionocyphon? TFIC sp 01	Scirtidae	7 (66)	10 (63)	1 (3)	3 (102)	21 (234)
Pseudomicrocara atkinsoni?	Scirtidae	6 (17)	4 (15)	2 (2)	3 (7)	15 (41)
Cryptamorpha TFIC sp 01	Silvanidae	3 (28)	8 (128)	4 (14)	10 (230)	25 (400)
Cryptamorpha victoriae?	Silvanidae	2 (2)	6 (9)	2 (3)	4 (7)	14 (21)
Aspidiphorus humeralis	Sphindidae	7 (19)	4 (24)	5 (17)	3 (8)	19 (68)
Aleocharinae TFIC sp 13	Staphylinidae	4 (6)	5 (36)	1 (1)	6 (11)	16 (54)
Aleocharinae TFIC sp 14	Staphylinidae	3 (3)	3 (62)	3 (3)	3 (63)	12 (131)
Aleocharinae TFIC sp 34	Staphylinidae	2 (2)	2 (2)	3 (5)	4 (6)	11 (15)
Aulonothroscus elongatus	Throscidae	6 (17)	7 (42)	3 (11)	3 (15)	19 (85)
Enhypnon tuberculatus	Zopheridae	9 (41)	10 (25)	8 (12)	8 (18)	35 (96)

6.3.2 Species richness

6.3.2.1 Species richness – standardised by log surface area

Species richness of large and small diameter logs did not differ significantly ($F_{1,55} = 2.9$, $p = 0.09$) when comparing the adjusted richness of small diameter logs standardised by surface area (41.4 ± 17.1 species per log) with species richness of large diameter logs (~33.5 ± 17.9 species per log). Note, however that the average surface area of small diameter logs (adjusted) (7.3 ± 2.5m^2 surface area) was still significantly less ($F_{1,59} = 20.7$, $p < 0.001$) than average surface area of large diameter logs (10.5 ± 2.4 m^2).

6.3.2.2 Cumulative species richness – log volumes and surface area

When cumulative species richness of logs grouped by log size/forest type treatments was compared based on equal wood volumes, the small diameter logs show a trend for supporting more species than large diameter logs (Figure 6.2a). This trend was similar, but less distinct when comparing species richness based on equal surface areas (Figure 6.2b).

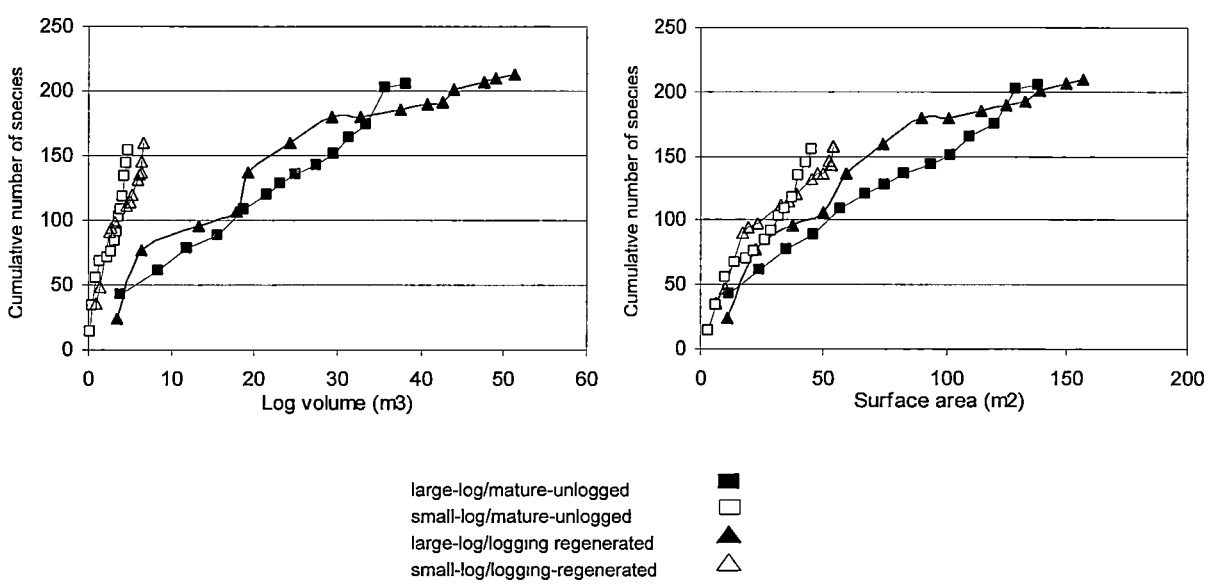


Figure 6.2. Cumulative number of saproxylic beetle species plotted against increasing a) sampled log volume and b) sampled surface area, grouped by log size/forest type treatments

6.3.2.3 Cumulative species richness – number of logs

In terms of comparing species richness based on equal numbers of logs, large diameter logs clearly hosted more species than small diameter logs, with little difference between forest types. This can be seen in Figure 6.2, where each point is an additional log. In particular, a total of 207 and 213 saproxylic beetle species had emerged from 14 and 15 large diameter logs in mature unlogged and logging regenerated forests respectively, of which 20 and 18 species were singletons. By contrast, 159 and 154 species emerged 15 and 12 small diameter logs in mature unlogged and logging regenerated forests respectively, of which of 28 and 29 species occurred as singletons.

6.3.2.4 Estimated species richness - number of individuals

Rarefied species richness was consistently lowest for small diameter logs in logging regenerated forests, whether considering all species (Figure 6.3a), obligate taxa only (Figure 6.3b) or facultative taxa only (Figure 6.3c). They hosted around 20 obligate species fewer than the other treatments. Rarefaction curves based on obligate species show a similar trend to curves based on all species. Small diameter logs in mature-unlogged forests had the highest estimated species richness of facultative beetles (Figure 6.3c).

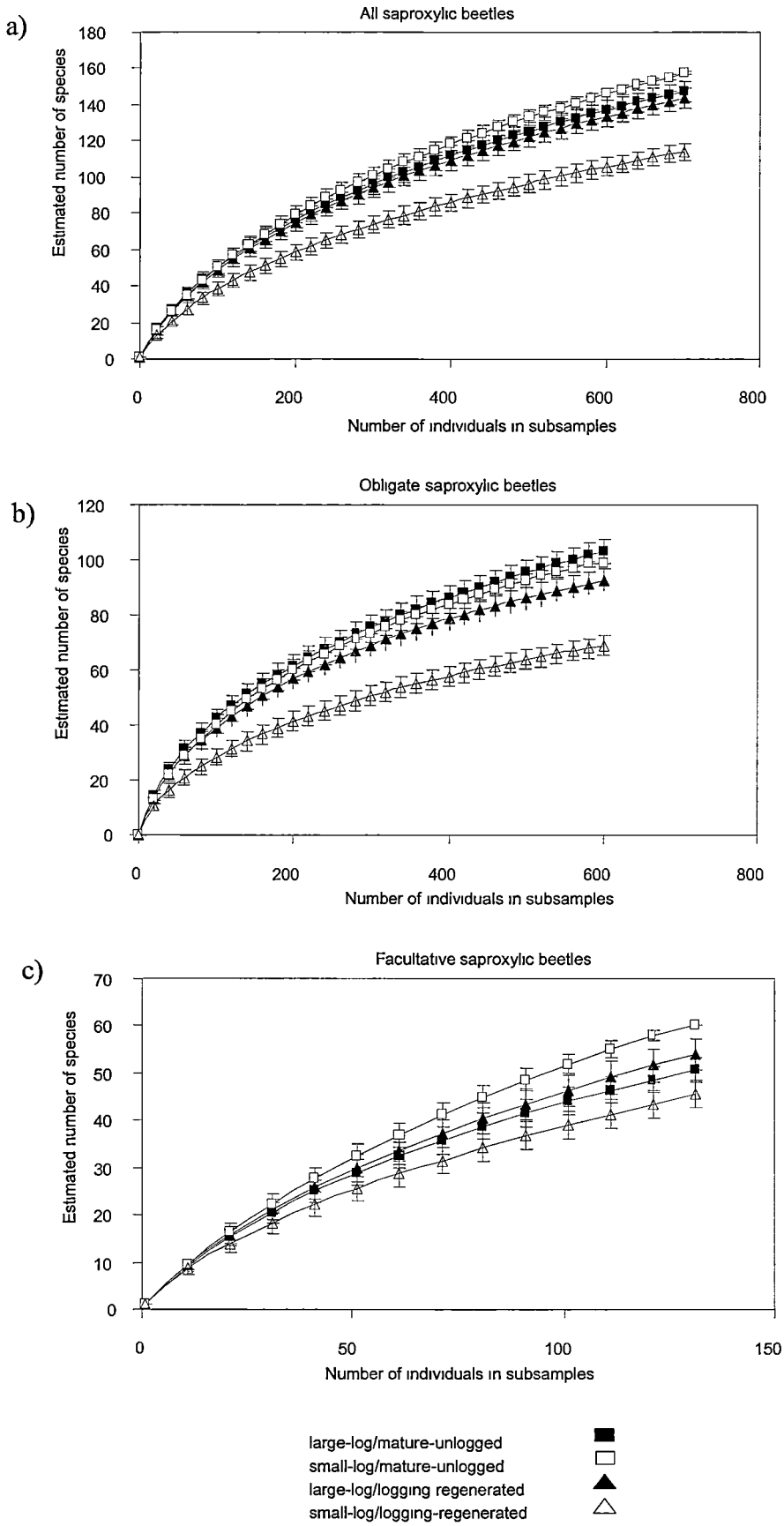


Figure 6.3 Rarefaction estimates of a) all, b) obligate and c) facultative saproxylic beetles species collected from logs grouped by log size/ forest type

6.3.3 Species diversity

Rank abundance plots from each log size/forest type treatment (Figure 6.4) generally revealed numerical dominance by just a few species, with a large number of uncommon species, and many rare species, including a high proportion of singletons. For large diameter logs, species abundance distributions were similar between forest types. In the logging regenerated forests, the logs, irrespective of log size, supported species that occurred in high abundances (> 200 individuals) (Figure 6.4, Table 6.2). Small logs in mature unlogged forests had the fewest abundant species.

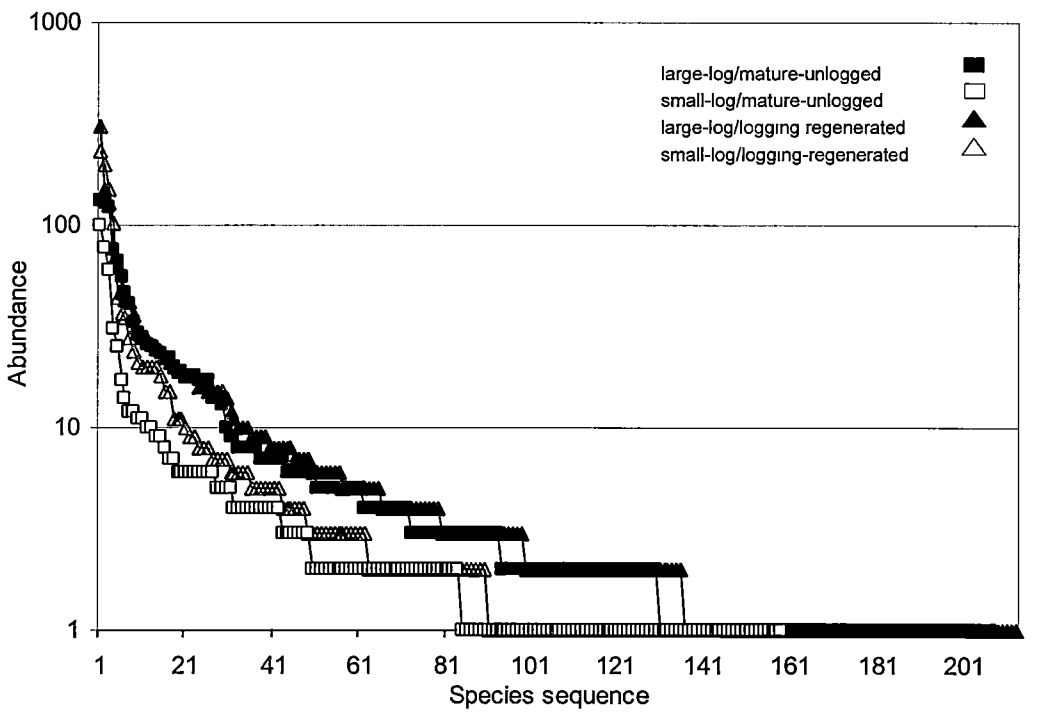


Figure 6.4. Rank abundance curves of saproxylic beetles from *Eucalyptus obliqua* logs pooled by log-size/forest type, collected using log emergence traps in southern Tasmania. Note that the y-axis is logarithmic

6.3.4 Beetle assemblage differences among log size/forest types

6.3.4.1 Unconstrained analyses

According to the PERMANOVA results, beetle assemblages of logs within mature unlogged forest sites differed significantly from those in the logging regenerated forest sites (Table 6.3). This can be seen in the NMS ordination plot, which shows a distinct, if incomplete, separation of logs along axis 2 (Figures 6.5a,b). *Ancytallia tarsalis* (Curculionidae) and *Aulonothroscus elongatus* (Throscidae) correlated with the ordination ($r^2 > 0.20$), in the direction along axis 2, which is towards logs in mature unlogged forests.

Beetle assemblages differed significantly between large and small diameter logs (Table 6.3, see Figure 6.5a along axis 1). *Enneaphyllus aeneipennis* (Cerambycidae) correlated with the ordination ($r^2 > 0.20$) towards the cluster of small diameter logs; and *Prionocyphon?* TFIC sp 01 (Scirtidae), *Aleocharinae* TFIC sp 13 (Staphylinidae), and *Decilaus striatus* (Curculionidae) correlated towards the cluster of large diameter logs. Note, that the separation of logs by forest type (squares versus triangle symbols) seemed greater than their separation by size (closed versus open symbols), as indicated by the overlap of log treatments (Figures 6.5a,b).

While it is possible that the assemblage differences between large and small diameter logs based on log transformed species abundance may be due to confounding effect of greater sampling effort for large diameter logs, repeating the NMS ordination using presence/absence data revealed a similar pattern. Large and small diameter logs seperated along Axis 3 (closed versus open symbols, Figure 6.6b). However, when based on presence/absence data, there appears little distinction in species composition between logs by forest type (Figure 6.6a,b).

Beetle assemblages, when based on species abundance data, varied significantly among sites (Table 6.3), and the effect of log size varied significantly among sites, as indicated by the significant site(forest type) by log size interaction (Table 6.3).

