The Influence of Forestry Practices on Insect Communities in the Karri and Jarrah Forests of South-Western Australia, as Indicated by Aerial Trapping

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SUMMARY

Insects were sampled in four regions of the south-west of Western Australia to examine the effects on aerial insect communities of forestry management practices.

At Pemberton and Manjimup regenerating karri forest was compared with mature karri forest. At Quilergup and Nannup pine plantations were compared with the jarrah forest communities they had replaced.

Sampling was conducted by night and day using light and Malaise traps respectively. The invertebrates trapped were classified to order level, the Hymenoptera, Coleoptera, Diptera, Lepidoptera and Hemiptera were classified to the family level (134142 individuals) and some Coleoptera and Lepidoptera were identified to the generic level.

The five orders identified to the family level yielded for each region the following numbers of individuals respectively: Pemberton 12163 (2478 to generic level); Manjimup 12686 (698); Quilergup 99559 (5115) and Nannup 9734 (1200).

The data are sequentially analysed using different levels of taxonomic resolution. The diversity, evenness, dissimilarity dendrograms, dominance-diversity curves and rarefaction are presented for the pooled data and for various sub-sets of the data to examine the response to various silvicultural practices.

At the order level of identification the impact of silvicultural practices cannot readily be separated from the 'noise' in the sampling. At the family and generic levels of identification different taxa often show grossly different responses to the treatments. Large differences are often apparent between the paired ridge and valley sites within treatments.

Different sampling methods may provide data which yield different interpretations of the community structure and the reasons for this are discussed in relation to the characteristics of the traps and the structural changes to the vegetation associated with the treatments.

At both the family and generic levels of identification taxonomic groups can be identified which seem especially susceptible to the treatments and which may prove to be useful indicator taxa on which to focus attention in future studies. There is considerable concordance between these taxa and those examined previously.

TABLE OF CONTENTS

Page

LIST OF FIGURES

1.   INTRODUCTION

Despite a long history of forestry and continual changes in forest management practices (Pentony and Kimber 1976) the invertebrate fauna of the forests of south-western Australia have been studied seldom (Christensen and Kimber 1975; Greenslade and Majer 1985; Koch and Majer 1980; McNamara 1955; Ridsdill Smith, Weir and Peck 1983; Springett 1973, 1979, Curry et al. 1985, Curry and Humphreys, 1987), mostly by phenological studies of surface and litter active animals. The forests of south-western Australia are subjected to three main management practices; fuel reduction burns in standing forest and, after felling, the regeneration of the forest from either seed trees or by replanting, and substitution of native forest by conifer plantations.

Replacement forests have a profound long term effect on the soils due to acidification of soils associated with coniferous forests, while regeneration forestry has profound short term effects which have been summarized elsewhere (Curry and Humphreys 1987), related to ashbed effects, soil compaction, and to changes in the flora, fauna, structure and biomass of the forest.

This study examines the effects of regrowth and replacement forestry practices on the insect communities, as indicated by aerial trapping of insects by both day and night. The regrowth forest resulted from the regrowth of karri (Eucalyptus diversicolor; see Curry and Humphreys 1987), while in the replacement forests conifers (Pinus radiata) replaced jarrah (Eucalyptus marginata) forest, all sites being the the south-west of Western Australia.

2.1   Trapping

Trapping was conducted mainly in spring and summer; it has been shown
elsewhere that most aerial activity, as determined by Malaise trap catches,
occurred in spring and that the greatest species richness was found in spring
and summer (Neumann 1979).

The treatment plot was sampled near the centre of the roughly ovoid cleared
area while the uncleared forest was sampled a similar distance into the forest
from the edge of the cleared area. Two types of traps were used to sample
flying insects, namely Malaise traps (Butler 1965; Gressitt and Gressitt 1962)
during the day and ultra-violet light traps at night (Southwood 1978; Curry
and Humphreys 1987); throughout the text these are referred to as day traps
and night traps respectively. The light traps were operated from sunset for 3
hours by a time switch.

2.2   Identification (Appendices 1 and 2)

All arthropods trapped were counted and classified to order for each sampling
period and site; Hymenoptera, Lepidoptera, Coleoptera, Diptera and Hemiptera
were classified to the family level by staff at the Department of Agriculture,
Perth. In addition, some of the samples of Lepidoptera and Coleoptera were
identified to the generic level. The number of days the traps were operated
was not standardized and the rarefaction analysis was used to overcome the
sample size disparities introduced by these changes in treatment of the data.

2.3   Analysis

2.3.1 Weekly Averages of Insect Orders from Light and Day Traps

Two analyses were conducted on the Department of Agriculture's Prime 750
computer using GENSTAT. The similarity of the taxonomic groupings between
areas was made using Kendall's rank correlation (τ) and the significance
tested against a normal distribution only if there were > 7 categories
(Ghent 1963) of data without very long tails of small counts. Abundance data
for 14 orders (Blattodea, Isoptera, Mantodea, Dermaptera, Orthoptera,
Psocoptera, Hemiptera, Neuroptera, Coleoptera, Mecoptera, Diptera,
Trichoptera, Lepidoptera and Hymenoptera) were analysed using a full
log-linear model and tested for significant site (ridge vs valley), area
(uncleared vs treatment) and interaction terms (site x area) against a
chi-squared distribution only if the minimal acceptable cell values (Siegal
1956) were present (D'Antuono 1983).

2.3.2 Analysis of Five Orders Pooled for the Sampling Period

The data were analysed by a number of methods to explore the differences in
taxonomic composition of the samples between sites both within and between
years and treatments. Indices of similarity are used to illustrate
numerically the differences between samples and dominance-diversity curves to
explore the structure of the community. The cluster analysis on the
dissimilarity matrices are given to show the magnitude of the differences
between samples. Diversity:- the index of information content (H_1; Shannon
1948) or the Berger-Parker dominance index (limits 0,1) was calculated

together with the evenness measure H_1/H_{max}; all followed usual algorithms (Southwood 1978). Dominance-diversity curves were plotted as the frequency of occurrence of taxa grouped into log base 2 (octave) classes of abundance; high values denote many taxa represented, to the left by few individuals and to the right by many individuals.

Rarefaction:- the expected number of taxa per given number of individuals collected (E_s: Sanders 1968) and its standard deviation were calculated using the corrected procedure and algorithms (Heck et al. 1975; Simberloff 1978); this procedure standardises the number of taxa to a given number of individuals and so tends to compensate for variation in sample size. Several rarefaction methods are shown to be similar analytically and the similarity holds not only for the expected number of species but also for the variance of the number of species (Smith, Stewart and Cairns 1985). Cluster analysis: two indices of association were used:- that of Jacaard for presence data and of Bray and Curtis for numeric data (Southwood 1978), the latter is a good index for the analysis of the successional type of changes being considered here (Huhta 1979). The indices were clustered from range scaled or Wisconsin standardised data using the WPGMA method (Sneath and Sokal 1973). In some cases the statistical significance of clusters was determined, following Strauss (1982), by taking the 95% occurrence of each node level following the accumulation of ca 3500 nodes derived from random data sets using the same clustering procedure. In the randomization process for presence data the species number per site was kept constant and the species present randomly allocated. Essentially the same procedure was followed for numeric data but the number of individuals of the species present was randomly allocated a number between 1 and the maximum value for that species in the original data set. Analysis of the numeric data is presented; in most cases the results of presence data yielded similar results.

Some analyses are not presented as they are inappropriate to the sample, the data are too sparse or yield results similar to other analyses.

2.4 Description of the Study Areas (Appendix 3)

PEMBERTON (33° 31 S, 115° 50 E; Table 1). The two study areas were 2-year old karri (Eucalyptus diversicolor) at Warren and 44-year old karri at Big Brook with both ridge and creek sites being sampled. The Warren site comprised 190 ha of 2-year old regenerated karri from which all seed trees had recently been removed; there was considerable shrub growth between the young trees about 1 m in height but reaching 2 m adjacent to the stream. The Big Brook site comprised 57 ha regenerated in 1930 (hence about 44 years old when the trapping programme was conducted). The area had not been burnt since the original regeneration burn in 1930 and there was considerable scrub cover up to 30 m high beneath the trees. The day traps were operated for 3 hours (1300-1600 hours) for 3 days in October and December 1974 and for 4 days in February and March 1975 and they were emptied daily. Night traps were operated for 4 hours (1830-2230 hours) for 7 nights (12 nights in early March 1975) in each month from October 1974 through May 1975, including late March. The data were pooled within each collection period.

MANJIMUP (natural; 34° 18 S, 115° 50 E: cleared; 34° 15 S, 115° 51 E Table 1). Insects were trapped at Manjimup (Pine Creek Road) from September 1974 to August 1975 in native karri (Eucalyptus diversicolor) forest and in karri forest which had been clear felled; sampling was conducted on ridge and creek sites in each area. At each site the day trap was operated for 3 hours between 13:00 and 16:00 hours on each of four days in November and December

1974 and February and March 1975; the night trap was operated between 18:30 and 22:30 hours for 7 nights in November, February, April and May, for 5 nights in December, for 6 nights in January and 9 nights in both early and late March.

In order to compare cleared and uncleared karri forest four areas were selected. Area 1: 53 ha cleared in 1972 leaving 4 seed trees per ha and a heavy accumulation of logging debris and some scattered undergrowth for future regeneration burning. Area 2: 50 ha virgin karri forest which had been subjected to regular prescribed burning, the last being in 1967 leaving ground vegetation which was 7 years old when the insect trapping programme was conducted.

QUILERGUP (33° 46 S, 115° 37 E; Table 1). Insects were trapped from 1975 to 1976 in native jarrah forest (Eucalyptus marginata) and in pine plantation (Pinus radiata) established one and two years previously (referred to as 2-year old in text) on cleared, disease affected, poor quality jarrah forest sites in the Donnybrook Sunklands south of Busselton; each area was sampled at both ridge and creek sites. The pines had by then had little effect on the regenerating native vegetation which had reached about 1 m in height. Sampling was not conducted in each pine area at the same time but were alternately sampled to ensure that cleared and uncleared sites could be compared. The uncleared forest was sampled by day traps for 7 hours (09:00-16:00 h) for five days (age in years of corresponding pine plantation sampled) in early (1) and late (2) October, and December (2), 1975, and in February (1), April (1), July (1) and August (2), 1976. The areas were sampled by night traps between 18:30 and 22:30 h for a variable number of days (age of corresponding pine plantation in years; number of nights sampled) in early (1; 7) and late (2; 7) and December, 1975, and in February (1; 7), April (1; 6) and July-August (2; 10), 1976.

NANNUP (uncleared; 33° 57 S, 115° 45 E: cleared; 33° 55 S, 115° 46 E Table 1). Insects were trapped at Nannup in native jarrah-forest (Eucalyptus marginata) which had been regularly control burnt and thus contained only a scattered understory, and in an 18-year old pine plantation (Pinus radiata) which contained little native vegetation with only a few scattered Melaleuca bushes. Day and night traps were operated at both ridge and creek sites in 1977. Day traps were operated between 13:00 and 16:00 h over 16 days in February 1977. The night traps were operated for 4 hours (18:30-22:30 h) over six nights in February 1977.

Table 1. Summary description of the locations sampled for insects. Each area was sampled at ridge and valley sites. The pines are Pinus radiata

Location	Brief description of areas sampled
Pemberton	2 year old and 44 year old karri forest
Manjimup	Uncleared and cleared karri forest
Quilergup	Uncleared jarrah forest and 2 year old pine plantation
Nannup	Uncleared jarrah forest and 18 year old pine plantation

3.   RESULTS AND DISCUSSION

The analysis is presented so that it progresses from the general to the
specific.   The overall picture is presented for the entire data base before
examining the influences of silvicultural practices on various subsets of the
data at both the familial and generic levels.

3.1   Pemberton

Total average counts for orders of insects: The average counts for the data
classified to the level of Orders showed, for the day samples, interaction
between areas and sites only for the second sampling period.   There were area
differences only in the first sampling period; otherwise area, site and
interaction terms were not significant.   For the night samples there was
interaction between sites and areas during the third and fourth sampling
periods, there were site differences in the tenth sampling period but
otherwise area, site and interaction terms were not significant.

Analysis of the pooled samples for the families in five orders: In the day
samples there were significant differences between areas on both ridge and
valley sites for Hymenoptera ($\tau = 0.11$ and 0.25 respectively) and Diptera
($\tau = -0.02$ and 0.24 respectively).   In the night samples the Coleoptera
showed significant differences on both ridge ($\tau = 0.17$)) and valley
($\tau = 0.44$) sites, whereas the Lepidoptera did not show differences between
areas on either the ridge ($\tau = 0.62$) or valley ($\tau = 0.59$) sites.

Pemberton Pooled Family Data

Numbers (Table 2): More families and many more individuals were trapped at
night than in the equivalent day samples.   More individuals were trapped by
both day and night in the 2 y.o. than in the 44 y.o. karri.

Table 2.   The total number of families and individuals trapped at Pemberton
            from 1974-5 in 2 year old and 44 year old karri

Site	Age (years)	No. families		No. individuals	
		Day	Night	Day	Night
Valley	1	41	42	416	3,415
Ridge	2	43	50	426	2,936
Valley	44	46	46	330	2,805
Ridge	44	35	50	221	1,614

Dominance (Table 3): The day samples from the 44 y.o. plots show increased
Berger-Parker dominance indices compared with their respective 2 y.o. plots
while the reverse is the case with the night samples which also show greater
dominance than the day samples.

Table 3. Berger-Parker dominance index for the pooled Pemberton data

Site	Age (years)	Day	Night
Valley	2	0.17	0.71
Ridge	2	0.22	0.47
Valley	44	0.21	0.44
Ridge	44	0.31	0.28

Dominance-diversity (Figure 1a): Day: The 2 y.o. samples have strongly
bimodal dominance-diversity curves whereas the curves from the 44 y.o. plots
were higher, steeper and unimodal, namely they had more uncommon families.
Night: All curves are bimodal with the second peak one octave to the right in
the 44 y.o. plots. The curves for the 2 y.o. plots have higher initial peaks,
that is they have more rare families.

Rarefaction (Figure 2a): All the day samples had greater E_s diversity than
the night samples. The day samples show little change in diversity with the
age of the stand or between valley and ridge sites. However, in the night
samples the ridge sites had greater familial diversity than the valley sites
and diversity was greater on the older plots than on the corresponding younger
sites.

Dendrogram (Figure 3a): The corresponding ridge and valley sites link most
closely in all cases. The day and night samples separate significantly into
two groups and the 2 y.o. plots separate from the 44 y.o. plots in each case
using both numeric and occurrence data.

Coleoptera Families from Pemberton

Dominance (Table 4): In the day samples the valley sites had greater
dominance than the corresponding ridge sites whereas the night samples showed
lower dominance in the 44 y.o. sites than in the 2 y.o. sites.

Table 4. Berger-Parker dominance index for the Coleoptera family data from
Pemberton

Site	Treatment	Day	Night
Valley	2 year old	0.50	0.38
Ridge	2 year old	0.17	0.26
Valley	44 year old	0.39	0.21
Ridge	44 year old	0.25	0.22

Dominance-diversity (Figure 1c): In the night samples the 44 year old sites
had lower origins and a shift to the left in the second peak than the
comparable 2 year old sites, indicating fewer rare taxa.

Dendrogram (Figure 3b): Both numeric and occurrence data separate into night and day samples. Whereas the night samples separate clearly according to the age of the stand, the day samples do not group by stand age or site location.

Lepidoptera Families from Pemberton

Dominance (Table 5): In the day samples the valley sites show much greater dominance than the ridge sites and the age of the stand was unrelated to Berger-Parker dominance. In the night samples the dominance was greater in the older stands of karri.

Table 5.   Berger-Parker dominance index for the Lepidoptera family data from Pemberton

Site	Treatment	Day	Night
Valley	2 year old	0.64	0.47
Ridge	2 year old	0.30	0.41
Valley	44 year old	0.63	0.65
Ridge	44 year old	0.33	0.45

Rarefaction (Figure 2b): In the day samples E_s in valley sites increased with stand age while the converse occurred on the ridge sites. The opposite changes were seen in the night samples with the effect being more marked on the valley sites.

Dendrogram (Figure 3c): The data separate clearly into night and day samples; the night samples link according to site location rather than stand age but the day samples link on neither category.

Hymenoptera Families from Pemberton

Dominance (Table 6): The night samples had much greater dominance values than the day samples and they were higher in the younger stands. In the day samples there was a marked change in dominance with stand age on the valley site but not on the ridge site.

Table 6.   Berger-Parker dominance index for the Hymenoptera family data from Pemberton

Site	Treatment	Day	Night
Valley	2 year old	0.25	0.99
Ridge	2 year old	0.75	0.99
Valley	44 year old	0.67	0.93
Ridge	44 year old	0.67	0.86

Rarefaction (Figure 2c): The day samples showed similar E_s diversity in all groups whereas the night samples showed greater diversity in the older stand.

Figure 1.   Dominance-diversity curves for Pemberton samples plotted as
             two-point moving averages. (a) combined family data, (b) pooled
             genera (right) and Lepidoptera genera (left), (c) Coleoptera
             families. V = valley sites; R = ridge site; N = night sample,
             D = day sample; 2 and 44 = 2 y.o. and 44 y.o. karri stands
             respectively.

