

Habitat Fragmentation: Impacts on Microarthropod Communities of the Pinelands

Sarah Rose Smith

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John Dighton

And approved by

John Dighton

Dennis Gray

William Saidel

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ABSTRACT OF THE THESIS

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Sarah Rose Smith

Thesis Director:

Dr. John Dighton

Soil microarthropods were surveyed for one year in order to see if the theory of island biogeography held true for micro-communities. Soil fauna were collected on a bi-monthly basis at a previously disturbed site in the New Jersey Pine Plains on natural regrowth islands. In conjunction with the survey an experimental survey was also conducted using defaunated soil patches, which were examined on a bi-monthly basis from September 2011- May 2011. Soil fauna on natural regrowth islands responded positively to island area and litter depth, and there was clear separation of soil fauna communities between the main lands the regrowth islands. Defaunated islands displayed changes in community assemblage over time and there were clear differences between soil fauna types and the ability to colonize new island habitats. There was a change in community structure over time as early colonizers were able to prosper for a short amount of time, followed by a slower dispersing suite of microarthropods that were able to establish and flourish in the defaunated habitat for a longer period of time. Overall, the study showed that soil microarthropod communities follow the assumptions of Mac Arthur and Wilson's theory of island biogeography and that certain species are limited by their dispersal capabilities.

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DEDICATION

For my Grandfather.
February 5, 1937- October 4, 2009

TABLE OF CONTENTS

Abstract	ii
Acknowledgements	iii
Dedication	iv
Table of Contents	v
List of Figures and Tables Chapter One	v
List of Figures and Tables Chapter Two	vi
List of Plates	ix
I. General Introduction	1
II. Chapter One	
Survey of microarthropod communities in a fragmented regrowth pygmy pine forest	
1. Introduction	9
2. Materials and Methods	13
3. Results	21
4. Discussion	31

III. Chapter Two

Investigation of colonization abilities of microarthropods in a fragmented system

1. Introduction	41
2. Materials and Methods	45
3. Results	50
4. Discussion	55
5. General Discussion	60
6. Figures and Tables	63
7 Appendix I	99
8. References	102

List of Figures and Tables Chapter One

Chapter 1

Figure 1.1	Microarthropod populations over time	64
Figure 1.2	Linear regression of functional groups over time	65
Figure 1.3	Fungivores and island size	66
Figure 1.4	Saprotrophs and island size	66
Figure 1.5	Effects of island distance on soil fauna density over time.	67
Figure 1.6	Effect of island distance on functional groups	68
Figure 1.7	Soil moisture % between habitat types	69
Figure 1.8	Linear regression of soil moisture and soil fauna	70

Figure 1.9	Organic matter % between habitat types	71
Figure 1.10	Linear regression of functional groups and organic matter %	72
Figure 1.11	Linear regression of litter depth and functional groups	73
Figure 1.12	Comparison of fungal hyphal length and island area	74
Figure 1.13	Comparison of fungal hyphal length and habitat	74
Figure 1.14	Linear regression of fungal hyphal length and soil fauna density on different habitat types	75
Figure 1.15	Linear regression of predators vs. prey	76
Figure 1.16	Litter decomposition rate between different Island habitats	77
Figure 1.17	Linear regression of soil respiration vs. Soil fauna densities	78
Figure 1.18	Comparison of soil respiration between habitats	79
Figure 1.19	PCA analysis of communities within different Habitats	80
Figure 1.20	PCA analysis of soil fauna communities within Island habitats	81

Table 1.1	Summary results of Figure 1.2	82
Table 1.2	Effect of island distance on microarthropod densities summary results of Figure 1.6	82
Table 1.3	Summary results of Figure 1.8-1.12	83
Table 1.4	Results of linear regression of Figure 1.10	84
Table 1.5	Results of linear regression of functional guilds Vs. Fungal hyphal length	84

List of Figures and Tables Chapter Two

Figure 2.1	Soil fauna densities over time	85
Table 2.1	Summary results of Figure 2.1	86
Figure 2.2	Functional guilds over time	87
Table 2.2	Summary results of Figure 2.2	88
Figure 2.3	Linear regression of organic matter content and functional guild densities for May 2011	89
Table 2.3	Summary results of Figure 2.3	90
Figure 2.4	Linear regression of soil moisture % and soil fauna densities	91
Table 2.4	Summary results of Figure 2.4	92
Figure 2.5	Soil respiration at different island distances	93
Figure 2.6	Linear regression of soil respiration and fauna	94
Table 2.5	Summary results of Figure 2.6	95
Figure 2.7	PCA analysis of time and soil fauna community Development	96
Figure 2.8	PCA of community development within defaunated Islands at different distances	97
Figure 2.9	Species richness and diversity over time and Habitat types	98
List of Plates		
Plate 1	Stylized map of natural islands	15
Plate 2	Stylized map of sterile islands	46

Appendix I

Figure 3.0	Parker Preserve treatments over time	99
Figure 3.1	Mites to Collembola ratio over time	100
Figure 3.2	Treatment effect on Collembola	101
Figure 3.3	Treatment effect on Mites	101

General Introduction

Habitat Fragmentation and microarthropod communities

Habitat isolation and fragmentation have been shown to have negative impacts on many different species (Hunter, 2002), including microarthropods (Hoyle et al, 2005). Hunter (2002) suggests that if space is the final frontier of ecological theory; fragmentation of space is the warped engine that drives research in spatial ecology. Research in the area of spatial interaction between organisms within fragmented systems has been receiving greater attention as landscapes are becoming altered through anthropogenic forces. Critical issues such as local extinction of bird populations (Renjifo, 2001; Robinson et al., 2001, Sekercioglu et al., 2002), declining populations of small mammals and herpetofauna (Maisonneuve & Rioux, 2001), declines in bee populations due to deforestation (Brown & Albrect, 2001; Cane, 2001), and the management of landscapes for preservation of insect biodiversity (Ehrlrich & Murphy, 1987) have all been receiving great attention in recent years. Yet in these fragmented landscapes, some insects prosper, in some instances at very high densities and diversity. The growing sense of urgency and awareness in understanding the role that habitat fragmentation plays in ecological processes is a prerequisite for sound science, policy and management (Hunter, 2002). Whether the goal is to predict the presence, absence or abundance of species in fragmented landscapes (Cowley et al., 2000), or conserve species (Fisher, 1998). The behavioral and dynamic responses of insects to landscape structure are key (Hunter, 2002) to gaining perspective on the issue of habitat fragmentation. The features of a landscape that influence the population and community ecology of species are well

known and documented. Edge effects (Chen & Wise, 1995; Radeloff et al., 2000), habitat isolation (Collinge, 2000), patch area dynamics were discussed in Kruess & Tscharrntke's 2000 paper. Patch quality (Hunter et al., 1996), patch diversity (Gathmann et al, 1994; Varchola & Dunn, 2001) and microclimate conditions (Braman et al, 2000) have all contributed significantly to the greater understanding of habitat fragmentation and the ecology of insects.

After fragmentation, habitats undergo a process of community disassembly or "relaxation" (Diamond, 1972) where the number of species that might be lost in the future is known as the "extinction debt" (Tilman et al, 1994). Spatially identifiable islands are expected to decrease over time in species richness to new equilibrium values. The degree of habitat fragmentation that maximizes species richness may depend on the stage in the relaxation process (Hoyle & Harbone, 2005).

Immediately following a disturbance event that leads to an altered fragmented landscape, the number of habitats and the proportion of species in common between subpopulations will be critical (Higgs, 1981). Un-naturally fragmented habitats that are dispersed over large areas are likely to have a greater range of habitat types verses a single large habitat patch of the same total area (Hoyle & Harbone, 2005). Macarthur and Wilson's (1967) publication of the theory of island biogeography setup the model for determining the affects of habitat isolation on species. In its simplest form the model predicts that the number of species on an island or similarly isolated area is a results of a dynamic equilibrium between immigrations and extinctions. Immigration rate is observed as a decreasing function of the numbers of species already present on an islands, whereas extinction rate is

an increasing function of the species number, with equilibrium occurs at the intersection of the two rate functions (Rey, 1984). Little is known about the effects of habitat fragmentation on forest insect communities and how land use changes affect the distribution and abundances of organisms (Gibbs & Stanton, 2001). Forests are increasingly fragmented worldwide (Groom and Schumaker, 1993) and many of the biological processes critical to forest ecosystem functioning including seed predation, pollination and decomposition are mediated by insects (Gibbs & Stanton, 2001).

Of particular interest to this thesis is the effect of habitat isolation on microarthropod communities. Microarthropods serve an important role in nutrient recycling of forest detritus (Coleman, Crossley and Herndrix, 2004). Large numbers of microarthropods live in forest soil. A square meter of temperate forest soil has been shown to contain hundreds of thousands of individuals representing thousands of different species (Coleman, Crossley and Hendrix, 2004). By sheer numbers microarthropods greatly influence soil processes. Soil microarthropods represent one of the most numerous groups of organisms on the planet, yet their behaviors and taxonomy remain largely under explored within scientific community. The significance of microarthropods becomes even more apparent when one takes a deeper look at the interactions between plant species that form ectomycorrhizal associates with fungal species present in the soil; the resulting mycorrhizal hyphae has been shown to be a substantial food source for fungivorous microarthropods (Newell, 1984; Baxter and Dighton, 2001).

Microarthropods form an important linkage in food webs and serve as both predator and prey. Microarthropods are prey items for spiders, beetles, ants, and centipedes. Smaller mega-fauna such as toads and salamanders have been known to feed upon microarthropods (Coleman, Crossley & Hendrix, 2004). Predatory mites are known to feed on nematodes and smaller microarthropod species (i.e. Collembola and juvenile mites) and larvae insects. Predators have a role influencing the population dynamics of smaller prey species.

Soil dwelling microarthropods are composed of several dominate groups of organisms. Mites are in the phylum Arthropoda, Order Acari possess four pairs of legs, sclerotized pigmentation, and have unique mouthparts that vary depending upon the fauna's feeding biology. Four major families of soil dwelling mites exist Oribatida, Mesostigmata, Prostigmata, and Astigmata. Oribatid mites are the most abundant of the families and are estimated to be in 1000 genera and 150 families, they are sometime referred to as a super family because of how large the family is (Norton, 1990). Populations have been estimated up to a hundred thousand individuals per square meter (Norton, 1990). Mesostigmata mites have been described to contain at least 120 genera and 30 families and are the predators of the soil. Over 1100 genera of Prostigmata mites exist. Over 400 genera and approximately 1300 species of Astigmata mites appear to be the least abundant group of microarthropods found in forest soils, contributing approximately 2.4% of total population of microarthropods found in temperate forest soils (Norton, 1990).

Collembolan are currently considered to be an order in the Class Entognatha of the Phylum Arthropoda although their exact taxonomic position is still the subject of

some debate (Hopkins, 1997). Approximately 6,500 species of Collembola have been described, but there is a general agreement that the number of collembolan species is significantly higher (Hopkins, 1997). The most recent estimates of total number of species of all organisms on earth quotes a figure between 13-14 million, only 13% of which have been described (Heywood, 1995). If the same ratio of described to undescribed species holds true for Collembola then there could be more than 50,000 species of springtail in the planet (Hopkins, 1997).