Table 6.3. PERMANOVA results on the basis of Bray-Curtis dissimilarities for saproxylic beetle assemblages (233 species) after $\log_{10}(x+1)$ transformation. Used 4999 unrestricted randomised permutations were used.

Source	Degrees of Freedom	Sum of Squares	Mean Squares	F-ratio	P(perm)
Forest type	1	1.013	1 013	1 731	0.0326
Site(Forest type)	8	4.6818	0.5852	2.1481	0.0001
Log size	1	0.5336	0.5336	1.5714	0.0337
Forest type x Log size	1	0.3382	0.3382	0.9959	0.4585
Site(Forest type) x Log size	8	2 7166	0.3396	1.2464	0 0058
Residual	36*	10.8975	0 2724		
Total	59	20 1807			

* Modified residual degrees of freedom because data from four logs were excluded from analyses.

6.3.4.2 Constrained analyses

As shown in the CAP ordination, beetle assemblage structure significantly related to forest type, with a squared canonical correlation of $\delta^2 = 0.68$ ($p = 0.0001$). It also significantly related to log size ($\delta^2 = 0.5$, $p = 0.0015$) (Table 6.4). Graphing the logs on the canonical axes corresponding to the two main effects showed that components of the assemblages were distinct among the four treatments (Figure 6.7). Logs grouped by forest type had a lower misclassification error than log size, as indicated by the leave-one-out allocation success diagnostic (Table 6.4). This implies that forest type has a greater effect on assemblage structure than does log size.

In terms of the joint plot of vectors of species correlating ($|r| > 0.35$) with the canonical axes for forest type and log size, this showed no species were correlating in the direction of small diameter (Figure 6.8)

Table 6.4. Results of two canonical analyses of principal coordinates (CAP), examining the effects of forest type, and of log size. %Var = percentage of the total variation explained by the first m principal coordinate axes. Allocation success = percentage of points correctly allocated into each group. δ^2 = squared canonical correlations.

Factor	m	% Var	Allocation success (%)			δ^2	p
			Group 1	Group 2	Total		
Forest type	18	82.14	88 89 (logging-regenerated)	79.31 (mature-unlogged)	83.93	0.68	0.0001
Log size	13	48.21	68.97 (large)	77.78 (small)	73.21	0.50	0.0015

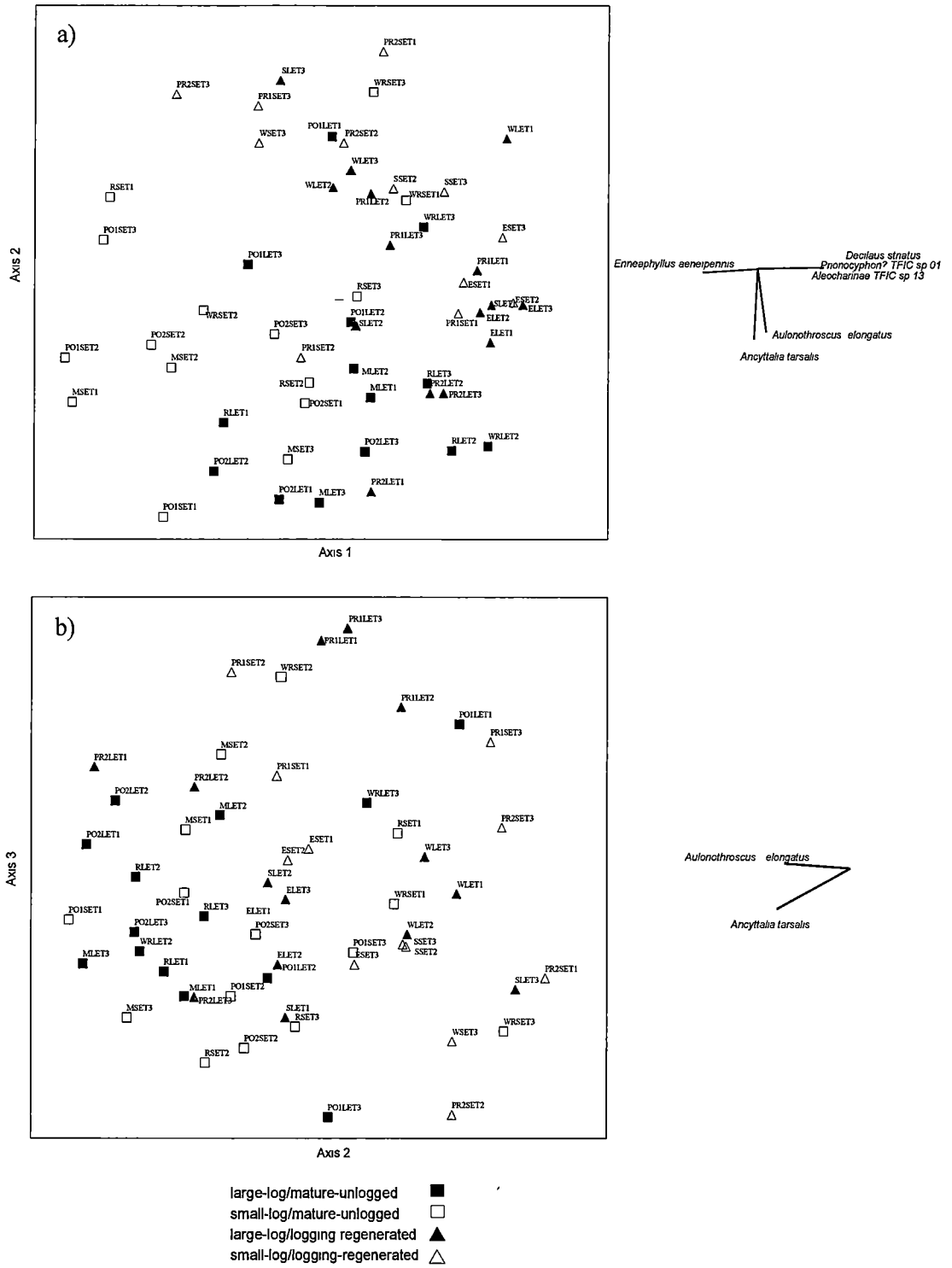


Figure 6.5. Non-metric multidimensional scaling (NMS) ordination plot for saproxylic beetle species abundance data from 56 log emergence traps at 10 study sites, showing axes a) 1 and 2, and b) 2 and 3. Symbols are log-size/forest type treatment group. Vectors are defined by beetle species abundance data; for greater clarity, these are displayed adjacent to the ordination. Vector scaling 100%. Only vectors with $r^2 > 0.2$ are shown. Species abundance data for each log were $\log_{10}(x+1)$ transformed. Singletons were excluded. N=233 species Stress = 20.7.

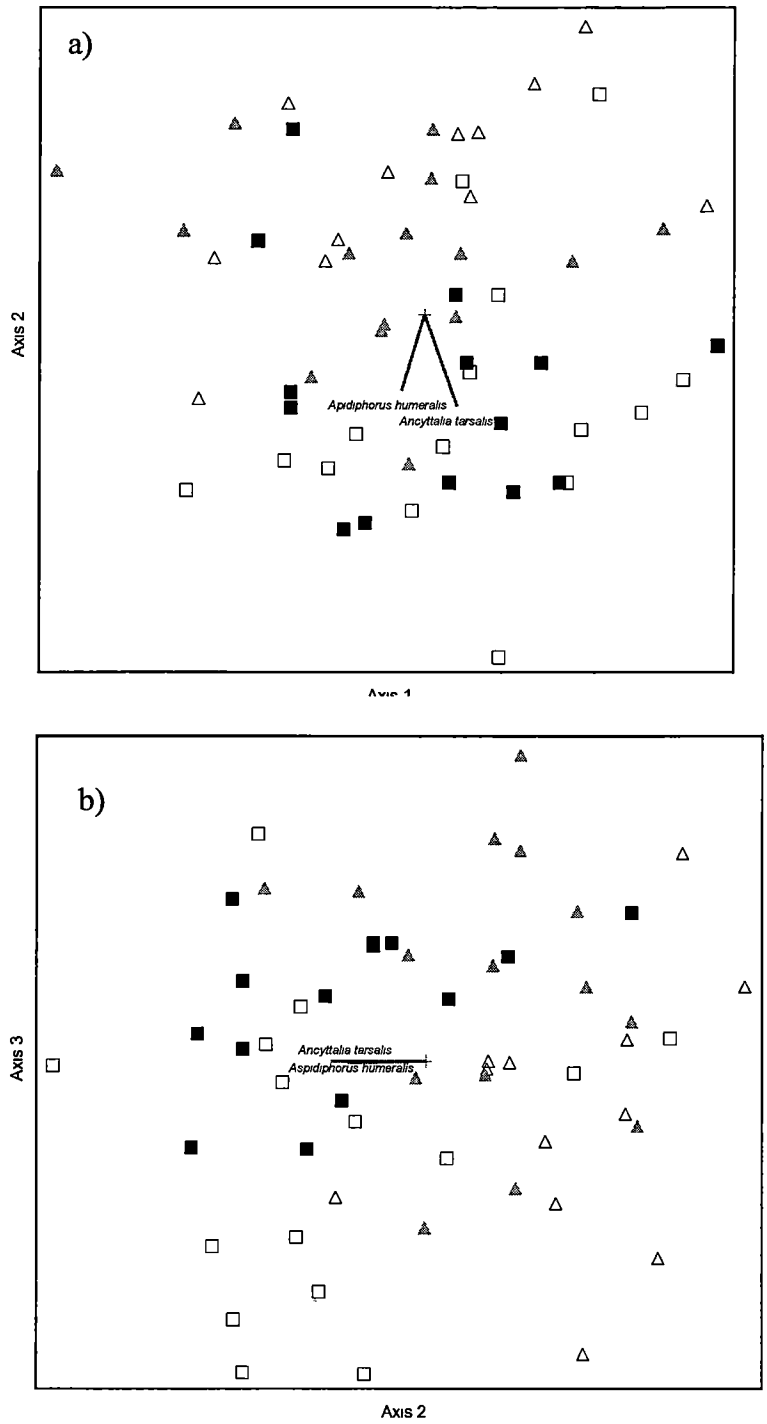


Figure 6.6. NMS ordination plot for saproxylic beetle presence/absence data from 56 log emergence traps at 10 study sites, showing axes a) 1 and 2, and b) 2 and 3. Symbols are log-size/forest type treatment group. Vectors are defined by beetle species abundance data and only vectors with $r^2 > 0.2$ are shown. Vector scaling 100%. Singletons were excluded. N=233 species. Stress = 23.9.

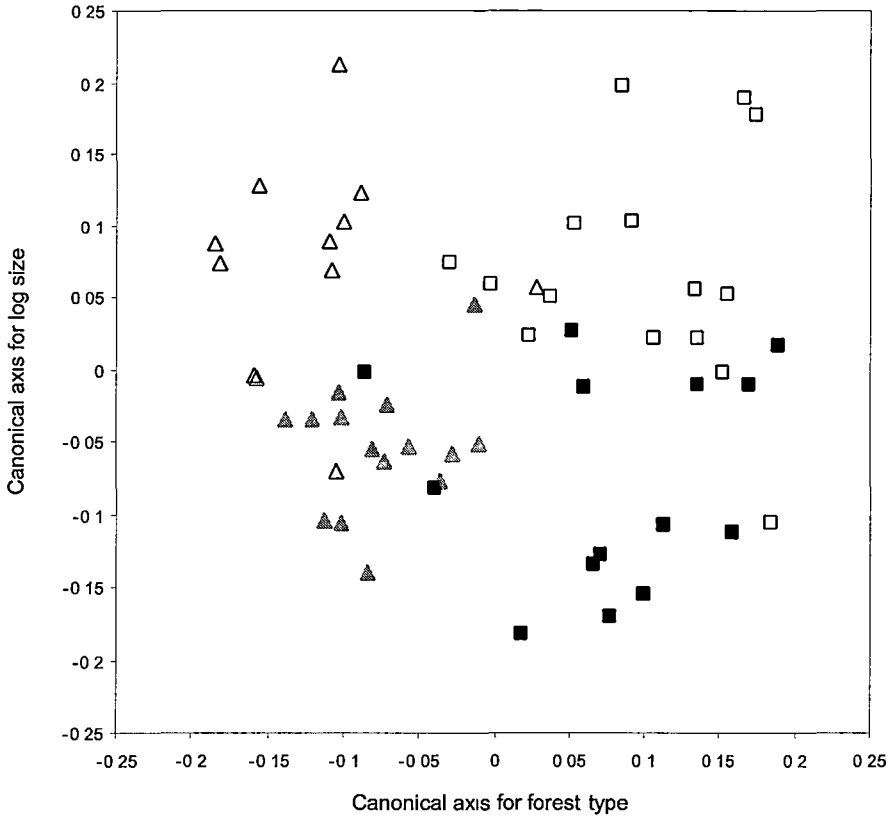


Figure 6.7. Two-dimensional scatter plot of the canonical axes for forest type and log size. N=233 species (singletons excluded), and data were $\log_{10}(x+1)$ transformed.