A

D2V   N2V
D44V   N44V
D2R   N2R
D44R   N44R

B

2V   2V
2R   2R
44V   44V
44R   44R

C

D2V   N2V
D44V   N44V
D2R   N2R
D44R   N44R
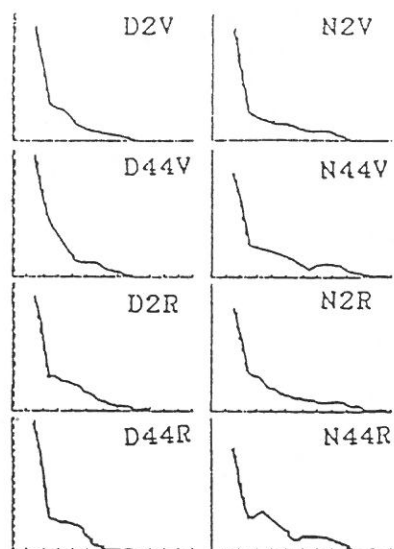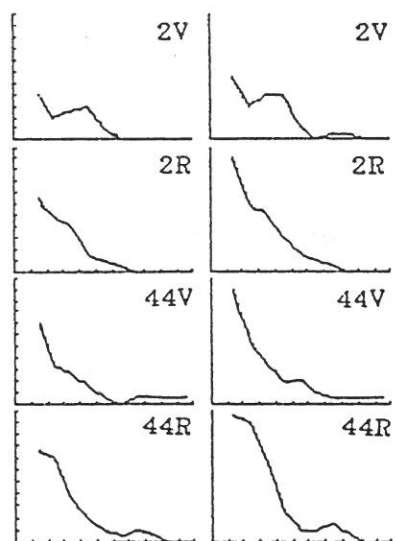
Figure 2.   Rarefaction of the Pemberton samples giving the estimated number
(E_S) of families or genera per given number of individuals.
(a) the combined number of families per 100, (b) Lepidoptera
families per 100, (c) Hymenoptera families per 100, (d) Diptera
families per 100, (e) Coleoptera genera per 100, (f) Lepidoptera
genera per 100.   V = valley sites; R = ridge site; N = night
sample, D = day sample; 2 and 44 = 2 y.o. and 44 y.o. karri stands
respectively.
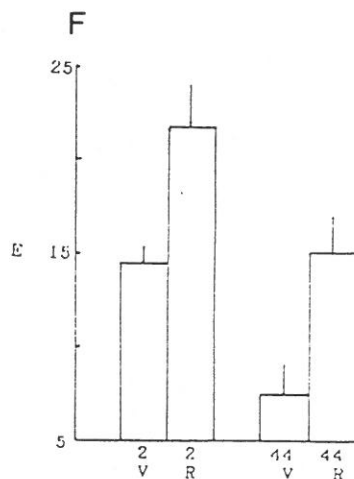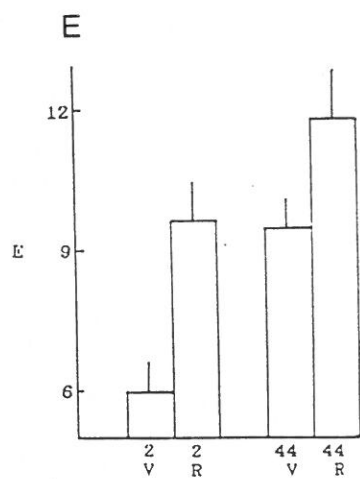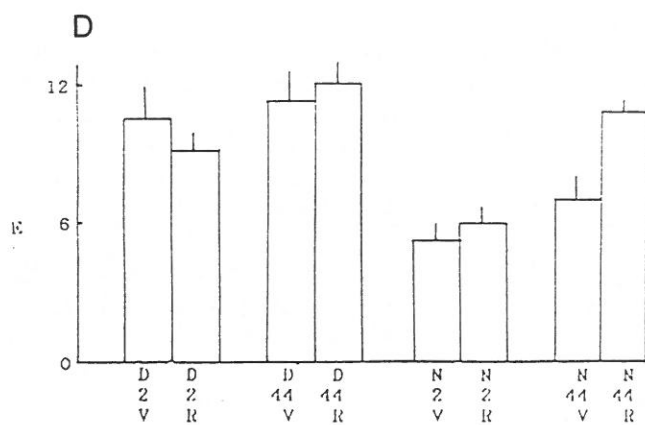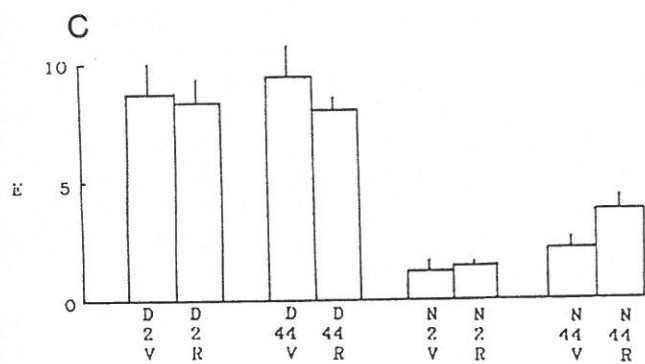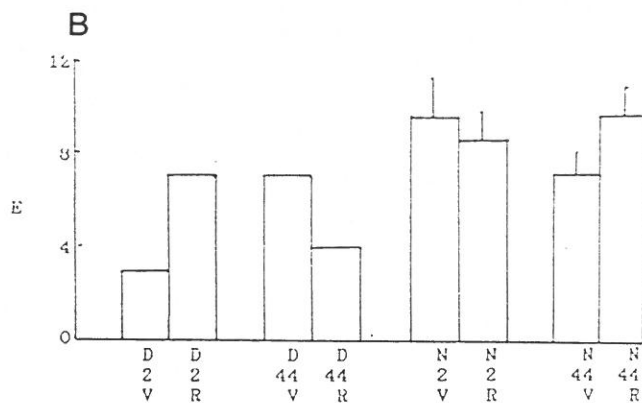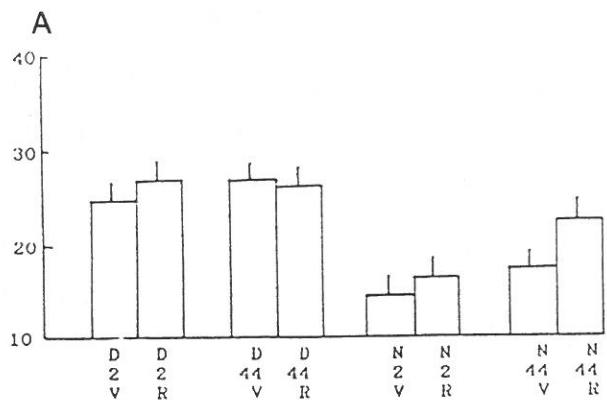
Figure 3.   Dendrograms of dissimilarity for the Pemberton samples.
(a) combined families based on numeric data where the solid lines
denote significant linkages at α = 0.05, (b) Coleoptera families
based on numeric data, (c) Lepidoptera families, numeric data,
(d) Hymenoptera families based on numeric data, (e) Diptera
families based on numeric data, (f) Hemiptera families based on
occurrence data, (g) pooled genera, (h) Coleoptera genera based on
numeric data, (i) Lepidoptera genera based on numeric. V = valley
sites; R = ridge site; N = night sample, D = day sample; 2 and
44 = 2 y.o. and 44 y.o. karri stands respectively.
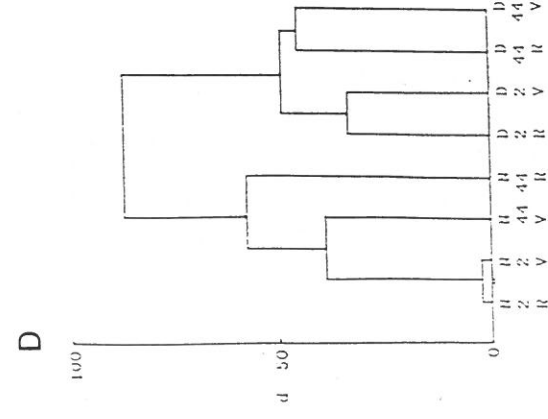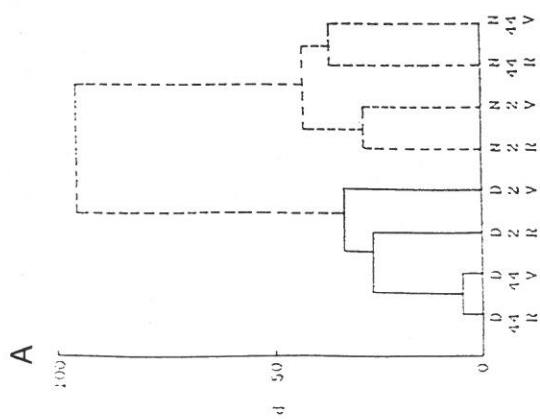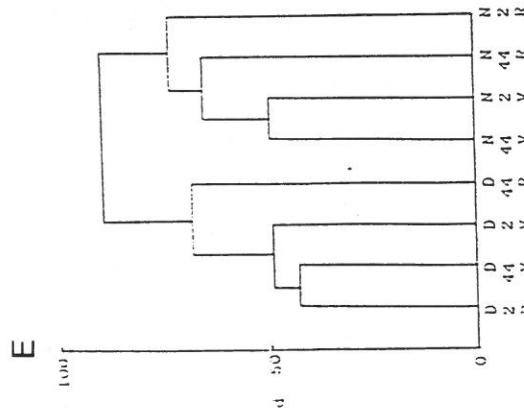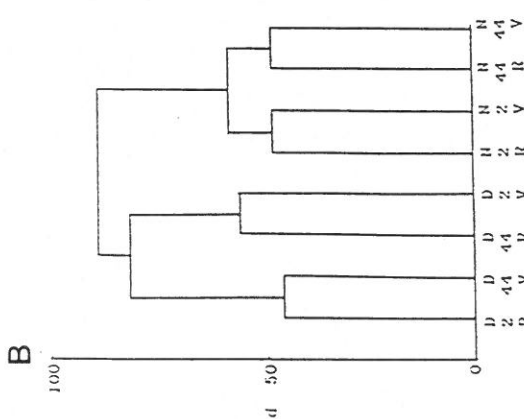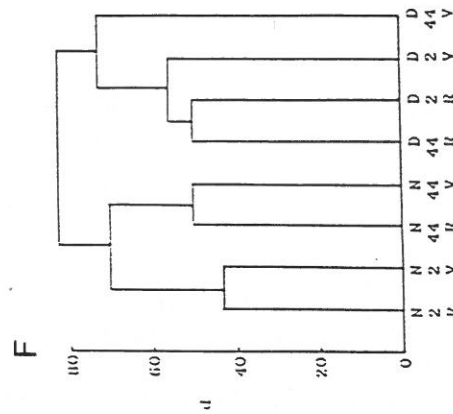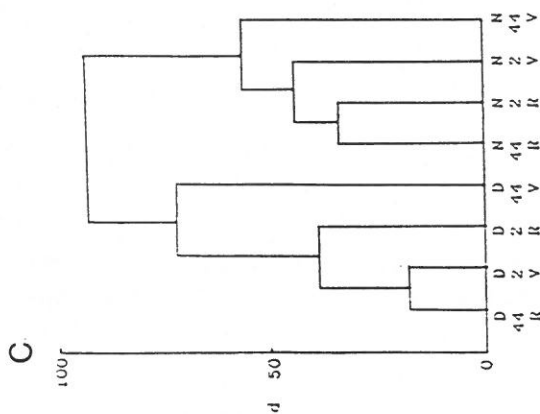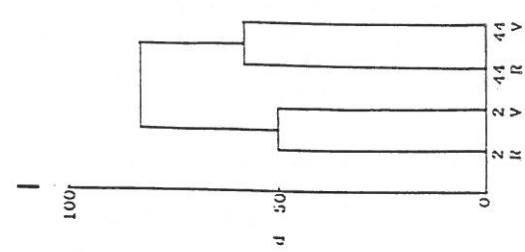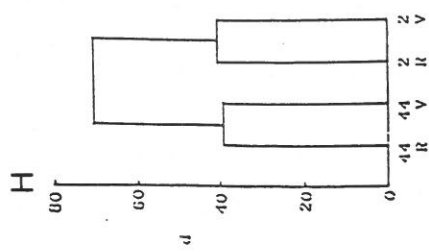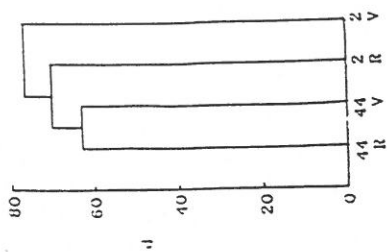
Dendrogram (Figure 3d): Both numeric and occurrence data separate clearly into day and night samples and within these groups the data link according to the age of the stand.

Diptera Families from Pemberton

Dominance (Table 7): In the day samples the sites in the older stand had greater dominance than their respective sites in the younger stand; in the night samples the reverse was the case but the effect was much more marked.

Table 7. Berger-Parker dominance index for the Diptera family data from Pemberton

Site	Treatment	Day	Night
Valley	2 year old	0.38	0.61
Ridge	2 year old	0.42	0.91
Valley	44 year old	0.40	0.48
Ridge	44 year old	0.48	0.61

Rarefaction (Figure 2d): Both day and night samples had greater E_s diversity on the 44 y.o. stands than in the comparable 2 y.o. stands, with the increase being more marked on the ridge sites.

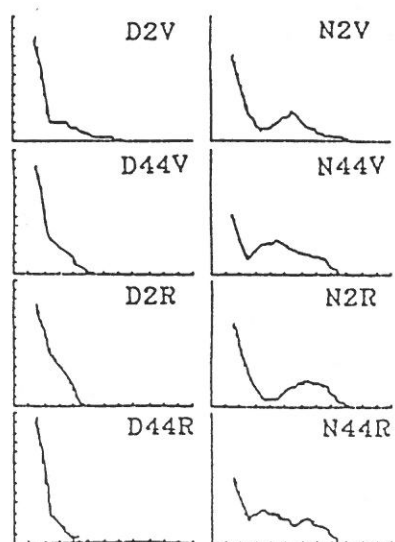Dendrogram (Figure 3e): The data separate clearly into day and night samples. Within this classification the night samples group by site location rather than stand age, while the day samples group by neither stand age nor site location.

Hemiptera Families from Pemberton

Dominance (Table 8): The Berger-Parker dominance index was related to neither stand age nor site location in the day samples but in the night samples the sites in the older stand had greater dominance indices than their respective younger sites.

Table 8. Berger-Parker dominance index for the Hemiptera family data from Pemberton

Site	Treatment	Day	Night
Valley	2 year old	0.66	0.35
Ridge	2 year old	0.43	0.69
Valley	44 year old	0.33	0.56
Ridge	44 year old	0.62	0.82

Dendrogram (Figure 3f): There is clear separation of the day from the night samples; the night samples link according to the age of the stand but the day samples do not group by either stand age or site location.

Numbers (Table 9): More genera and substantially more individuals were trapped in the 44 y.o. stand than in comparable sites in the 2 y.o. stand.

Table 9. The total number of genera and individuals trapped at Pemberton from 1974-5 in 2 year old and 44 year old karri

Site	Treatment	Number of	
		Genera	Individuals
Valley	2 year old	22	283
Ridge	2 year old	34	257
Valley	44 year old	33	1,359
Ridge	44 year old	39	579

Diversity (Table 10): Sites in the older stand had lower H_1 and H_1/H_{max} diversities than the comparable sites in the younger stand and ridge sites had much greater diversities than valley sites.

Table 10. H_1 and H_1/H_{max} diversity indices for the pooled generic data from Pemberton

		H_1	H_1/H_{max}
Valley	2 year old	2.7	5.9
Ridge	2 year old	3.7	12.3
Valley	44 year old	1.8	3.3
Ridge	44 year old	3.1	7.2

Dominance-diversity (Figure 1b, right): The 44 y.o. sites exhibited steeper curves with longer tails than the 2 y.o. sites, namely they had more rare genera as well as more common genera.

Dendrogram (Figure 3g): The numeric and occurrence data link by site according to stand age.

Coleoptera Genera from Pemberton

Diversity (Table 11): Valley sites, but not ridge sites, showed greater H_1 and H_1/H_{max} diversity in the older aged stand.

Table 11. H_1 and H_1/H_{max} diversity indices for the Coleoptera generic data from Pemberton

		H_1	H_1/H_{max}
Valley	2 year old	1.32	1.4
Ridge	2 year old	1.94	3.3
Valley	44 year old	1.80	3.7
Ridge	44 year old	1.90	3.0

Rarefaction (Figure 2e): E_s diversity was greater on sites in the older aged stand than the comparable sites in the younger aged stand; however, the diversity overlapped between stands of different age.

Dendrogram (Figure 3h): The data group strongly according to the age of the stand; however, notice that the ridge and valley sites have dissimilarity values of about 40% compared with between stand age dissimilarity of 70%.

Lepidoptera Genera from Pemberton

Diversity (Table 12): The 44 y.o. stands exhibited much lower H_1 and H_1/H_{max} diversities than the 2 y.o. stands and the ridge sites had higher diversities than the comparable valley sites.

Table 12. H_1 and H_1/H_{max} diversity indices for the Lepidoptera generic data from Pemberton

		H_1	H_1/H_{max}
Valley	2 year old	3.2	13.2
Ridge	2 year old	3.6	13.4
Valley	44 year old	1.8	1.8
Ridge	44 year old	2.4	4.3

Dominance-diversity (Figure 1b, left): The 44 y.o. sites exhibited steeper curves with much longer tails than the 2 y.o. sites.

Rarefaction (Figure 2f): E_s is considerably lower in the samples from the 44 y.o. stands than in the comparable 2 y.o. stands and higher on ridge than on creek sites.

Dendrogram (Figure 3i): The data group strongly according to the age of the stand; however, notice that the ridge and valley sites have dissimilarity values of about 50% compared with between stand age dissimilarity of 82%.

Discussion of the Pemberton Data

The differential resolution of community data analysed at various levels of taxonomic resolution has been discussed elsewhere in relation to other parts of this study (Curry and Humphreys 1987). In addition consideration was given

to the problems of sampling habitats having very different structural
characteristics, as seen here when sampling mature forest and sites recently
cleared of forest (ibid.). These factors lead to constraints on the data and
subsequent analyses which may be exacerbated by the contamination of samples
from adjacent untreated areas. The question arises whether the noise in the
system is sufficient to mask any effects of the treatment.

Analysis of the numeric data classified to Orders for each sampling time shows
that the data have very low resolution with few significant effects seen in
either the day or night samples. Analysis of the numeric data for the pooled
family samples for five orders showed that both Hymenoptera and Diptera were
significantly different between treatments in the day samples and the
Coleoptera in the night samples.

Many more individuals were trapped at night and in the 2 year old sites but
this increase in numbers had little effect on the number of families trapped
(Table 2). It is unknown whether the numeric differences result from the
concentration of insects in one stratum in cleared sites, compared with many
strata in the uncleared sites. However, it will be shown later, from the
Manjimup data, that this effect is, in itself, insufficient to explain the
changes in numbers trapped, as at that location many more insects were trapped
on uncleared forest sites than on cleared sites. Nevertheless here the
overall dominance on the cleared site was lower by day and higher at night
(Table 3). A breakdown of these results shows that there is a differential
response between the Orders (Tables 4, 5, 6, 7 and 8). Whereas valley sites
had higher dominance for Coleoptera and Lepidoptera (day; Tables 4 and 5),
ridge sites had greater dominance for Hymenoptera and Diptera (day; Tables 6
and 7), and the uncleared forest had greater dominance for Hemiptera (night;
Table 8). The generic data showed overall higher dominance in the 2 year old
sites and on the ridges (Table 10), mainly caused by the Lepidoptera (Table
12) which showed clear and marked between area differences.

Overall there was lower E_s diversity in the night samples in which E_s was
greater in the uncleared areas (Figure 2a). For Lepidoptera E_s was greater
at night (Figure 2b) but was lower for Hymenoptera (Figure 2c; greater in
uncleared areas) and for Diptera (Figure 2d), where E_s was greater in the
uncleared areas by both day and night. The generic data showed higher E_s
for Coleoptera (Figure 2e) and lower E_s for Lepidoptera (Figure 2f) in the
uncleared sites than on comparable cleared sites.