One of the most obvious features of Collembola is the jumping organ known as the furca. The furca evolved through basal fusion of a pair of appendages on the fourth abdominal segment and is capable of propelling some springtails many times their own body length in a fraction of a second; the furca is used as an escape mechanism to avoid predation (Hopkins, 1997). Species of Collembolan that are confined to the soil have a reduced furca to ease their movements through the soil particles; some even lose the organ all together. Deeper dwelling Collembolan also tend to have reduced or no pigmentation, but this feature does not hold true for all species and certain outliers are found (Hopkins, 1997). The majorities of collembolan feed on fungal hyphae or decaying plant material and have been shown to influence the growth of mycorrhizae and control fungal distribution (Newell, 1984). A number of Collembolan are carnivorous and eat nematodes, rotifers, and even other Collembolan (Cassagnau, 1972). Evidence exist that Collembola are abundant on human corpses during the early stages of decomposition (Folsom, 1902). Many Collembolan live all their lives in the soil, others live on trees and are abundant in suspended soils (Guilbert et al., 1995). Extreme habitats seem to support few

species of Collembola but sites with many niches have a diverse springtail fauna (Hopkins, 1997). Collembolan appear to follow the general rule that diversity increases are inversely related to latitude (Villalobos, 1990). More species of springtail exist in the tropics than in temperate zones. Collembolan exhibit dominance patterns typical of most groups of terrestrial arthropods, meaning that the majority of individuals are usually represented by a small number of common species (Hopkins, 1997). In most terrestrial ecosystems they are extremely abundant occurring at densities of 10^4 - 10^5 m⁻². Collembolan have a critical role at the basal level in soil processes and their diversity provides good reason for studying their biology and role in the soil.

The impacts of habitat fragmentations on microarthropods have been observed in a few key studies (Hertzberg, 1997; Rantalainen et al., 2005; Astrom & Bengtsson, 2011). Fragmentation may occur by natural or anthropogenic causes (e.g. roadways or development that requires a forest to be clear cut). Aerial imagery permits one to visualize habitat fragmentation. Forested areas abruptly come to an end on the edge of a housing development or a farm field and shrubland turns into parking lots, sewn together by a thread of asphalt highway systems. The consequences of fragmentation can have major impacts on biodiversity and genetic diversity (Dixon et al., 2009), and is currently under investigation with Pine Snakes in the NJ Pinelands (Dr. Walter Bien *pers comm*). The effects of fragmentation may be more exaggerated/ more visible in larger species such as snakes or small mammals when compared to microarthropods, but the underlying model of reduction in diversity is the same at either scale.

Certain taxa of microarthropods are more sensitive to changes in their physical environment, particularly Collembolan, and will aggregate in areas that are more favorable to them. Microarthropods live within the litter layer of the soil and depend on that environment for providing habitat, food resources and maintaining the appropriate level of humidity and soil moisture. Alterations in the microhabitat can lead to changes in the community structure. Disturbance to the forest floor that can lead to or create isolated habitats include deforestation, clear-cut harvesting along with post-harvest residue removal. These process involved the physical removal of the litter layer and organic materials necessary to soil fauna. This practice also produces severe soil disturbance and compaction. The removal of litter and organic materials from the forest floor alters the density and structure of microarthropod communities (Dighton et al., 2012) and soil compaction has been shown to have negative impacts on microarthropods (Coleman, 2004).

In a separate study in the New Jersey Pinelands at the Parker Preserve site the physical removal of understory vegetation, soil disturbance and tree thinning appears to have alter the soil fauna community, leading to lower levels of diversity and abundances in the disturbed plots compared to control sites (Figures 3.0-3.3), the results of the Parker Preserve study are still preliminary and need further investigation.

Dispersal capabilities of microarthropod species and their ability colonize new habitats have been documented to some extent by (Hertzberg et al., 1997; Rantalainen et al., 2005; Astrom and Bengtsson, 2011),).The intense level of sampling needed to fully grasp both the identification and number of samples

required to observe such relationships a daunting challenge even for expert taxonomists. Due of limited research in this area it is imperative that more research continue investigating microarthropods in communities in order to understand more of their life histories, questions of colonization and dispersal abilities, aggregation within the soil , feeding guilds and taxonomy. Microarthropods are one of the most biologically diverse groups organisms on the planet; yet very little known about individual species behaviors and biology. New species are continually discovered in a range of new habitats from tree canopies to the deepest known terrestrial arthropod ever found to date in a cave at a depth of over 2km below ground level (Jordana et al., 2012).

Chapter One

Survey of microarthropod communities in a fragmented regrowth pygmy pine forest

This survey was performed in conjunction with a study investigating soil fauna movements using sterile patches of organic material as regrowth islands surrounded by a sandy matrix surrounding natural regrowth islands. The regrowth islands consisted of dwarf pitch pine (*Pinus rigida*) trees, which make up the majority of the surrounding forest. This terrestrial ecosystem provided a model where the theory of island biogeography could be tested using microarthropods. Islands of regenerating forest appear in a “sea of sand”, which appears to be a hostile barrier to the migration of soil microarthropods. The regrowth islands were within a previously disturbed area of Warren Grove Gunnery Range, a sandy gravel matrix created through the disturbance event. Historically, the landscape was used as a former target site. The gravel pit occupies 2.4 hectares of former pine plain habitat that was cut and excavated sometime between the years of 1974-1976 and lacked vegetation until 1997 (Zolkewitz, 2010). A restoration project was performed in 2001 and newly planted seeded native grasses. When the site was visited in 2011 new patches of pitch pine had grown and formed isolation regrowth islands. The new regrowth islands were the subject of this study and are referred to as natural island habitats. The surrounding main forest consisted of an undisturbed portion of dwarf pitch pine that had not been physically disturbed, but undergoes periodically intense fires (Forman, 1998) however the immediate adjacent area where the study was performed was cleared of vegetation between 1974-1976 as observed from historical aerials.

Environmental and edaphic factors significantly affect soil microarthropod populations and communities. Differences between the soil environments of the mainland and island communities may lead to relative differences in population and community composition of microarthropods. Microclimatic conditions such as soil temperature, soil moisture, resource quality and litter depth are some important drivers of microarthropod communities (Madson, 2003). One of the most important factors affecting microarthropod populations is soil moisture (Madson, 2003). Several studies have shown a positive correlations between soil moisture and the abundances of microarthropods (Wallwork 1970, Usher 1976, Vannier 1978, Whitford 1989, Asikidis and Stamou 1991). Soil temperature is a driving feature of soil microarthropod populations, where extreme temperatures adversely affect soil microarthropods. Wallwork, 1970 proposed that a range of intermediate temperatures is preferred by certain soil taxa. Other factors are soil organic matter content, which influences density and diversity of microarthropod assemblages (Fujikawa 1970, Santos et al., 1978, Anderson 1988, Scheu and Schulz 1996). Usher, 1976 suggested food resources drive the patchiness observed in microarthropod populations. Leonard and Anderson, 1991 successfully demonstrated this relationship in laboratory studies on preferential feeding of microarthropods. Isolated habitats are likely to have very different microclimatic conditions compared to the richer main forest. Differences in habitat resources between the isolated islands and the main forest dictate which soil fauna groups are able to establish communities. The mobility of soil fauna also influences the community structure of isolated islands. Dispersal capabilities of soil organisms are

still poorly known (Wardle 2002). However empirical research shows a stark between the mobility of different groups of microarthropods (Bengtsson et al 1994; Sjorgren 1997; Ojala and Huhta 2001) for instance, some mite groups were able to migrate 10-20 cm in a day, while others are limited by porosity, temperature and soil moisture to a much smaller range. In a study conducted by Berthet, (1964) radioactive tagging was used to study the mobility of Oribatida (Acari) mites and found that the average daily displacement varied from one day to another. Berthet, (1964) found a significant correlation between the average daily displacements of *Steganacarus magnus* Nic. and the mean precipitation of the two previous days.

The mobility of soil fauna was examined using sterilized patches of soil at different distances in the field (see Chapter 2). To the best of my knowledge and upon review of literature MacArthur & Wilson's (1967) island biogeography theory has not been directly tested natural islands and sterilized patches of organic soil horizons as surrogate islands in the Pine Barrens. Using natural islands of forest regrowth in a previously highly disturbed area of the New Jersey Pine Barrens, I examined the populations and communities of microarthropods in forest islands and the neighboring mainland forest by addressing the following hypotheses as predicted by Mac Arthur and Wilson's theory:

- a. Islands that are closer to the main forest will have increased population densities of microarthropods than small islands.
- b. Large islands that are nearer will have higher population densities of microarthropods than large islands that are further.

- c. The surrounding main forest will have the greatest density and diversity of microarthropods.

Materials and Methods

Study site description

The study was located at the Warren Grove Gunnery Range in Burlington County, NJ (39.6928928°N, -74.3905961°W). The location of the field site is in the NJ Pine Plains within the Pinelands National Reserve along the Outer Atlantic Coastal Plain physiographic province. The study site is a reclaimed abandoned gravel pit. The gravel pit is located on the western boundary of the Warren Grove Range. The gravel pit occupied 2.4 hectares of a formerly pine plains habitat that was cut and excavated between 1974 and 1976. This site remained un-vegetated until 1999 when restoration was performed on a 1.7-acre portion of the gravel pit, 0.81ha of the gravel pit was used by the military as a helicopter-landing zone. By the late 1990's the area became unsuitable for use due to severe erosion and gulying (Zolkewitz 2010).

The Pine Plains are upland forested area characterized by dry, sandy, oligotrophic and acidic soils of the Woodmainie-Lakehurst association. Wildfire is a major driver of the Pine Plains ecosystem and this section of the Pine Barrens has had a long history of forest fires (Forman, 1998). The soils are nutrient poor and have low soil moisture content supporting uniquely adapted plant and animal communities. Many of the plant species are mycorrhizal and depend on symbiotic fungi to assist in the acquisition of nutrients from the soil. The dominant trees species present are Dwarf Pitch Pine (*Pinus rigida*), and shrub oak (*Quercus marilandica* & *Quercus ilicifolia*). The predominant understory vegetation of the main forest consisted of

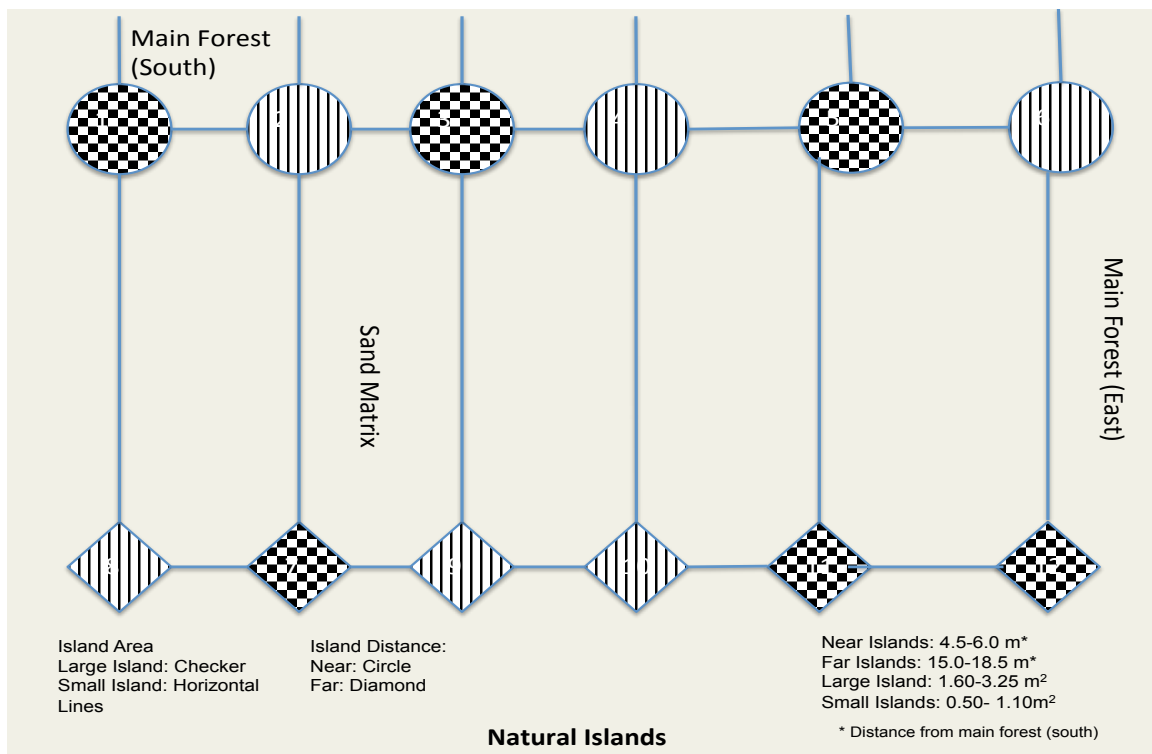
ericaceous species such as *Gaylussacia baccata*, *Gaylussacia frondosa*, *Kalamia latifolia* & *Vaccinium palidum*.