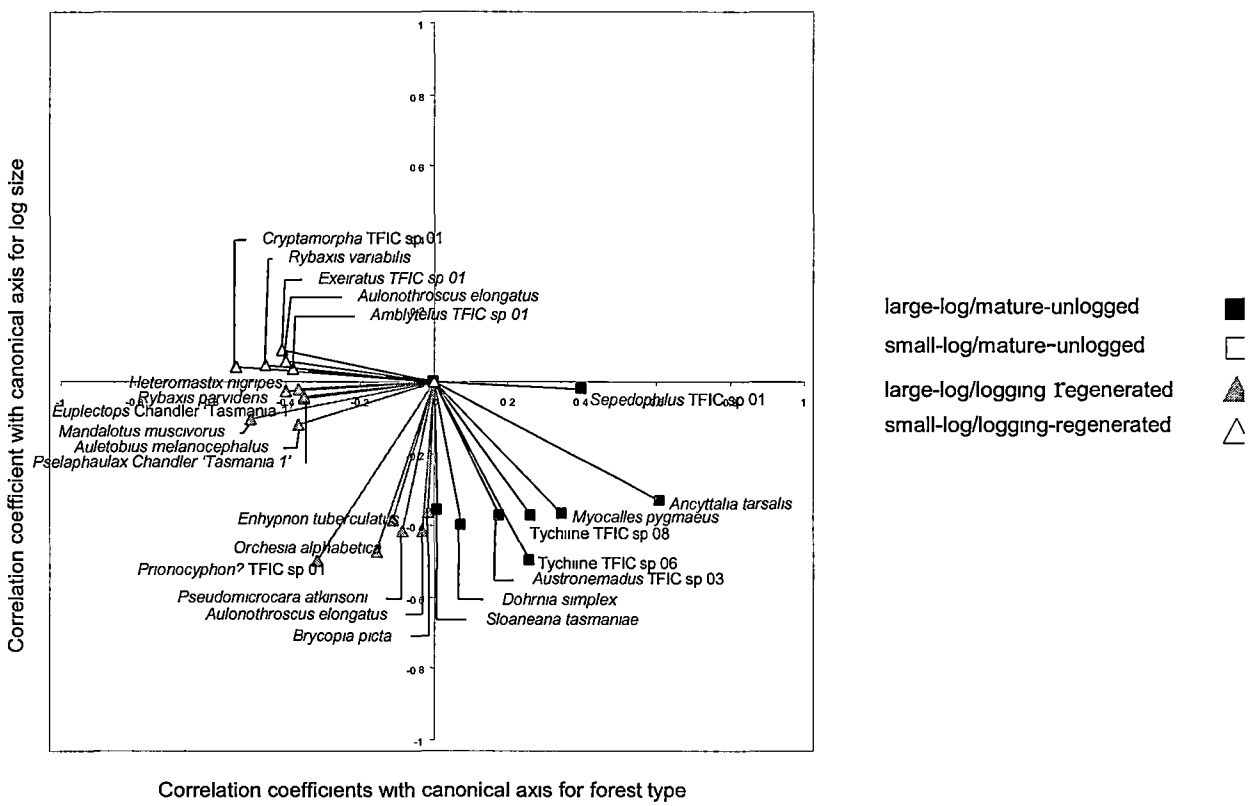


Figure 6.8. Joint plot of species correlated ($r > 0.35$) with the canonical axes for forest type (x-axis) and log size (y-axis).

6.3.5 Species habitat preferences

Species habitat preferences were investigated using Indicator Species Analysis. Many of these species with a habitat preference (IndVal >25, $p < 0.05$) had also correlated ($| r | > 0.30$) with the canonical discriminant axis from CAP of the same treatment, and so this data is also presented with the corresponding species.

By combining the results of the five indicator species analysis for i) forest type, ii) log size, iii) log size within mature unlogged forest, iv) log size within logging regenerated forest and v) site (Table 6.5 – 6.8), as described in Section 6.2.6, as well as checking the raw species abundance scores by treatment (Table 6.2), species were grouped into one of five categories. Raw species abundance scores by treatment are listed in Appendix 6.1 and species with an IndVal > 25, $p < 0.05$ are marked in bold. The five categories are 1) specialists of a forest type (irrespective of log size); 2) specialists of a log size class (irrespective of forest type); 3) specialists of a certain forest type (irrespective of log size) while being specialists of large diameter logs in the other forest type; 4) specialists of large diameter logs within a certain forest type only; 5) and species that showed a strong affinity with a particular site.

6.3.5.1 Specialist of a forest type

Four species were indicative of mature unlogged forests, two of which were also indicative of large diameter logs: *Ancyttalia tarsalis* (Curculionidae) and *Chylnus ater (Carabidae).*

Ancytallia tarsalis was indicative of the mature unlogged forests (Table 6.5), and this was indicative of large diameter logs when individuals were present in logging regenerated forests (Table 6.7) - found in six of the 15 large diameter logs in logging regenerated forests but absent in all small diameter logs in logging regenerated forests (Table 6.2). *Chylnus ater* (Carabidae) was also indicative of mature unlogged forest, and was collected from two large diameter logs in logging regenerated forest (Table 6.2).

Six species were indicative of logging regenerated forests (Table 6.5). Of which, *Cryptamorpha* TFIC sp 01 (Silvanidae), *Mandalotus muscivorus* (Curculionidae),

Aleocharinae TFIC sp 13 (Staphylinidae) and *Decilaus lateralis* (Curculionidae) were common across all logging regenerated sites (See Appendix 6.1). *Decilaus lateralis,* which was also indicative of large diameter logs was in six large diameter logs in mature unlogged forests, and absent on all six small diameter logs in mature unlogged forest (Table 6.2, Appendix 6.1). *Cryptamorpha TFIC sp 01* was also indicative of site E (Table 6.8).

Table 6.5. Combined results of Indicator species analysis for the effect of forest type and corresponding correlation analyses based on canonical axis derived from CAP analysis for forest type. Species in bold had also showed preferences for a particular log size class – see Table 6.5.

	Species name	Family	Indicator species analysis		Correlation coefficient with canonical axis for forest type
			IndVal	p - value	
Mature unlogged forest	***Chylnus ater***	Carabidae	25.6	0.031	0.2279
	Ancyttalia tarsalis	Curculionidae	64	0.001	0.6113
	Exithius capucinus	Curculionidae	29.6	0 032	0 3221
	Myocalles pygmaeus	Curculionidae	31.7	0 018	0.3463
Logging regenerated forest	*Cryptamorpha TFIC sp 01*	Cryptophagidae	56.7	0.002	-0 5342
	Decilaus lateralis	Curculionidae	27 4	0.041	-0 2518
	Exeiratus TFIC sp 01	Curculionidae	30 5	0.022	-0 4069
	Mandalotus muscivorus	Curculionidae	48.5	0.001	-0.4901
	Aleocharinae TFIC sp 13	Staphylinidae	36.4	0.01	-0.3253
	Startes CHANDLER 'Tasmania 1'	Staphylinidae Pselaphinae	27.9	0.009	-0.3791

6.3.5.2 Specialist of a log size class

No species were indicative of small diameter logs (Table 6.6). By contrast, nine species were indicative of large diameter logs.

When analysing only data from the mature unlogged forests, 9 species were indicative of large diameter logs and none for small diameter logs (Table 6.7). This included *Lissotes subcaeruleus,* which was also indicative of site M (Table 6.8).

When only analysing data from the logging regenerated forests, 3 species were indicative of large diameter logs and none for small diameter logs (Table 6.7). This included *Ancytallia tarsalis,* which when analysing all data combined, was indicative of the mature unlogged forest (Table 6.6).

Table 6.6. Combined results of of Indicator species analysis for the effect of log size and corresponding correlation analyses based on canonical axis derived from CAP analysis for log size. Species in bold also showed preferences for a particular forest type – see Table 6.5. Species abundance data for each species is listed in Appendix 6.1

	Species name	Family	Indicator species analysis		Correlation coefficient with canonical axis for log size
			IndVal	p value	
Large diameter logs	***Chylnus ater***	Carabidae	25 6	0.038	-0 3435
	Trechimorphus diemenensis	Carabidae	37.7	0.047	-0 3545
	Ancyttalia tarsalis	Curculionidae	43	0 039	-0.3315
	Decilaus lateralis	Curculionidae	29 9	0 012	-0.2802
	Tychiinae TFIC sp 08	Curculionidae	28	0.011	-0.3743
	Orchesia alphabetica	Melandryidae	47.9	0.01	-0.4697
	Dohrnia simplex	Oedemeridae	42.4	0.025	-0 3976
	Platypus subgranosus	Platypodinae	25.9	0.043	-0 1742
	Aulonothroscus elongatus	Throscidae	35.7	0.048	-0 4415

Table 6.7. Results of indicator species analyses for the effect of log size within a particular forest type. Species in bold also showed preference to either a certain forest type (see Table 6.5), or log size class irrespective of forest type - see Table 6.6. Species abundance data for each species is listed in Appendix 6.1

Species name	Family	IndVal	p - value
Large diameter logs in mature unlogged forest			
Chylnus ater	Carabidae	39.9	0 032
Decilaus nigronotatus	Curculionidae	59 8	0 044
Dinichus terreus	Curculionidae	28.6	0.043
Tychiinae TFIC sp 08	Curculionidae	44 8	0.013
Austronemadus TFIC sp 03	Leiodidae	28.6	0 048
Lissotes subcaeruleus	Lucanidae	28.6	0 036
Melandryidae TFIC sp 04	Melandryidae	28.6	0 045
Dohrnia simplex	Oedemeridae	69	0 002
Prionocyphon? TFIC sp 01	Scirtidae	48	0 01
Large diameter logs in logging regenerated forest			
Ancyttalia tarsalis	Curculionidae	40	0.023
Denticollinae TFIC sp 01	Elateridae	33.3	0.051
Orchesia alphabetica	Melandryidae	64 7	0 005

6.3.5.3 Specialists of a particular study site

Twenty-seven species were indicative of a particular study site (IndVal >= 40, p <= 0.01). Species and their associated sites are listed in Table 6.8.

Table 6.8 Results of indicator species analyses for the effect of site. Site codes refer to sites in Figure 2.1. Underlined species also showed preference to a certain forest type - see Table 6.5. Species abundance data for each species is listed in Appendix 6.1

SITE	Species name	Family	IndVal	p - value
E	*Heteromastix nigripes*	Cantharidae	98.8	0.001
	Amblytelus TFIC sp 01	Carabidae	66.7	0.001
	Decilaus nigronotatus	Curculionidae	51.4	0 001
	Dryophthorus TFIC sp 02	Curculionidae	42.8	0 012
	Metriorhynchus ?erythropterus	Lycidae	41 2	0.019
	Scirtidae YEE sp 14	Scirtidae	43 7	0.014
	Cryptamorpha TFIC sp 01	Silvanidae	73.9	0.001
	Anotylus TFIC sp 03	Staphylinidae	50	0 009
	Pselaphaulax CHANDLER 'Tasmania 1	Staphylinidae – Pselaphinae	83.3	0 001
	Euplectops CHANDLER 'Tasmania 1'	Staphylinidae – Pselaphinae	66 7	0 001
	Palimbolus victoriae	Staphylinidae – Pselaphinae	58 3	0.001
	Rybaxis variabilis	Staphylinidae – Pselaphinae	80 3	0.001
	Rybaxis parvidens	Staphylinidae – Pselaphinae	100	0.001
M	*Pedilophorus multicolor*	Byrrhidae	50	0 008
	Lissotes subcaeruleus	Lucanidae	46 5	0 005
PO1	*Enneaphyllus aeneipennis*	Cerambycidae	50	0.006
	Aridius costatus	Latridiidae	50	0.002
R	*Anthribidae TFIC sp 02*	Anthribidae	50	0.007
	Aporocera lagopus	Chrysomelidae	50	0.005
	Brycopia coelioides	Tenebrionidae	40 7	0.01
S	*Microchaetes scoparius*	Byrrhidae	40	0.012
	Aleocharinae TFIC sp 29	Staphylinidae	61.3	0 001
WR	*Mandalotus sp nr vacillans*	Curculionidae	40	0 011
	Notobrachypterus TFIC sp 01	Nitidulidae	80	0 001
	Staphylinidae YEE sp 02	Staphylinidae	45.7	0.003
	Brycopia hexagona	Tenebrionidae	40	0.017

6.4 DISCUSSION

This study clearly showed that the assemblage compositions of saproxylic beetles from emerging logs differ significantly for each of the effects of forest type, log diameter and site. This chapter discusses these results, while the long term implications of this for conservation and management of saproxylic beetles in production forests are discussed in Chapter 7.

6.4.1 CBS logging regeneration versus mature unlogged forests

This study demonstrates that many saproxylic beetle species can successfully colonise *Eucalyptus obliqua* logging debris left from CBS silviculture after 20-30 years of forest regeneration. This was indicated by similar numbers of species emerging from logs in the logging regenerated forest to those in mature unlogged forests though.

However, the assemblages of beetle emerging from logs within the logging regenerated forests differed significantly to those within the mature unlogged forest, with some species showing a preference for a specific forest type. To some extent, differences in assemblage composition are not surprising as there are many environmental differences between these forest types that could affect their suitability for particular individual species. These differences can be grouped into factors concerning current forest conditions, such as forest age and succession; and factors concerning the history of the decomposing log in relation to the effects of burnt wood, and insect and fungal successional processes. It is likely that a combination of factors is responsible for the resulting differences in assemblage compositions.

6.4.1.1 The effects of forest succession and age

In this study, the logging regenerated forests are considerably younger than mature unlogged forests with a difference in 'time since disturbance' of over 35 years. Not only are these forests of different successional stages, which is also reflected by different vascular plant floristics (see Section 2.9.1, Hickey 1994), but logging-regenerated forests are also more open. Average canopy cover in the logging regenerated sites range between 48.1 and 65.3% compared to 51.8 and 85.9% in the mature unlogged forest sites (Section 2.9.1). It is unlikely that most of the species within the logging

regenerated forest are still responding to the initial clearfell disturbance event. Various studies on the recovery of arthropods following fire show total recovery in less than six years (Collett 1999; Coy 1994; Michaels & McQuillan 1995; Oliver *et al.* 2000; York 1994, 1999b).

Various studies overseas have demonstrated that dead wood dependent fauna vary in relation to forest successional age. For example, Setala & Marshall (1994) demonstrated that Collembola inhabiting log stumps in Canadian Douglas Fir forest varied in relation to the surrounding forest successional age. More recently, Hammond *et al.* (2004) documented the succession of saproxylic beetle assemblage variation in native boreal aspen forests of different stand ages in western Canada; and similarly Similä *et al.* (2002) did so for sub-xeric pine forests in eastern Finland. Moretti & Barbalat (2004) provide a detailed description of xylophagous saproxylic beetle successions relative to wildfire in deciduous forests in Switzerland. However, it is still unclear whether such patterns relate to the successional age of the forest *per se*, to the microclimatic conditions of the forest (Moretti & Barbalat 2004), to log microclimate, or to a combination of these factors.

Species that were specific to the logging regenerated forests in this study may represent a fauna adapted to early successional forest, and/or possibly have a higher tolerance to withstanding greater insolation, and greater temperature and moisture extremes. The numerically dominant species *Cryptamorpha* TFIC sp 01 (Silvanidae) emerged in greater numbers and frequency from logs in the logging regenerated forests than the mature unlogged forest, and further was also more prevalent in the small diameter logs in the logging regenerated forest. This species has often been observed flying during sunny days in summer (pers. obs). Conversely, the apparent specialists of mature unlogged forests are likely to be shade-tolerant, especially for the flightless species (e.g. Meggs & Munks 2003; Moretti & Barbalat 2004).

However, given the dearth of life history information of the majority of species collected, their limited sample size, and the relatively limited area in which this study was conducted, it is not possible to confidently define an individual species habitat preference. For example, it is unknown why the flightless species *Mandalotus*

muscivorus, Decilaus nr striatus/subfasciatus and *D. nigronotatus* were either indicative or at least more abundant in logging regeneration. Though, for some species, the data presented, limited as it is, does support preconceived habitat requirements. For example, *Lissotes subcaeruleus* had only been collected from mature unlogged forests at site M. This species is a flightless obligate saproxylic species that is considered a mature forest specialist due to its sensitivity to environmental conditions typical of older forests, such as dead wood in shaded, moist forest, and is highly sensitive to high light levels (Bornemissza pers. comm). In this study, this species remained absent from logged forests after 20 years of regeneration despite sites being in close vicinity of less than one hundred metres away from source populations.