The change in the structure of the communities is shown in the
dominance-diversity curves, the form of which changes substantially between
treatments in the pooled data (Figure 1a), Coleoptera (Figure 1c) and for the
generic data (Figure 1b).

All dendrograms give complete separation of the day and night samples (Figure
3a-f). Overall the effects of the clearing is seen in the dendrogram for the
pooled data (Figure 3a), in which, within the day and night samples, the data
segregate according to the treatments. This is also the case for some subsets
of the data; for Coleoptera (night; Figure 3b), Hymenoptera (day and night;
Figure 3d) and Hemiptera (night; Figure 3f). Some samples, however, segregate
according to site location (ridge vs valley; these include Lepidoptera, night;
Diptera, night and Hemiptera, day), whereas other segregate according to
neither treatment nor site (Coleoptera, day; Lepidoptera, day and Diptera,
day). Note that in all cases where the data segregate by treatment the
dendrograms form without chaining; in all other cases, bar one (Coleoptera,
day; Figure 3b), the dendrograms form chains within the day and night samples
indicating poor resolution of the data. The generic data show clear
segregation of the samples according to treatment (Figure 3g-i), with only the
pooled generic data exhibiting chaining.

-17-

In the day samples the Colletidae and Syrphidae increased significantly in numbers on the replanted karri sites while the Chironomidae disappeared (Table 41). In the night samples 8 families decreased, and 2 families increased, significantly in numbers on the replanted plots compared with the uncleared karri forest (Table 41). Note that the Chironomidae apparently became entirely nocturnal in the cleared areas, perhaps reflecting a change in microclimate. Of the families represented in the samples 13% were significantly changed in numbers on the cleared and replanted sites compared with the uncleared forest (Table 42).

Seven genera had significantly different numbers on the treatment plots with about equal numbers increasing and decreasing (Table 43). Chlorocoma (Geometridae), which feeds on the foliage of small trees, was the predominant lepidopteran genus in mature karri but was reduced substantially in numbers on the regrowth plots (Table 43). Other genera were reduced [Anobium (Anobiidae) and Acidalia (Geometridae)] or absent [Simplicia (Noctuidae)] on regrowth plots, while Orgyia (Lymantriidae; a predominantly tree feeding genus), Onthophagus (Scarabaeinae), Liparetrus (Melolonthinae) and Pantydia (Noctuidae) were significantly adavantaged on the regrowth plots (Table 43).

3.2   Manjimup

Total average counts for orders of insects: The average counts for the data classified to the level of orders showed, for the day samples, no area x site interaction in any sampling period. There were significant site effects in the first two samples and a significant area effect in the fourth sample. In the night samples there was significant interaction (samples 2, 6 and 9), area (samples 1, 2, 4) and site (sample 2, 4, 7) effects.

Analysis of the pooled samples for the families in five orders: τ was unsuitable for all the day samples. In the night samples the Coleoptera showed significant differences on both ridge ($\tau = 0.36$) and valley ($\tau = 0.24$) sites, whereas the Lepidoptera showed significant differences between the valley ($\tau = 0.42$) but not the ridge ($\tau = 0.06$) sites.

Pooled Family Data from Manjimup

Numbers (Table 13): There is little difference in the numbers of families or individuals sampled by day in cleared and uncleared forest. However, in the night samples there was a substantial reduction in both the numbers of families and individuals in the cleared forest.

Table 13. The total number of families and individuals trapped at Manjimup
           from 1974-5

Site	Treatment	No. families		No. individuals	
		Day	Night	Day	Night
Valley	Uncleared	43	41	359	3,769
Ridge	Uncleared	30	44	163	5,615
Valley	Cleared	36	35	320	1,314
Ridge	Cleared	33	39	192	954

Dominance (Table 14): In the day samples there was a marginal increase in dominance in cleared sites relative to the comparable uncleared sites. In the night samples there was a substantial reduction in dominance in the cleared forest sites.

Table 14. Berger-Parker dominance index for the pooled Manjimup data

Site	Treatment	Day	Night
Valley	Uncleared	0.20	0.69
Ridge	Uncleared	0.21	0.92
Valley	Cleared	0.33	0.27
Ridge	Cleared	0.22	0.21

Dominance-diversity (Figure 4a):

In both the day and night samples there is a reduction in height of the second peak in the dominance-diversity plots for the cleared sites compared with the comparable uncleared sites.

Rarefaction (Figure 5a): E_S diversity was much greater in all the day samples than in those taken at night. While day samples showed rather constant E_S values, in the night samples the cleared sites had much greater E_S values than uncleared forest sites.

Dendrogram (Figure 6a): The data separate clearly into day and night samples with the day samples grouping according to whether the sites were cleared or not. The night samples do not group according to site location or treatment.

Coleoptera Families from Manjimup

Dominance-diversity (Figure 4b): In both the day and night samples there is a reduction in height of the second peak in the dominance-diversity plots for the cleared sites compared with the comparable uncleared sites.

Rarefaction (Figure 5b): In the day samples E_S diversity is greater in the cleared sites than in the comparable uncleared sites while the reverse is the case in the night samples.

Dendrogram (Figure 6b): The data separate clearly into day and night samples with the day samples grouping according to whether the sites were cleared or not. The night samples do not group according to site location or treatment.

Lepidoptera Families from Manjimup

Dominance (Table 15): The Berger-Parker dominance indices are similar through all samples and show no clear separation between sampling time or treatments.

Table 15. Berger-Parker dominance index for the Lepidoptera family data from
           Manjimup

Site	Treatment	Day	Night
Valley	Uncleared	0.45	0.44
Ridge	Uncleared	0.60	0.43
Valley	Cleared	0.50	0.63
Ridge	Cleared	0.50	0.39

Dominance-diversity (Figure 4c): In the night samples there is an increase in
origin height and a smaller area under the left side of the dominance
diversity plots in the cleared relative the comparable uncleared sites,
showing a decrease in the number of rare taxa in the cleared plots.

Rarefaction (Figure 5c): E_S is much greater in the night samples and lower
on cleared sites than in samples from comparable uncleared sites.

Dendrogram (Figure 6c): The data separate clearly into day and night samples
with the night samples grouping according to whether the sites were cleared or
not. The day samples do not group according to site location or treatment.

Hymenoptera Families from Manjimup

Dominance (Table 16): The Berger-Parker dominance index shows complete
dominance by one family in the night samples and low values in the day samples
with no consistency by site location or treatment.

Table 16. Berger-Parker dominance index for the Hymenoptera family data from
           Manjimup

Site	Treatment	Day	Night
Valley	Uncleared	0.21	0.99
Ridge	Uncleared	0.44	0.99
Valley	Cleared	0.45	0.99
Ridge	Cleared	0.35	0.99

Dominance-diversity (Figure 4d): In the day samples there is a reduction in
the dominance of the second peak in the cleared sites. In the night samples
the cleared sites both have a peak of common taxa not present in the uncleared
sites.

Rarefaction (Figure 5d): E_S is much greater in the day samples in which
there is a reduction in E_S diversity in the cleared sites. In the night
samples there is an increase in E_S diversity in the cleared sites relative
to the comparable uncleared sites.

Dendrogram (Figure 6d): The data separate clearly into day and night samples
with the day samples grouping according to whether the area was cleared or
not. The night samples group according to site location.

Diptera Families from Manjimup

Dominance (Table 17): The Berger-Parker dominance was greater in night
(> 0.76) than day (> 0.66) samples. The night samples show greater
dominance in the uncleared forest.

Table 17. Berger-Parker dominance index for the Diptera family data from
Manjimup

Site	Treatment	Day	Night
Valley	Uncleared	0.37	0.92
Ridge	Uncleared	0.50	0.90
Valley	Cleared	0.66	0.77
Ridge	Cleared	0.49	0.85

Dominance-diversity (Figure 4e): In the day samples there is a more rapid
decline in the dominance-diversity curve for the cleared sites than for the
comparable uncleared sites, but there are no consistent differences in the
night samples.

Rarefaction (Figure 5e): The day samples had greater E_S diversity than
night samples, with the cleared sites having lower E_S diversity than the
uncleared forest. In night samples the cleared sites had greater E_S
diversity than comparable uncleared sites.

Dendrogram (Figure 6e): The data separate clearly into day and night samples
with both the day and night samples grouping according to whether the sites
were cleared or not.

Hemiptera Families from Manjimup

Dominance (Table 18): Dominance is mostly greater in the day samples but
there is no association with site or treatment.

Table 18. Berger-Parker dominance index for the Hemiptera family data from
Manjimup

Site	Treatment	Day	Night
Valley	Uncleared	0.25	0.48
Ridge	Uncleared	0.75	0.50
Valley	Cleared	0.67	0.50
Ridge	Cleared	0.66	0.39

Figure 4.   Dominance-diversity curves of the Manjimup samples plotted as
two-point moving averages. (a) pooled families, (b) Coleoptera
families, (c) Lepidoptera families, (d) Hymenoptera families,
(e) Diptera families, (f) genera: left, pooled; centre,
Lepidoptera; right Coleoptera. Codes denote: V = valley sites;
R = ridge site; N = night sample, D = day sample; N = uncleared;
C = cleared.
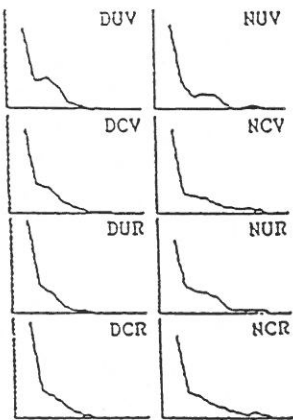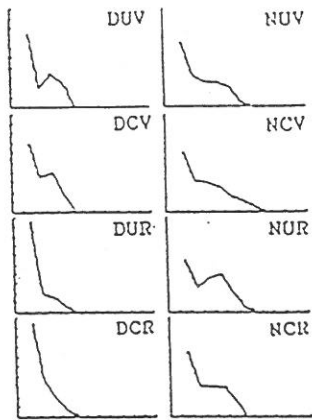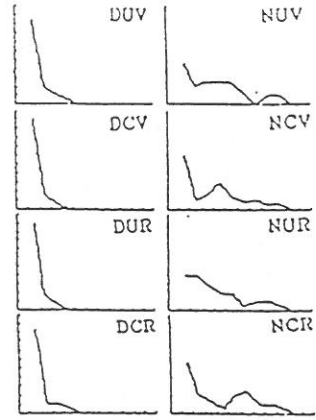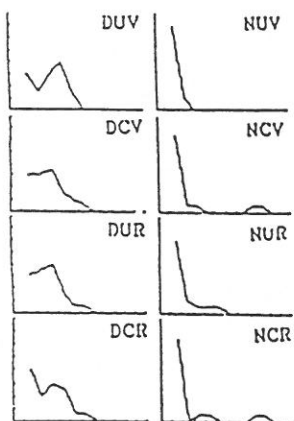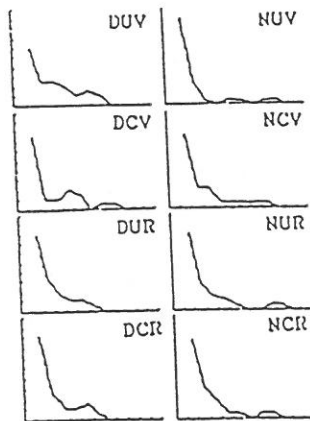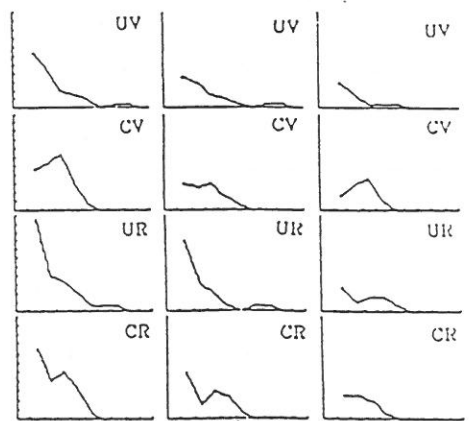
Figure 5.   Rarefaction of the Manjimup samples giving the estimated number
            (E_s) of families or genera per given number of individuals.
            (a) the combined number of families per 100, (b) Coleoptera
            families per 10, (c) Lepidoptera families per 50, (d) Hymenoptera
            families per 50, - note change of scale for the day and night
            samples, (e) Diptera families per 50, (f) genera per 100,
            (g) genera per 30 Coleoptera, (h) genera per 50 Lepidoptera.
            Codes denote: V = valley sites; R = ridge site; N = night sample,
            D = day sample; N = uncleared; C = cleared.
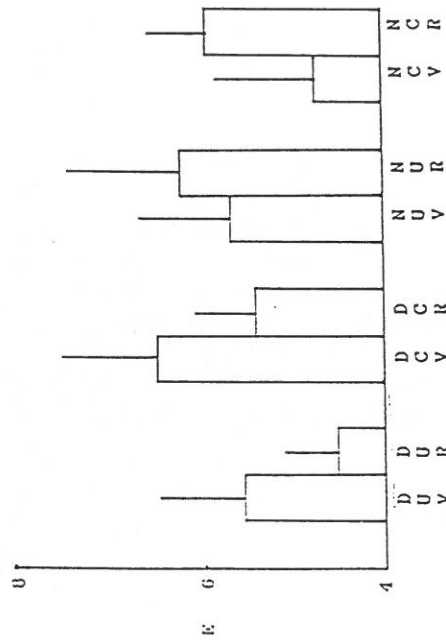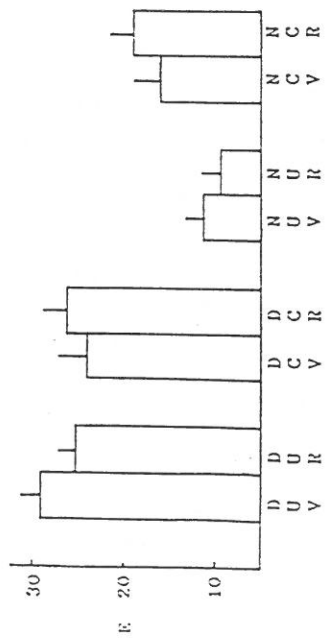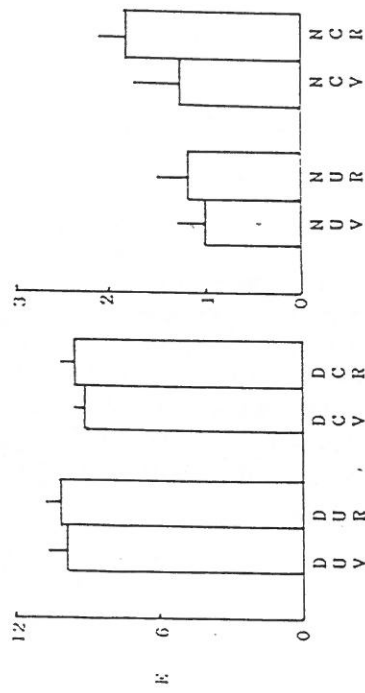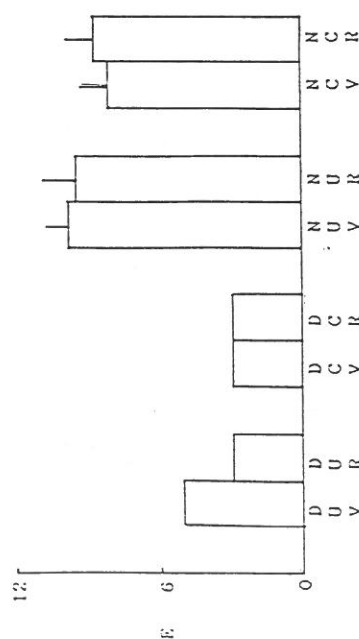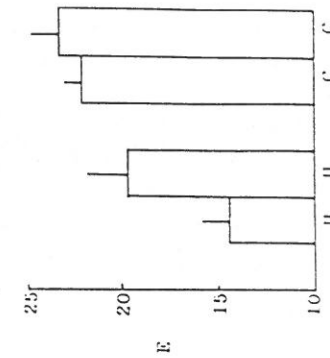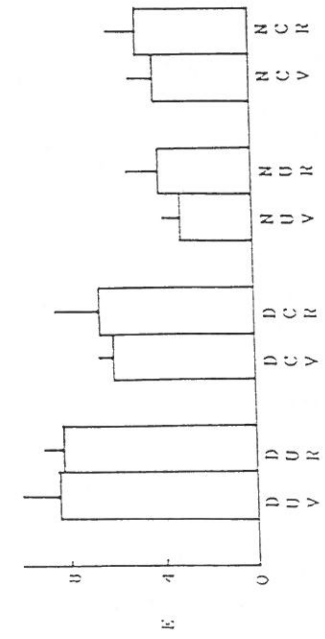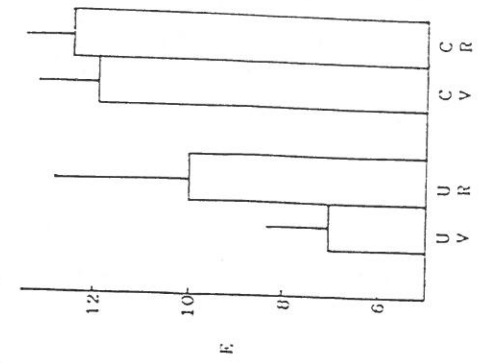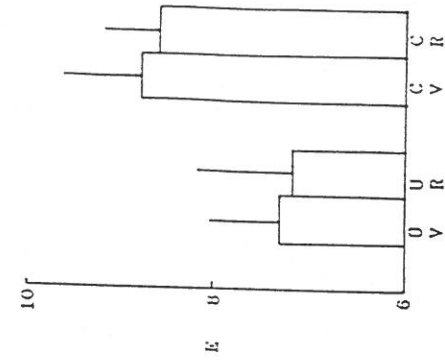
Figure 6.   Dendrograms of dissimilarity values for the Manjimup samples.
(a) Pooled families based on numeric data, (b) Coleoptera
families based on numeric data, (c) Lepidoptera families based on
numeric data, (d) Hymenoptera families based on numeric data, (e)
Diptera families based on occurrence data, (f) Hemiptera families
based on numeric data, (g) pooled genera based on numeric data,
(h) Coleoptera genera based on numeric data, (i) Lepidoptera
genera based on numeric data. Codes denote: V = valley sites;
R = ridge site; N = night sample, D = day sample; N = uncleared;
C = cleared.
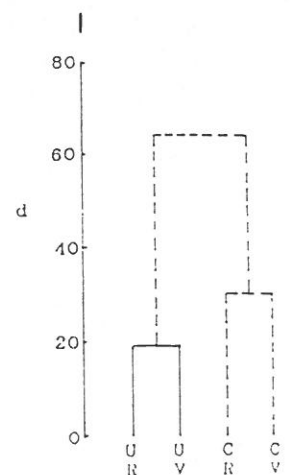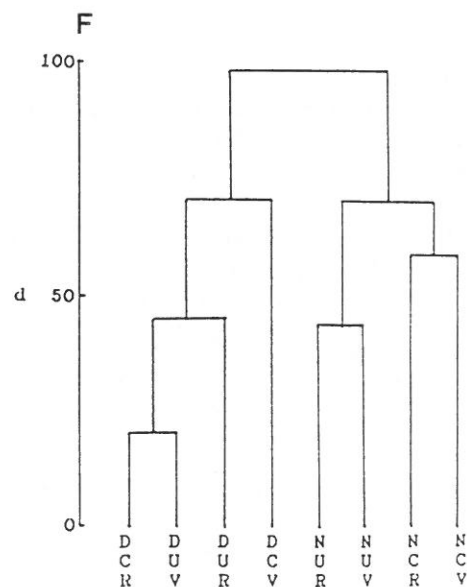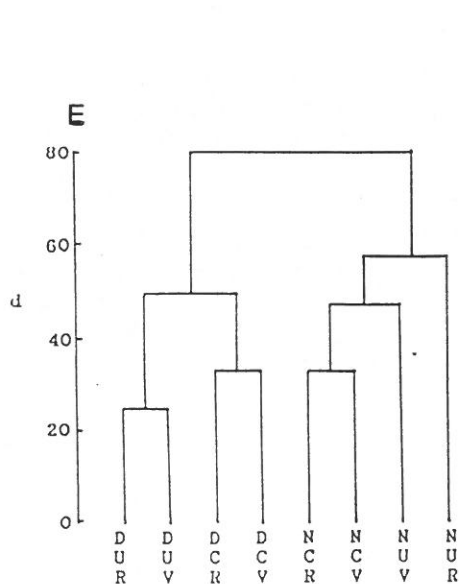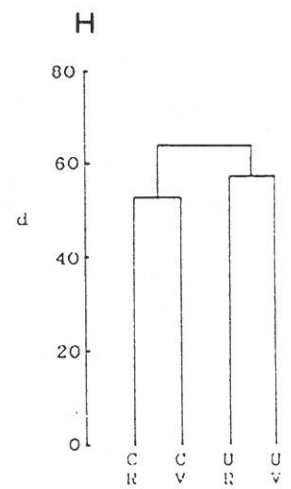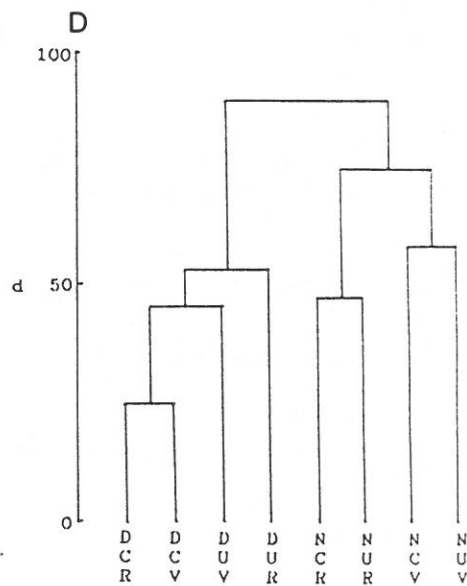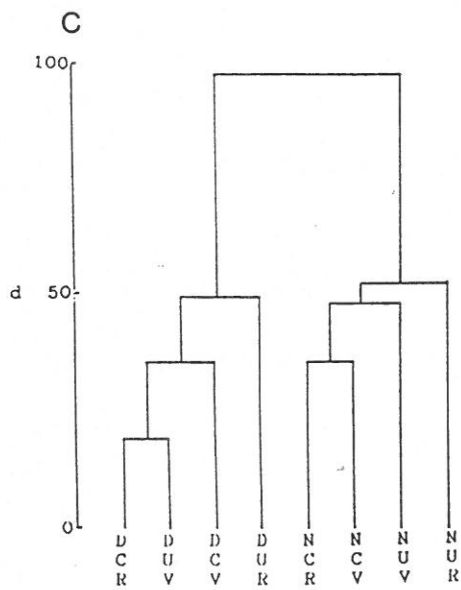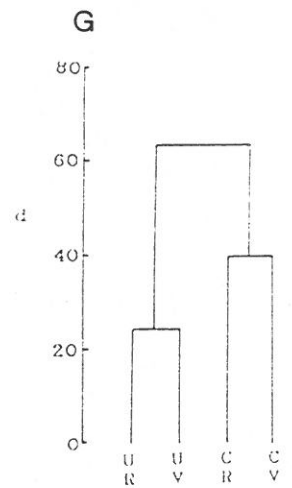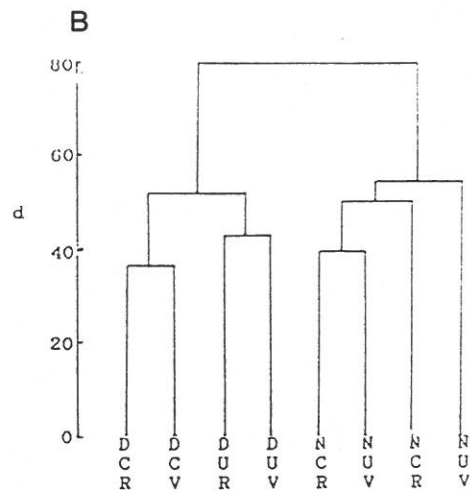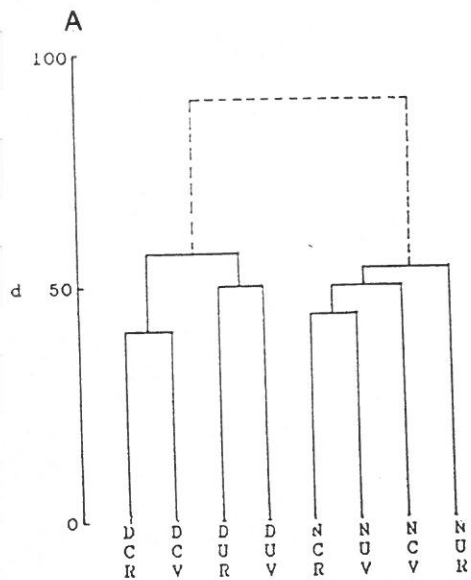
Dendrogram (Figure 6f): The data separate clearly into day and night samples
with the day samples grouping according to whether the area was cleared or
not. The night samples do not group according to site location or treatment.