During the summer of 2011, the site was evaluated for its usefulness in determining the effects of habitat patchiness and island biogeography on soil microarthropod communities. The site was evaluated on its level of disturbance history, the presence of natural island-like habitats (comparable sites), distance from main forest and area. An area of undesirable habitat was necessary in order to test whether microarthropods would be limited in dispersal. The unique sandy matrix gives the site a “desert-like” environment, which provides little or no escape from high temperature and desiccating conditions during the summer months. Islands were classified as large - close, large - far, small - close, small - far; hypothesizing that the natural islands furthest away from the main stretch of forest will host a smaller population of microarthropods. Also, being investigated was the effect of habitat size on microarthropod populations.

Natural island description and experimental design

Twelve natural island habitats were identified. Islands were selected based on two factors, distance to mainland and island area. Natural islands were classified as either near or far to the mainland. Islands that were located between 4.5-6.0 m away from the main forest were categorized as “near islands”; islands that were located 15.0-18.5 m away from the mainland were categorized as “far islands”. Islands were further classified as being either large or small based on area. Islands that had

an area of between 0.50-1.10m² were classified as small islands; islands that had an area between 1.60-3.25m² were classified as a large island.



away from the main forest. Large islands were between 1.60-3.25m² and small islands were between 0.50-1.10m².

Soil Microarthropod Extraction

Microarthropods were extracted using a modified MacFayden high gradient extractor (MacFayden, 1961) funnel method of extraction over a period of 5 days with increasing temperatures via a light heat source driving soil fauna towards cooler temperatures into collection vial. One core per island was taken during each of the six sample periods, islands were replicated three times, three cores from the main forest were taken during each sampling period. Three cores from the sand matrix were taken during each sample period (N=18). The fauna were stored in 70% ethanol solution for further identification and enumeration using stereomicroscopy.

Specimen Identification

Extracted microarthropods were enumerated and identified to family Mesostigmata, Prostigmata, Astigmata and the super family of Oribatida using stereomicroscopy at 20x and 50x magnification. All Oribatid mites were further identified to genera level. Identification reference material was obtained by using the Soil Biology Guide (Dindal, 1990). Collembolan were identified to the genera level using multiple resources (Dindal, 1990 and Hopkins, 1997). Soil fauna were identified using the characteristics such as body size, shape, mouthparts, and pigmentation to identified members of families. Furthermore, soil arthropods were classified according to their functional grouping (Norton, 1990, Hopkins, 1997). Microarthropods were classified as fungivores, generalists, predators, saprotrophs,

or unknown feeding guild (Norton, 1990, Hopkins, 1997). Fungivores consisted mainly of Oribatid mites and included the following genera *Oppoidea spp.*, *Mycobatidae spp.*, *Brachythoidea spp.*, *Carabodoidea spp.*, *Oribatulidea spp.*, *Nanhermannoidea spp.*, *Tectocephus spp.*, *Pelopidea spp.*, *Scleroribatidae spp.* Fungivores feed on fungi growing on plant roots and decomposing materials. Generalists consisted mostly of Collembolan, but included the following families of Oribatid *Nothroidea spp.* (mite). Juvenile mites were not identified but were enumerated and classified as generalists. The following collembolan family groups were classified as generalists, *Isotomidae spp.*, *Poduridae spp.*, *Onychiuridae spp.*, *Entomobryidae spp.*, *Hypogasturinae spp.*, *Folsomidae spp.*, *Sminthuridae spp.* Generalist feeders do not have a specific feeding preference and feed on readily on decomposing organic materials, while there are some families of collembolan that do feed on fungi predominately (Hopkins, 1990). For the purpose of this survey all collembolan were ordered as generalist. Predatory mites consisted of the following suborder groups *Mesostigmatidea spp.*, and *Prostigmatidea spp.* These predatory mites feed on smaller arthropods, collembolan and arthropod larva. Saprotrophs consisted of *Phthiracaridae spp.*, and *Galumonidea spp.*, Saprotrophs feed on dead and dying plant or animal material. The last group consisted of mites that have an unknown/ undetermined functional guild: *Eulohmannoidea spp.*, *Hydrozedia spp.*, and *Astigmatidea spp.* Classification of soil arthropods into functional group categories is a common way of determining their role in an ecosystem by highlighting their feeding preferences and role in nutrient cycling (Wallwork, 1970; Dindal, 1990; Hopkins 1997). Since species identification using taxonomic methods

is often difficult and time consuming many soil ecologists utilizes this method of classification.

Methods for investigating environmental parameters on natural islands

Soil Moisture

Soil moisture was measured in September 2011 and May 2012 using the following formula: $\text{soil moisture (\%)} = (\text{wet weight} - \text{dry weight}) / \text{wet weight} \times 100$ was measured by drying soil at 70°C for 24 hours and comparing the wet: dry ratio.

Soil Organic Matter Content

Soil organic matter (May 2011) was calculated by measuring loss on ignition method which involved taking a ~ 5g subsample of mixed soil in a crucible, placing it into a muffle furnace at 550°C. This method converts the organic materials into CO₂, ash and mineral soil particles. Organic matter content was calculated using the following formula: $\text{dry weight} - \text{ash weight} / \text{dry weight} \times 100 = \% \text{ organic matter}$.

Fungal Hyphal Length

Fungal hyphal length measured during May 2011 was measured using line intercept method. Approximately 1 g of soil was suspended in 50 ml of water, a 15ml aliquot of the suspended soil was taken and a few drop of methylene blue added to the solution. The suspension was vacuum filtered through a cellulose nitrate membrane filter (1µm pore size and 25 mm diameter. The filter was mounted onto a microscope slide with a drop of Cargill Type A immersion oil. For

determinations of the total fungal biomass in soil it is common practice to determine total hyphal length and calculate biomass from those values (Hanssen, 1974). The membrane filtration method was utilized for the purpose of determining the biomass of fungal hyphae in the soil. Hyphal length was calculated using the number of times fungal hyphae crossed the grid line of an eyepiece graticule adapted from Oslen grid line intersect method (Hanssen, 1974; Tennant, 1975). The slide was examined at 10 different fields of view using a Zeiss microscope with a 20 x 20 eyepiece grid graticule at 25x magnification. The formula for calculating fungal hyphal length per field of view (R) is $R = \{(11/14)\} * N * L$, where N= total number of intersections between hyphae and all vertical and horizontal grid lines. L= length of side of one grid square.

Soil Respiration

Soil respiration was measured during May 2012 for each island, the main forest and the sand matrix using Infra-Red Gas Analysis using the PP system EGM- soil respiration chamber. Soil respiration was measured every 8 seconds for 120 seconds on each island. Measurements were taken in the morning and afternoon for each location.

Decomposition Rate

Litterbags were placed on the twelve natural islands to measure the rate of decomposition at six months and one year using 5 grams of dried (green) Pygmy Pine needles. Needles were dried for 24 hours at 70°C, in order to prevent

introduction of new species to the islands. The difference in the amount of litter remain in the litterbag at each collection was calculated into the percent of material decompose. Decomposition rate was calculated using the following formula $\ln(M_0/M_t) = k \cdot t$, where M_0 = Mass of litter at time; M_t = mass of litter at time t ; t = time of incubation (0.5/1.0); k = decomposition rate constant, 0.5 is equivalent to 6 months and 1.0 is equivalent to 12 months.

Data Analysis

Data was analyzed using SAS 9.2 statistical software, Graph Pad Prism 6.0 and PC-ORD. Linear regression analysis was used to determine the strength between environmental factors and soil microarthropod communities and functional group. Two-way ANOVA was used to determine the effect of time and habitat type and the soil microarthropod and functional group. Unpaired t-test was used to determine the differences between environmental parameters based on habitat type and location. Results were declared statistically significant at an alpha level of 0.05. Principle component analysis (PCA) was conducted by classifying microarthropod populations into large-close (LC), large-far (LF), main forest (MF), and sand categories. Testing the effect of habitat type on microarthropod taxa. Results of the PCA analysis will test which taxa were associated with a particular habitat type.

Results

Island area and microarthropod density

Regression analysis of bi-monthly fauna collection data revealed that island area did reveal a significant correlation with the density of the mean number of microarthropods. Figure 1.1 displays the faunal density for each sample date regressed against the island area/m². A significant relationship between island area and the mean number of microarthropods found on a island based on area for the month of July 2011-May 2012 was not observed based on the R square values and deviation from the non-zero slope. July 2012 was the only month to display a relationship between island area and microarthropod density. ($r^2 = 0.4318$, $F=7.599$, $P=0.0202$).

Functional groups of microarthropods and the effect of island size and sample date

As described earlier microarthropods were classified into functional groups in order to analyze any relationships between island size and microarthropod functional groups. Using two-way ANOVA different functional groups were analyzed for the effects of island size (large or small) and sample date. The graphs displayed in Figure 1.2 reflect the changes in population density for each sample period. Fungivores had significantly higher population densities in large islands (Figure 1.3 and Table 1.1, $P = 0.0463$, $F = 5.166$). Predator population density did not differ significantly when comparing island size ($P = 0.7792$, $F = 0.07931$). The results revealed significant differences between the sample date and the density of predatory mites ($P = 0.0003$, $F = 5.451$), with maximum abundance in January 2012

(Fig. 1.2; table 1.1). Saprotrophs showed significantly higher population densities in large islands compared to small islands (Figure 1.4 and Table 1.1, $P = 0.0021$, $F = 10.35$). The analysis also revealed significant differences of population density between sample dates ($P = <0.0001$, $F = 11.20$), again densities are observed to peak in January 2012 (Fig. 1.2). The unknown functional group did not show a significant difference in populations between island sizes Table 1.1 ($P = 0.1209$, $F = 2.475$). Population densities differed significantly among sample dates ($P = 0.0003$, $F = 3.404$). Interaction between the unknown functional groups density and the two variables (sample date and island size) was shown to be significant ($P = 0.0633$, $F = 2.226$). Interaction between the densities of the unknown guild of microarthropods is related to both island size and time of sampling, why this is a significant interaction is questionable since a similar pattern was not observed between any other functional guild. Unknown functional guild density peaked in January 2012 for small islands and continued to increase from January through May 2012 in the large islands (Figure 1.2). Generalist microarthropods did not respond differently to island size (Table 1.1, $P = 0.5654$, $F = 0.3342$) and therefore were not influenced by island area. Sample data did show significant difference in population densities of generalist ($P = <0.0001$, $F = 12.07$). The lack of significant interaction for saprotrophs, generalists, predators and fungivores populations indicates that despite the differences in population density between islands of differing size, and changes in population density over time, the microarthropod population dynamics of the two different size islands do not differ.