6.4.1.2 The effects of clearfelling on log successional processes

A major difference in dead wood types between forest types is that in the logging regenerated forests, logs are subject to a high intensity regeneration burn where insect and fungal succession, and thus the decomposition processes, initially occurred under sun-exposed conditions. By contrast, logs in unlogged forests of a mature forest age would be recruited by natural causes: some by tree-fall of fire-killed trees, but many from rot and windfalls, and most logs would have effectively began decomposition and succession within relatively closed forest conditions.

It is highly probable that decomposing logs within mature unlogged forests undergo different initial log successions from those in the logging regenerated forests. Burnt wood is likely to be favourable to certain fungi and beetles that benefit from the flush of nutrient and food resources after fire (Coy 1994 - fungi and bacteria; Dajoz 2000; Esseen *et al.* 1997; Penttilä & Kotiranta 2001 - beetles and fungi; Wikars 1992 - beetles; Wikars 2001, 2002). Studies in northern Europe have demonstrated that sun-exposed dead wood undergoes different colonisation of insect and fungal assemblages compared to dead wood occurring in shaded conditions (Buisson 1999; Jonsell *et al.* 1998; Kaila *et al.* 1997; Lindhe 2004; Martikainen 2001; Ranius & Jansson 2000; Sverdrup-Thygeson & Ims 2002- saproxylic beetles in stags; Lindhe *et al.* 2004 - wood decay fungi in logs and high stumps). In wet eucalypt forests that have evolved with wildfire, it is probably a combination of both burnt and open forest conditions that drive the colonisation of early successional specialists. This has been demonstrated in a Swedish

experimental field study (Wikars , 2002), which compared burnt and unburnt spruce and birch logs in burnt and open unburnt forests.

Because the present study has only be been conducted at one point in time, it remains unclear as to whether past log successions can influence the occurrence of saproxylic beetle species decades after log decomposition was initiated. However, initial insect and fungus colonisers of dead wood both theoretically and empirically determine the subsequent succession of wood decay fungi (Boddy 2001; Rayner & Boddy 1988), arthropods (Swift & Boddy 1984), possible rotten wood types (see Section 4.4.4); and saproxylic beetles can be intimately associated with these factors (Chapter 5, e.g. Kaila *et al.* 1994).

6.4.2 Large versus small diameter logs

This study was particularly concerned with understanding the specific ecological roles of large diameter logs at maintaining saproxylic beetle biodiversity. In summary, this study showed that although small diameter logs showed an indication that they might support more species on the basis of equal surface area and/or equal log volumes, large diameter logs irrespective of forest type supported distinct assemblages of saproxylic beetles, with species showing a greater occurrence for small diameter logs. In addition, in the logging regenerated forest, there was a lack of apparent mature forest specialists in small diameter logs, yet such species were present in large diameter logs.

6.4.2.1 Species richness and diversity in relation to log diameter class

It is often considered that large diameter logs host higher number of species than small diameter logs (e.g. Kappes & Topp 2004; Kleinevoss *et al.* 1996; Kolström & Lumatjärvi 2000). In this study, species richness varied depending on whether trap samples were compared based on standardised surface area (Section 6.3.2.1), equal surface area and volume (Section 6.3.2.2), equal numbers of logs (Section 6.3.3.3), or equal numbers of individuals collected (Section 6.3.3.4). It may be more important, however, to consider the ecological implications of these results. Combining the results of these analyses suggests that species richness increases more clearly with log surface area than with log volume, and increases more clearly with number of individual logs *per se* than with log volume. Higher animal activity occurring on the outer layers of the

log is one possible explanation for this result, as has been suggested by Kappes & Topp (2004), who sampled beetles emerging from beech wood in a German forest. The litter/surface layer was found to be a productive microhabitat for saproxlic beetle species associated decomposing *Eucalyptus obliqua* logs (see Section 3.3.2.2 and Section 5.3.2). Such higher productivity may relate to the rich and diverse food types, such as fungi (Bader *et al.* 1995; Niemelä *et al.* 1995), cryptogams (Andersson & Hytteborn 1991; Kruys *et al.* 1999; Turner 2003), bacteria and micro- and macroarthropods colonising and sheltering on the log surface, as well as this being an easily accessible microhabitat type for colonisers.

The findings also indicate that small diameter logs show a trend for supporting more species than large diameter logs. This trend, however, should be interpreted with caution. It is unknown as to what point species saturation point occurs for small diameter logs. Moreover, increasing the amount (volume, surface area) or number of small diameter logs may still not support those species that were indicative of large diameter logs.

6.4.2.2 Large diameter logs support distinct suites of species

For species indicative of large diameter, logs, there is a dearth of information of their life-histories, but it is likely that their habitat requirements vary among species. For some species though, log size preference can be explained by their apparent association for certain log decomposition processes strongly associated with a log diameter class. For example, members of the Scirtidae family, particularly *Prionocyphon? TFIC sp 01,* are associated with the wet cracks, which commonly occur in large diameter logs. *Dohrnia simplex* (Oedemeridae), which was indicative of large diameter logs, is associated with red-brown blocky fibrous and discoloured wood rots, which are rots more prevalent in large diameter logs.

Based on the results of Chapter 5, it was expected that the four species *Cossonus simsoni* (Curculionidae), *Prostomis atkinsoni* (Prostomidae), *Dryophthorus* TFIC sp 01 (Curculionidae) and *Pycnomerus* TFIC sp 02 (Zopheridae), which are associated with inner brown rot would have exhibited a preference for large diameter logs based on this association (discussed in Section 5.4). They were however not collected in sufficient

numbers to confirm or reject this hypothesis. The low sample size is likely to be an artefact of sampling by emergence traps. From destructive sampling, they were among the most common species found, and field and laboratory observations suggest that these species have low emergence rates (see Section 5.4). Thus, the lack of observed habitat preference possibly reflects the limitations associated with using log emergence traps to sample beetles with low emergence rates or long development times (see Section 3.4.4).

Interestingly, no species were indicative of small diameter logs. A similar phenomenon was found by Hammond *et al.* (2004) for *Populus* spp. snags of different diameters in boreal aspen forests in Canada. It should be noted that while *Enneaphyllus aeneipennis* (Cerambycidae) was expected to be indicative of small diameter logs as it is associated with white outer heartwood rots (Section 5.3.3), which are rots markedly more common in small diameter logs (Section 4.3.2), it had only emerged from small diameter logs. In general though, one may conclude that because of the non-specificity towards small diameter *E. obliqua* decomposing logs, these logs support beetles with more general habitat requirements. That is, rather than supporting its own specific fauna or certain species at the same population levels as those found in large diameter logs. This implies that although small diameter logs function as important habitat for saproxylic beetles, retaining them alone as a means to mitigate the loss of large diameter logs might not cater for the conservation of species indicative of large diameter logs.

6.4.2.3 Large diameter logs as legacy habitats - spatial and temporal stepping stones in disturbed forests

Large diameter logs, and not small diameter logs, in the logging regenerated forests shared two species which were otherwise indicative of mature unlogged forest, irrespective of log size. This could suggest that large diameter logs represent a similar habitat type, irrespective of forest succession or age (least after 20 years of forest regeneration) to some species. The flightless carabid predator *Chylnus ater* is considered a mature forest specialist (Darlington 1961; Michaels 1999; Michaels & McQuillan 1995). It showed a strong preference for mature-unlogged forests, particularly large diameter logs, but was also found in large diameter logs within the logging regenerated forest. Similarly, *Ancytallia tarsalis* showed a strong association

with mature-unlogged forests, occurring in 80% of logs sampled within mature unlogged forests sampled. When present in the logging regenerated sites though, it only occurred in large diameter logs. Conversely, large diameter logs in mature unlogged forests shared similar species (e.g. *Aleocharinae* TFIC sp 13 and *Decilaus lateralis*) to those indicative of logs in logging regenerated forest, irrespective of log size. However, no explanation can be given for this phenomemon.

Large diameter logs generally hold more moisture than smaller sized logs (Amaranthus *et al.* 1989; Harmon *et al.* 1986), have lower decay rates (Harmon *et al.* 1986 ; Mackensen *et al.* 2003; Stone *et al.* 1998), can be less affected by fire damage (Slijepcevic 2001), and have a greater potential for internal decay to be present at the time of their recruitment (see Section 4.4.2.1). These factors, combined with their sheer size infers that large diameter logs potentially provide a greater buffer against desiccation and extreme local climatic (temperature, light and moisture) conditions, which are typical of recently clearfelled forests (Florence 1996). Thus, large diameter logs may provide a more stable microclimate irrespective of the external forest conditions. This would be important for species with larvae that are sensitive to these extremes. Topp (1994) shows that the larval stages of many forest floor dwelling beetles are susceptible to desiccation and have higher survival rates in saturated habitats.

The presence of apparent mature forest specialist in large diameter logs within logging regenerated forests further support the idea that log microclimate is an important determining factor of habitat occupancy of species, in addition to the forest condition or forest age *per se*. If so, then this suggests that large diameter logs may function as important spatial or temporal stepping stones (see Bennett 1999) in early to mid successional forests where open forest conditions prevail, especially for species limited by their requirements for stable (micro) climatic conditions, irrespective if such conditions are provided by the log, or the forest. In other words, large diameter logs may provide suitable habitat for species to disperse through a regenerating forest, or persist in one until such a stage as tree-canopy closure. However, without quantitative data on log temperature or moisture variability in different sized logs under different forest conditions, nor information on species developmental responses to fluctuating microclimatic conditions, this remains a hypothesis warranting further investigation.

Saproxylic beetle assemblages were more similar among logs within sites (within $50m^2$ study plot) than those between sites, irrespective of forest type or log size (within this $10km^2$ range). This possibly indicates a founder effect during colonisation events, as has been suggested from Swedish genetic studies on the saproxylic beetle *Bolitophagus reticulates* (e.g. Jonsson *et al.* 2003; cf. Knutsen *et al.* 2000). Wikars (2002), when comparing burnt and unburnt logs at three burnt sites, also found assemblage response to site effects more stronger than the effect of dead wood type, further implying a founder effect for some species.

6.5 CONCLUSION

The results of this study showed that many saproxylic beetle species could successfully colonise *Eucalyptus obliqua* logging debris after 20-30 years of forest regeneration in wet eucalypt forests. However, assemblage composition differed significantly from that of mature unlogged forest. There are many interrelated differences between 20-30 year old CBS disturbed and more mature wildfire disturbed forest stands that may explained this result. Viewing the forest as a regenerating system in which forest successional processes operate, the differences between forest types can be grouped into those relating to current conditions, and those relating to past conditions. The present study, however, reflects a snap-shot approach. As the biology and habitat requirements of most species collected in this study are unknown, the extent to which current and historical factors (relating to log decomposition processes), influence their habitat occupancy is unknown.

This study clearly showed that large diameter logs play a specific ecological role, different from that of small diameter logs. Not only were different saproxylic beetle assemblages supported to that of small diameter logs, but such logs when present within logging regenerated forest hosted some apparent mature forest/ or stable microclimate specialists that remained to be absent from adjacent small diameter logs. Thus indicating that large diameter logs could be important in providing continuity of habitat for the re-establishment of certain species (such as mature forest specialists/ or stable microclimate specialists) following stand level disturbances, whether indicated by logging or by wildfire.

6.6 APPENDICES

Appendix 6.1 Taxanomic list of saproxylic beetles collected from 56 *Eucalyptus obliqua* logs in in wet eucalypt forest in southern Tasmania using emergence trapping. The Number of logs in which species were present in, and the total number of Individuals collected [N(I)] is listed for each site by log size (SITECODE.LOGSIZE) treatment. Site codes E, S, W, PR1, PR2, M, PO1, PO2, R, and WR refer to sites in Figure 2.1. Note, sites are grouped by forest type. Log size: L = large diameter logs, S = small diameter logs. Three logs were sampled for each site by log size treatment. Though, for W.S group, data from only one log was analysed. For S.S group, data from only two logs were analysed, and for WR.L group, data from only two logs were sampled. See section 6.2.2 for explanation. Singletons have been excluded from the list. Species marked in bold were either indicative of of a forest type, log size, log size within forest type, or site. Species are listed in taxanomic order.