Pooled Genera from Manjimup

Numbers (Table 19): About twice as many individuals were trapped in the
uncleared areas as in the cleared areas but the number of genera was similar
between treatments, there being more genera on ridge sites.

Table 19. The total number of genera and individuals trapped at Manjimup from
1974-5

Site	Treatment	Number of Genera	Number of Individuals
Valley	Uncleared	20	228
Ridge	Uncleared	30	220
Valley	Cleared	23	120
Ridge	Cleared	26	130

Diversity (Table 20): Both H_1 and H_1/H_{max} diversity were much greater
in the cleared sites than in the uncleared sites.

Table 20. H_1 and H_1/H_{max} diversity indices for the pooled generic data
from Manjimup

| H_1		H_1/H_{max}	
Valley	Uncleared	2.1	2.0
Ridge	Uncleared	2.8	4.5
Valley	Cleared	4.0	28.0
Ridge	Cleared	3.9	22.2

Dominance-diversity (Figure 4f, left): The plots for the uncleared forest
samples have higher origins and longer tails than those for the cleared area.
The latter are strongly bimodal compared with the unimodal plots from the
uncleared area.

Rarefaction (Figure 5f): The cleared sites had much greater E_s diversity
than samples from uncleared forest and the values were greater on ridge sites.

Dendrogram (Figure 6g): The data separate into two groups according to the
treatment with the uncleared sites being more similar (74%) than the cleared
sites (62%).

Coleoptera Genera from Manjimup

Diversity (Table 21): Cleared sites showed much greater H_1 and H_1/H_{max} diversity and lower dominance than samples from the uncleared forest; in uncleared forest the ridge sites are more diverse than valley sites but the reverse is the case in cleared areas.

Table 21. H_1 and H_1/H_{max} diversity indices for Coleoptera genera from Manjimup

Site	Treatment	H_1	H_1/H_{max}	B-P
Valley	Uncleared	2.0	3.6	0.555
Ridge	Uncleared	2.4	6.1	0.392
Valley	Cleared	2.9	10.7	0.272
Ridge	Cleared	2.7	8.3	0.323

Rarefaction (Figure 5g): Cleared sites showed much greater E_s values than the uncleared forest sites.

Dendrogram (Figure 6h): The data separate according to the treatment but the similarity of the paired sites is low (ca 45%).

Lepidoptera Genera from Manjimup

Diversity (Table 22): Both H_1 and H_1/H_{max} diversity were much greater in samples from the cleared than in samples from uncleared forest.

Table 22. H_1 and H_1/H_{max} diversity indices for Lepidoptera genera from Manjimup

H_1	H_1/H_{max}		
Valley	Uncleared	1.5	1.9
Ridge	Uncleared	1.1	2.5
Valley	Cleared	2.5	11.4
Ridge	Cleared	3.3	13.0

Dominance-diversity (Figure 4f, centre): The plots for the uncleared forest samples are higher, have longer tails and are less strongly bimodal than those for the cleared area, namely there are more rare genera in the uncleared forest.

Rarefaction (Figure 5h): E_s diversity values were greater in the samples from the cleared area than in samples from the uncleared forest and ridge sites had greater E_s diversity than the comparable valley sites.

Dendrogram (Figure 6i): The data separate into two groups according to the treatment and show a large separation between treatments; the uncleared sites were more similar (80%) than the cleared sites (70%).

Discussion of the Manjimup Data

Analysis of the numeric data classified to Orders for each sampling time shows that the data has moderate resolution with some significant site, area and interaction terms. Analysis of the numeric data for the pooled family samples for five orders showed that both Coleoptera and Lepidoptera were significantly different between treatments.

Many more individuals were trapped at night and in the uncleared sites which also resulted in a greater number of families being trapped (Table 13). This results in the overall dominance being much greater on uncleared sites at night (Table 14). A breakdown of these data shows that there is no clear association between dominance of families within an Order and site or treatment (Tables 15, 16, 17, and 18), unlike the situation in the Pemberton study area. For the generic data more individuals, but not families, were trapped on the uncleared sites (Table 19), resulting in greater dominance on the cleared sites (Table 20). For both the Coleoptera (Table 21) and Lepidoptera (Table 22) generic dominance was greater on the cleared sites.

Overall there was lower E_s diversity in the night samples in which E_s was greater in the cleared areas (Figure 5a). For Coleoptera E_s was greater by day on cleared sites but the reverse was the case in the night samples (Figure 5b). For Lepidoptera E_s was greater at night and on uncleared sites (Figure 5c). E_s was lower for Hymenoptera (Figure 5d) and Diptera (Figure 5e) at night being greater on cleared sites, whereas the reverse was the case in the day samples. The generic data overall showed higher E_s on cleared sites (Figure 5f), and for the Coleoptera (Figure 5g) and Lepidoptera (Figure 5h) alone.

The change in the structure of the communities is shown in the dominance-diversity curves, the form of which changes substantially between treatments in the pooled data (Figure 4a), Coleoptera (Figure 4b), Lepidoptera (Figure 4c, night), Hymenoptera (Figure 4d), Diptera (Figure 4e) and for the generic data (Figure 4f).

All dendrograms give complete separation of the day and night samples (Figure 6a-f). Overall the effects of the clearing is seen in the dendrogram for the pooled data (Figure 6a), in which, within the day samples, the data segregate according to the treatments, but not in the night samples in which chaining is seen. Clear separation between treatments is seen also for some subsets of the data; for Coleoptera (day Figure 6b), Lepidoptera (night; Figure 6c), Hymenoptera (day Figure 6d), Diptera (day and night; Figure 6e) and Hemiptera (night; Figure 6f). However, the Hymenoptera at night segregate according to site location (ridge vs valley; Figure 6d), whereas others segregate according to neither treatment nor site (pooled samples, night; Coleoptera, night; Lepidoptera, day and Hemiptera, day: Figures 6a, 6b, 6c, and 6f respectively).

In the day samples the Muscidae, Scutelleridae, Aradidae and Coccinellidae were more abundant on the cleared plots, the latter two families being absent in the uncleared forest (Table 41). In the night samples one family increased (Noctuidae) and three families (Formicidae, Geometridae and Melolonthinae) significantly decreased in numbers on the cleared sites (Table 41). Of the families represented in the samples 8% were significantly changed in numbers on the cleared and replanted sites compared with the uncleared forest (Table 42).

Two genera were significantly altered in numbers on the treatment plots. Chlorocoma (Geometridae), which feeds on the foliage of small trees, was the predominant lepidopteran genus in mature karri but was reduced substantially in numbers on the regrowth plots. Onthophagus (Scarabaeinae) was significantly advantaged on the regrowth plots, being absent in uncleared forest sites (Table 43).

3.3   Quilergup

Total average counts for Orders of insects: The average counts for the data classified to the level of Orders showed, for the day samples, interaction between areas and sites in all sampling periods except 4, 5, 7 and 8. There were area differences in sampling periods 5, 7 and 8 and site differences in sampling periods 4, 5, 7 and 8. For the night samples there was interaction between sites and areas in all but the fifth sampling period in which an area difference was apparent.

Analysis of the pooled samples for the families in five orders: In the day samples there were significant differences beyween areas on both ridge and valley sites for Hymenoptera ($\tau = 0.43$ and 0.50 respectively) and Diptera ($\tau = 0.45$ and 0.40 respectively), for only one site in the Lepidoptera (valley; $\tau = 0.57$) and the Coleoptera (ridge; $\tau = 0.44$). For the night samples only the Diptera from the ridge sites ($\tau = 0.40$) were significantly different.

Pooled Families from Quilergup

Numbers (Table 23): More families but substantially fewer individuals were trapped by day than by night. There was no consistent influence of pine planting on the numbers of families or individuals trapped.

Table 23.   The total number of families and individuals trapped at Quilergup from 1975-6

Site	Treatment	No. families		No. individuals	
		Day	Night	Day	Night
Valley	Uncleared	83	58	4,069	12,323
Ridge	Uncleared	67	70	1,745	50,649
Valley	2 year old pine	80	62	4,530	16,696
Ridge	2 year old pine	78	54	2,004	7,543

Dominance (Table 24): The night samples have higher Berger-Parker dominance indices than the day samples but there is no consistent relationship between dominance and treatment.

Table 24. Berger-Parker dominance index for the pooled family data from
          Quilergup

Site	Treatment	Day	Night
Valley	Uncleared	0.24	0.50
Ridge	Uncleared	0.13	0.85
Valley	2 y.o. pine	0.19	0.50
Ridge	2 y.o. pine	0.27	0.40

Dominance-diversity (Figure 7a): In the day samples pine sites have a lower
origin and are less strongly bimodal than comparable uncleared sites. For the
night samples the pine sites have lower origins than comparable jarrah plots,
namely they have fewer rare families.

Rarefaction (Figure 8a): Day samples had much greater E_s diversity than
night samples and the latter show greater E_s diversity in the pine plots.

Dendrogram (Figure 9a): The data separate clearly into day and night samples;
within these groups the night samples link according to forest type while the
day samples link according to site locality.

Coleoptera Families from Quilergup

Dominance (Table 25): Dominance in the night samples is always greater than
in the paired day samples and valley sites had greater dominance than the
comparable ridge sites. Dominance was always greater in the pine plantation
than in the comparable uncleared forest sites.

Table 25. Berger-Parker dominance index for the pooled Coleoptera family data
          from Quilergup

Site	Treatment	Day	Night
Valley	Uncleared	0.59	0.76
Ridge	Uncleared	0.34	0.52
Valley	2 y.o. pine	0.62	0.79
Ridge	2 y.o. pine	0.37	0.67

Rarefaction (Figure 8c): The day samples have greater E_s diversity than the
night samples and E_s is greater on the pine sites. In the night samples
E_s is less on the pine sites.

Dendrogram (Figure 9b): The data group clearly into day and night samples.
Within these groups the data link by site locality rather than forest type
using either numeric or occurrence data.

Lepidoptera Families from Quilergup

Dominance (Table 26): Both the night and day samples show greater dominance on the pine sites than on the comparable jarrah forest sites.

Table 26. Berger-Parker dominance index for the pooled Lepidoptera family data from Quilergup

Site	Treatment	Day	Night
Valley	Uncleared	0.34	0.29
Ridge	Uncleared	0.37	0.40
Valley	2 y.o. pine	0.61	0.46
Ridge	2 y.o. pine	0.38	0.52

Rarefaction (Figure 8b): E_s is greater in the day samples and on uncleared forest sites than in comparable sites in the pine plantation.

Dendrogram (Figure 9c): The samples separate clearly into day and night samples and then according to whether the sample came from pine or native forest.

Hymenoptera Families from Quilergup

Dominance (Table 27): Night samples had very high dominance and the day samples low dominance. There is no consistent difference in dominance according to forest type.

Table 27. Berger-Parker dominance index for the Hymenoptera family data from Quilergup

Site	Treatment	Day	Night
Valley	Uncleared	0.22	0.99
Ridge	Uncleared	0.38	1.00
Valley	2 y.o. pine	0.36	0.98
Ridge	2 y.o. pine	0.28	0.95

Rarefaction (Figure 8d): E_s is greater in the day samples and lower in uncleared forest sites than in comparable sites in the pine plantation.

Dendrogram (Figure 9d): The data separate clearly into day and night samples. The night samples group according to forest type but the day samples group according to neither forest type nor site locality.

Diptera Families from Quilergup

Dominance (Table 28): Both day and night samples show moderate to low dominance; within the night samples those from pine forest had greater dominance than the jarrah forest.