Effects of habitat type and sample date on mean microarthropod populations

Microarthropod population densities were analyzed in order to determine if microarthropod densities were different on mainland, sand, close and far islands (Figure 1.5). The mean microarthropod density for each habitat was compared for each sample date and habitat type. Analysis including the mainland and sand communities showed a significant difference in fauna density between habitat types (Figure 1.5 and Table 1.2). Further analysis using two-way ANOVA, excluding the mainland and sand communities did not express a significant difference ($P=0.2880$, $F=1.146$) between island distance and the density of soil microarthropods. Significant differences between sample time and the density of microarthropods ($P<0.0001$, $F=8.032$) was observed for all habitats.

Effects of island distance on microarthropod functional groups

Mean density of microarthropods observed in each of the functional guilds was used in the analysis for two-way ANOVA investigating the effects of island distance and sample date. The analysis revealed that for functional guilds the difference in density is not related to island distance. Microarthropods densities do not appear to be driven by the distance away from the main forest when comparing natural regrowth islands (Figure 1.6, Table 1.3). Sample date did have a significant effect on the number of microarthropods collected as shown in (Table 1.3) indicating that population fluctuations of different functional guilds are more temporally dependent rather than spatially dependent.

Soil Moisture

Soil moisture samples were collected in September 2011 and May 2012. Mean fauna densities of microarthropods collected on those sampling dates were regressed against the % soil moisture. Results of a one-way ANOVA did not reveal a significant difference between habitat type and soil moisture for either sample date September and May (Figure 1.7, September $P = 0.0951$, $F = 3.001$; May $P = 0.5396$, $F = 0.6506$).

There was a trend for islands to be drier than the mainland forest. A trend was observed indicating that the regrowth islands had less soil moisture than the main forest for both September 2011 and May 2012 (Figure 1.8, $P = 0.6702$, $F = 0.1925$, $r^2 = 0.0188$; $P = 0.2207$, $F = 1.624$, $r^2 = 0.0921$).

Organic Matter

Results of a one-way ANOVA comparing habitat types and organic matter content revealed that the main forest had significantly more organic matter content than small islands, large island and sand matrix area (Figure 1.9, $P = 0.0017$, $F = 8.703$).

Mean microarthropod densities were calculated for all islands and regressed against the percentage of soil organic matter present. The results of the linear regression did not reveal any significant relationship between soil organic matter and soil fauna densities.

Further investigation of functional group relationships with organic matter content and island size did not reveal a significant relationship. Fungivores did not show a significant correlation between organic matter and mean population density

on either island type (Large: $r^2=0.0762$, $P=0.3852$, $F=0.8245$; Small: $r^2=0.1314$, $P=0.4802$, $F=0.6049$). Slopes were not significantly different for fungivores between large and small islands; the slopes were essentially identical ($P=0.2766$, $F=1.2817$). Since the slopes for large and small were not significantly different, all data can be combined to a slope that equals 176.98. The unknown functional guild on large islands showed significant negative relationship with the percent soil organic matter on large islands ($r^2=0.6921$, $P=0.0400$, $F=8.990$) a similar correlation on small islands was not observed ($r^2=0.0563$, $P=0.6508$, $F=0.2386$). The slopes of both the large and small islands were identical over all ($P=0.392$, $F=0.8186$). Therefore, the combined pooled slope and calculated to be -288.343.

Generalist microarthropods on both large and small islands were not significantly correlated with the percent of soil organic matter (Large: $r^2=0.0008$, $P=0.9589$, $F=0.0030$; Small: $r^2=0.0495$, $P=0.6718$, $F=0.2083$) and the slopes of both large and small islands were essentially identical ($P=0.8963$, $F=0.0181$). Therefore, the combined slope was calculated to be 288.944. Saprotrophs on both large and small islands did not show a significant relationship between mean population density and percent soil organic matter (Large: $P=0.7269$, $F=0.1404$, $r^2=0.0339$; Small: $P=0.4689$, $F=0.6387$, $r^2=0.1377$), the slopes of the two island habitats were not significantly different ($P=0.9706$, $F=0.0014$). The a pooled slope was calculated at -100.74. A summary table of the results of the linear regression is found in Table 1.4 and the graphs of the linear regression for all functional groups are found in Figure 1.10 and Table 1.4.

Litter Depth

Three measures of litter depth for each island were taken and the mean value was used for each of the six large, six small islands and the main forest. Islands were compared by island size since distance was assumed not to be a factor in litter depth. The results of a two-way ANOVA revealed a significant difference between litter depth and habitat type (Figure 1.11, $P = <0.0001$, $F = 75.57$). The main forest contained the highest level of litter depth (mean 13.6), followed by large islands (mean 7.92) and small islands (mean 2.33). Functional groups were analyzed by linear regression and the results revealed in Figure 1.11 display a strong trend between the mean numbers of fungivores found on natural islands the litter depth ($P = 0.07$, $F = 4.14$, $r^2 = 0.30$). Generalists and predatory mites did not show a significant relationship between litter depth and fauna density ($P = 0.25$, $F = 0.95$, $r^2 = 0.09$; $P = 0.32$, $F = 1.1$, $r^2 = 0.09$). Saprotrophic mites (Figure 1.11 $P = 0.002$, $F = 18.4$, $r^2 = 0.65$) showed a significant positive relationship between litter depth and the mean density of fauna. The regression model for saprotrophic mites is $y = 38.68 * x + 8.280$ and 64.8% of saprotrophic mite occurrence can be explained by litter depth. The relationship between microarthropods and litter depth is interesting because the microarthropods live in the litter layer and therefore one would expect the two to be highly correlated.

The unknown function guild also showed a significant relationship between litter depths and population density ($r^2 = 0.40$, $P = 0.03$, $F = 6.5$) and 40% of the occurrence of the unknown functional are related to litter depth. Since unknowns do not have an determined feeding guild this finding is interesting because it gives insight as to

which environmental parameters more correlated with higher abundances of this group in islands.

Fungal Hyphal Length

Fungal hyphal length differed significantly between the main forest and the natural islands. The main forest had significantly more fungal hyphae (Figure 1.13, $P < 0.0001$, $F = 35.87$). The four of the functional groups known to feed on fungal hyphal were regressed against the fungal hyphal length calculated using the Olsen grid line intersect method of fungal hyphal length estimation. The results of the linear regression, showed no significant relationship between fungivores and fungal hyphal length on large & small islands or the main forest (Figure 1.14 & Table 1.5, Large: $r^2 = 0.04410$; Small: $r^2 = 0.2326$, MF $r^2 = 0.6033$). An interesting result of the linear regression revealed that the behavior of fungivorous soil animals in large and small islands responded similarly to fungal hyphal length, their slopes did not differ significantly ($P = 0.4425$, $F = 0.8938$).

Fungivores could be utilizing other types microorganisms that were not accounted for by looking only at fungal hyphal length. Generalists did show a relationship between small islands and fungal hyphal length but did not show a relationship with large islands or the main forest (Figure 1.14 & Table 1.5, Large: $r^2 = 0.1334$; Small: $r^2 = 0.6818$, MF: $r^2 = 0.1540$). Saprotrophs did not show a relationship between fungal hyphal length and the population densities within any of the habitats (Figure 1.14 & Table 1.5, Large: $r^2 = 0.2790$; Small: $r^2 = 0.04127$, MF: $r^2 = 0.7550$). The final group tested was the unknown functional guild and they did not show a significant

relationship between fungal hyphal length and population density within any of the habitat types (Figure 1.14 & Table 1.5, Large: $r^2=0.3082$; Small: $r^2=0.1360$, MF: $r^2=0.1721$).

Predator-Prey Interaction

Mean predatory mite population densities were regressed against the mean densities of two prey sources, Collembolan and juvenile mites (Figure 1.15). The results of a linear regression did not reveal any significant relationship between predators and collembolan and juvenile mites (Figure 1.15, $P=0.2642$ $F=1.399$ $r^2=0.12227$; $P=0.7638$, $F=0.0954$, $r^2=0.0094$). The lack of relationship between the potential prey sources tested and predatory mites suggests that predators may be utilizing other prey items, such as nematodes.

Decomposition Rate

The rate of decomposition was significantly higher in large islands at the six-month mark (Figure 1.16 $P=0.0236$, $F=1.806$). However, the mean abundance of microarthropods on different island sizes and decomposition rate did not show a relationship. Linear regression of the mean fauna density on large and small islands (Figure 1.16) did not reveal a significant relationship between decomposition rate and fauna density for the six month and one-year mark ($P=0.2572$, $F=1.447$, $r^2=0.1262$; $P=0.8034$, $F=0.0654$, $r^2=0.0064$). Soil fauna do not appear to be significantly contributing to the rate of decomposition and the two parameter examined are not correlated. Some evidence of a trend is observed between the six-

month period and the mean density of microarthropods present was not significant (Figure 1.16, $P=0.2572$, $F=1.447$, $r^2=0.1262$).

Soil respiration

Results of a linear regression using the mean number of fauna collected in May 2011 regressed against CO_2 efflux for both AM and PM sampling events showed a significant relationship between the density of fauna and soil respiration. The results of the AM and PM measurements showed that soil respiration significantly varied with the density of soil fauna during both sampling events of May 2011 (Figure 1.17, $P=0.0322$, $F=5.505$, $r^2=0.2560$; $P=0.0027$, $F=12.52$, $r^2=0.4391$). Further analysis between island size and respiration using an unpaired t-test showed that there was not a significant difference between large and small islands with regards to soil respiration. (Figure 1.18, $P=0.5730$, $F=1.369$).

Microarthropod Community Composition

Abundance data for microarthropods were analyzed using Principle Component Analysis (PCA both with and without the inclusion of the main forest communities. A PCA analysis for all islands and the mainland shown is displayed in Figure 1.19. The combined first two axes account for 73% of the variance. It is clear that the mainland arthropod community is significantly different from the islands by greater abundances of Sminthuridae (Collembola), Onychiuridae (Collembola), Poduridae (Collembola) and Hydrozetidae (mite-unknown functional guild). Although there is no significant separation of Large-Close islands from the rest (separation on Axis 2).

One can infer from the PCA analysis that Large and Close islands were dominated by Nanhermanoidae (mite), Scleroribatidae (mite), Mycobatidae (mite), and Caraboidea (mite) compared to the other habitats investigated. This dominance becomes clearer if the mainland communities are excluded from the analysis and differences between islands only are investigated (Figure 1.20). Between islands the first two PCA axes account for only 57.6% of the variance with separation between sites along Axis 1 only. The large close islands have significantly difference fauna community dominated by Caraboidea, Oppoidea, Scleroribatidae and Nanhermanoidae, which have the highest negative eigenvector loadings on Axis 1. Species richness, diversity and evenness did not differ significant between habitat types. Investigation of the number of taxa observed and habitat did not reveal differences between sites over the course of the experiment. July 2012 has an anonymously lower number of taxa collected, excluding the July 2012 sample date showed that differences in taxa collected exist between habitat types. Testing this effect using two-way ANOVA confirmed that this result was significant (Figure 1.21, $P < 0.001$, $F = 143$).