Family	Species name	LOGGING REGENERATED FOREST SITES										MATURE UNLOGGED FOREST SITES									
		E L	E S	S L	S S	W.L	W S	PR1 L	PR1 S	PR2 L	PR2 S	M L	M S	PO1 L	PO1 S	PO2 L	PO2 S	R L	R S	WR L	WR S
Carabidae	*Amblytelus placidus*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Carabidae	***Amblytelus TFIC sp 01***	**1(1)**	**3(4)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**
Carabidae	***Chylnus ater***	**0(-)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**	**0(-)**	**2(4)**	**1(1)**	**0(-)**	**1(1)**	**2(15)**	**0(-)**	**1(3)**	**0(-)**	**1(3)**	**0(-)**
Carabidae	*Notonomus politulus*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	1(1)	0(-)	1(1)	1(1)
Carabidae	*Percodermus niger*	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)
Carabidae	*Percosoma carenoides*	0(-)	2(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Carabidae	*Promecoderus tasmanicus*	1(1)	1(1)	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)
Carabidae	*Pterocyrtus tasmanicus*	0(-)	0(-)	2(5)	1(1)	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(19)	1(1)	1(1)	1(1)
Carabidae	*Rhabdotus reflexus*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(2)	1(1)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Carabidae	*Scopodes intermedius?*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Carabidae	*Sloaneana tasmaniae*	0(-)	0(-)	2(7)	0(-)	0(-)	0(-)	0(-)	1(2)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(8)	1(1)	1(6)	1(1)
Carabidae	*Stichonotus leai*	0(-)	0(-)	2(6)	0(1)	1(2)	0(-)	0(-)	0(-)	1(2)	2(5)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	2(6)	0(-)	1(1)	1(1)
Carabidae	***Trechimorphus diemenensis***	**2(16)**	**2(3)**	**2(5)**	**2(5)**	**1(2)**	**0(-)**	**1(1)**	**1(3)**	**2(3)**	**0(-)**	**0(-)**	**1(1)**	**2(12)**	**0(-)**	**2(3)**	**0(-)**	**2(4)**	**2(2)**	**0(-)**	**0(-)**
Ptiliidae	*Ptiliidae TFIC sp 01*	0(-)	0(-)	1(1)	1(-)	1(1)	1(1)	1(1)	0(-)	0(-)	1(1)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	1(1)	1(2)	1(1)
Ptiliidae	*Ptiliidae TFIC sp 03*	1(1)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Ptiliidae	*Ptiliidae TFIC sp 04*	1(1)	0(-)	2(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(2)	1(1)	0(-)	1(1)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Leiodidae	*Austronemadus TFIC sp 01*	2(3)	2(3)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(4)	0(-)
Leiodidae	***Austronemadus TFIC sp 03***	**0(-)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(2)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**1(2)**	**0(-)**	**1(5)**	**0(-)**
Leiodidae	*Leiodidae TFIC sp 02*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)
Leiodidae	*Myrmicholeva ligulata*	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	1(5)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Leiodidae	*Nargomorphus jeanneli*	1(1)	0(-)	1(1)	0(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Leiodidae	*Nargomorphus TFIC sp 01*	0(-)	1(1)	0(-)	1(1)	1(1)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Leiodidae	*Neopeltops TFIC sp 01*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	1(2)	0(-)	0(-)	1(22)	0(-)	0(-)	0(-)
Leiodidae	*Paragyrtodes percalceatus*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(2)	0(-)	0(-)	1(1)	0(-)
Scydmaenidae	*Scydmaenidae TFIC sp 03*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(2)	0(-)	0(-)
Scydmaenidae	*Scydmaenidae TFIC sp 04*	0(-)	1(2)	1(1)	0(-)	0(-)	0(-)	0(-)	1(3)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)
Scydmaenidae	*Scydmaenidae TFIC sp 05*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	1(1)	0(-)	1(1)	0(-)	0(-)
Scydmaenidae	*Scydmaenidae TFIC sp 06*	1(1)	1(1)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)

Family	Species name	LOGGING REGENERATED FOREST SITES										MATURE UNLOGGED FOREST SITES									
		E L	E S	S L	S S	W L	W S	PR1 L	PR1 S	PR2 L	PR2 S	M L	M S	PO1 L	PO1 S	PO2L	PO2 S	R.L	R S	WR L	WR S
Scydmaenidae	*Scydmaenidae* TFIC sp *07*	1(4)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(2)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Scydmaenidae	*Scydmaenidae* TFIC sp *10*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	1(8)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	2(2)
Scydmaenidae	*Scydmaenidae* TFIC sp *11*	2(2)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Scydmaenidae	*Scydmaenidae YEE sp X*	2(4)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Staphylinidae	*Aleocharinae* TFIC sp *01*	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(14)	1(2)	1(1)	0(-)
Staphylinidae	*Aleocharinae* TFIC sp *04*	0(-)	0(-)	0(-)	1(-)	1(1)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Staphylinidae	*Aleocharinae* TFIC sp *10*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(2)	2(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	1(1)	0(-)	0(-)
Staphylinidae	***Aleocharinae* TFIC sp *13***	**2(14)**	**3(3)**	**0(-)**	**3(7)**	**1(19)**	**0(-)**	**0(-)**	**1(1)**	**2(3)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**2(4)**	**1(1)**
Staphylinidae	*Aleocharinae* TFIC sp *14*	2(2)	2(33)	0(-)	2(13)	2(59)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	0(-)	0(-)	0(-)	1(1)	1(1)	0(-)	1(1)	1(1)
Staphylinidae	*Aleocharinae* TFIC sp *15*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	2(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Staphylinidae	*Aleocharinae* TFIC sp *26*	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	2(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(2)	1(1)	0(-)
Staphylinidae	***Aleocharinae* TFIC sp *29***	**0(-)**	**0(-)**	**2(4)**	**2(2)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**	**0(-)**	**1(1)**
Staphylinidae	*Aleocharinae* TFIC sp *33*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	1(1)	0(-)	0(-)
Staphylinidae	*Aleocharinae* TFIC sp *34*	0(-)	1(2)	1(1)	2(2)	1(1)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	1(1)	1(1)	0(-)	0(-)	0(-)	1(1)	2(4)	0(-)	0(-)
Staphylinidae	*Aleocharinae* TFIC sp *35*	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Staphylinidae	*Anabaxis* CHANDLER 'Type 1'	2(4)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)
Staphylinidae	***Anotylus* TFIC sp *03***	**1(1)**	**2(6)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**
Staphylinidae	*Anotylus* TFIC sp *04*	1(1)	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Staphylinidae	*Aulaxus* CHANDLER 'Tasmania 1'	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	1(2)	0(-)	0(-)	0(-)	0(-)
Staphylinidae	*Baeocera* TFIC sp *01*	2(3)	2(3)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(8)	0(-)
Staphylinidae	*Chalcoplectus depressus*	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Staphylinidae	*Chichester CHANDLER 'Tasmania 1'*	1(1)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Staphylinidae	*Eupinella dentiventris*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)
Staphylinidae	***Euplectops* CHANDLER 'Tasmania 1'**	**2(2)**	**2(3)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**
Staphylinidae	*Falagria* TFIC sp *04*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Staphylinidae	*Ischnosoma* TFIC sp *01*	1(1)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Staphylinidae	*Logasa* CHANDLER 'Tasmania 1'	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Staphylinidae	*Macroplectus tasmaniae*	0(-)	0(-)	0(-)	0(-)	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)
Staphylinidae	***Palimbolus victoriae***	**1(1)**	**3(6)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**
Staphylinidae	*Protoplectus* CHANDLER 'Tasmania 1'	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Staphylinidae	***Pselaphaulax CHANDLER 'Tasmania1'***	**2(3)**	**3(3)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**
Staphylinidae	*Quedius* TFIC sp *04*	0(-)	1(1)	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)
Staphylinidae	***Rybaxis parvidens***	**3(6)**	**3(20)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**
Staphylinidae	***Rybaxis variabilis***	**2(9)**	**3(23)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**

Family	Species name	LOGGING REGENERATED FOREST SITES										MATURE UNLOGGED FOREST SITES									
		E L	E S	S L	S S	W L	W S	PR1 L	PR1 S	PR2 L	PR2.S	M L	M S	PO1 L	PO1 S	PO2 L	PO2 S	R L	R S	WR L	WR S
Staphylinidae	*Sagola CHANDLER 'Tasmania 2'*	2(6)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	1(3)	0(-)	0(-)	1(1)
Staphylinidae	*Sagola rugicornis*	0(-)	2(3)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)
Staphylinidae	*Scaphisoma indutum*	1(1)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(3)	0(-)	0(-)	0(-)	0(-)	0(-)
Staphylinidae	*Sepedophilus* TFIC sp *01*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(3)	2(8)	0(-)	1(1)	0(-)	0(-)	1(1)	1(1)	1(4)	0(-)
Staphylinidae	*Staphylinidae ANIC 88-0088*	0(-)	1(1)	1(4)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(2)	1(2)	2(3)	0(-)
Staphylinidae	***Staphylinidae YEE sp 02***	**0(-)**	**0(-)**	**0(-)**	**1(-)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(2)**	**2(2)**
Staphylinidae	*Staphylinidae YEE sp 63*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(2)
Staphylinidae	*Staphylininae* TFIC sp *10*	1(1)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Staphylinidae	***Startes CHANDLER 'Tasmania 1'***	**2(3)**	**2(3)**	**1(6)**	**2(2)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**
Staphylinidae	*Tasmanityrus newtoni*	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)
Staphylinidae	*Washpool CHANDLER 'Tasmania 1'*	0(-)	0(-)	0(-)	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(3)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	2(4)	0(-)	0(-)
Lucanidae	*Lissotes cancroides*	3(10)	1(3)	1(1)	1(1)	1(2)	0(-)	1(3)	0(-)	0(-)	2(2)	0(-)	0(-)	1(2)	1(1)	0(-)	1(1)	2(2)	1(1)	1(18)	2(3)
Lucanidae	*Lissotes curvicornis*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	3(6)	0(-)	0(-)	0(-)	0(-)	1(1)	1(3)	0(-)	0(-)	1(5)	0(-)	0(-)
Lucanidae	***Lissotes subcaeruleus***	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**3(16)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**	**0(-)**
Lucanidae	*Syndesus cornutus*	2(8)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	2(4)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	1(1)
Clambidae	*Clambus bornemisszai*	2(6)	0(-)	1(1)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	1(2)	0(-)
Clambidae	*Sphaerothorax tasmani*	1(1)	0(-)	0(-)	1(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	1(1)
Scirtidae	***Prionocyphon?* TFIC sp *01***	**3(10)**	**2(103**	**2(7)**	**1(1)**	**2(20)**	**0(-)**	**2(21)**	**1(4)**	**2(11)**	**0(-)**	**2(3)**	**0(-)**	**1(3)**	**0(-)**	**3(42)**	**1(3)**	**2(55)**	**0(-)**	**1(5)**	**0(-)**
Scirtidae	*Pseudomicrocara atkinsoni?*	0(-)	2(5)	1(1)	0(-)	1(1)	0(-)	0(-)	1(2)	2(13)	0(-)	0(-)	0(-)	1(2)	2(2)	2(4)	0(-)	2(10)	0(-)	1(1)	0(-)
Scirtidae	*Pseudomicrocara* TFIC sp *01*	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(2)	0(-)	0(-)	0(-)	0(-)	0(-)	1(6)	0(-)
Scirtidae	*Pseudomicrocara* TFIC sp *02*	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(2)
Scirtidae	*Scirtidae YEE sp 11*	0(-)	1(35)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)
Scirtidae	***Scirtidae YEE sp 14***	**2(5)**	**1(2)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**
Scirtidae	*Scirtidae YEE sp 15*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	1(1)	0(-)
Byrrhidae	*Microchaetes bryophilus*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(4)	0(-)	0(-)	1(1)	0(-)	1(1)	0(-)	0(-)	1(2)	1(1)
Byrrhidae	*Microchaetes scoparius*	0(-)	0(-)	2(2)	0(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Byrrhidae	*Microchaetes hystricosus*	2(2)	3(8)	1(2)	1(-)	1(1)	0(-)	0(-)	0(-)	2(5)	0(-)	0(-)	0(-)	1(1)	1(1)	1(1)	0(-)	1(1)	1(3)	0(-)	0(-)
Byrrhidae	*Microchaetes scoparius*	0(-)	0(-)	2(2)	0(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Byrrhidae	*Pedilophorus griffithi*	1(5)	0(-)	1(3)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Byrrhidae	***Pedilophorus multicolor***	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**2(4)**	**1(6)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**
Byrrhidae	*Pedilophorus nr ANIC sp 04*	2(3)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)

Family	Species name	LOGGING REGENERATED FOREST SITES										MATURE UNLOGGED FOREST SITES									
		E L	E S	S L	S S	W L	W S	PR1 L	PR1 S	PR2.L	PR2 S	M L	M S	PO1 L	PO1 S	PO2 L	PO2 S	R L	R S	WR L	WR S
Eucnemidae	*Aderus acaciae*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Throscidae	***Aulonothroscus elongatus***	**3(25)**	**0(-)**	**1(4)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**2(3)**	**3(13)**	**0(-)**	**1(1)**	**2(10)**	**0(-)**	**0(-)**	**2(6)**	**1(1)**	**2(7)**	**0(-)**	**1(3)**	**0(-)**
Throscidae	*Aulonothroscus YEE sp 02*	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	1(2)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Throscidae	*Aulonothroscus YEE sp 03*	1(1)	0(-)	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Elateridae	*Agrypnus TFIC sp 01*	1(1)	0(-)	0(-)	0(-)	1(1)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(4)	0(-)	1(1)	0(-)
Elateridae	*Conoderus australasiae*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)
Elateridae	***Denticollinae TFIC sp 01***	**3(7)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**1(2)**	**0(-)**	**1(3)**	**1(1)**	**1(1)**	**0(-)**	**1(2)**	**1(1)**	**1(3)**	**1(1)**	**0(-)**	**1(1)**
Elateridae	*Elateridae TFIC sp 20*	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)
Elateridae	*Elateridae TFIC sp 21*	2(4)	0(-)	1(2)	0(-)	0(-)	0(-)	0(-)	1(2)	0(-)	2(4)	2(2)	2(4)	0(-)	1(1)	0(-)	0(-)	1(1)	3(4)	0(-)	1(1)
Elateridae	*Elateridae TFIC sp 23*	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)
Elateridae	*Enischnelater specularis*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)
Elateridae	*Enischnelater TFIC sp 01*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Elateridae	*Parablax ooliekirra*	1(4)	2(8)	0(-)	0(-)	1(1)	0(-)	1(1)	2(3)	0(-)	0(-)	2(4)	1(1)	1(1)	0(-)	1(1)	1(1)	1(1)	2(2)	0(-)	1(2)
Lycidae	***Metriorhynchus ?erythropterus***	**2(4)**	**1(3)**	**0(-)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**
Lycidae	*Metriorhynchus rhipidius*	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Lycidae	*Metriorhynchus TFIC sp 01*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Lycidae	*Metriorrhynchus TFIC sp 03*	2(2)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	1(1)	0(-)
Cantharidae	***Heteromastix nigripes***	**3(46)**	**3(37)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**
Canthandae	*Heteromastix TFIC sp 01*	2(16)	2(3)	1(1)	1(-)	1(2)	0(-)	1(2)	1(1)	1(1)	0(-)	3(4)	0(-)	1(2)	1(1)	3(3)	2(2)	0(-)	1(1)	1(9)	1(2)
Anobiidae	*Dorcatoma TFIC sp 01*	1(1)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	0(-)	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)
Anobiidae	*Hadrobregmus areolicollis*	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	1(1)	0(-)
Trogossitidae	*Rentoniinae TFIC sp 01*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)
Cleridae	*Lemidia subaenea*	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	1(3)	0(-)	1(1)	0(-)	1(1)	2(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)
Melyridae	*Dasytes TFIC sp 01*	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)
Sphindidae	*Aspidiphorus humeralis*	1(2)	1(1)	1(1)	0(-)	0(-)	0(-)	0(-)	1(3)	2(3)	0(-)	3(6)	1(4)	0(-)	1(7)	1(1)	1(2)	1(1)	1(1)	2(2)	1(3)
Brachypteridae	***Notobrachypterus TFIC sp 01***	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**2(2)**	**2(3)**
Nitidulidae	*Epuraea victoriensis*	2(2)	2(2)	0(-)	2(1)	2(3)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	2(2)
Nitidulidae	*Thalycrodes cylindricum*	2(3)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	1(1)	0(-)
Nitidulidae	*Thalycrodes pulchrum*	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	1(1)	1(1)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Silvanidae	***Cryptamorpha TFIC sp 01***	**3(66)**	**3(202**	**1(2)**	**2(15)**	**2(4)**	**1(1)**	**2(20)**	**3(13)**	**0(-)**	**0(-)**	**0(-)**	**1(3)**	**0(-)**	**0(-)**	**1(3)**	**0(-)**	**1(1)**	**1(2)**	**1(24)**	**2(9**
Silvanidae	*Cryptamorpha victoriae?*	2(3)	1(2)	1(2)	1(1)	2(2)	0(-)	1(2)	1(3)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	1(1)	1(2)
Phalacridae	*Litochrus ?alternans*	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	1(1)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Cryptophagidae	*Cryptophagidae TFIC sp 01*	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)
Cryptophagidae	*Cryptophagus sp nr gibbipennis*	0(-)	0(-)	1(1)	0(1)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Cryptophagidae	*Cryptophagus tasmanicus*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(2)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)