Figure 7.   Dominance-diversity curves of the Quilergup samples plotted as
two-point moving averages. (a) pooled families, (b) pooled
genera. Codes denote: N = night; D = day; N = uncleared jarrah
forest; P = 2 year old pine; R = ridge; V = valley.
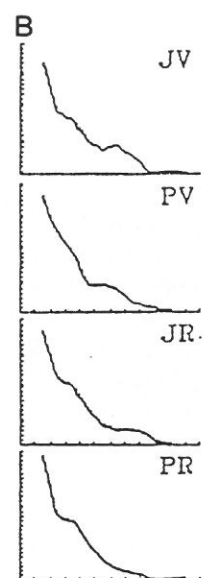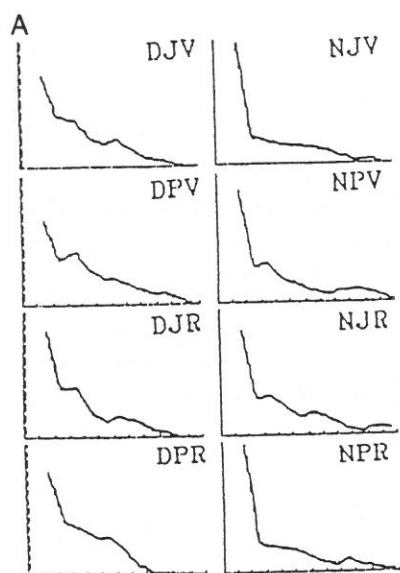
Figure 8. Rarefaction of the Quilergup samples giving the estimated number
(E$_s$) of families or genera per given number of individuals.
(a) the combined number of families per 100, (b) Lepidoptera
families per 60, (c) Coleoptera families per 100, (d) Hymenoptera
families per 100, (e) Diptera families per 50, (f) Hemiptera
families per 30. Codes denote: N = night; D = day; N = uncleared
jarrah forest; P = 2 year old pine; R = ridge; V = valley.
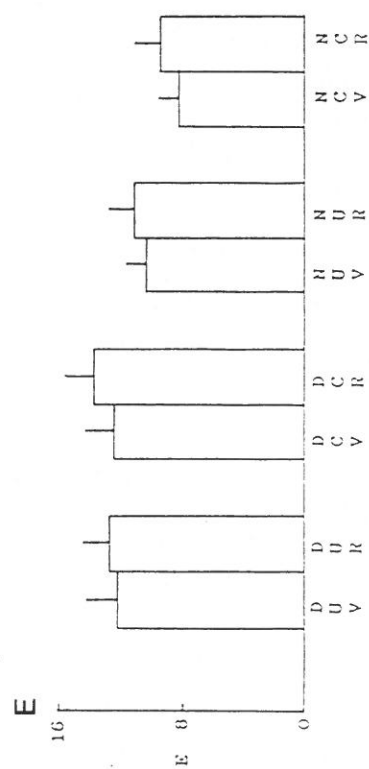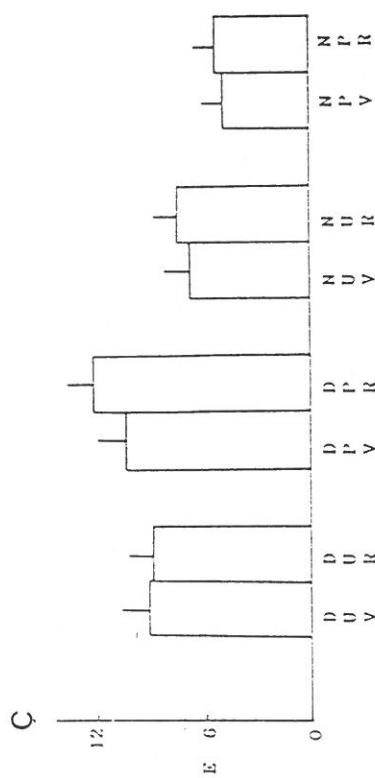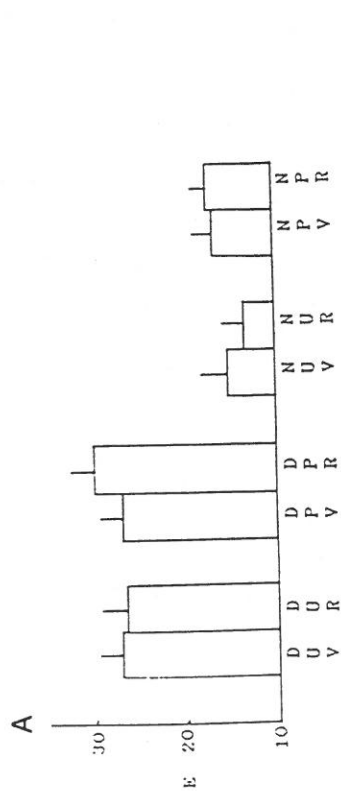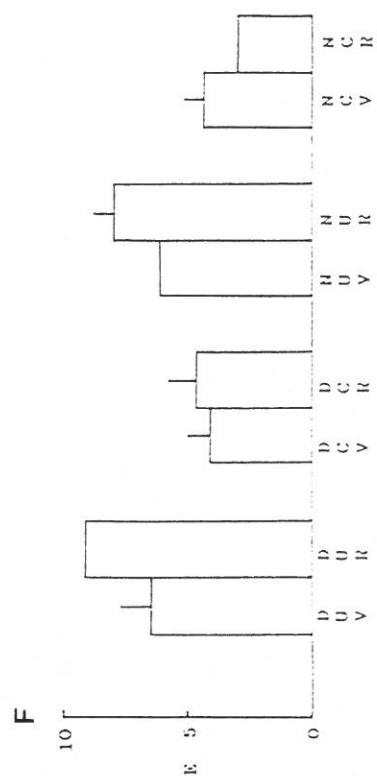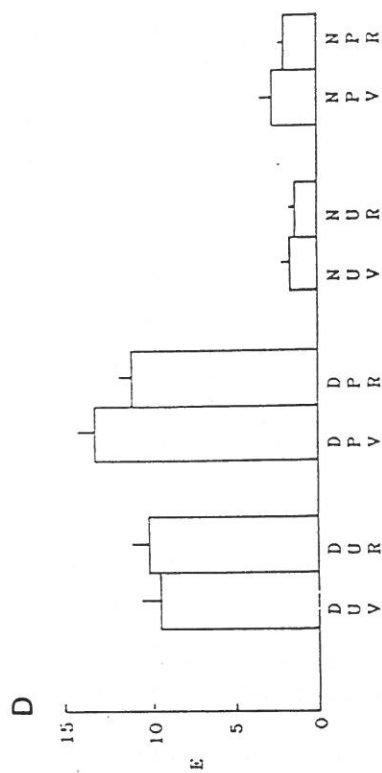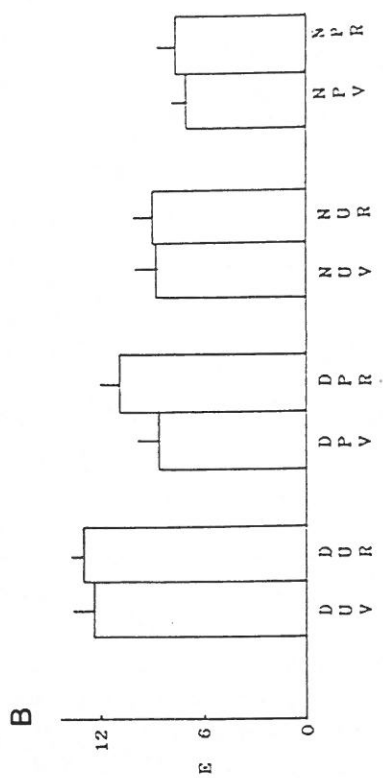
Figure 9.   Dendrograms of dissimilarity values for the Quilergup samples.
(a) Pooled families based on numeric data, (b) Coleoptera families
based on numeric data, (c) Lepidoptera families based on numeric
data, (d) Hymenoptera families based on numeric data, (e) Diptera
families based on numeric data, (f) Hemiptera families based on
numeric data, (g) pooled genera based on numeric data,
(h) Coleoptera genera based on numeric data, (i) Lepidoptera genera
based on numeric data. Codes denote: N = night; D = day;
N = uncleared jarrah forest; P = 2 year old pine; R = ridge;
V = valley.
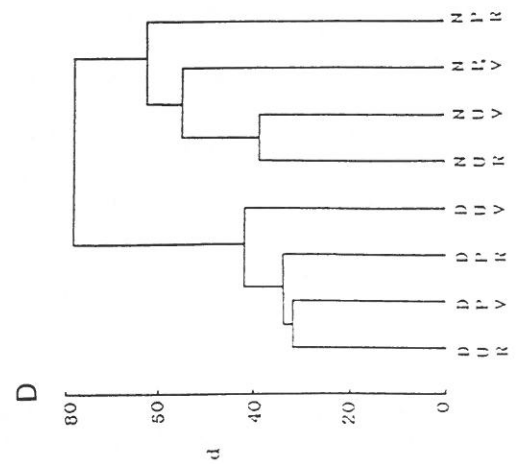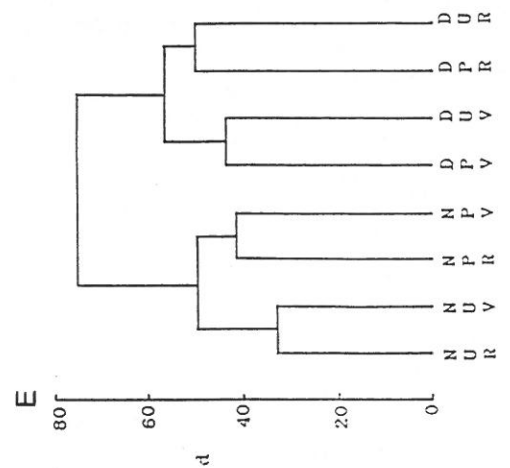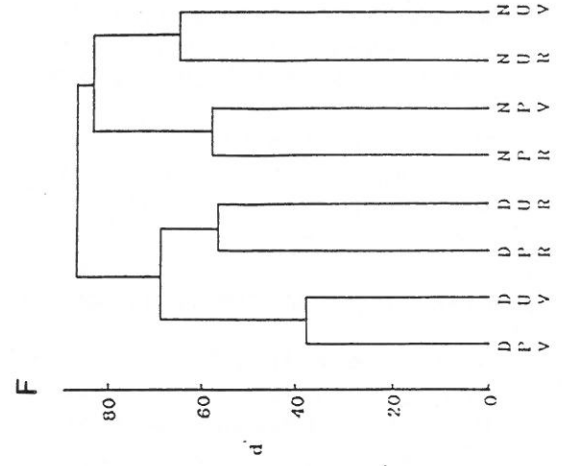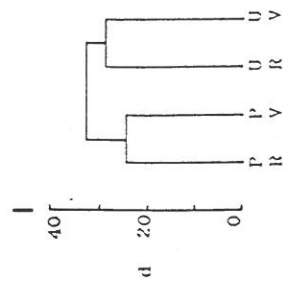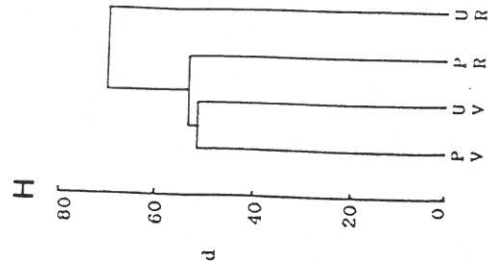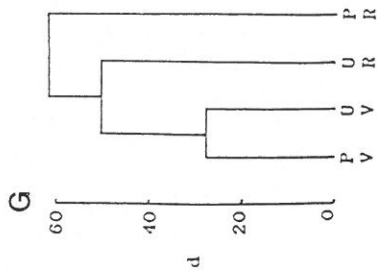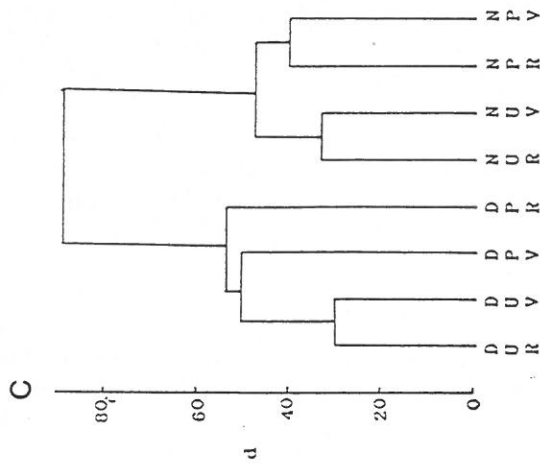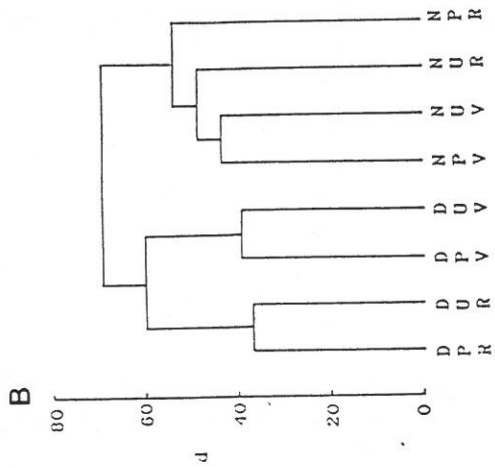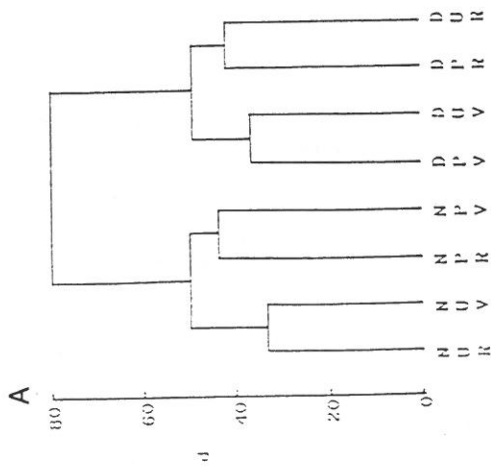
Table 28. Berger-Parker dominance index for the pooled Diptera family data from Quilergup

Site	Treatment	Day	Night
Valley	Uncleared	0.27	0.21
Ridge	Uncleared	0.26	0.26
Valley	2 y.o. pine	0.23	0.43
Ridge	2 y.o. pine	0.38	0.36

Rarefaction (Figure 8e): E_S is greater in day, than in night samples and on ridge than creek sites. In night samples E_S is greater on the uncleared sites than in the pine plantation.

Dendrogram (Figure 9e): The data group clearly into day and night samples; the night samples group according to forest type but the day samples group according to forest type using occurrence data and by site locality using numeric data.

Hemiptera Families from Quilergup

Dominance (Table 29): In both the day and night samples the pine sites showed much greater dominance than sites from the jarrah forest, the differences being more marked in the day samples.

Table 29. Berger-Parker dominance index for the pooled Hemiptera family data from Quilergup

Site	Treatment	Day	Night
Valley	Uncleared	0.41	0.45
Ridge	Uncleared	0.29	0.34
Valley	2 y.o. pine	0.74	0.74
Ridge	2 y.o. pine	0.82	0.52

Rarefaction (Figure 8f): E_S is similar in night and day samples on comparable sites but E_S is much higher in uncleared jarrah forest than in the pine plantation.

Dendrogram (Figure 9f): The data separate clearly into night and day samples; while the night samples group by forest type the day samples group according to site location.

Pooled Genera from Quilergup

Numbers (Table 30): Similar numbers of genera but fewer individuals were trapped in the pine plantation than in the jarrah forest.

Table 30.   The total number of genera and individuals trapped at Quilergup
            from 1975-6

| Site | Treatment | Number of | |
		Genera	Individuals
Valley	Uncleared	58	1,552
Ridge	Uncleared	60	1,295
Valley	2 y.o. pine	61	1,161
Ridge	2 y.o. pine	52	1,107

Dominance-diversity (Figure 7b): Pine sites have more steeply declining
curves with lower tails than comparable jarrah sites.

Dendrogram (Figure 9g): Using either numeric or occurrence data the
dendrogram chains with the valley sites forming the first linkage.

Coleoptera Genera from Quilergup

Dendrograms (Figure 9h): Using either numeric or occurrence data the
dendrogram chains with the valley sites forming the first linkage.

Lepidoptera Genera from Quilergup

Dendrogram (Figure 9i): The samples separate clearly according to forest
types.

Discussion of the Quilergup Data

Analysis of the numeric data classified to orders for each sampling time shows
site x area interaction present in some day samples and common in the night
samples. The data have moderate resolution, showing, where interaction was
not significant, a large number of significant site and treatment (area)
effects. Analysis of the numeric data for the pooled family samples for five
orders showed that the day samples were more consistent than the night
samples, with four of the five Orders showing significant differences,
compared with only one (Diptera) in the night samples.

Both the number of individuals and the number of families show no consistent
pattern by day or night related to either site or area (Table 23). This
results in a lack of pattern in the dominance of the pooled samples (Table
24). However, subdivision of the data by order resolves some of the data; in
both Hymenoptera (Table 27) and Coleoptera (Table 25) dominance was much
greater at night. In the Coleoptera dominance was greater in valley than in
ridge sites, and greater on the pine sites than on the comparable uncleared
forest sites. The Lepidoptera (Table 26) and Hemiptera (Table 29) showed
higher dominance on pine sites by both day and night, and the Diptera (Table
28) only at night.

Overall there was lower E_s diversity in the night samples with E_s being
greater in the pine plantation (Figure 8a). Resolving the data to the Order
level shows that E_s was greater by day for the Coleoptera (Figure 8c;
greater in pine plantation by day and the uncleared forest at night),
Lepidoptera (Figure 8b; greater in uncleared forest by day and night),

-41-

Hymenoptera (Figure 8d; greater in the pine forest by day and night) and Diptera (Figure 8e; greater in uncleared forest at night). The Hemiptera had much greater E_S values in uncleared forest than in pine plantation (Figure 8f).

The change in the structure of the communities is shown in the dominance-diversity curves, the form of which changes substantially between treatments in the pooled family (Figure 7a) and generic data (Figure 7b).

All dendrograms for the family data separate into day and night samples (Figure 9a-f). Of all areas sampled in this study the sampling regime used on these sites were the least standardised and this is probably reflected in the following analyses which give little clear separation of the data according to forest type despite the large sample sizes in both the family and generic analyses. The night data mostly group according to forest type (Figure 9a,c,e and f), as do the Lepidoptera generic data but only the Lepidoptera and Diptera (presence data) do so for the day samples (Figure 9 c and e). The remaining samples cluster according to whether the samples were taken from valley or ridge sites (Figure 9a,b,f,g and h). Hence, in these samples also, the clearest grouping of the data according to forest type has been obtained from the night samples and reflects the much greater numbers of individuals trapped in these samples.

In the day samples the Lycaenidae (Lepidoptera); Tipulidae, Syrphidae, Sepsidae (Diptera); Scutelleridae (Heteroptera) and Aphididae (Homoptera) were more abundant on the 2 y.o. plots, while three families [Calliphoridae, Culicidae (Diptera); and Curculionidae (Coleoptera)] were less abundant (Table 41). In the night samples 3 families increased [Chironomidae, Sphaeroceridae (Diptera); Melolonthinae and Hydrophilidae (Coleoptera)] and 9 families [Formicidae, Braconidae (Hymenoptera); Tineidae, Oecophoridae, Xyloryctidae, Geometridae, Hepialidae (Lepidoptera); Elateridae (Coleoptera) and Flatidae (Homoptera)] significantly decreased in numbers on the cleared sites, the latter family being absent (Table 41).

Of the families represented in the samples 18% were significantly changed in numbers on the cleared and replanted sites compared with the uncleared forest (Table 42).