Discussion

Island Area and Fauna Populations

The results of this study suggest that defined by their participation in a specific functional group a relationship exists between density and island area. Fungivores were significantly more numerous in large islands versus small islands (Figure 1.3, $P = 0.0027$, $F = 9.780$). Saprotrophs also showed significantly greater populations on large islands compared to small islands (Figure 1.4, $P = 0.0021$, $F = 10.35$). Large islands had significantly greater litter depths (Figure 1.11, $P < 0.0001$, $F = 75.57$). Saprotrophs were positively correlated with litter depth (Figure 1.11). The relationship between saprotrophs and litter depth accounts for nearly 65% of their distribution and is one of the driving forces influences saprotrophs distribution among natural regrowth islands.

Litter provides a food source, habitat as well as aiding in maintaining a stable microclimate for microarthropods. The amount of litter present can have significant effects on microclimatic conditions by holding more moisture and providing substrate for fungi to growth. Although there was no significant difference between fungal hyphal length island area (Figure 1.12, $P = 0.4608$, $F = 2.102$). The main forest was found to have significantly more fungal hyphae present and exceeded the amount of fungal hyphae present on regrowth islands (Figure 1.13, $P < 0.001$, $F = 35.87$). The main forest consists of a more complex plant (over story tree community and shrub layer community) compared to the natural regrowth islands. Resource quality is known to have a positive effect on the diversity of microorganisms (Wardle, 2002). Fungivores did not display a significant

relationship between fungal hyphal length and density for any of the habitat types (Table 1.1). This result was surprising because I expected that fungivores would be positively correlated with fungal hyphal length. Fungivores consisted mostly of Oribatid mites whose feeding habits still remain elusive, despite numerous detailed feeding studies (Luxton, 1972, 1975, 1979; Mueller et al., 1990; Walter and Proctor, 1999). Many Oribatids appear to be indiscriminate fungal feeders that ingest fungal hyphae or fruiting bodies of a variety of species (Mitchell and Parkinson, 1976; Sieple and de Ruiter-Dijkman, 1993). Some studies that find selective feeding within specific species of Oribatida, Anderson, 1975, by studying the gut analysis of two species of Oribatida and found that when isolated the two species used similar food sources, but that when confined together in soil-litter microcosms, the two species changed their feeding and their utilization of habitat space. One species moved in the litter (A_0) layer while the other species increased in population density in the F (A_i) layer. Other studies using evidence through gut analysis revealed that Oribatids consume both plant material and fragments of Collembolan (Behan-Pelletier and Hill, 1983; Kaneko, 1988). Although classified as fungivores, Oribatids have the potential and digestive capabilities (Siepel and de Ruiter-Dijkman, 1993) to utilize different food resources and may not be as constrained to fungal feeding as previously thought.

Saprotrophs play an important role in micro-fragmentation by grazing on decaying plant litter (Krantz, 1978). These animals did not show a significant relationship between fungal hyphal length within the large island and main forest (Figure 1.14, Table 1.5), but did show a significant relationship within small island habitats.

Saprotrophs that feed on dead and decaying litter materials would be expected to respond more to litter depth than fungal hyphal length because of their known feeding guild (Krantz, 1990). Saprotrophs responded positively to litter depth within the different habitat types (Figure 1.11, $P=0.0016$, $F=18.43$, $r^2=0.6483$). Saprotrophs may have responded positively to fungal hyphal length within small islands may be due to the limited amount of high quality resources available on smaller habitats. With limited resources saprotrophic fauna may utilize any food sources available. The main forest and larger islands, there is a greater diversity of resources available due to larger area and more complex plant communities

Generalist feeders consisted of members of the order Collembolan there is evidence that suggests (Gunn and Cherrett, 1993) that Collembolan will feed on a variety of different food sources. Gut analysis of field-collected specimens revealed a wide variety of materials, including fungi, plant debris, and animal remains.

Selective grazing studies demonstrate that selectiveness of Collembolan grazing upon fungal hyphae influences the fungal community (Newell, 1984). Therefore, for the purpose of this study collembolans may be classified as generalists since one cannot specify a unique specific food source. Generalist feeders would not be expected to display a significant relationship with fungal hyphal length, because of their feeding habits. Generalists have the capacity to break down different food resources and would be expected to be able to exploit different resources in the soil, including fungal hyphae (Hopkins, 1997). In a limited resource area, such as an island fungal hyphae may play a more critical role in nutrient allocation through ectomycorrhizal, if generalists are able to “tap in to” and feed off of the fungal

hyphae there would be a benefit from the transfer of nutrients from another location (i.e. main forest) to the growing tree on the regrowth island. The allocation of nutrients into the natural islands via ectomycorrhizae may be one of the underlying drivers that support soil fauna life on natural regrowth islands. Generalists on small islands had a positive relationship between the amount of fungal hyphae present and the population density (Figure 1.14).

A similar non-significant trend was observed on the large islands (Figure 1.14). Generalists might be more dependent on fungal hyphae on smaller islands because of less resources to choose from and less dependent on fungal hyphae as a major food source on larger islands, which would have a more complex suite of resources.

The final group investigated was fauna that fall into the unknown functional group category. The unknown taxa of fauna do not have a determined feeding preference in the soil (Krantz, 1990) and included members of the Acari order *Eulohmannoidea spp.*, *Hydrozetidae spp.*, and the sub-order Astigmatidae. All of the members of this guild are mites. Since this group does not have a determined feeding guild it was of interest to determine what environmental factors maybe influencing their distribution. None of the members of the unknown functional group responded significantly to fungal hyphal length (Figure 1.14, Table 1.5), although there seems to be a slightly upward trend in large islands. Members of the unknown guild did respond positively to litter depth (Figure 1.11), which gives some insight into what environmental factors drive this group of fauna.

There are bottom-up controls and top down forces that might influence the decomposer community. When carbon resources are readily available, the microbial

biomass almost always increases rapidly (Anderson and Domsch, 1978; Nordgren, 1992). Setälä and Mikola (1998) found that with the additions of glucose (carbon source) in soil microcosms soil fauna abundances increased significantly. The effects of basal resource addition on major soil fauna taxa explored in the field by Chen and Wise (1999). The results of their study show that amended soils (446 g/m² of detritus addition) had significantly more soil fauna present after 107 days in the field. Regardless of their trophic positions all soil fauna responded positively to resource addition (Chen and Wise, 1999).

Time of sampling affects soil moisture and consequently influences the amount of soil moisture observed. Samples taken during this research project represent a snapshot of the fluctuation in soil moisture with in this system. Ecological characteristics of Woodmainsie soils can be found in Forman (1979). Woodmainsie soils are described as being xeric (low moisture and dry) with excessive drainage, very low water capacity, rapid permeability, low organic matter content on surface soil and a combined litter and humus thickness of 0-5 cm (Forman, 1979). The definitions presented in Forman's description of Woodmainsie soils are consistent with the observations of this study. The low soil moisture observed may also explain the lower abundances of microarthropods in theses soil compared with other studies, which have shown microarthropod abundances as high as several hundred thousand per square meter (Wallwork 1970, Norton 1990). Examples of densities of microarthropods in other sections of the Pinelands, such as the work conducted in Parker Preserve (Appendix 1, Figure 3.0-3.3) demonstrates that microarthropod

densities are much greater in the lowland pitch pine forests compared to the pine plains.

The fluctuations in microarthropod populations over the course of the study may be linked to changes in soil moisture and temperature and may explain why higher populations were found during the winter and spring months when soil moisture is generally higher and temperature are lower allowing for less evaporation. Temporal patterns have been observed in microarthropod populations and fauna with peaks occurring during the late autumn/early winter months and with the lower densities occurring during mid-summer (Wallwork 1970, Fujikawa 1970, Anderson 1988). Temporal patterns have been related to soil moisture and temperature because as spring transitions into summer, there is a shift from wet to dry season and with this a decrease in soil moisture and increase in soil temperature (Madson, 2003). During the fall, the wet season begins again which leads to an increase in soil moisture and a decrease in soil temperature. The data shows a bell shaped curve for microarthropod populations with lowest populations during the summer and early autumn months and highest populations during the cooler fall-winter and early spring months (Figures 1.5 and 1.6). Microarthropods densities were significantly different based on habitat type when including the mainland and sand communities ($P < 0.001$; $F = 14.68$). Excluding the mainland and sand community values does not show a difference in microarthropod abundance between near and far islands (Figure 1.5, $P = 0.2880$; $F = 1.146$). The certain taxon separated out significant based on habitat type as displayed in the PCA analysis (Figure 1.19).

Decomposition was measured at six months and one year. Large and small islands were significantly different in their rates of decompositions (Figure 1.16, $P=0.0236$, $F=1.806$), large islands displayed a higher rate of decomposition in during the first six months and a slower rate in the one-year litterbags. When the litterbags were collected at the one-year mark, the differences between the decomposition rates were not significantly different between island sizes (Figure 1.16, $P=0.0902$, $F=5.327$). Regression analysis did not reveal a significant relationship between microarthropod densities and decomposition rate. An upward trend is observed in the six-month analysis (Figure 1.16, $P=0.2572$, $F=1.447$, $r^2=0.1262$) and a similar trend is not observed for the one-year collection. The decomposition of plant residues is influenced by the chemical composition of the plant material, the physical-chemical environment and the abilities the decomposer community (Swift et al., 1979). The physical and chemical conditions include both climate and soil parent material, which in turn, influence litter quality and ultimately the activity and composition of microbial and invertebrate communities (Wardle and Lavelle, 1997; Gonzales and Seastedt, 2000). Decomposition is the result of combination of soil fauna and larger invertebrates both of who are important in conditioning the litter for the microbial actions that lead ultimately to uptake by plants. Faster rates of decomposition observed in the litter bags during the first six months is may be due to the higher resource quality of green litter. As decomposition continued the quality of the litter becomes reduced as various members of the decomposer community extract nutrients from the decomposing material.

Soil respiration was positively correlated with microarthropod densities. The result is not surprising because soil arthropods have been shown to contribute to a small amount of soil respiration <2% (Petersen & Luxton, 1982). The relationship observed between soil fauna and soil respiration is likely due in part to soil fauna aggregating in areas of higher environmental quality (high% soil moisture & % organic matter). Greater resource quality will not only attract microarthropods, but will also attract other soil organisms (i.e. fungal biomass, bacterial mass, root mass), which will lead to an increase in total soil respiration. The attractiveness of an area of high resource quality would lead to increased amount of organisms respiring.

Principle component analysis of communities revealed that the mainland forest separated significantly from the natural regrowth islands (Figure 1.19). The following families of microarthropod were collected primarily in the mainland, Sminthuridae (C), Onychiuridae (C), Poduridae (C), and Hydrozetidae (M). The separation of communities is reflective of the dispersal capabilities of the certain species. Three families of Collembolan were not observed on regrowth islands and one family of Oribatida. The four taxa microarthropods are some of the smallest microarthropods that were collected all <2mm during this survey. Collembolan are soft-bodied and were lacked the dispersal capabilities needed to cross the sandy matrix. The sand is acting like barrier between the islands. The inability of certain genera of Collembola to disperse is important because it suggests that a disturbed area (sand) is acting as a hostile barrier to this group. The sand matrix creates a barrier the natural islands and the mainland preventing the dispersal of these four groups of microarthropods. Large and close islands showed clear separation of four

different genera of the superfamily Oribatida, Nanhermanoidae, Scleroribatidae, Mycobatidae, and Carabodidae. This group of fauna is interesting because they have highly pigmented sclerotized exoskeleton, which helps to reduce the effects of desiccation and the effects of UV radiation (Norton, 1990). Pigmentation would be advantageous in dispersal to new islands. Mites were found at greater densities on regrowth islands compared to collembolan throughout the course of the survey. Mites have a hard exoskeleton compared to a Collembolan, which have a soft-thin cuticle that is susceptible to desiccation (Hopkins, 1997).