Family	Species name	LOGGING REGENERATED FOREST SITES										MATURE UNLOGGED FOREST SITES									
		E L	E S	S L	S S	W L	W S	PR1 L	PR1 S	PR2 L	PR2 S	M L	M S	PO1 L	PO1 S	PO2 L	PO2 S	R L	R S	WR L	WR S
Cerylonidae	*Philothermus tasmanicus*	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	1(1)	2(5)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Coccinellidae	*Rhyzobius TFIC sp 05*	1(1)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Coccinellidae	*Rhyzobius TFIC sp 14*	1(1)	1(1)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Coccinellidae	*Rhyzobius TFIC sp 15*	1(16)	2(4)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	2(2)	0(-)	2(2)	1(1)	2(2)	1(1)	0(-)	0(-)	1(1)
Coccinellidae	*Rhyzobius TFIC sp 16*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(2)	1(1)
Coccinellidae	*Rhyzobius TFIC sp 20*	1(1)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Corylophidae	*Corylophodes YEE sp 03*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(13)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Corylophidae	*Holopsis TFIC sp 01*	3(8)	3(8)	1(1)	2(1)	1(1)	0(-)	0(-)	3(3)	1(1)	1(2)	3(19)	3(4)	0(-)	2(3)	2(2)	3(11)	2(5)	2(13)	2(3)	0(-)
Corylophidae	*Sericoderus TFIC sp 02*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)
Corylophidae	*Sericoderus TFIC sp 05*	1(1)	0(-)	0(-)	0(-)	0(-)	1(1)	2(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	1(1)
Latridiidae	***Aridius costatus***	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**2(3)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**
Latridiidae	*Aridius nodifer*	2(9)	3(7)	0(-)	2(1)	2(5)	0(-)	1(1)	1(1)	0(-)	1(1)	0(-)	0(-)	2(3)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	3(5
Latridiidae	*Corticaria TFIC sp 02*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)
Latridiidae	*Cortinicara TFIC sp 02*	2(7)	1(1)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	2(2)	0(-)	0(-)	0(-)	0(-)	0(-)	2(3)	1(1)	0(-)	1(1)
Latridiidae	*Enicmus TFIC sp 01*	0(-)	0(-)	0(-)	1(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)
Melandryidae	***Melandryidae TFIC sp 04***	**1(3)**	**1(2)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(2)**	**1(1)**	**1(1)**	**0(-)**	**1(1)**	**0(-)**	**2(2)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(3)**	**0(-)**
Melandryidae	*Orchesia ?australina*	1(2)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Melandryidae	***Orchesia alphabetica***	**3(62)**	**3(8)**	**2(4)**	**1(-)**	**2(5)**	**0(-)**	**2(6)**	**0(-)**	**2(5)**	**1(4)**	**0(-)**	**0(-)**	**1(9)**	**1(3)**	**0(-)**	**1(4)**	**2(15)**	**0(-)**	**2(24)**	**2(2)**
Melandryidae	*Orchesia TFIC sp 01*	2(7)	0(-)	2(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(2)	0(-)
Melandryidae	*Orchesia TFIC sp 02*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)
Zopheridae	*Coxelus gibbicollis*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)
Zopheridae	*Enhypnon TFIC 'sp nov' 01*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(3)	0(-)
Zopheridae	*Enhypnon tuberculatus*	3(7)	2(4)	2(3)	2(5)	2(7)	0(-)	2(6)	2(6)	1(2)	1(2)	3(4)	2(3)	2(5)	1(1)	0(-)	2(5)	2(9)	1(1)	2(23)	2(2)
Zopheridae	*Enhypnon YEE sp 01*	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)
Zopheridae	*Latometus differens*	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	1(9)	1(1)	0(-)
Zopheridae	*Pycnomerus TFIC sp 02*	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	2(6)	1(1)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	1(1)
Tenebrionidae	*Adelium abbreviatum*	1(1)	2(2)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(5)	0(-)
Tenebrionidae	***Brycopia coelioides***	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**2(3)**	**2(2)**	**1(1)**	**0(-)**
Tenebrionidae	***Brycopia hexagona***	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**	**1(1)**
Tenebrionidae	*Brycopia picta*	1(2)	0(-)	2(3)	0(-)	0(-)	0(-)	0(-)	0(-)	1(2)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	2(5)	0(-)	0(-)	1(1)
Tenebrionidae	*Corripera deplanata*	1(3)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	1(1)	1(1)	0(-)	0(-)	0(-)	0(-)	1(2)	1(1)	0(-)	1(3)	1(2)
Prostomidae	*Prostomis atkinsoni*	0(-)	1(4)	0(-)	1(1)	1(1)	0(-)	0(-)	1(1)	1(3)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	2(6)	1(1)	0(-)	0(-)
Oedemeridae	*Dohrnia miranda*	0(-)	0(-)	1(4)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	2(5)	0(-)	0(-)	0(-)

Family	Species name	LOGGING REGENERATED FOREST SITES										MATURE UNLOGGED FOREST SITES									
		E L	E S	S L	S S	W L	W S	PR1 L	PR1 S	PR2 L	PR2 S	M L	M S	PO1 L	PO1 S	PO2 L	PO2 S	R L	R S	WR L	WR S
Oedemeridae	***Dohrnia simplex***	**0(-)**	**2(12)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**2(23)**	**2(6)**	**2(2)**	**0(-)**	**3(19)**	**0(-)**	**1(3)**	**0(-)**	**2(6)**	**1(1)**	**3(25)**	**1(1)**	**1(6)**	**1(3)**
Aderidae	*Aderidae TFIC sp 03*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(5)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Scraptiidae	*Scraptia laticollis*	2(3)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	1(1)	0(-)	0(-)
Scraptiidae	*Scraptia TFIC sp 01*	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	2(5)	0(-)	0(-)	0(-)	0(-)	2(7)	0(-)	0(-)	1(1)	0(-)	0(-)	1(1)	2(3)	0(-)
Cerambycidae	*Dorcadida TFIC sp 01*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)
Cerambycidae	***Enneaphyllus aeneipennis***	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**3(4)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**
Cerambycidae	*Mecynopus cothurnatus*	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)
Cerambycidae	*Toxeutes arcuatus*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(2)	0(-)	0(-)	0(-)
Chrysomelidae	*Aporocera viridis*	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	1(1)	1(1)	1(1)	0(-)	1(2)	1(1)	0(-)	0(-)
Chrysomelidae	*Cryptocephalinae TFIC sp 02*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	1(1)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	2(3)	0(-)	1(1)	0(-)
Chrysomelidae	*Cryptocephalinae TFIC sp 24*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(3)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Chrysomelidae	*Microdonacia truganina*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	1(1)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Chrysomelidae	*Monolepta TFIC sp 01*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(2)	1(1)	0(-)	0(-)
Anthribidae	***Anthribidae TFIC sp 02***	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**	**2(11)**	**0(-)**	**0(-)**
Anthribidae	*Xynotropis micans*	2(4)	2(2)	2(4)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	0(-)	1(1)	0(-)	1(1)	1(1)	1(2)	1(1)	0(-)
Attelabidae	*Auletobius melanocephalus*	0(-)	2(14)	0(-)	0(-)	0(-)	0(-)	3(14)	1(7)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Attelabidae	*Auletobius suturalis/varicollis?*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)
Curculionidae	*Ancyttalia oleariae*	1(3)	0(-)	3(3)	1(1)	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	2(100)
Curculionidae	***Ancyttalia tarsalis***	**2(11)**	**0(-)**	**2(2)**	**0(1)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**2(5)**	**0(-)**	**2(7)**	**2(2)**	**2(6)**	**2(8)**	**3(12)**	**3(6)**	**3(15)**	**3(7)**	**1(7)**	**2(2)**
Curculionidae	*Cossoninae TFIC sp 06*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(7)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Curculionidae	*Cryptorhynchinae TFIC sp 17*	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Curculionidae	*Cryptorhynchinae TFIC sp 28*	0(-)	0(-)	2(3)	0(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(3)	0(-)	1(1)	0(-)	2(3)	1(1)	0(-)	0(-)
Curculionidae	*Cryptorhynchinae TFIC sp 30*	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)
Curculionidae	*Cryptorhynchinae TFIC sp 31*	2(3)	2(3)	0(-)	1(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	0(-)	0(-)	1(1)	1(1)	1(1)	0(-)	0(-)	0(-)
Curculionidae	*Curculionidae TFIC sp 10*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(2)	1(1)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Curculionidae	*Decilaus albonotatus*	2(13)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	2(2)	0(-)	2(2)	2(2)	0(-)	0(-)	1(1)	1(1)	0(-)	1(1)	1(3)	0(-)
Curculionidae	***Decilaus lateralis***	**3(21)**	**3(15)**	**1(7)**	**1(5)**	**1(1)**	**0(-)**	**1(2)**	**1(1)**	**2(9)**	**1(1)**	**2(7)**	**0(-)**	**1(2)**	**2(4)**	**1(2)**	**0(-)**	**0(-)**	**0(-)**	**2(18)**	**1(3)**
Curculionidae	***Decilaus nigronotatus***	**3(259)**	**3(46)**	**2(35)**	**3(63)**	**3(9)**	**1(5)**	**0(-)**	**0(-)**	**2(2)**	**2(2)**	**2(4)**	**1(4)**	**2(8)**	**1(3)**	**2(8)**	**2(9)**	**3(56)**	**3(51)**	**0(-)**	**1(2)**
Curculionidae	*Decilaus nr striatus/subfasciatus*	3(83)	3(39)	3(22)	3(85)	3(20)	1(3)	0(-)	1(34)	2(7)	2(27)	3(51)	1(2)	2(11)	0(-)	2(16)	2(18)	3(4)	2(7)	2(38)	2(6

Family	Species name	LOGGING REGENERATED FOREST SITES										MATURE UNLOGGED FOREST SITES									
		E L	E S	S L	S S	W L	W S	PR1 L	PR1 S	PR2.L	PR2 S	M L	M S	PO1 L	PO1 S	PO2 L	PO2 S	R L	R S	WR L	WR S
Curculionidae	*Decilaus TFIC sp 02*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(6)	2(4)	0(-)	0(-)	0(-)
Curculionidae	***Dinichus terreus***	**1(1)**	**2(5)**	**1(3)**	**0(3)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**2(12)**	**0(-)**	**1(5)**	**0(-)**
Curculionidae	***Dryophthorus TFIC sp 02***	**1(2)**	**2(11)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**
Curculionidae	*Dryophthorus TFIC sp 01*	1(18)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(31)	0(-)	1(2)	0(-)	0(-)	0(-)
Curculionidae	*Elleschus wellingtoniensis?*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(2)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Curculionidae	*Emplesis TFIC sp 01*	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)
Curculionidae	*Eugnomini TFIC sp 16*	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	2(2)	0(-)	1(1)	0(-)	2(2)	0(-)	1(1)	0(-)	1(2)	1(1)
Curculionidae	*Exeiratus TFIC sp 01*	2(2)	2(2)	0(-)	0(-)	0(-)	1(1)	1(3)	2(2)	0(-)	2(3)	2(2)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)
Curculionidae	***Exithius capucinus***	**0(-)**	**2(2)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**	**2(4)**	**1(3)**	**1(2)**	**2(4)**	**2(4)**	**0(-)**	**0(-)**	**1(7)**	**1(2)**
Curculionidae	*Exithius loculiferus*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(6)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)
Curculionidae	*Mandalotus arciferus*	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)
Curculionidae	***Mandalotus muscivorus***	**1(1)**	**2(7)**	**1(9)**	**2(3)**	**1(1)**	**0(-)**	**2(4)**	**1(7)**	**2(6)**	**2(3)**	**0(-)**	**0(-)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**	**1(1)**	**0(-)**
Curculionidae	***Mandalotus sp nr vacillans***	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**1(2)**	**1(1)**
Curculionidae	*Miocallus pygmaeus*	1(1)	1(2)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	1(3)	1(1)	2(4)	2(2)	2(3)	1(1)	1(7)	0(-)
Curculionidae	*Platypus subgranosus*	3(26)	0(-)	1(1)	1(2)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(21)	0(-)	0(-)	1(2)	1(1)	0(-)	0(-)	0(-)
Curculionidae	*Poropterus alboscutellaris*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)
Curculionidae	*Poropterus antiquus*	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	0(-)	0(-)	0(-)	0(-)
Curculionidae	*Poropterus TFIC sp 05*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	1(1)	1(1)	1(3)	0(-)	0(-)	0(-)	0(-)
Curculionidae	*Roptoperus tasmaniensis*	3(13)	1(1)	2(19)	2(6)	0(-)	0(-)	0(-)	1(1)	0(-)	1(1)	1(2)	1(3)	0(-)	0(-)	0(-)	0(-)	1(1)	2(6)	2(4)	1(1)
Curculionidae	*Tychiinae TFIC sp 05*	1(2)	2(3)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	2(2)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	1(1)	0(-)
Curculionidae	*Tychiinae TFIC sp 06*	0(-)	0(-)	1(3)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	2(2)	2(2)	2(2)	0(-)	1(3)	0(-)
Curculionidae	***Tychiinae TFIC sp 08***	**1(2)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**0(-)**	**2(4)**	**1(1)**	**0(-)**	**0(-)**	**0(-)**	**1(2)**	**0(-)**	**0(-)**	**0(-)**	**1(1)**
Curculionidae	*Tychiinae TFIC sp 22*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	2(3)	2(4)	0(-)	0(-)	0(-)	1(2)	1(1)
Curculionidae	*Tychiinae TFIC sp 26*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	1(1)	0(-)
Curculionidae	*Tychiinae TFIC sp 27*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)
Curculionidae	*Tyrtaeosus ustulatus*	0(-)	0(-)	1(4)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(6)	0(-)	0(-)	0(-)
Unknown	*Coleoptera unknown YEE sp 13*	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	0(-)	1(1)	0(-)	0(-)	0(-)	0(-)	0(-)	1(2)	1(1)	0(-)	0(-)

7 SAPROXYLIC BEETLE CONSERVATION AND MANAGEMENT IN WET EUCALYPT PRODUCTION FORESTS

ABSTRACT

This chapter discusses the implications of the thesis findings in inform conservation management of saproxylic beetles in Tasmanian wet eucalypt forests. A precautionary and multi-scaled approach towards dead wood management is advocated, with particular consideration of the temporal scale at which the dynamics of the forests operate. From a better understanding of wet eucalypt forest saproxylic beetle biodiversity (Chapter 3), log decomposition processes relating to log size (Chapter 4), beetle species associations to the resulting rotten wood types (Chapter 5), and beetle assemblage responses to forest age and disturbance histories (Chapter 6), the thesis findings help discuss some immediate (over one rotation) and potential long-term (over several rotations) conservation impacts associated with standard clearfell logging on 90-year rotations. In line with current conservation management paradigms, retention of some trees during harvesting to improve stand structure complexity and future dead wood supply is strongly recommended as one means of mitigating potential negative impacts. The planning of trees for retention should aim to provide sufficient oldgrowth features as well as regrowth to lead to sufficient quantities and continuity of dead wood types, throughout successive forest regeneration cycles. Given the highly diverse, yet localised patterns of fauna, at the landscape scale, managing the production forest matrix as a habitat mosaic is recommend. This would allow opportunities for adaptive management to be applied. Directions for future research that would assist in better understanding the ecology of saproxylic beetles and better ensuring their conservation in the matrix are also suggested.