Eight genera were significantly altered in numbers on the treatment plots. Lagria (Coleoptera); Chilo, Agrotis and Acidalia (Lepidoptera) were significantly more abundant on the regrowth plots, the latter genus being absent on uncleared forest sites. Liparetrus, Rhinoplethes (Coleoptera); Fraus and Thalamarchis (Lepidoptera) were less abundant in the cleared forest sites (Table 43).

3.4   Nannup

Total Average Counts for Orders of Insects

The only significant effects were interaction between areas and sites in one of each of the day and the night samples.

Analysis of the Pooled Samples for the Families in Five Orders

In the day samples there were significant differences beyween areas on both ridge and valley sites for Hymenoptera (τ = 0.31 and 0.17 respectively) and Diptera (τ = 0.08 and 0.33 respectively). In the night samples only the ridge sites for Diptera were significantly non-similar (τ = 0.18).

-42-

Pooled Families from Nannup

Numbers (Table 31): Similar numbers of families were trapped in the jarrah forest and in the 18 year old pine plantation. More individuals were trapped at night than by day on comparable sites. By both day and night the ridge sites had substantially greater numbers of families in the jarrah forest than in the pine plantation.

Table 31. The total number of families and individuals trapped at Nannup in 1977

Site	Treatment	No. families		No. individuals	
		Day	Night	Day	Night
Valley	Jarrah	51	46	934	1,564
Ridge	Jarrah	48	52	1,399	2,034
Valley	18 year old pine	53	44	1,260	1,577
Ridge	18 year old pine	37	38	467	499

Dominance (Table 32): Dominance was greater at night than by day on comparable sites. The night samples showed greater dominance in the pine plantation than on comparable sites in the jarrah forest.

Table 32. Berger-Parker dominance index for the pooled family data from Nannup

Site	Treatment	Day	Night
Valley	Uncleared	0.12	0.18
Ridge	Uncleared	0.14	0.20
Valley	18 y.o. pine	0.12	0.21
Ridge	18 y.o. pine	0.20	0.30

Dominance-diversity (Figure 10a): In both day and night samples there is an evident decline in the number of rare families on pine sites relative to comparable uncleared sites.

Rarefaction (Figure 11a): Day samples had higher E_s diversity than night samples but there are no consistent changes in diversity with treatment.

Dendrogram (Figure 12a): There is clear separation betweeen the day and the night samples. There is chaining in both these groups with the two jarrah forest sites forming the first link in each case. Using occurrence data the day samples separate clearly according to forest type.

Coleoptera Families from Nannup

Dominance (Table 33): In the day samples there is little change in dominance with treatment or site differences. The night samples show markedly greater dominance in the jarrah forest than in the pine plantation.

Table 33.   Berger-Parker dominance index for the Coleoptera family data from Nannup

Site	Treatment	Day	Night
Valley	Uncleared	0.57	0.62
Ridge	Uncleared	0.56	0.62
Valley	18 y.o. pine	0.41	0.33
Ridge	18 y.o. pine	0.56	0.32

Rarefaction (Figure 11b): day samples had lower E_s diversity than night samples and the latter showed greater E_s diversity on pine sites than on uncleared forest sites.

Dendrogram (Figure 12b): There is clear separation between day and night samples. Within these groups the data are grouped by forest type although there is chaining in the night samples.

Lepidoptera Families from Nannup

Dominance (Table 34): All the ridge sites show greater dominance than the comparable valley sites. In the night samples the pine sites show greater dominance than the jarrah sites.

Table 34.   Berger-Parker dominance index for the Lepidoptera family data from Nannup

Site	Treatment	Day	Night
Valley	Uncleared	0.57	0.43
Ridge	Uncleared	0.64	0.32
Valley	18 y.o. pine	0.37	0.62
Ridge	18 y.o. pine	0.63	0.48

Rarefaction (Figure 11c): Night samples had higher E_s diversity on uncleared forest sites than did the pine plantation.

Dendrograms (Figure 12c): Using either numeric or occurrence data there is clear separation of the day and night samples. Using numeric data the night samples separate clearly by forest type but the day data chain; the latter link by pine site using occurrence data.

Hymenoptera Families from Nannup

Dominance (Table 35): Within the day samples the pine sites show much greater dominance than the comparable jarrah sites although there is a marked change in dominance according to site location. In the night samples the ridge sites showed substantially greater dominance than comparable valley sites.

Table 35. Berger-Parker dominance index for the Hymenoptera family data from Nannup

Site	Treatment	Day	Night
Valley	Uncleared	0.26	0.52
Ridge	Uncleared	0.36	0.90
Valley	18 y.o. pine	0.37	0.46
Ridge	18 y.o. pine	0.63	0.94

Rarefaction (Figure 11d): Day samples had higher E_s diversity than night samples and uncleared forest sites had higher E_s diversity than those from the pine plantation.

Dendrogram (Figure 12d): There is complete separation of the day and night samples. The night samples group by site locality using numeric data but by forest type using occurrence data. By neither method of analysis do the day samples group by site locality or forest type.

Diptera Families from Nannup

Dominance (Table 36): The night samples show greater dominance than comparable day samples. Both day and night samples show greater dominance in comparable sites in the pine plantation than in jarrah forest, most markedly on ridge sites.

Table 36. Berger-Parker dominance index for the Diptera family data from Nannup

Site	Treatment	Day	Night
Valley	Uncleared	0.21	0.29
Ridge	Uncleared	0.19	0.35
Valley	18 y.o. pine	0.22	0.33
Ridge	18 y.o. pine	0.42	0.43

Rarefaction (Figure 11e): There is little variation in E_s diversity with either sampling time or treatment.

Figure 10. Dominance-diversity curves of the Nannup samples plotted as
two-point moving averages. (a) Combined family data, (b) pooled
generic data. V = valley; R = ridge; N = night and D = day
samples; U = uncleared jarrah forest; P = 18 year old pine
plantation.
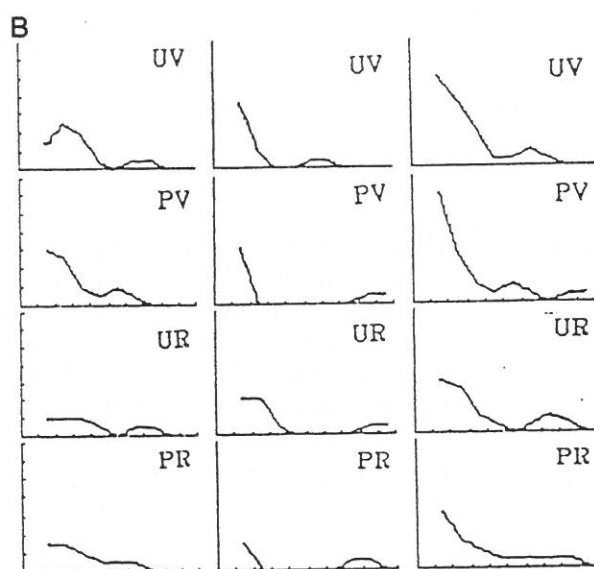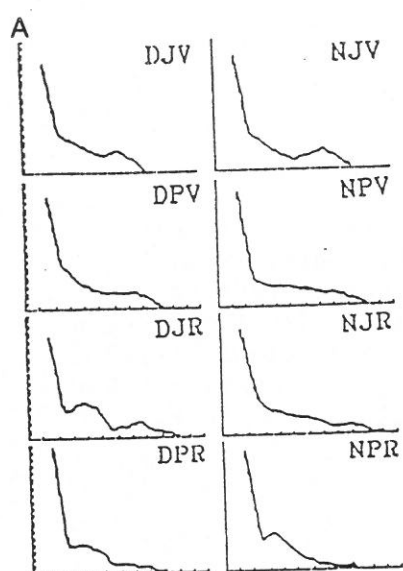
Figure 11. Rarefaction of the Nannup samples giving the estimated number
(E_s) of families or genera per given number of individuals.
(a) the combined number of families per 100, (b) Coleoptera
families per 50, (c) Lepidoptera families per 50, (d) Hymenoptera
families per 50, (e) Diptera families per 50, (f) genera per 50,
(g) Lepidoptera genera per 50. Codes denote: N = night; D = day;
N = uncleared jarrah forest; P = 2 year old pine; R = ridge;
V = valley.
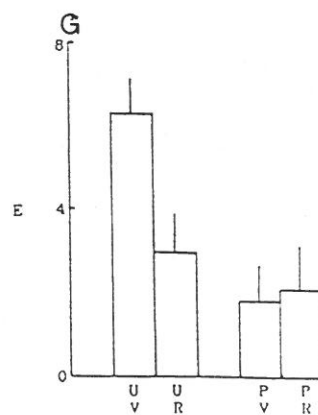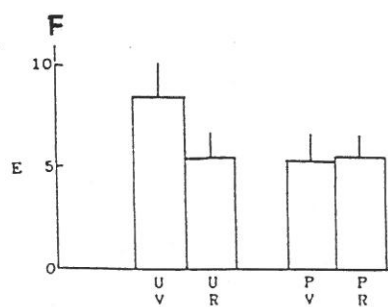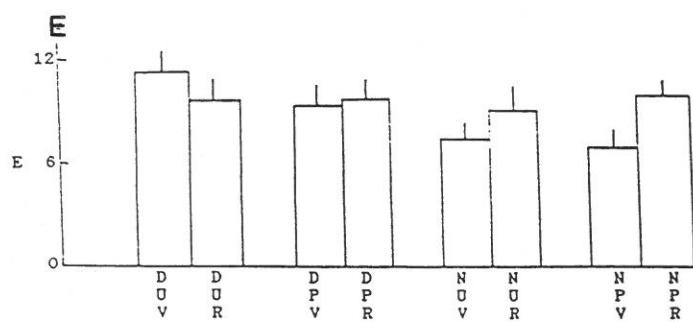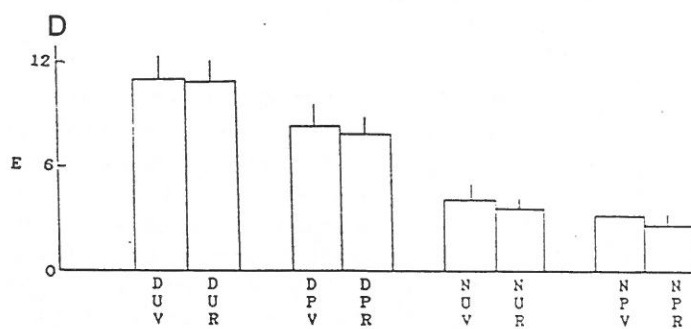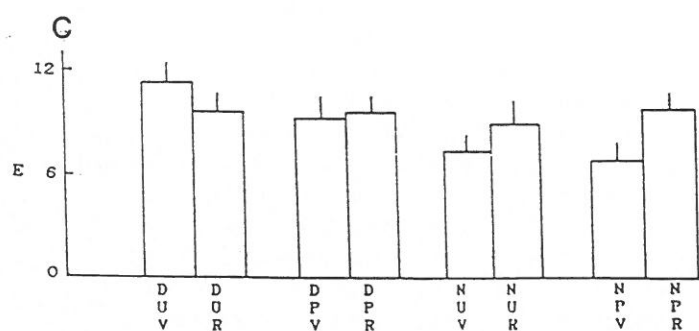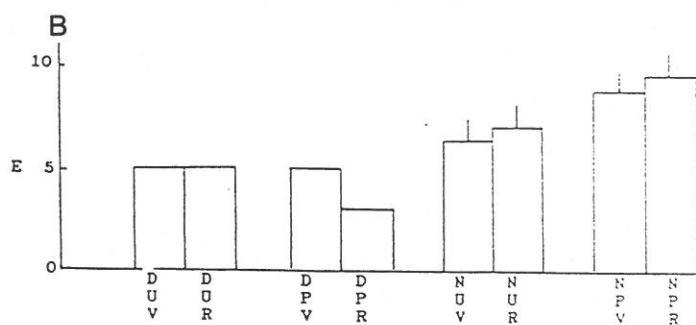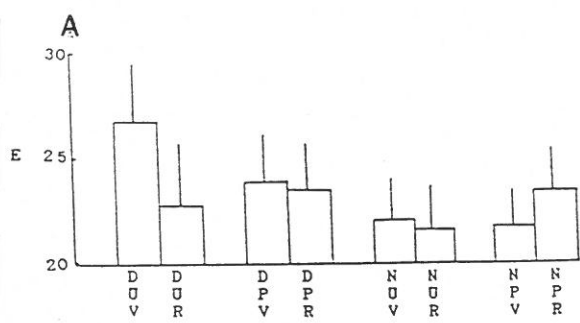
Figure 12.   Dendrograms of dissimilarity values for the Nannup samples.
(a) Pooled families based on numeric data, (b) Coleoptera
families based on occurrence data, (c) Lepidoptera families based
on numeric (night) and occurrence (day) data, (d) Hymenoptera
families based on numeric data, (e) Diptera families based on
occurrence data, (f) Hemiptera families based on numeric data,
(g) pooled genera based on numeric data, (h) Coleoptera genera
based on numeric data, (i) Lepidoptera genera based on numeric
data.   Codes denote: N = night; D = day; N = uncleared jarrah
forest; P = 2 year old pine; R = ridge; V = valley.
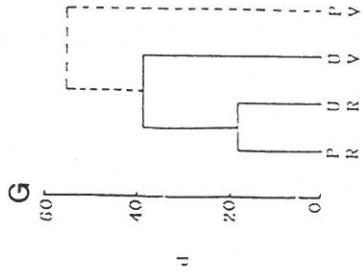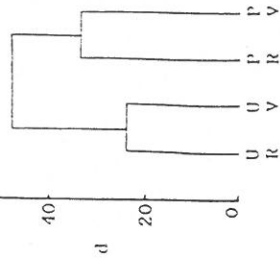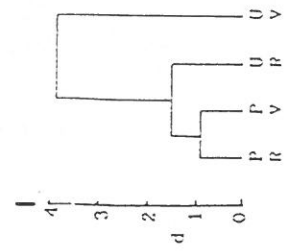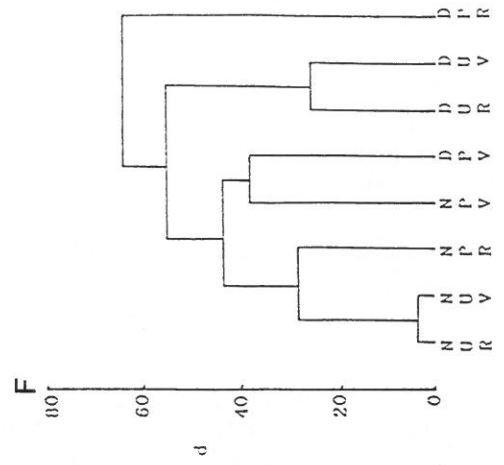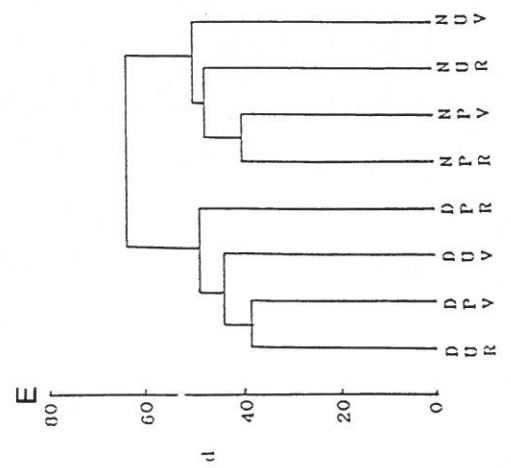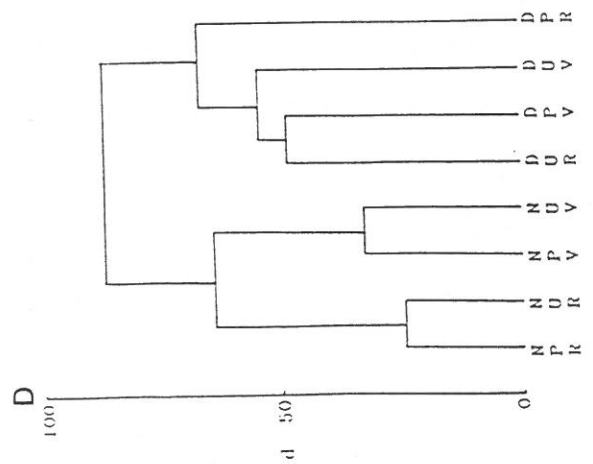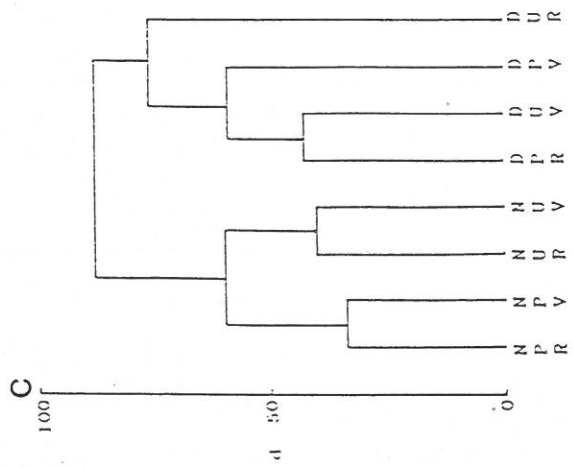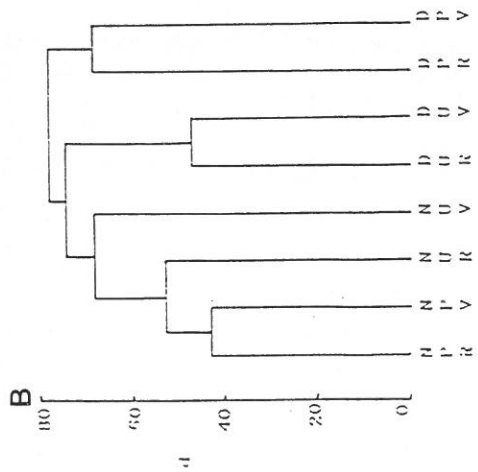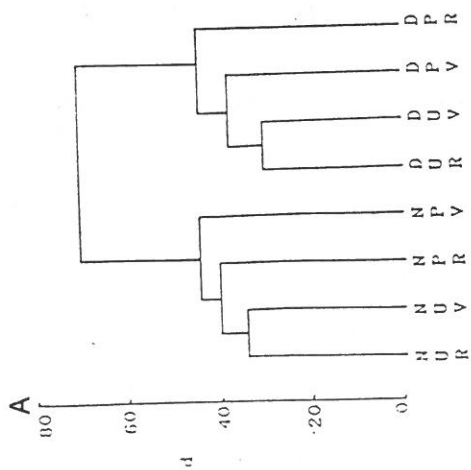
Dendrogram (Figure 12e): There is clear separation between day and night samples but there is chaining within both these groups; in the night samples the pine sites link first.