Overall, the results of the survey displayed that indeed larger islands supported the greatest populations of microarthropods when compared to the smaller islands. The findings are consistent with the hypothesis of MacArthur and Wilson's theory of island biogeography; larger islands hosting larger populations. Larger islands are able to support more individuals and therefore the rate of extinction will go down with increasing area (Mac Arthur and Wilson, 1967). Seasonal fluctuations were observed within each functional group and significant differences occurred between the density of microarthropods collected and sample date (Figure 1.6 & Table 1.6). The greatest population density was observed during January 2012 during which a sharp increase in the populations was observed. This result is consistent with others who have demonstrated that soil fauna reach greatest population densities during the cooler months. (Wallwork 1970; Fujikawa 1970; Anderson 1988; Madson 2003). The average temperature for the month of December 2011 was 10.5° C and the maximum temperate reached during December 2011 was 17.8° C. During January 2012 the average temperature was 7.7° C and the maximum temperature recorded

was 18.8° C. The spike in populations observed could be related to the mild conditions observed during these two months.

Aerial imagery did not show the natural regrowth islands present at the site before 2002 (Google earth inc.). One can assume that the animals collected from the regrowth natural islands during the survey had to migrate into these islands from the main forest sometime after 2002. Soil arthropods would have had to traverse a long distance relative to their body size, so the migration to these newly formed islands, likely took a significant amount of time and energy. Fauna most likely only migrated to these islands once enough growth and accumulation of organic material was present to support a community. However, one can not rule out the possibility that the organism could have been transported to the islands through passive dispersal (wind, water, or phoresy animals) which can play a significant role in dispersal (Siepel, 1994; Dighton et al., 1997). Resource dependent migration represents the underlying principle that MacArthur and Wilson (1967) suggested in the theory of island biogeography. Not only are island size and distance important drivers of diversity and abundance, but that resource quality is also a fundamental driver of diversity.

Chapter Two

Introduction

Experimental approach to island biogeography using defaunated patches

Habitat destruction and fragmentation influence ecosystems both directly and indirectly and are considered to be one of the major threats to biodiversity and the maintenance of ecosystem functioning (Astrom and Bengtsson, 2011). The dispersal capabilities of an organism have important implications when considering the effects of habitat fragmentation. Dispersal is important for understanding the characteristics of a meta-community and good estimates of dispersal rates in the field are often lacking (Astrom and Bengtsson, 2011).

Only a few authors have previously studied differences in the dispersal capabilities of microarthropods and more information is necessary to understand the complex nature of soil microarthropods (Berthet, 1964; Behan-Pelletier & Hill, 1983; Norton, 1990 & 1994, Hopkin, 1997; Rantalainen, Fritze, Ojala and Huhta, 2001; Haimi, Pennanin, & Setälä, 2005). Examining the effects of patch size versus distance from a mainland (Astrom and Bengtsson, 2011) found mixed effects on the dispersal abilities of Acari: Oribatida and Collembolan in an experimentally fragmented system consisting of bryophytes on a bare rock surface. The results of the 10 week long experiment showed that Oribatid mites were severely dispersal limited within the time frame of the experiments even at isolation distances of only 5 cm. They also found that Collembolan did not show any dispersal limitation over distances as far as 300 cm. They also found that the mainland had a relatively large influence on

microarthropod occurrence, even at 300 cm distance. Overall, suggested that fragmentation can strongly influences species occurrence and abundance in natural systems that are limited by dispersal (Astrom and Bengtsson, 2011).

Soil fauna have been shown to have the capabilities of inhabiting and colonizing suspended soil patches in the canopies of trees (Behan-Pelletier et al., 2008). Soil fauna were sampled and certain species were found to be more associated with certain lichen species versus tree species and indication that microhabitat conditions may influence aboreal microarthropods (Behan-Pelletier et al., 200). Suspended soils can act like islands especially for microscopic organisms. Therefore there is much interest in understanding the dispersal abilities of these organisms and there colonization behaviors.

Studies considering the impacts of corridor connectivity on microarthropods and they found that corridors are positively correlated with abundances of microarthropod species (Rantalainen et al, 2005; Hoyle, 2006). Others showed mixed effects of habitat corridors on the dispersal capabilities of soil fauna and have found varying degrees of differences among the different groups of microarthropod investigated (Hoyle & Harbone, 2005).

Microarthropods search for suitable microhabitats as required by the demands of various life stages (Norton, 1994). Gravid female microarthropods travel in order to find favorable oviposition sites of higher resource quality (Norton, 1994). When leaving a patch, microarthropods may search in a way that maximizes their chances of finding suitable habitat, perhaps using cues such as pheromone trails (Verhoef et al., 1977). Usher (1975) suggested that microarthropods are able to find

conspecifics since they are considered to be generally aggregated at high densities. Other methods of dispersal can include phoresy the phenomenon in which an animal actively seeks out and attaches to the outer surface of another animal for a limited time during which the phoretic ceases both feeding and ontogenesis in an attempt that results in dispersal from areas unsuited for further development of itself or progeny, has been documented in mites (Binns, 1982; Sieple, 1994). Berhet (1964) measured the movements of Oribatid mites in the soil and found that they moved an average of two to four centimeters per day. Ojala and Huhta (2001) study showed dispersal capabilities by Collembola were lower (0.5-10cm per week) than for Oribatids (1-20 cm per week in soil). The limited information on the dispersal and colonization abilities of micrarthropods shows the increased need for more studies considering these aspects which are necessary in order to understand the biology and ecology of soil fauna.

There is much debate on the factors influencing the distribution of soil organisms. The physical, chemical, climatological and geomorphic factors are considered to be the most heavily influential on animal and plant community assemblages, but also on interspecific relationships, such as competition, predation, or processes related to growth and development (Gutierrez-Lopez et al., 2010). Environmental factors such as soil moisture have been shown to be positively correlated with soil fauna populations (Rantalainen et al., 2005). Isolated habitats may have differences in soil properties and therefore may influence the microarthropod community strongly. Investigation of environmental parameters in isolated habitats is an important

measure that should be considered when investigating community structure of fragmented habitats.

In conjunction with the natural island survey, an experimental approach was adopted to investigate colonization rates and community assemblage characteristics in comparable islands at contrasting distances from a common mainland location.

H1: With Patches located closest to the the main forest. They will have the greatest density and diversity of microarthropods present.

H2: With Patches located furthest from the main forest . They will have the least density at first, but will eventually reach a density equilibrium that is similar to the the patches nearest to the main forest.

H3: Distant patches will display a lower diversity due to the inability of certain microarthropod species to migrate far distances.

The experimental portion of this study will complement the survey of natural islands and help to detail which groups of soil were able to initially colonize the regrowth islands during the early stages of habitat succession. The combination of the studies will provide detailed information and data on the dispersal capabilities of different groups of soil arthropods.

Materials and Methods

Sterile Island Patches

Sterile islands were created by isolating pieces of soil from the main forest described in chapter 1. Soil patches were 45 cm(L) X 22 cm(W) X 5cm(D) and consisted of organic material and rich hummic material. The soil patches were brought back to the lab for a sterilization procedure. Soil patches were immediately placed into a drying oven at 70C for 72 hours in an attempt to kill most of the soil fauna. The patches were then returned to the field site after 3 days and “planted” into the sandy matrix. Sterilized patches were placed 7.m and 15. m from the main forest (Plate 2.1). The patches were placed 1 m away from the closest regrowth island. The patches were placed 1 m away from the nearest islands because thereby defining a standard distance to be applied to all separation between patches. Placing the sterilize patches at varying distances from natural regrowth islands would have led to some sterile patches being closer to islands than other patches, therefore a standard of 1 meter was applied. The sterile patches were sampled bimonthly for microarthropod fauna from September 2011-May 2012 for microarthropods using a 58 mm soil corer. One core per patch was extracted bimonthly and examined.

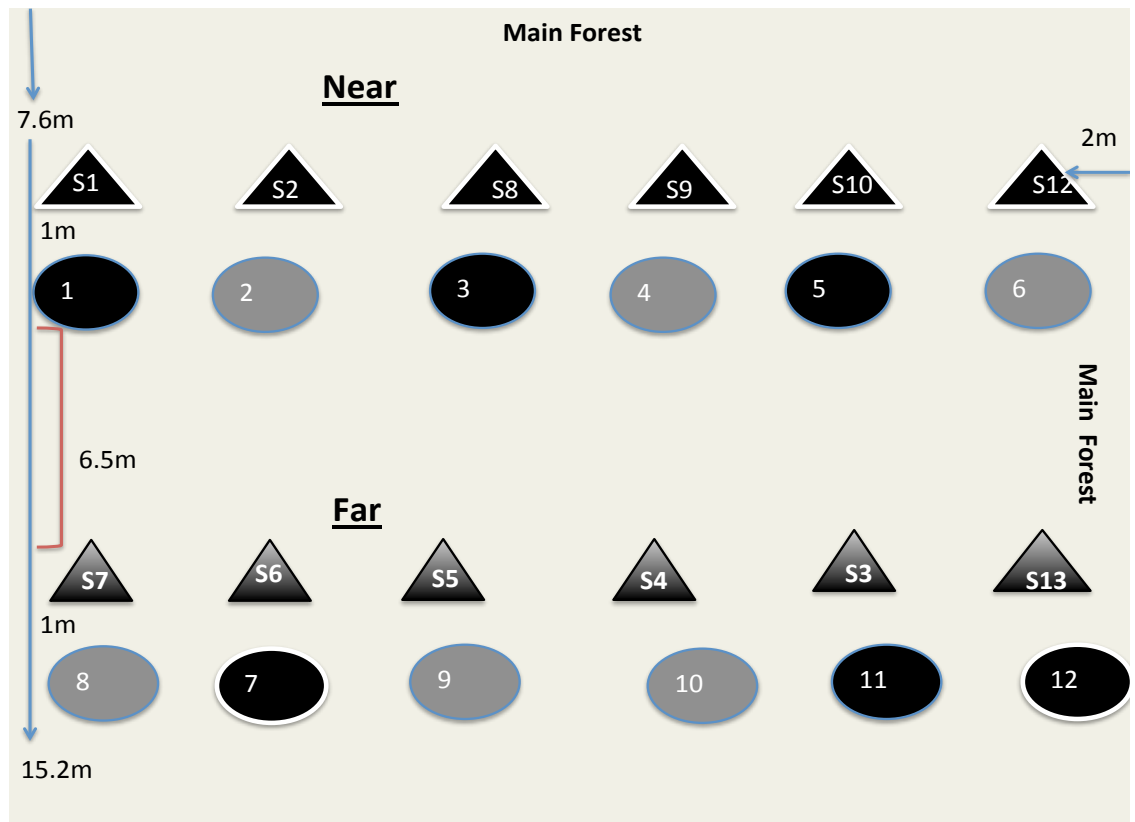


Plate 2.1: Stylized map of sterile island patches located within the gravel pit where the natural regrowth islands were surveyed. Black triangles represent the sterilized patches of soil. Circles represent the natural regrowth islands, black circles represent large islands and gray circles represent small islands.