7.1 OBJECTIVES OF THIS CHAPTER

This thesis is the first study in Tasmania to comprehensively document the saproxylic beetle fauna. It provides important baseline data from which future studies can build upon, and thus has made a significant contribution to the previously limited knowledge of saproxylic beetles in Tasmania's wet eucalypt forest. The study investigated relationships between saproxylic beetle assemblage compositions and forest ecological processes (wood decomposition and forest succession), and where possible the biological attributes and habitat requirements of individual beetle species. The study however is albeit still limited given the sheer diversity of this fauna. While information of the biology and habitat requirements of the more common species was gained, the majority were either too 'cryptic'; collected in too few numbers; and/or not previously known to be definite about their life history and habitat requirements. Therefore, a more precautionary approach has been taken to interpolating the findings to inform discussion on the longer-term implications of standard clearfell harvesting practices on the conservation of saproxylic beetles.

The intent of this chapter was to synthesise the results of the preceding chapters and interpret their implications for forestry within the context of current conservation management strategies currently adopted or explored by Tasmanian government agencies. This chapter has been written as a discussion paper, where by the main results of the thesis, and their flow-on ecological implications, are clearly stated at the beginning. These are then discussed with respect to: the importance of off-reserve conservation management; multi-scaled approach to managing the production forest matrix; and managing the structural components of the forest, with particular focus on a temporal approach to conservation planning, for the conservation of saproxylic beetles in wet eucalypt forests. Throughout this chapter, further research needs are identified.

Many forests, including wet eucalypt forests in Southern Tasmania, are multiple-use forests managed for many values that include conservation values, which has been the focus of this thesis. But such forests are primarily managed for wood production. It should be noted that altering systems by changing CWD dynamics, or even increasing the amounts of dead wood to mitigate habitat loss could potentially lead to unprecedented increases in populations of certain wood feeding species resulting in pest

outbreaks. As seen in Scandinavia, declines or alterations in certain saproxylic invertebrates can lead to increases in bark beetle pest outbreaks (Heliövaara and Väisänen 1984; Weslien and Schroeder 1999). While this has not been the scope of this thesis, it important to be aware of this issue when managing for the different values of these forests.

7.2 SUMMARY OF THESIS RESULTS

As written in the preceding chapters, a survey of saproxylic beetle fauna associated with decomposing *Eucalyptus obliqua* logs of an intermediate decomposition stage was undertaken, and the assemblage compositions between large and small diameter logs in mature-unlogged and logging regenerated forests compared. Assemblage relationships with log decomposition processes (rot types), and to some extent forest succession and logging disturbance processes were explored.

The main results and ecological implications of them are:

1. Three hundred and sixty saproxylic beetle species from 54 families were collected from 54 large (100cm) and small (30-60cm) diameter *Eucalyptus obliqua* logs of an intermediate decompositon on stage in wet eucalypt forests (Chapter 3). Species occurrence and abundance varied greatly; with species being highly mobile and wide ranging, occurring in most study sites, to flightless, collected only from a particular site (Chapter 3,6). This clearly indicates that decomposing *Eucalyptus obliqua* logs at an intermediate decomposition stage are an essential habitat for an exceptionally species rich and functionally diverse fauna that have a diverse range of life histories and dispersal capabilities. Some species are dead wood habitat generalists, while others have specialised habitat requirements making use of the range of ecological niches provided by dead wood heterogeneity.

2. Rotten wood types formed by particular log decomposition processes significantly vary between logs of different sizes, and to some extent they vary between forests of different age/disturbance histories, and among different sites (Chapter 4). It is apparent that dead wood is a highly heterogeneous resource that is maintained by the ecological processes such as disturbance, regeneration and decomposition processes. The type of decomposition processes within a log seems to depend on the

logs' history: as a living tree, during senescence, as a dying tree, and as a log on the forest floor (Chapter 4). The greater prevalence of inner brown heartwood rot within large diameter logs probably relates to an already present butt or heartrot within the senescent and dying tree.

3. Saproxylic beetle assemblages differ between large and small diameter logs (Chapter 5& 6), and for some species this can partly be attributed to their association to certain rotten wood types/log decomposition processes (Chapter 5). This implies that for some species, their occurrence depends in part on the types of decomposition processes and resultant rotten wood types present within that log at that point in time.

4. Saproxylic beetle assemblages significantly differ between large and small diameter logs, with several species indicative of large diameter logs, while only one species *Enneaphyllus aeneipennis* indicative of small diameter logs (Chapter 5 & 6), meanwhile species richness standardized by sampling effort did not differ. This implies that small diameter logs can support a rich fauna of saproxylic beetles equal to that of large diameter logs, though this fauna comprises species with more general habitat requirements. Whereas large diameter logs have unique habitat qualities as reflected by exclusive or greater occurrence and abundance of certain species in large diameter logs.

5. Saproxylic beetle assemblages significantly differ between forests of different age/disturbance histories, yet species richness does not differ between forest types (Chapter 6). This implies that logs left after a single clearfell, burn and sow harvesting event can support a rich saproxylic beetle fauna equivalent to that within mature unlogged forests, though some of the species are likely to be mid-early successional forest specialists and/or are adapted to withstand more open and exposed environements.

6. Some apparent mature forest species were present in large diameter logs within logging regenerated forests, but were absent from small diameter logs of the same forest type. This suggests that some species are responding to the microclimate of

the log *per se* rather than the forest *per se;* and, given large diameter logs provide a greater buffer against exposure and dessication, sucg logs could potentially play an important role in re-establishing populations of certain species, including mature forest specialists, to a regenerating disturbed forest (Chapter 6).

7.3 ADEQUACY OF THE RESERVE SYSTEM FOR SAPROXYLIC BEETLE CONSERVATION IN TASMANIA

Conservation of forest biodiversity in Tasmania is partially reliant on a network of formal and informal reserves. Large tracts of forests are protected in World Heritage Area, National Parks, Forest Reserves and additional reserves were established under the Regional Forest Agreement (RFA) (Commonwealth of Australia 1997). The RFA adopted the JANIS criteria to ensure the establishment of a Comprehensive Adequate and Representative (CAR) forest reserve system, aimed at permanently protecting representative areas of the various vascular plant communities, their associated biodiversity and natural ecological processes. Note though, the adequacy of vascular plant communities as surrogates for saproxylic biodiversity has yet to be assessed. Moreover, several studies have demonstrate a lack of congruence between the distributions of invertebrate species or communities and vegetation communities (e.g. Cranston & Trueman 1997; Oliver *et al.* 1998; Taylor *et al.* 1994; c.f. Yen 1987; York 1999a).

Although reserves clearly play a crucial role in biodiversity conservation, in isolation they are likely to be inadequate to maintain saproxylic beetle biodiversity without concurrent conservation efforts in areas of forest available for timber harvesting (Lindenmayer & Franklin 2002). This is referred to as off-reserve management, where the production forest matrix is managed for conservation as well as for timber and other forest products (Lindenmayer & Franklin 1997, 2002).

There are two particular reasons to advocate off-reserve management for saproxylic beetle conservation. First, it is plausible that many of the species collected in this study would also have limited distribution ranges, as local endemism is typical of many flightless log dwelling Tasmanian invertebrate species (e.g. Mesibov 1994; Mesibov & Ruhberg 1991). Much of their restricted distributions would then lie outside the CAR

reserve system, and in areas subject to intensive forestry practices that directly threaten their habitat (Grove & Meggs 2003; Meggs 2003). This has already been well illustrated by three threatened Tasmanian saproxylic stag beetle species (*Hoplogonus simsoni, Lissotes latidens and Lissotes menalcas*) (*Tasmanian Threatened Species Protection Act, 1995*). This work involved extensive field surveys to define distribution and habitat requirements and modelling to predict their potential range (Meggs 2003; Meggs & Munks 2003; Meggs *et al.* 2003; Meggs & Taylor 1999). Managers are thus able to consider the conservation of these species when developing timber-harvesting plans. However, the resources required to enable this were substantial, and accurate determination of the distributional range for most saproxylic species is infeasible.

From an invertebrate perspective, Tasmania comprises distinct biogeographical zones, separated by faunal breaks (Mesibov 1994). The topography and geology within and between these zones is highly variable, with high (>1000m) mountain ranges and intersecting rivers characterising the landscape. Considering that around 25% of saproxylic beetle species collected in the present study seemed to disperse by 'crawling' (Section 3.3.2.4), these geographical features almost certainly act as barriers to dispersal for many species. Furthermore, collection records of specimens held at the Australian National Insect Collection (CSIRO Entomology, Canberra) and Tasmanian Forest Insect Collection (Forestry Tasmania, Hobart) also support this inference in showing that some species have only been collected within the Southern Ranges bioregion. Therefore, if species are responding to additional factors not reflected purely by vegetation changes, such as fine-scale biogeographical boundaries (as illustrated by genetic studies of a saproxylic collembolan species in south east New South Wales (Garrick *et al.* 2004), then the reserve system alone will not cater for the full range of saproxylic beetle species native to the wet eucalypt forest type.

The second reason to advocate off-reserve management for conservation of saproxylic beetle biodiversity relates to their apparent requirement for disturbance events such as wildfire to maintain habitat (see Section 7.2). Wildfire ensures the maintenance of a range of different forest successional stages, and their flow-on ecological processes, and hence continual availability of different dead wood types in different forest conditions. It is currently unknown whether reserves within the existing reserve system are large

enough to fulfil these requirements. In any case, it is highly likely that the integrity of reserves would greatly benefit from a surrounding 'permeable' matrix to ensure the availability of source populations for recolonisation after disturbance, and to ensure connectivity between reserve areas and the movement of saproxylic beetles (Lindenmayer & Franklin 2002). With little assessment as to whether the reserve system is adequately conserving areas within the range of all species, or protecting the natural heterogeneity of dead wood necessary to maintain populations, off-reserve management within the logging matrix thus seems an essential element of conserving saproxylic beetle species.

7.4 ADEQUACY OF STANDARD CLEARFELLING PRACTICES FOR SAPROXYLIC BEETLE CONSERVATION

The most concerning potential impact of forest management practices on biodiversity relates to habitat loss and habitat fragmentation that disrupt species emigration and colonisation processes such that localised populations of a given species become isolated and more prone to extinction events (Bennett 1999). For saproxylic organisms, habitat loss will arise from a reduced availability of suitable dead wood types, a phenomenon that occurs at the stand level. Because some species were associated with large diameter logs, or had only emerged from such logs, albeit in low numbers, harvesting practices that appear inadequate for saproxylic beetle conservation include operations that lead to:

- the elimination of oldgrowth structures, in particular large diameter logs;
- the cumulative reduction in dead wood volumes over time; and
- disruption to dead wood recruitment processes during forest regeneration.

7.4.1 Loss of oldgrowth structures – large diameter logs

The study showed that large diameter logs play a specific ecological role, different from that of small diameter logs (see Section 6.4.2), and so the absence of these structures (after successive rotations) would likely affect the species that showed a preference for these logs and/or the rotten wood types present within such logs (see Section 5.4 and Section 6.2.2.2). While only tens of species were found indicative of large diameter logs for whichever reason, this is likely a gross underestimate given that this could only be determined for common species. Four beetle species (*Cossonus simsoni*, *Dryophthorus*

TFIC sp 01 , *Pycnomerus* TFIC sp 02 and *Prostomis atkinsoni*) were particularly highlighted as being of conservation importance, based not only on a rotten wood type, and thus large diameter log association, but also on their apparent low dispersal rates and because each species belongs to a genus with European representatives which were once common and widespread but which are now regionally threatened with extinction (see Section 5.4).

The loss of large diameter logs could severely compromise the effectiveness of logging regenerated forests as a permeable matrix, since these structures appear to be important natural spatial and temporal stepping stones that allow specialist species to disperse, or persist under the more open forest conditions prior to canopy closure (Section 6.2.2.3). This assertion is based on the scenario that certain species disperse through the matrix and need stable microclimatic conditions to successfully breed, but can do so whenever such conditions are provided by the log habitat, regardless of the condition of the forest. Reduction in numbers, or elimination, of large diameter logs after CBS harvesting could negatively affect the recolonisation or dispersal of stable microclimate specialists through regenerating forest. Thus, it would be important for future studies to determine whether apparent mature forest saproxylic beetle specialists respond to forest microclimate conditions, log microclimate conditions, or both.

7.4.2 Cumulative reduction of dead wood volumes

Predictive models indicate there will be an over two-fold reduction of dead wood volumes in forests successively harvested at 100-year intervals by clearfelling compared to stand-replacing wildfire of the same periodicity (Grove *et al.* 2002). Increased pressures may also be placed on dead wood resources should recent proposals to utilise them for biofuel eventuate (Grove *et al.* 2002). In the absence of mitigation measures, the cumulative effects of these practices at a local to forest regional scale would increase the likelihood that distance between suitable dead wood types is greater than the dispersal ability of dependent species, especially short-range dispersers. Thus leading to fragmentation effects at the local scale and subsequent local population species extinctions. If such practices extend throughout the matrix, the possible many local population extinctions would lead to a greater chance of regional extinction for a

given species. Species most likely to be affected by this are short-range dispersers (see Section 3.1, Schiegg 2000a).