Hemiptera Families from Nannup

Dominance (Table 37): Night samples had greater dominance than comparable day samples but there is no other consistent pattern in these samples.

Table 37. Berger-Parker dominance index for the Hemiptera family data from Nannup

Site	Treatment	Day	Night
Valley	Uncleared	0.75	0.79
Ridge	Uncleared	0.47	0.75
Valley	18 y.o. pine	0.52	0.76
Ridge	18 y.o. pine	0.57	0.66

Dendrogram (Figure 12f): Using either numeric or occurrence data no complete separation of the data by sampling time, forest type or site locality was obtained. However, in both analyses most of the data group according to the first two criteria.

Pooled Genera from Nannup

Numbers (Table 38): Valley sites contained more genera than ridge sites but the number of genera did not differ between treatments. There is interaction between sites and forest type in the number of individuals.

Table 38. The total number of genera and individuals trapped at Nannup in 1977

Site	Treatment	Number of	
		Genera	Individuals
Valley	Uncleared	16	214
Ridge	Uncleared	10	279
Valley	18 y.o. pine	17	492
Ridge	18 y.o. pine	10	215

Diversity: For both H_1 and H_1/H_{max} diversity the jarrah sites have greater values than their comparable pine sites.

Dominance-diversity (Figure 10b): Valley sites have much higher and steeper curves than the comparable ridge sites, namely they contain more rare genera, but they have tails of comparable length.

Rarefaction (Figure 11f): Only the jarrah valley site clearly separates from the other sites, having greater E_s diversity than other sites.

Dendrogram (Figure 12g): Using either numeric or occurrence data the dendrogram chains with the ridge sites linking first.

Coleoptera Genera from Nannup

Diversity (Table 39): Pine sites had higher H_1 and H_1/H_{max} diversity than comparable jarrah sites; in both forest types the diversity measures were higher in the valley than on the corresponding ridge sites.

Table 39. H_1 and H_1/H_{max} diversity indices for the Coleoptera genera from Nannup

Site	Forest type	H_1	H_1/H_{max}
Valley	Jarrah	1.3	1.7
Ridge	Jarrah	0.9	1.6
Valley	Pine	2.0	4.0
Ridge	Pine	1.4	1.9

Dendrogram (Figure 12h): The data group according to forest type with strong separation between the forest types. The paired sites were more similar in the jarrah forest (77%) than in the pine plantation (67%).

Lepidoptera Genera from Nannup

Diversity (Table 40): Both H_1 and H_1/H_{max} diversity were substantially greater in the jarrah plots than in either of the pine plots and the difference was more marked for the vally sites.

Table 40. H_1 and H_1/H_{max} diversity indices for Lepidoptera genera from Nannup

H_1	H_1/H_{max}		
Valley	Jarrah	0.92	1.07
Ridge	Jarrah	0.38	0.40
Valley	18 y.o. pine	0.15	0.15
Ridge	18 y.o. pine	0.18	0.19

Rarefaction (Figure 11g): E_s diversity was lower on pine plots than on comparable jarrah plots.

Dendrogram (Figure 12i): Using either numeric or occurrence data the dendrogram chains with the pine sites joining first.

Discussion of the Nannup Data

Analysis of the numeric data classified to Orders for each sampling time shows that the data has very low resolution with few significant effects seen in either the day or night samples.

Analysis of the numeric data for the pooled family samples for five Orders showed significant between area (forest type) differences in the Hymenoptera (day) and Diptera (day) for both valley and ridge sites, while in the night samples only the Diptera ridge sites were significantly different.

Many more families were trapped on the ridge site in jarrah forest than in 18 year old pine plantation but this was not reflected in the valley sites (Table 31). Many more individuals were trapped on ridge sites in jarrah forest but in valley sites in the pine plantation. Overall, however, there was greater dominance in the pine plantation than in the jarrah forest (Table 32) and this is reflected in the lower number of rare families in pine (Figure 10a). This dominance is order related with Hymenoptera and Diptera (Tables 35 and 36) being more dominant in pine by day and Lepidoptera and Diptera by night (Tables 34 and 36), while the Coleoptera were more dominant in the jarrah forest by night (Table 33). These results are mostly supported by the rarefaction analyses of the same data (Figure 11a-e).

The dendrograms give complete separation of the day and night samples (Figure 12a-e), with the exception of the Hemiptera (Figure 12f). The dendrograms illustrate considerable noise in the data with few clear separations by forest type, some grouping by site locality, frequent chaining of the dendrograms and often conflicting results when occurrence and numeric data were compared. This is the noisiest data set examined in the course of this study.

In the day samples 4 families [Formicidae (Hymenoptera), Lygaeidae (Heteroptera), Aleyrodidae and Aphididae (Homoptera)] were more abundant on the pine plots, the latter being absent in uncleared forest, while 8 families were less abundant [Scoliidae (Hymenoptera), Colletidae, Asilidae and Dolichopodidae (Diptera)] or absent (Apidae, Chrysididae, Oecophoridae and Melolonthinae) on the regrowth plots (Table 41).

Table 41. The response of different insect families to silvicultural practices in four study areas in south-western Australia. The values in the table are the ratio of the number of individuals on the combined treatment plots divided by those on the uncleared or older plots. Numerals in ordinary type denote values which are significantly different (^{2}; P < 0.05) for both ridge and creek sites separately; these values give the sub-totals and totals for the number (this Table) and percentage (Table 42) of families in which the number of individuals was significantly reduced (<) or increased (>) on the treatment plots compared with the control plots. Numerals in bold type denote values where > = 10 individuals occur in the combined ridge and valley sites of either the treatment or control groups but are absent in the alternative group. Taxa marked * were distributed with significant numerical disproportion on treatment plots at Crowea (Curry and Humphreys 1987)

ORDER Family	Pemberton Day	Night	Manjimup Day	Night	Quilergup Day	Night	Nannup Day	Night
HYMENOPTERA								
*Ichneumonidae	-	-	-	-	-	-	-	0.32
*Tiphiidae	-	-	-	-	-	-	0.03	-
Colletidae	5.00	-	-	-	-	-	-	-
*Apidae	-	-	-	-	-	-	0	-
*Formicidae	-	11.66	-	0.07	-	0.01	3.36	0.34
Braconidae	-	-	-	-	-	0.04	-	-
Chrysididae	-	-	-	-	-	-	0	-
Scoliidae	-	-	-	-	-	-	0.04	-
LEPIDOPTERA								
*Tineidae	-	-	-	-	-	0.23	-	-
*Oecophoridae	-	-	-	-	-	0.25	0	0.08
*Xyloryctidae	-	-	-	-	-	0.32	-	0.32
*Geometridae	-	0.08	-	0.42	-	0.36	-	0.13
*Noctuidae	-	0.38	-	2.38	-	-	-	-
Lymantridae	-	0.28	-	-	-	-	-	-
Lycaenidae	-	-	-	-	2.68	-	-	-
Hepialidae	-	-	-	-	-	0.15	-	-
DIPTERA								
*Tipulidae	-	0.07	-	-	2.20	-	-	-
*Chironomidae	0	2.85	-	-	-	6.10	-	-
*Syrphidae	2.28	-	-	-	3.13	-	-	-
*Sphaeroceridae	-	-	-	-	-	3.29	-	-
*Muscidae	-	0.25	1.73	-	-	-	-	0.05
*Calliphoridae	-	-	-	-	0.63	-	-	-
Culicidae	-	-	-	-	0.01	-	-	-
Sepsidae	-	-	-	-	1.83	-	-	-
*Asilidae	-	-	-	-	-	-	0.11	-
*Dolichopodidae	-	-	-	-	-	-	0.30	-

ORDER Family	Pemberton Day	Night	Manjimup Day	Night	Quilergup Day	Night	Nannup Day	Night
COLEOPTERA								
*Staphylinidae	–	–	–	–	–	–	–	30.0
*Melolonthinae	–	–	–	0.25	–	13.72	0	0.24
Dermestidae	–	0.05	–	–	–	–	–	–
*Hydrophilidae	–	1.82	–	–	–	2.99	–	–
Anobiidae	–	0.11	–	–	–	–	–	–
Coccinellidae	–	–	∞	–	–	–	–	–
*Elateridae	–	–	–	–	–	0.15	–	–
*Curculionidae	–	–	–	–	0.39	–	–	–
HEMIPTERA								
*Reduviidae	–	0.35	–	–	–	–	–	–
Aradidae	–	–	∞	–	–	–	–	–
Scutelleridae	–	–	29.0	–	34.0	–	–	–
Aphididae	–	–	–	–	43.27	–	14.0	–
*Lygaeidae	–		–	–	–	–	32.0	–
Flatidae	–		–	–	–	0	–	–
*Cicadellidae	–		–	–	–	–	–	0.23
*Miridae	–	–	–	–	–	–	–	0.07
Aleyrodidae	–	–	–	–	–	–	∞	–

		Pemberton Day	Night	Manjimup Day	Night	Quilergup Day	Night	Nannup Day	Night
Hymenoptera	<	–	–	–	1	–	2	2	2
	>	1	1	–	–	–	–	1	–
Lepidoptera	<	–	3	–	1	–	5	–	3
	>	–	–	–	1	1	–	–	–
Diptera	<	–	2	–	–	2	–	2	1
	>	1		1	–	3	2	–	–
Coleoptera	<	–	2	–	1	1	1	–	1
	>	–	1	1	–	–	2	–	–
Hemiptera	<	–	1	–	–	–	1	–	2
	>	–	–	1	–	1	–	1	–
Total 36	<	0	8	0	3	3	9	4	9
20	>	2	3	3	1	5	4	2	0

Table 42. Percentage of all families showing significant changes between treatment and control plots after burning and after replanting by day and night. < and > denote that the treatment plots contained respectively fewer or greater numbers of individuals than the uncleared forest plots

Order		Pemberton Day	Night	Manjimup Day	Night	Quilergup Day	Night	Nannup Day	Night
Hemiptera	<	–	8.3	–	–	–	9.1	–	25.0
	>	–	–	10.0	–	5.9	–	14.3	–
Coleoptera	<	–	10.0	–	6.3	5.9	5.3	–	5.3
	>	–	5.0	7.7	–	–	10.5	–	–
Diptera	<	–	13.3	–	–	6.5	–	8.0	5.6
	>	5.9	6.7	8.3	–	9.7	8.0	–	–
Lepidoptera	<	–	15.8	–	5.9	–	27.8	–	25.0
	>	–	–	–	5.9	5.6	–	–	–
Hymenoptera	<	–	–	–	20.0	–	40.0	11.8	33.3
	>	7.7	33.3	–	–	–	–	5.9	–
No. families		66	69	54	55	99	78	69	63
All families	<	–	11.6	–	5.4	3.0	11.5	5.8	14.3
	>	3.0	4.3	5.6	1.8	5.1	5.1	2.9	–
No. families		99		88		119		95	
All families	<	8.1		3.4		10.0		13.7	
	>	5.1		4.5		7.6		2.1	

In the night samples the Staphylinidae (Coleoptera) increased, and 9 families [Ichneumonidae, Formicidae (Hymenoptera); Oecophoridae, Xyloryctidae, Geometridae (Lepidoptera); Muscidae (Diptera), Melolonthinae (Coleoptera), Cicadellidae (Homoptera) and Miridae (Heteroptera)] significantly decreased in numbers on the cleared sites (Table 41). Of the families represented in the samples 16% were significantly changed in numbers on the cleared and replanted sites compared with the uncleared forest (Table 42).

Three genera were significantly altered in numbers on the treatment plots. Hydatotrephus (Coleoptera) was more, and Liparetrus (Coleoptera) and Fraus (Lepidoptera) less abundant on the regrowth plots (Table 43).

Table 43. The response of different insect genera to silvicultural practices in four study areas in south-western Australia for the night samples only, except where specified. The values in the table are the ratio of the number of individuals on the combined treatment plots divided by those on the uncleared or older plots only for those which are significantly different (χ^2; $P < 0.05$) for both ridge and creek sites separately. The totals give the numbers and percentage of genera in which the number of individuals was significantly reduced (<) or increased (>) on the treatment plots compared with the control plots. Some genera were present on only the uncleared (0) or the treatment sites ( ). Genera marked * were distributed with significant numerical disproportion on treatment plots at Crowea (Curry and Humphreys 1987)

ORDER	Pemberton regrowth/ karri	Manjimup regrowth/ karri	Quilergup pine/ jarrah	Nannup pine/ jarrah
COLEOPTERA				
Onthophagus	5.00	∞		
Hydatotrephes				7.50
*Liparetrus	4.54		0.13	0.49
Anobium	0.11			
Lagria			2.17	
Rhinoplethes			0.08	
LEPIDOPTERA				
*Chlorocoma	0.03	0.15		
Chilo			2.27	
Acidalia	0.10		∞	
Orgyia	6.67			
*Agrotis			2.17	
*Simplicia	0			
*Pantydia	2.56			
Fraus			0.16	0.49
Thalamarchis			0.05	
Total 50% <	3	1	5	1
50% >	4	1	4	1

3.5 General discussion

Botanists long have used short cut methods to examine the structure and classify vegetation (Webb, Tracey and Williams 1976; Dale and Clifford 1976) and have shown that low level taxonomic classification may yield useful interpretation of the data, even at the order level (Hartley and Slater 1960; Maarel 1972; Pryor 1959; Walther 1972; Webb et al. 1970). While invertebrate zoologists often analyse data pooled above the species level, frequently as orders, analysis of the consequences of such low resolution data on the interpretation of the data are not attempted (see Curry and Humphreys 1987). This analysis has been conducted from the more general to the most specific

level of identification available to determine the efficacy of these different levels in answering questions about the nature of silvicultural practices on the forest insect community.

This paper considers two rather unrelated aspects of forestry management, namely the age of regrowth karri forest and the differences between jarrah forest and pine plantation established on areas previously occupied by jarrah forest. Of the taxa considered 34% were found only in one sampling area, 27% in two, 22% in three and only 16% of taxa were common to all four sampling areas (Appendix 1).

As found elsewhere (Neumann 1978; Curry and Humphreys 1987) the information content is very low of insect material classified only to the order level and is insufficient to separate clearly the uncleared forest from the treatment areas. Samples classified to the family, and especially to the generic, level contain adequate information to detect the gross effects of the forestry management practices. Analysis of the numeric data for the pooled family samples showed 13 significant between site effects of a possible 28 in which T was a suitable statistic; there were 8 in day and 5 in night samples, namely Diptera (3 day, 2 night), Hymenoptera (3D, 0N), Coleoptera (1D, 2N) and Lepidoptera (1D, 1N).

Even these low resolution data separate clearly, for the most part, the uncleared forest areas from both regrowth forest and from pine plantations. While the numbers of insects trapped may be greater (Table 2) or less (Tables 9, 13, 19 and 30) in the treatment plots, there was commonly a reduction in the number of rare familes (Figs 1a, 7a and 10a) or genera (Figs 1b, 4f) in treatment plots (pine or younger forest), as well as lower family (Figs 2a, 2c, 2d, 5b:night, 5c, 5d, 5e:night, 8c:night, 8b, 8e:night, 8f, 11c:night, 11d) and generic (Figs 2e, 11g) E_S diversity.

There is, nevertheless, considerable variation in the response of the different sites to disturbance which can be seen by perusing the various measures over all areas. In the karri areas more families and individuals were trapped at night in Pemberton and more individuals were trapped in the 2 y.o. plots than in mature karri (Table 2). At Manjimup, however, the numbers of families and individuals differed little between the day and night samples but there was a substantial reduction in both numbers of individuals and families in cleared sites (Table 13). In the jarrah areas more families, but substantially fewer individuals, were trapped at Quilergup by day than at night but pine planting had no consistent effect on either (Table 23). At Nannup, on the other hand, more individuals were trapped at night than by day on comparable sites. On ridge sites, however, substantially more families and individuals were trapped in jarrah forest than in pine plantation (Table 31); this is probably associated with the loss of the understorey and a decrease in light levels as the pines mature (Neumann 1978, 1979), the former being especially marked on ridge sites.

The various orders showed differential responses to the forestry management practices. Whereas the Hymenoptera showed greater E_S diversity in natural forest than in the treatment areas, except at Quilergup, the Coleoptera, at both Quilergup and Manjimup, E_S diversity in treatment plots was greater by day than at night.

For all regions except Nannup the pooled generic data show that substantially more genera, individuals or both were trapped in native forest than in the treatment areas.

Compared with the data previously presented from Crowea (Curry and Humphreys 1987) the data from the four sites considered here have low resolution because their sample sizes are much smaller. To what extent do the dendrograms group by treatment by chance rather than by site? The data overall show 37 linkages by treatment and 12 by site with an expected number of 36 each, showing a considerable excess of linkages by treatment over linkages by site (^{2} = 7.928; P = 0.0039). Hence although the differences between ridge and valley sites are large, they are insufficient to mask the treatment effects.

Generally night samples were much larger than day samples and so should yield more consistent data as the stochastic effects of small sample size are less important. While greater sample size may be expected to yield more families (Table 13) this was not necessariy the case (Table 32) and dominance measures may be related directly or inversly related to sample size.

The most consistent effect is the greater between site variation in the treatment areas compared with that seen in uncleared forest. This probably reflects the loss of environmental buffering associated with the forest cover, especially changes in insolation and soil moisture characteristics.

There is a trend in the data, from all four studies considered, for the day and night samples to differ in their response to treatment. In the day samples more families showed a significant numerical advantage on the treatment sites than were disadvantaged, whereas in night samples the reverse was the case; this effect was shown more strongly in the night samples (contingency ^{2} = 7.711; P = 0.002). This result indicates that the taxa collected by light traps are more severely affected by the disturbance of native forest than are those collected in Malaise traps and hence that Malaise traps are a poor technique for detecting changes to forest insects resulting from forest management practices.

This conclusion may, at first sight, seem counter-intuitive as one may expect that the light traps (which are strongly attractive to insects) would work better in young forest than Malaise traps, which work mainly by interception. This question cannot be resolved for reasons which were discussed at length elsewhere (Curry and Humphreys 1987). Among the relevant factors are the operating time of traps, whether they are active or passive traps, trap efficiency and selectivity between taxa and changes in vegetation structure, which affect, inter alia, free flight paths of insects and the distance from which they are attracted and the proportion of vegetation being sampled. The factors are relevant also to sampling changes in faunal composition associated with vegetation development and with successional changes. The unknown area sampled by the traps and the short sampling period could cause the different interpretation of the data taken by each trap type. In Oregon forests, not only were there significant seasonal trends in abundance of taxa but also in the structure of the community, probably reflecting the life history patterns of the included species; this was associated with considerable fine scale patchiness (in the order of metres) in the community (Schowalter et al. 1986).