Exclusion Cage Design

In order to test whether all microarthropods, larva and eggs were eradicated from the sterilized patches of soil, an exclusion cage was set up in the field. The cage consisted of a plastic bin, which was partially buried in the sand matrix so that it would cover the sterilized patch of soil. The top of the bin was cut off and replaced with screen (2mm) that allowed the patch exposure to the elements but would prevent most microarthropods from colonizing the sterilized patch since the only patch of exposure was by the top lid. I assumed that microarthropods would not be able to climb up the sides of the plastic bin. The exclusion cage was sampled during each sampling event. The exclusion cage was placed in the field in July 2011. When the site was visited for sampling in September 2011, the exclusion cage had been blown away, most likely due to Hurricane Irene which occurred during late August 2011. A new patch of soil was collected from the main forest and prepared using the same method of sterilization and placed in the field from September 2011- May 2012. During the time between the May 2012 and July 2012 sample dates the field an ATV vehicle disturbed site. The exclusion cage was removed and dug up by trespassers; the exclusion cage was not sampled during July 2012 for soil fauna. The exclusion cage was sampled each time the sterile islands were sampled and did not harbor microarthropods. Since microarthropods were found in the exclusion cage I can say with a degree of certainty that the sterilized patches of soil did not contain microarthropods when placed out into the field.

Soil Microarthropod Extraction and Identification

Methods used in Chapter One pages 16-17 detail the methods and materials used for the extraction and identification of soil microarthropods. Sterile patches were sampled for soil fauna bi-monthly from September 2011- May 2012.

Wind Dispersal of Microarthropods

In order to access if microarthropods were actually physically walking to the sterilized patches, sticky traps were placed on sterile patches 12.5 cm above the ground. The sticky traps consisted of a standard 20 x 25 cm (8x10 inch paper) overhead projection paper mounted onto a cardboard backing for stability. The overhead projection paper was coated with a thin film of Vaseline. Six sticky traps were created and placed at three near and three far islands. The sticky traps were left out for 48 hours during March 2012 and were collected and examined for microarthropods using stereomicroscopy. Overhead project paper was used because of its transparency would allow for easy observation using stereomicroscopy.

Organic Matter Content of Sterile Patches

Materials and methods used in Chapter One page 18 detail the procedure for soil organic content measurements. Soil organic matter was measured during May 2012.

Soil Moisture

Soil moisture was measured using the same methods found on page 18 of Chapter One. Soil moisture was measured for sterile islands during May 2012.

Soil Respiration

Soil respiration methodology can be found on page 20 of chapter one. Measurements were taken during May 2012.

Fungal Hyphal Length

Fungal hyphal length sampled were collected for the sterile islands during March 2011, however greater than half of the majority of the fungal hyphal samples were unable to be used because of cluttering on the microscope slide due to debris. Therefore, fungal hyphal length data could not be used for analysis of the sterile patches.

Results

Island Distance

The effect of island distance on microarthropod community development was measured over the course of the experiment. In order to test if distance from the main forest effected the abundances observed on near and far islands an unpaired t-test was used to compare the mean density of microarthropods extracted from close and far islands (Figure 2.1 and Table 2.1). The only month that showed a significant difference in mean population densities between close and far islands was January 2012 ($p=0.0616$; $F= 6.391$), where the faunal abundance was higher in close islands. Mean abundance of functional groups was tested between near and far islands for each sample period (Figure 2.2 and Table 2.2) using two-way ANOVA . Distance and sample time were tested and a significant interaction was observed between fungivores ($p<0.05$, $F= 2.49$), generalists ($p<0.0001$, $F= 17.20$), and saprotrophs ($p<0.0001$, $F= 9.44$) Significant differences in microarthropod densities between island distance and time are found by comparing the effect distance from all dates. Significant differences between distances by time indicate that the density of microarthropods on near and far islands varies over time. Interaction between functional guild densities by time and distance indicate that communities may be changing over time. Generalists ($p<0.0001$, $F= 24.80$) and saprotrophs ($p<0.0001$, $F=21.75$) showed significant separation between near and far islands. Significant differences in density between each sample time for generalists, ($p<0.0001$,

F=40.50) saprotrophs ($p<0.0001$; $F=47.92$) and fungivores ($p=0.0003$, $F=6.30$) were observed.

Microarthropods in Figure 2.2 display an interesting change in population densities on near and far between the November 2011 and January 2013 sample periods. In particular fungivores, generalist, and predators all show an increase in density for near and far islands leading up to the January 2012 sample date. Saprotrophs behaved interestingly because their density was much lower during the January 2012 sample date. The only group that did not behave this way was the unknown functional guild. Near islands increased between November 2011 and January 2012 but did show a similar increase on far islands. Some supporting research indicated that microarthropods have been shown to have higher densities during the winter months when gravid females search for locations to oviposit (Madson, 2003). Predators did not show a significant difference in density between distances, but did display significant differences in density based on sample date (Figure 2.2, $P<0.0001$, $F=7.400$).

Wind dispersal

Wind dispersal was investigated to determine if microarthropods were being blown onto islands via wind dispersal. After examining the sticky did not contain microarthropods on the traps for both near and far. Therefore, it can be inferred that the soil fauna collected on the sterile patches presumably immigrated to the patches. Furthermore, the exclusion cage remained free of microarthropods during

each sample date. Therefore the microarthropods did not originate from within the sterile patches.

Soil matter content

Soil organic matter content was measured during May 2012 for each sterile patch. Near and far islands did not differ significantly (Figure 2.3, $P=0.3707$, $F=12.29$). No significant relationship was observed between the organic matter content and the density of microarthropods for any of the defined functional groups (Figure 2.3 & Table 2.3). The results of a linear regression did not reveal any significant trends between the density of microarthropods present in a patch and the amount of organic matter detected. Furthermore, the slopes of the regression lines did not differ significantly, so a high population was equally probable in both areas of high organic matter content and low organic matter content on both near and far islands.

Soil moisture

Soil moisture percentage was analyzed in relation to the number of soil microarthropods collected during May 2012. No significant difference was found between near and far islands soil moisture percentage (Figure 2.4, $P=0.2308$, $F=1.044$). Functional groups were regressed against the soil moisture percentage and the mean number of microarthropods on near and far islands. None of the functional groups showed a relationship with soil moisture content and density (Table 2.4). Furthermore, the slopes of the regression lines for near and far islands lacked significance.

Soil respiration

Soil respiration was measured during the May 2011 sample time using the IRGA method. Comparison of near and far islands using an unpaired t-test showed that no significant differences in the rate of CO₂ respiration between near and far patches during the AM sample round (Figure 2.5 P=0.8602, F=1.611). No significant difference between the rates of CO₂ respiration during the PM measurement for near and far islands (P=0.8602, F=1.611). Linear regression of the mean number of microarthropods collected during May 2012 and soil respiration was conducted to determine if a relationship between microarthropod density and the amount of CO₂ respiration emitted from a soil patch existed. The analysis revealed a significant relationship between the density of microarthropods on near islands and the amount of CO₂ respired both in the AM (Table 2.5, P=0.0175, F=15.22) and in the PM (Table 2.5, P= 0.0323, F= 10.37) A similar relationship was not observed for far islands and CO₂ respiration.

Community analysis

Sterile island soil fauna communities differed over time, with no significant difference based on the distance from islands to the main forest (Figure 2.7). A PCA analysis of the collective data over all times gives 50.25% of the variance on Axis 1 and 9.74% and 7.08% on Axes 2 and 3 respectively. A MANOVA was also run on both Axis 1 and Axis 2 looking at the effects of distance on the community. Significant separation of microarthropods communities was not apparent between close and distance islands (Figure 2.7, axis 1 p<0.163, F= 2.0, axis 2 p=0.608, F=0.22,

Wilk's lambda $p=0.333$, $F= 1.12$). Community development over time revealed differences between close and far islands in terms of species richness (total number of taxonomic groups) and diversity with the Shannon Wiener diversity index. The September and January sample dates is represented by T1 and T3 respectively had significantly different soil fauna communities. These communities consisted mainly of Astigmatidae mites in September Phthiracaridae, Tectocepheus and Mycobatidae mites in January (Figure 2.8). Richness and diversity increased with time, (Figure 2.9). Regression analysis suggested that species accumulation and diversity increased more rapidly in distance islands versus close islands. Overall, diversity for all islands showed a trend (non-significant) to increase with time.

Discussion

Factors that influence the mobility of a microarthropod are body size and exoskeleton. Mites have a sclerotized exoskeleton that provides a protective barrier against desiccation and UV radiation that is likely to be encountered while migrating and expanding to new areas of greater resource quality. Collembolan are softer-bodied organisms with a soft exocuticle that is not as efficient at preventing desiccation and therefore collembolan are generally more restricted to soils that have a higher moisture content (Hopkins, 1997). Large body size is a limiting factor for microarthropods migrating vertically, but in this experiment only horizontal migration is being considered. Therefore one would be expected that large bodied microarthropods would be able to migrate greater distances because of their large body size.

The environmental parameters did not reveal any strong correlations between soil moisture and organic matter content (Figures 2.3 & 2.4) and the abundance of microarthropods from different functional guilds. Distance from the mainland also did not appear to be a driving factor in the community development of the patches. Rather, the most important factor in determining the microarthropod community within defaunated patches was time based on (Figure 2.8). Isolated habitats as predicted by Mac Arthur and Wilson's, 1963 model undergo processes of isolated equilibrium, which shapes the community assemblage of an isolated habitat (Mac Arthur and Wilson, 1963; Rey, 1981). Early colonizers are able to take advantage of low competition for resources and expand their populations until they are able to colonize the next new habitat. Species richness and diversity among isolated islands

will tend to be less than on close islands. In a patch dynamics system, species occurrence is a result of the balance between local extinctions and colonization events. In the sterile island patch communities, the community structure shifted over time (Figure 2.7) through an increase in diversity. The fauna that were able to colonize the patches were able to traverse a long distance relative to their body size. Despite the adverse conditions of low soil moisture and resources, microarthropods were able to colonize sterile patches at both near and far distances at great densities. With the investigation considering the wind dispersal capabilities of microarthropods, wind was not a dispersing agent. This is a pronounced effect and indicated that the main mode of dispersal of mites and Collembola was not aerial. I conclude that random ground based movements including walking or jumping, is the main colonizing mode and is in agreement with two other studies that have considered alternative dispersal modes (Wanner and Dunger, 2002; Astrom and Bengtsson, 2011). Since the patches were inhabited by microarthropods, it can be assumed that the patches were of favorable quality and thus a suitable habitat for the majority of organisms living in these habitats although abundances of fauna in patches were lower than abundances in the main forest and regrowth islands.

Understanding the differences in the colonization rates of the sterile patches gave insight into the initial colonization of the natural regrowth islands indicating that certain groups of fauna are able to migrate and reside faster to newly formed patches. This group can be likened to early successional species. They represent groups of organisms that are able to initially establish, but eventually become outcompeted by more other species. Fauna groups that were slower to colonize the

patches represent groups that are able to persist over a longer period of time and establish a long term populations. Of great interest are the types of microarthropods that colonize the patches. The expectation that members of the order Acrai would be the first colonizers of sterile island patches as previously shown in empirical research (Norton R.,1994; Ojala & Huhta, 2001.