From other studies, short dispersive movements seems a common trait of many log dwelling saproxylic animals; e.g. *Tasmanipatus barretti* –disperses up to 20m net/ year (Barclay, 2000 -cited in Fox *et al.* 2004), several saproxylic beetles species disperse <100m (Knutsen *et al.* 2000; Starzomski & Bondrup-Nielsen 2002; Sverdrup-Thygeson & Midtgaard 1998); and as indicated by the high relatively proportion of flightless taxa, similar traits are likely to be apparent for saproxylic beetles in wet eucaypt forests. Moreover, these saproxylic beetles have evolved in forest where dead wood volumes are naturally high (reviewed in Woldendorp *et al.* 2002a) and decay rates are low (Yin, 1999 - cited in Grove *et al.* 2002), and thus some species would have had less selection pressure to evolve long inter-patch dispersal abilities.

At this stage, no relationships between dead wood amounts (number of logs or log volumes) and saproxylic beetle populations have been established in wet eucalypt forests. However, there are a number indications that less dead wood could be an issue for conservation management in the future if such a situation occurs in the absence of mitigation measures. These include:

- Decreasing volumes of dead wood increases the chance of fewer dead wood types, especially those that are naturally rare dead wood types, thus affecting dependent species.

- European forestry provides many examples that demonstrate a relationship between decreasing volumes of dead wood, or increasing spatial distance of dead wood types, with local species extinctions of saproxylic beetles (Schiegg, 2000 – dead wood, Jonsell *et al.* 1999; Jonsson *et al.* 2003; Martikainen *et al.* 2000; Siitonen 1994a; Sippola *et al.* 1998; Sverdrup-Thygeson & Midtgaard 1998; Thunes *et al.* 2000 – wood decay fungal sporocarps).

- Several studies elsewhere (e.g. Martikainen *et al.* 2000; Sippola *et al.* 1998; Siitonen *et al.* 2000), including in the tropical forests of far North Queensland

(Grove 2002c), show that forest stand volumes of dead wood as a strong positive correlate of saproxylic beetle speces richness.

Future autecological studies should focus on understanding the population structure of short-range dispersing saproxylic beetle species with high habitat specialisations (e.g. specific to a certain decomposition state within a decomposing log), and determine how they move through, and perceive the natural forest matrix and previous fire histories (e.g. Meggs & Munks 2003; Meggs *et al.* 2003; Schmuki 2003; Watson 2003; Nash 2004)

7.4.3 Disruption to dead wood recruitment processes

Standard CBS silviculture disrupts the dead wood recruitment process, thus resulting in a discontinuity of suitable dead wood types within the stand. Clearfelling usually fells (and mostly removes) all trees in a forest stand in a single operation (Hickey & Savva 1992). Therefore, aside from the input of self-thinned trees during forest regeneration (Jacobs 1955), the bulk of larger dead wood would mostly arise from the initial harvesting event: severely burnt harvesting debris all of which commenced decomposition and log succession under similar conditions – with open exposure and associated extreme microclimatic conditions (see Section 4.4.4). This fundamentally differs from dead wood recruitment processes in naturally disturbed forests. Even after stand-replacing wildfire events, standing and fallen dead tree volumes are high, and survival of a proportion of living trees is also common (Hickey 1994; Hickey *et al.* 1999b). This ensures a continual supply of dead wood for many decades (Grove *et al.* 2002; Woldendorp *et al.* 2002a).

Since dead wood arising from a CBS harvesting event is synchronous, with limited continual dead wood recruitment, a temporal discontinuity of suitable dead wood types can be expected to prevail: a type of fragmentation effect in time. For example, many species collected in this study were specialists of decomposing large diameter logs that contained brown inner heartwood rotten wood types (Section 5.4). As log decomposition proceeds, the habitat quality for these specialist species inevitably diminishes. If all dead wood types within the forest stand, and possibly in surrounding forest stands, are of the same decomposition stage, then this species must disperse

further to find a new supply of suitable dead wood, which for flightless species, is likely to be beyond their dispersal range. Disruption of dead wood recruitment processes may lead to a reduction in unburnt dead wood undergoing its initial stages of decomposition in relatively moist and closed forests, and so this may be detrimental to saproxylic beetles dependent on this type of dead wood. While specialists of this dead wood have not been the subject of this study, such dead wood most likely undergoes specific fungal and insect successions (Section 4.4.4), and so could potentially represent a unique dead wood type for subsequent successions of saproxylic beetles (see Section 6.4.1.2).

Simply extending logging rotation periods is unlikely to be sufficient to conserve saproxylic beetles unless stand structures are also retained. This is evident from the extensively managed forests of northern Europe, where the assemblage compositions of saproxylic beetles and flies in mature aged managed forests differs significantly from similar aged semi-natural or oldgrowth forests (Martikainen *et al.* 2000- southern Finland; Økland 1994; Økland 1996b - Norway; Sverdrup-Thygeson 2002), and this difference correlates with the stand's dead wood quality and quantity (includes wood in all decay stages, especially large diameter logs at late stage of decay). Consequently, conservationists in Europe consider 'ecological continuity' (defined in Nórden & Appleqvist 2001) as a prime criterion for the selection of forest reserves for biodiversity conservation (see Rolstad *et al.* 2002). Because ecological continuity relates to the history of the forest, which is difficult to discern from current conditions, identifying indicators of this attribute is being given increased attention (e.g. Ås 1993; Jonsell & Nordlander 2002; Sverdrup-Thygeson 2001; Sverdrup-Thygeson & Lindenmayer 2003). Identifying particular saproxylic beetle species indicative of ecological continuity in wet eucalypt forests is likely to become an issue for future conservation management.

7.5 RECOMMENDATIONS – Implementing dead wood and tree retention strategies within the framework of multi-scaled and adaptive management

In coupes planned for harvesting, the retention of trees and the protection of rotting logs is prescribed to mitigate habitat loss for several hollow-dependent and log dependent threatened animal species (*Threatened Fauna Adviser* 2001). Though, as suggested by

this thesis, such prescriptions need to be applied more widely and not only in response to threatened species conservation. This is warranted because of the exceptionally high and yet still unknown diversity of saproxylic beetles, the likely limited distribution range and dipersal ability of many species, the limited life-history information known, and their association with a habitat that requires decades, if not centuries to develop. Restoring certain dead wood types in the forests would obviously take at least the same length of time that was required for their development, including the successive processes of tree growth, heartrot decay, tree death and log decomposition (see Section 4.4.3). If a break in habitat continuity arises, it would be at least a century before such dead wood types could be renewed, and even then this may not be possible as breaks in continuity may result in local extinction of particular wood decay fungi that are integral in the formation of particular rotten wood types (e.g. Bader *et al.* 1995; Sippola & Renvall 1999).

Tree retention should include retaining both mature-age and regrowth trees when felling mature multi-aged forests. Mature trees are the main generators of dead wood (Grove 2002). Retaining these structures not only ensures the presence of mature (large) structures, but because they continue to shed relatively large volumes of wood throughout their senescent years, they also better ensure that suitable dead wood types are in sufficient proximity (connectivity and continuity) to each other throughout the silvicultural cycle. Meanwhile, regrowth trees should be allowed to mature, undergo natural heartrot decay processes, and fall down at their own rates, thereby guaranteeing the persistence of mature (large) structures and their associated microhabitats within appropriate time frames.

The requirements for tree retention and dead wood retention should employ a range of volume prescriptions, modelled on those naturally occurring under natural disturbance regimes (Lindenmayer & McCarthy 2002; Lindenmayer 1999). Some early data demonstrate that natural dead wood levels in wet eucalypt forests are high, but vary between 203 and 1235 m^3 ha^{-1} (reviewed in Woldendorp *et al.* 2002a). This variation depends largely on wildfire intensity, time since last wildfire, interval times between previous wildfire events, and site productivity (Grove *et al.* 2002). While the retention of 'semi-natural' dead wood volumes is possible, given that high volumes of logging

debris are produced from harvesting a mature forest stands (see Section 2.9), the greater challenge will be retaining sufficient numbers of living standing trees to ensure continuity of dead wood habitat over time.

In Tasmania, a number of alternative silvicultural systems that include tree retention strategies are currently in development and review (Hickey *et al.* 2001). These have been developed in concordance with the similar biodiversity and conservation concerns in North American and Scandinavian modern forestry (Franklin *et al.* 1997; Kolström & Lumatjärvi 2000; Ranius *et al.* 2003; Sullivan *et al.* 2001) in terms of improved stand structure complexity and future dead wood supply. The alternative silvicultural systems are, in part, based on a growing understanding of the ecology and dynamics of the Tasmanian wet forest system, and most have some degree of green tree retention. Retained trees may be dispersed throughout the harvested area, aggregated, or concentrated in strips. These systems are being evaluated on their ability to allow continued wood production, on whether they retain oldgrowth species and structures at the stand level, on their associated safety and increased fire risks, and on their social acceptability (Forestry Tasmania 2004; Hickey *et al.* 2001).

Selection of silvicultural systems and the spatial and temporal arrangement of harvesting coupes is a major challenge for modern forestry and biodiversity conservation. This challenge could be met through modelling forest dynamics and species biological data (e.g. Kolström & Lumatjärvi 2000 - Sweden). However, understanding how stand structure and dead wood dynamics relate to the different disturbance regimes (natural and silvicultural) in wet eucalypt forests is still in its infancy (Grove *et al.* 2002; Su *et al.* 2001). In addition, there is still a dearth of biological and ecological information about individual species' habitat requirements, habitat specificity, and dispersal abilities. The scale at which saproxylic beetles perceive patch heterogeneity (McIntyre & Wiens 1999; Økland *et al.* 1996b), and how they respond to forest conditions and ecological processes associated with disturbance events (e.g. wildfire), is also unknown for most individual species. Because saproxylic beetles have evolved to cope with forest conditions and dynamics in the absence of timber harvesting, it is possible that determining the dispersal ecology of a few key species of different life histories could help. Hopefully this approach would facilitate the

conservation of a wide range of dead wood dependent taxa within the production forest matrix.

Wet eucalypt forests are naturally dynamic ecosystems that occur in a landscape of varying geomorphology and topography. Across the landscape, the forest comprises a mosaic of fire-disturbed stands of different successional ages and stand structure complexities, and these aspects of the forest continually change over time (Hickey *et al.* 1999b; Lindenmayer *et al.* 2000a; Lindenmayer *et al.* 1999a). Such changes are in response to interdependent ecological processes that drive forest dynamics, such as disturbance events, forest regeneration and succession processes at the stand-level scale; and tree growth, tree death and wood decomposition processes at the stand-structure scale. Theoretically, species that have evolved within this dynamic forest ecosystem are adapted to, and thus are maintained by, the spatial and temporal heterogeneity at these different scales (Bennett 1999; Haila 1999).

Employing a range of the most promising silvicultural regimes seems the most precautionary approach to the conservation of saproxylic beetles (and many other taxa) within the production forest matrix (Lindenmayer & Franklin 2002). This would ensure a degree of forest stand structural complexity and heterogeneity over a range of spatial and temporal scales. This approach also spreads the risk of adopting a single silvicultural practice that could have unforeseen detrimental effects. It also allows forest management to be more adaptive (Lindenmayer & Franklin 2002; Lindenmayer *et al.* 2002). Treating each stand as a replicate within a silviculture experiment enables managers to test various hypotheses, with adequate replication, at the scale at which forest operations and stand level ecological processes operate. Such hypotheses may include determining how saproxylic beetle assemblages in forests of similar ages respond to the ecological processes (e.g. forest regeneration and succession) associated with wildfire compared to those of the various silvicultural systems. This approach could provide conservation management with a tool for observing, studying, understanding, and feeding back ideas for developing forest practices that better meet the goals of ecologically sustainable forestry.

7.6 SUMMARY AND CONCLUSIONS

Humans have made innumerable changes to the forest ecosystem, and they continue to do so as demands for wood resources increase. The effects of European forestry provide a striking example of how altering forest ecological processes and structural composition can lead to the extinction of a large, albeit cryptic, component of the forest's biodiversity. Production forestry in Tasmanian wet eucalypt forests is entering a phase in which management practices could either prevent, or if inappropriate, then cause, such ecological changes and associated species extinctions. However, obtaining knowledge of the saproxylic beetle fauna, and other dead wood dependent organisms, the forest's natural disturbance dynamics and how these relate to stand structural complexity remains an ongoing process.

This thesis is the first comprehensive study of saproxylic beetles associated with *Eucalyptus obliqua* logs in Tasmanian wet eucalypt forests. Though the study was confined to Tasmania's Southern Ranges bioregion, the ecological outcomes are still relevant to wet eucalypt forests in other bioregions, including those in mainland Australia. The high diversity of saproxylic beetles occurring within a small geographical range (10km^2 area), and the high variability in species composition among forests of different age and disturbance histories, and in different sized logs, all support the need for implementing a precautionary and multi-scaled ecosystem approach to managing dead wood (Grove *et al.* 2002; Lindenmayer 1999). Based on the thesis findings, harvesting practices that lead to the elimination of oldgrowth structures (in particular large diameter logs), cumulative reductions in dead wood volumes over time, and disruption to dead wood recruitment processes during forest regeneration, are identified as key threats for saproxylic beetle conservation within the production forest matrix.

At the coupe level, recommendations to management focus on retention of dead wood, especially large diameter logs after harvesting, and retention of living trees for provision of oldgrowth structures undergoing natural decay processes and natural rates of treefall. This would provide a continuous supply of dead wood throughout the rotation, support unique microhabitat (rotten wood) types necessary for specialised species, and potentially play an important functional role in the recolonisation of saproxylic

communities after stand level disturbance. At the landscape level, recommendations focus on employing a range of silvicultural regimes modelled on natural disturbance regimes to emulate the natural range of forest age, and stand structural complexity and heterogeneity over a range of spatial and temporal scales. These regimes should be employed within the framework of adaptive management, whereby biota are monitored to assess how well they respond to such regimes. Results from this, the results and ideas of such assessments can feed into developing and refining forest practices that better meet the goals of ecologically sustainable forestry.

The conservation of saproxylic beetles in wet eucalypt forests requires an increased awareness of saproxylic beetles among the wider community, conservationists and forest managers. Conservation of saproxylic beetles in Tasmanian wet eucalypt forests can benefit not only from the lessons learnt from the relatively dire situation in northern Europe, but can also benefit from newly emerging scientific-based paradigms that are being used to develop modern forestry in Australia and elsewhere. Hopefully the findings in this thesis can contribute towards meeting the goals of ecologically sustainable forestry, and the continued survival of Tasmania's saproxylic beetle species.

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