Some families are present entirely, or predominantly, in the samples only by day or by night. Dominant by day are nearly all Hymenoptera, 3 families of Coleoptera (Mordellidae, Cerambycidae, Curculioninae) and 13 families of Diptera (Tipulidae, Cecidomyiidae, Mycetophilidae, Stratiomyidae, Asilidae, Bombyliidae, Empidae, Dolichopodidae, Phoridae, Syrphidae, Platystomatidae, Muscidae, Tachinidae). Dominant by night are 13 families of Coleoptera (Carabidae, Dytiscidae, Hydrophilidae, Silphidae, Staphylinidae, Trogidae, Aphodinae, Melolonthinae, Elateridae, Anobiidae, Tenebrionidae,

Cryptorrhynchinae and Amalactinae) and 9 families of Lepidoptera (Cossidae, Psychidae, Tineidae, Xyloryctidae, Zygaenidae, Pyralidae, Lycaenidae, Lasiocampidae and Arctiidae). The diversity of the response of some families to the various silvicultural treatments used in the karri and jarrah forests can be seen in Table 41. While many families do not show treatment differences, solely due to their small sample size, many families responded strongly to the treatments, some being absent in treatment plots in one or more areas [Apidae, Chrysididae (Hymenoptera); Oecophoridae (Lepidoptera), Chironomidae (Diptera), Melolonthinae (Coleoptera) and Flatidae Homoptera)] or reduced numerically to less than 10% [e.g. Tiphiidae, Formicidae, Braconidae, Scoliidae (Hymenoptera); Oecophoridae, Geometridae (Lepidoptera); Tipulidae, Muscidae, Culicidae (Diptera); Dermestidae (Coleoptera) and Miridae (Heteroptera)], while others were only recorded after treatment [e.g. Coccinellidae (Coleoptera), Aradidae (Heteroptera) and Aleyrodidae (Homoptera)] or increased numerically by magnitudes greater than one order [e.g. Formicidae (Hymenoptera), Staphylinidae, Melolonthinae (Coleoptera); Scutelleridae, Lygaeidae (Heteroptera); and Aphididae (Homoptera)].

In the pooled data from all orders, areas and sampling times, more families (36) were reduced numerically by the treatments than were increased (20: Table 41). Analysis of the families within orders, however, shows that the response within orders varied widely. Many more instances of a significant reduction in numbers with treatment occurred in the Lepidoptera (86%) and Hymenoptera (70%), the percentage declining through the Coleoptera (60%), Hemiptera (57%) and Diptera (47%: Table 41, sub-totals).

Hence even the low level of taxonomic resolution achieved in this study has revealed a range of responses amongst the families to the forestry management practices. In the four treatment areas (Table 42) the proportion of families significantly decreased numerically by the treatment is, in ascending rank order, Coleoptera (6.6%; mean of four areas), Diptera (8.4), Hemiptera (14.1), Lepidoptera (18.6) and Hymenoptera (28.0). This ranking is a measure of the impact of the treatment on the orders, with the Hymenoptera families being the most affected (cf. Crowea where Diptera were most affected; Curry and Humphreys 1987). The proportion of families significantly increased numerically by the treatment are, in ascending rank order, Lepidoptera (5.8%), Diptera (7.7%), Coleoptera (7.7%), Hemiptera (10.1%) and Hymenoptera (15.6%); again the Hymenoptera were the most affected (cf. Crowea where Diptera were most affected; Curry and Humphreys 1987).

In the pooled data from all orders, areas and sampling times more families (36) were reduced numerically by the treatments than were increased (20: Table 41). Analysis of the families within orders, however, shows that the response within orders varied widely. Many more instances of a significant reduction in numbers with treatment occurred in the Lepidoptera (86%) and Hymenoptera (70%), the percentage declining through the Coleoptera (60%), Hemiptera (57%) and Diptera (47%: Table 41, sub-totals).

The overall impact of the silvicultural practices (both numerical increases and decreases) on the various orders can be judged from the combined ranking of the number of families within an order significantly numerically different between treatment and unclearedforests. The combined ranking in ascending order is Hemiptera = Coleoptera (5), Hymenoptera = Lepidoptera (6) and Diptera (8); this indicates high sensitivity of the Diptera to the perturbation inherent in forestry practices, the higher the ranking the more sensitive should be the families within the order as indicator organisms; at Crowea families within the Diptera and Lepidoptera were the most sensitive (Curry and Humphreys 1987).

-61-

A similar analysis to the above shows that the mean percentage of families significantly changed numerically by the management practice was 5.3% on jarrah regrowth sites and 8.4% on pine plots which had replaced jarrah. Of the taxa showing significant numerical disproportion between the uncleared forest and the treatment sites, 61% of the families (Table 41) and 33% of the genera (Table 43) are in common with those showing the same disproportion between karri forest and treatment sites at Crowea (Curry and Humphreys 1987).

In considering the taxa representing potentially useful indicator groups, the most sensitive are those families present only on either the uncleared plots [e.g. Apidae, Chrysididae (Hymenoptera); Oecophoridae (Lepidoptera), Chironomidae (Diptera), Melolonthinae (Coleoptera) and Flatidae (Homoptera)] or treatment plots [e.g. Coccinellidae (Coleoptera), Aradidae (Heteroptera) and Aleyrodidae (Homoptera)] as their mere presence or absence may provide the necessary information relating to the perturbation. These are followed at lower sensitivity, as numeric data are required, by those families increasing numerically to the treatments by more than one order of magnitude [e.g. Formicidae (Hymenoptera), Staphylinidae, Melolonthinae (Coleoptera); Scutelleridae, Lygaeidae (Heteroptera) and Aphididae (Homoptera)].

At higher resolution some genera were present only on uncleared [Simplicia: (Lepidoptera)] or on treatment [Onthophagus (Coleoptera), Acidalia (Lepidoptera)] plots or differed numerically between treatment and uncleared plots more than one [Rhinoplethes (Coleoptera); Thalamarchis, Chlorocoma (Lepidoptera)] or half an order of magnitude [Liparetrus, Onthophagus, Anobium, Hydatotrephes (Coleoptera); Orgyia, Fraus (Lepidoptera)] in either direction (Table 43). As the feeding habits may vary widely within the higher classification used here no comment can be made on any changes in the trophic structure of the community associated with silvicultural practices.

Curry and Humphreys (1987) discussed at length the problems associated with the low level of taxonomic resolution obtainable from insect surveys of the type conducted here; this results from the bulk of material obtained as well as the low level of taxonomic knowledge of the forest insects of south-western Australia. By its design this study was intrinsically unable to yield high level ecological information and so high taxonomic resolution was not needed. The finding that the treatments had a major effect on the forest insect communities can be ascertained from the analysis of the data classified to orders. At the family level considerably greater information was available on appropriate taxa to examine for evidence of indicator taxa and further analysis of these families should lead to indicator species for the rapid evaluation of the impact of silvicultural practices on karri forest.

The two sampling methods yield similar conclusions despite the differences in detail between them. The various treatments had profound effects on the structure (dominance-diversity curves) and composition (dendrograms of similarity) of the arthropod community compared with the uncleared forest sites but this was not necessarily reflected in the broad scale taxonomic richness of the community (rarefaction and diversity measures). That such marked changes are being detected, despite the crude level of taxonomic classification, suggests that the changes resulting from the forestry practices are profound and that analysis of samples to the species level would reveal that a major loss of insect diversity has resulted from these practices.

Diversity indices are the most accessible measure of community structure and thus are used widely for the assessment of environmental conditions, especially for the impact of perturbations (Bakelaar and Odum 1978; Vance 1979), but they have more recently been challenged on heuristic grounds (Poole

1974), as being of little use (Hurlbert 1971) and shown in many cases to be inferior, or redundant, to other methods of data presentation (Green 1979, Dritschilo and Erwin 1982). The use of diversity indices for impact assessment has been challenged due to their insensitivity and/ or the misleading conclusions to which they may lead (Dritschilo and Erwin 1982). In this study, at all levels of analysis, the diversity indices showed only slight changes resulting from silvicultural practices, whereas the dominance diversity plots and the cluster analyses consistently showed major changes to the communities with the former identifying the differential responses of the different taxa as well as the different collection methods and/or times.

It must be emphasized that a study of this type cannot identify the immediate causes of the changes to the insect fauna because there are a number of compounding effects due to the treatments used at Crowea, inter alia:- clearing is the mass removal of faunal and floral biomass leading to changes in microclimate and the nutrient pool due to the removal of biomass, together with possible disturbance to, and compaction of, the soil. Burning forest residues produces high surface temperatures (Humphreys and Lambert 1965) which removes the unincorporated surface organic cover and exposes the soil to nutrient loss by erosion and leaching, and changes the soil microbiology and the form of soil nutrients for several years (Theodorou and Bowen 1982). No measure was made of fire intensity although it can be gauged by its effect on the understorey shrubs and trees (Cheney 1981; McArthur and Cheney 1966).

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6.   APPENDICES

Appendix 1.   The proportion of samples that were identified to the generic level from the night samples from four areas of forest in south-western Australia

Area	Forest type	Sample size	% identified	No. genera	No. in common	Main genera	%
Nannup	Jarrah	1,462	16	10		Endotricha	93
	Pine	695	77	7	5	Endotricha	98
Manjimup	Uncleared Karri	1,253	29	26		Chlorocoma	75
						Cidaria	8
	Cleared Karri	1,019	15	32	14	Chlorocoma	27
						Cidaria	15
Quilergup	Jarrah	6,239	13	53		Hednota	29
						Agrotis	29
	Pine	4,586	15	44	30	Agrotis	35
						Hednota	24
Pemberton	2 y.o. Karri	1,414	17	39		Caradrina	19
						Cidaria	13
						Chlorocoma	11
	44 y.o. Karri	2,956	57	35	24	Chlorocoma	68
						Cidaria	18
						Pantydia	2

Appendix 2.   The level of identification of various insect taxa trapped at
Pemberton (P), Nannup (N), Quilergup (Q) and Manjimup (M)

Order	Family	Genus	Location
Ephemeroptera			P M Q
Odonata			P M Q
Blattodea			P M Q N
Isoptera			P M Q N
Mantodea			N
Dermaptera			P M Q N
Plecoptera			P M Q
Orthoptera			P M Q N
Psocoptera			N
Hemiptera			
Homoptera	Cixiidae		P M
	Eurybrachyidae		Q
	Fulgoridae		Q
	Ricaniidae		Q
	Flatidae		P M Q N
	Dictyopharidae		P M Q
	Cercopidae		P M Q N
	Cicadidae		P M
	Cicadellidae		P M Q N
	Eurymelidae		P Q N
	Membracidae		P M Q
	Aphididae		Q N
	Aleyrodidae		N
Heteroptera	Nabidae		N
	Miridae		P Q N
	Tingidae		M
	Reduviidae		P M Q
	Aradidae		P M Q
	Coreidae		Q
	Alydidae		P Q N
	Lygaeidae		P M Q N
	Scutelleridae		M Q
	Cydnidae		P Q
	Pentatomidae		P M Q N
	Gelastocoridae		P Q
	Notonectidae		P Q
	Corixidae		P Q
Thysanoptera			P M
Megalopter			P M Q
Neuroptera			P M Q
Coleoptera	Carabidae		P M Q N
		Chlaeniu	Q
	Dytiscidae		P
		Rhantus	Q N
		Lancester	N
		Cybister	M
	Gyrinidae		
	Hydrophylidae		P M
		Hydatotrephes	Q N
	Silphidae	Ptomaphila	P M Q N
	Staphylinidae		P M Q N
	Lucanidae	Syndesus	P M N
		Lamprima	Q

Order	Family	Genus	Location			
	Trogidae	Trox	P		Q	N
	Scarabaeidae:					
	Aphodiinae	Aphodius	P	M	Q	N
	Scarabaeinae	Onthophagus	P	M	Q	
	Melolonthinae	Liparetrus	P	M	Q	N
		Colpochila	P	M	Q	N
		Diphucephala			Q	
		Maechidius	P			
		Colymbomorpha			Q	
		Haplonycha				N
		Phyllocerus				N
	Dynastinae	Cryptodus	P	M	Q	
		Heteronychus	P	M	Q	
		Semanopterus				N
		Neodon		M		
	Buprestidae		P	M		
		Stigmodera			Q	
		Cisseus			Q	
	Elateridae		P		Q	N
		Pseudotetralobus		M		N
	Lampyridae		P	M	Q	
		Trichalus			Q	
	Cantharidae		P			N
	Lycidae	Metriorrhynchus			Q	
	Dermestidae		P	M	Q	
	Anobiidae	Anobium	P			N
	Bostrychidae		P			
		Bostrychopsis			Q	
		Xylopsocus			Q	
	Cleridae		P			N
		Natalis		M	Q	
		Trogodendron			Q	
		Eleale			Q	
	Lymexylidae			M		
	Coccinellidae		P			N
		Orcus		M	Q	
	Tenebrionidae					N
		Chalcopterus			Q	
		Adelium			Q	
	Lagriidae	Lagria			Q	
	Alleculidae		P		Q	
	Mordellidae	Mordella				
	Rhipiphoridae		P	M		
	Oedemeridae		P	M		
	Meloidae					N
	Cerambycidae:		P	M		
	Prioninae	Dioclides			Q	N
		Sceleocantha			Q	
	Cerambycinae	Phoracantha			Q	
		Coptocercus		M	Q	
		Uracanthus			Q	N
		Bardistus	P		Q	

Order	Family	Genus	Location
	Lamiinae	Ancita	Q
	Chrysomelidae		N
		Paropsis	P M Q
		Ditropidus	Q
	Belidae		P M
		Belus	
	Curculionidae:		P M N
	Erirrhininae	Desiantha	Q
	Gonipterinae	Oxyops	Q
	Amycterinae	Acantholophus	P Q
		Euomus	Q
		Aedrioides	Q
	Aterpinae	Rhinaria	P
		Rhinoplethes	Q
		Pelororhinus	Q
	Amalactinae	Tranes	P M Q N
	Leptopiinae	Catasarcus	Q
		Polyphrades	P M Q
		Cherrus	P Q
		Leptopius	Q
	Scolytinae	Xyleborus	N
Mecoptera			P M Q
Diptera	Tipulidae		P M Q N
	Psychodidae		Q N
	Culicidae		P M Q
	Chironomidae		P M Q N
	Ceratopogonidae		Q N
	Simuliidae		Q N
	Anisopodidae		P M Q
	Cecidomyiidae		Q N
	Sciaridae		M Q N
	Mycetophilidae		Q N
	Tabanidae		P M Q N
	Stratiomyidae		M Q
	Therevidae		P M Q N
	Asilidae		P M Q N
	Apioceridae		M
	Bombyliidae		P M Q N
	Empididae		Q N
	Dolichopodidae		Q N
	Phoridae		Q N
	Syrphidae		P M Q N
	Conopidae		P Q N
	Platystomatidae		Q N
	Pyrgotidae		P M Q N
	Neriidae		P M
	Micropezidae		P Q N
	Sepsidae		P M Q
	Lauxaniidae		P
	Sphaeroceridae		Q N
	Agromyzidae		Q N
	Ephydridae		Q N

Order	Family	Genus	Location
	Drosophilidae		Q N
	Milichiidae		N
	Muscidae		P M Q N
	Calliphoridae		P M Q N
	Sarcophagidae		P Q
	Tachinidae		P M Q N
Trichoptera			P M Q N
Lepidoptera			
	Hepialidae	Fraus	P M Q
		Aenetus	P
		Trictina	Q
	Cossidae		P Q
	Tortricidae		P M Q N
		Arotrophora	Q
	Psychidae		P Q
		Plutoreotis	Q N
	Tineidae		P M Q
		Moerarchis	P Q N
		Thalamarchis	Q N
	Lyonetiidae	Opogona	M
	Yponomeutidae		P M
	Oecophoridae		P M N
		Wingia	Q
		Garrha	P
		Thudaca	Q
	Xyloryctidae		P M Q N
	Zygaenidae	Pollanisus	P M Q
	Limacodidae		N
		Doratifera	P M Q
	Pyralidae		P N
		Urisephita	M Q
		Chilo	Q N
		Hednota	P M Q
		Endotricha	M N
	Hesperiidae		P Q N
		Anisynta	M
	Pieridae		P M Q
	Nymphalidae		P Q N
	Lycaenidae		P Q N
		Candalides	M
	Geometridae		N
		Chlorocoma	P M Q
		Arthodia	Q
		Hypographa	Q
		Oenochroma	Q
		Ciampa	P M Q
		Acidalia	P M Q
		Cidaria	P M
		Thalaina	P M
		Xanthorrhoe	P M
		Mnesampela	P
		Crypsiphonia	P

Order	Family	Genus	Location			
		Ophiographa			Q	
		Taxeotis			Q	
		Dichromodes			Q	
		Boarmia			Q	
	Lasiocampidae			M		N
		Digglesia	P			
		Entometa	P		Q	N
	Anthelidae	Pterolocera	P	M	Q	
		Anthela	P			
	Saturniidae	Antheraea	P			
	Sphingidae	Hippotion	P		Q	
	Notodontidae	Hylaeora	P	M		
		Trichocercus			Q	N
		Epicoma	P	M	Q	
		Teara		M		
		Discophlebia	P	M		
		Stenadelpha			Q	
		Ochrogaster			Q	
		Oenosanda			Q	
	Lymantriidae	Orgyia	P	M	Q	N
		Porthesia		M		
	Arctiidae					N
		Nyctemera		M	Q	
		Spilosoma	P	M	Q	
	Noctuidae	Agrotis	P	M	Q	N
		Heliothis	P	M	Q	
		Persectania	P	M	Q	
		Simplicia	P	M	Q	
		Pantydia	P	M	Q	N
		Plusia	P		Q	N
		Peripyra	P	M	Q	
		Cosmodes		M		N
		Caradrina	P	M		
		Omphaletis	P	M		
		Proroeopis	P	M		
		Radinogoes	P		Q	
	Agaristidae				Q	N
Hymenoptera	Pergidae			M	Q	
	Ichneumonidae		P	M	Q	N
	Braconidae					
M Q N						
	Evaniidae		P	M	Q	N
	Gasteruptiidae		P	M		N
	Torymidae					N
	Chrysididae		P	M	Q	N
	Cleptidae					N
	Pompilidae		P		Q	N
	Scoliidae					N
	Mutillidae		P	M	Q	N
	Tiphiidae		P	M	Q	N
	Masaridae		P			
	Eumenidae		P		Q	N

Appendix 2 continued ...

Order	Family	Genus	Location
	Sphecidae		P M Q N
	Colletidae		P M Q N
	Halictidae		M
	Megachilidae		Q N
	Anthophoridae		M Q N
	Apidae		P M Q N
	Formicidae		P M Q N

Total number of insects in night and day traps = 134,142

Appendix 3. Map showing the location of the four study areas.

BUNBURY

• Quilergup

Nannup •

34°S –

Manjimup •

• Pemberton

116° E