The community detected in the first sample was dominated by Collembolan in genera *Folsomia spp.*, along with two types of Oribatid mites, Nanhermannoidea and Carabodidea (Figure 2.8). Hutson (1980) found that the fast buildup of Collembola and Oribatid abundances at newly formed reclaimed industrial sites was due to decreased pressure from predators, and therefore these early successional groups were able to persist for some time. The community then shifted to community dominated by predatory mites Mesostigmata, a member of the unknown functional guild, and smaller Oribatid mite from the family Oppoidea. The latter community assemblage persisted until the end of the study and did not differ significantly from time T2-T5, (Figure 2.7). The greatest level of species richness was achieved during the month of January (T3, Figure 2.7 and 2.8) in which 23 different species of fauna were observed during that sampling event. January 2012, T3, could indicate a shift in the community from the early colonizers to a new group of later successional colonizers to the patches. Oribatid mites representing the Oribatid family groups of Phthiracaridae, Tectocephus and Mycobatidae were the dominant groups associated with the patches during T3, (Figure 2.7). Overall, distance from the mainland did not dictate which patches would contain the highest species diversity or abundance. Rather the amount of time that the sterile patches were left in the

field highlighted the shifts in community assemblage (Figure 2.8). Astrom and Bengtsson (2011) found similar results in their experiment. They also found that the mainland influenced the dispersal much more than neighboring islands. At 5 cm away from the mainland, sterile patches seemed to contributed much more to Oribatid abundance than did neighbor patches, and at 300 cm, they seemed to contribute roughly the same, indicating that mainland dispersal was relatively more important than island-to-island dispersal, (Astrom and Bengtsson, 2011). This finding suggests that the mainland is acting as the “seed stock” for the fragmented habitats and therefore the ecological integrity of mainland patches may be more valuable than maintaining fragmented patches (Anstrom and Bengtsson, 2011). Overall, the defaunated patches did not react as expected in my hypothesis. I had originally hypothesized that islands closest to the mainland would be the most diverse due to the proximity of the island to the main forest, but expectation was not found for the sterile patches. Defaunated islands did not different significantly in richness or diversity based on distance from the mainland. Overall, microarthropods did not behave as originally hypothesized and distance did not act to separate patches based on faunal communities. Oribatid mites and surprisingly Collembola were some of the first colonizers of the patches. Mites were hypothesized to be some of the first colonizers to the patches. The presence Collembolan were surprising due to their softer body which was thought to be a limiting factor in dispersal due to the risk of desiccation in a low moisture environment such as the sandy matrix.

The simple act of observing a particular group of organisms over time provides valuable insight into those organisms' behaviors and life histories. Ecologists have long studied the happenings of the natural world from Fabre studies of the wasps of his backyard (Fabre, 1921) to more elaborate studies that investigate the genetic makeup of a community. Microarthropods represent a group of organisms that may be one of the most diverse groups of fauna on the planet but remain one of the many groups of organisms that are in desperate need of further research. Every new piece of research on this group adds a little more detail to the overall understanding of their function and ecological importance. While their total impact in nutrient cycling may be relatively small, they still represent a group that should be studied and valued. This study has demonstrated that certain species are distinct in their abilities or inabilities to colonize new habitat. There was very clear evidence that certain groups of microarthropods were only associated with the main forest and were not found in other habitats (Chapter 1, Figure 1.19). Species that were unable to migrate to the isolated may be the most vulnerable to habitat fragmentation because they lacked the ability (or need) to disperse into the new regrowth islands. Species that were able to successfully colonize the regrowth islands may be less vulnerable to the effect of habitat fragmentation.

General Discussion

Habitat fragmentation has been shown to reduce biodiversity (Fahrig, 2003). The amount of literature on the topic of habitat fragmentation reveals over 1,800 research papers using the web of knowledge and countless studies have displayed similar results, the more heavily fragmented a landscape, the greater the risk for loss of diversity on the fragmented pieces. There are different ways of conceptualizing fragmentation, either by loss of area or separation from a mainland source of diversity, thus island biogeography. Habitat fragmentation has been described as a process during which a large expanse of habitat is transformed into a number of smaller patches of smaller total area, isolated from each other by a matrix of habitats unlike the original (Wilcove et al., 1986).

The site used for this study had been previously disturbed (total vegetation removal in the late 1960's) and was not subsequently physically disturbed. Therefore, the community that subsequently reestablished had a significant amount of time between disturbance and sampling for soil fauna. The natural regrowth islands can only be estimated how long they had actually been established, so it is not possible to estimate from the regrowth islands which fauna were the early colonizers and actively mobile. Regrowth islands have more chance of passive dispersal of microarthropods to contribute to the populations since they have been established longer. Therefore, including the sterile islands in the survey complements the study and helps to answer questions on dispersal capabilities.

Soil microarthropod communities (combined) were not influenced by distance from mainland in either study, as is predicted in MacArthur and Wilson (1967).

When individual taxa were investigated further information was drawn from the data that showed certain taxa were more closely associated with a particular habitat. The taxa displayed in (Figure 1.19) on Axis 2 are of interest because they are more closely associated with large and close islands. The four taxa are mites of the Family Oribatida, it would be interesting to investigate the various genera of Oribatida that were observed and look at separation of specific families of microarthropods between habitat types. Within a given family group exaggerated differences between different genera may exist based on habitat and environmental conditions. Parameters such as litter depth showed positive relationships for microarthropods combined and for specific functions groups (Saprotrophs, Unknown) and further data mining may uncover which genera relate most strongly to the environmental conditions tested.

Colonization and dispersal capabilities of certain genera of microarthropods were interesting because shifts in the community were observed between different groups of microarthropods over time (Figure 2.8). Further investigation into early colonizers would be interesting since one of the early colonizers was a Collembolan and this result was not expected due to their body type. Collembolans have been shown to take advantage of low predator abundances for a short time followed by a decrease in abundance once predators are introduced (Hopkins, 1997).

The applicability of this study to large-scale land management practices is likely limited due to the differences in the aggregation of soil fauna as well as their demands for space versus a larger animal such as an elephant on a nature preserve. The simple model of increasing species diversity with greater area is true for almost

every organism. Given the right set of conditions with the appropriate level of resources populations will grow. Provide there are enough resources to go around. Once the species area equilibrium is reached populations will regress downward to the next equilibrium.

Changes to this study that may make the results more applicable to a land and resource management would be investigating the dynamic of microarthropods as sources of prey for threatened and endangered species Litter dwelling microarthropods are an important prey item to beetles and other larger invertebrates (Hopkins, 1997). Microarthropods that live deeper in the soil horizon would not be accessible to larger fauna. Kruess and Tschardtke (1994) showed the negative effects of fragmentation were magnified in predator populations and Rey, (1981) also had similar results, with predators being more vulnerable to fragmentation. By thinking about microarthropods in prey role and considering the adaptations that some predators may have evolved in order to capture this unique group of organisms, one can see how the removal of the habitat that is suitable for microarthropods may in turn negatively affect a species that is concern.

There are many amphibians that are specialized predators of microarthropods, predators that traverse through the litter layer in search of collembolan and mites. Fragmenting forests for whole tree harvest, residue removal and forest road creation remove the litter layer, which has been shown in this study to have a positive relationship soil fauna densities. The litter also serves an important function for the predators of microarthropods in providing camouflage for smaller predators such as frogs, toads and salamanders that may use the litter to avoid their

predators, such as hawks and large mammals. Overall, while microarthropods are small and the extent of their contribution is not fully understood, their impacts on a healthy ecosystem should not be underestimated. Further studies into the interactions with other organisms would provide more insight into their role as regulators and drivers of diversity.

Figures and Tables: Chapter One

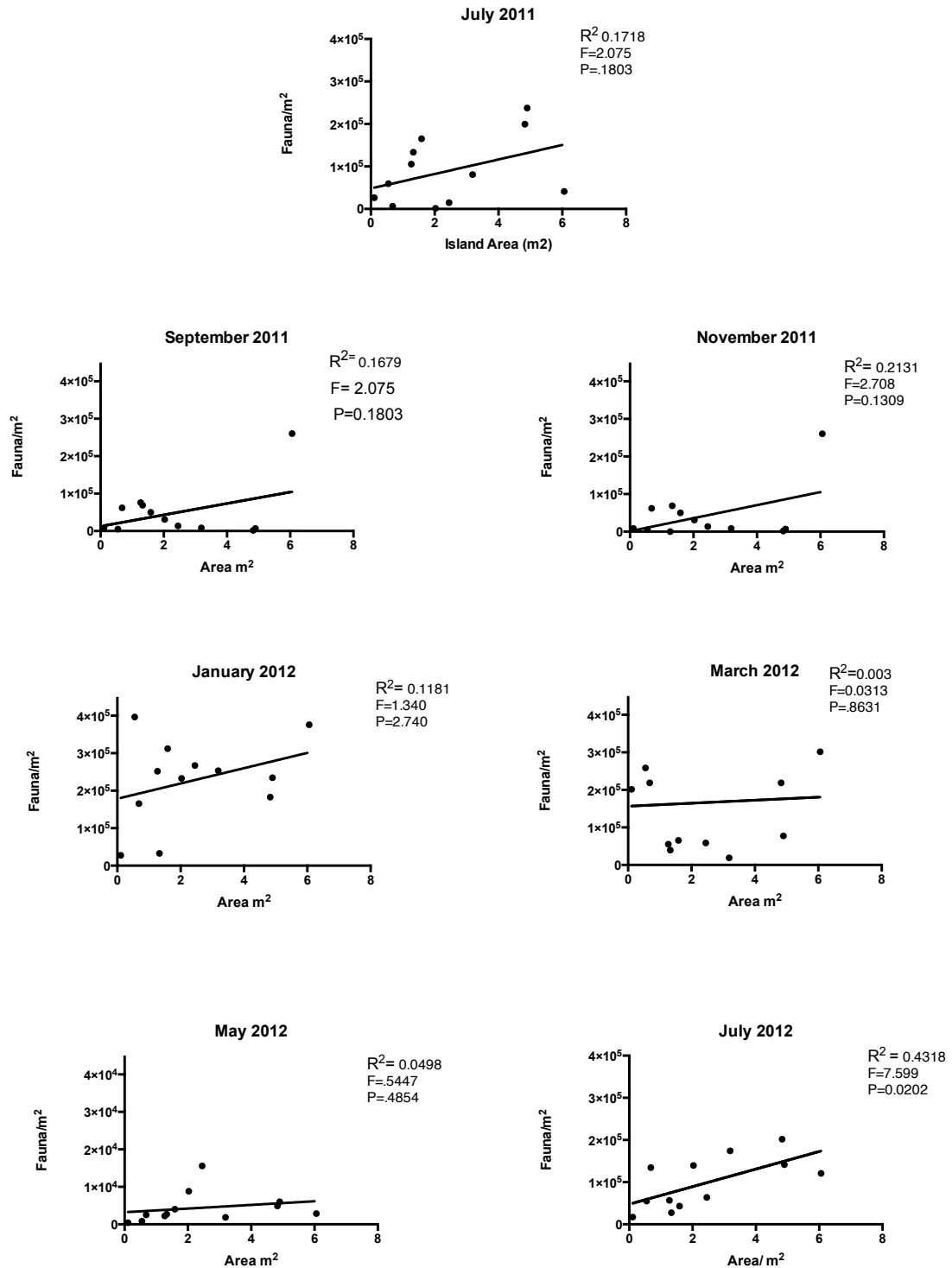


Figure 1.1: Linear regression of the mean number of microarthropods collected during each sample period regressed against island area.

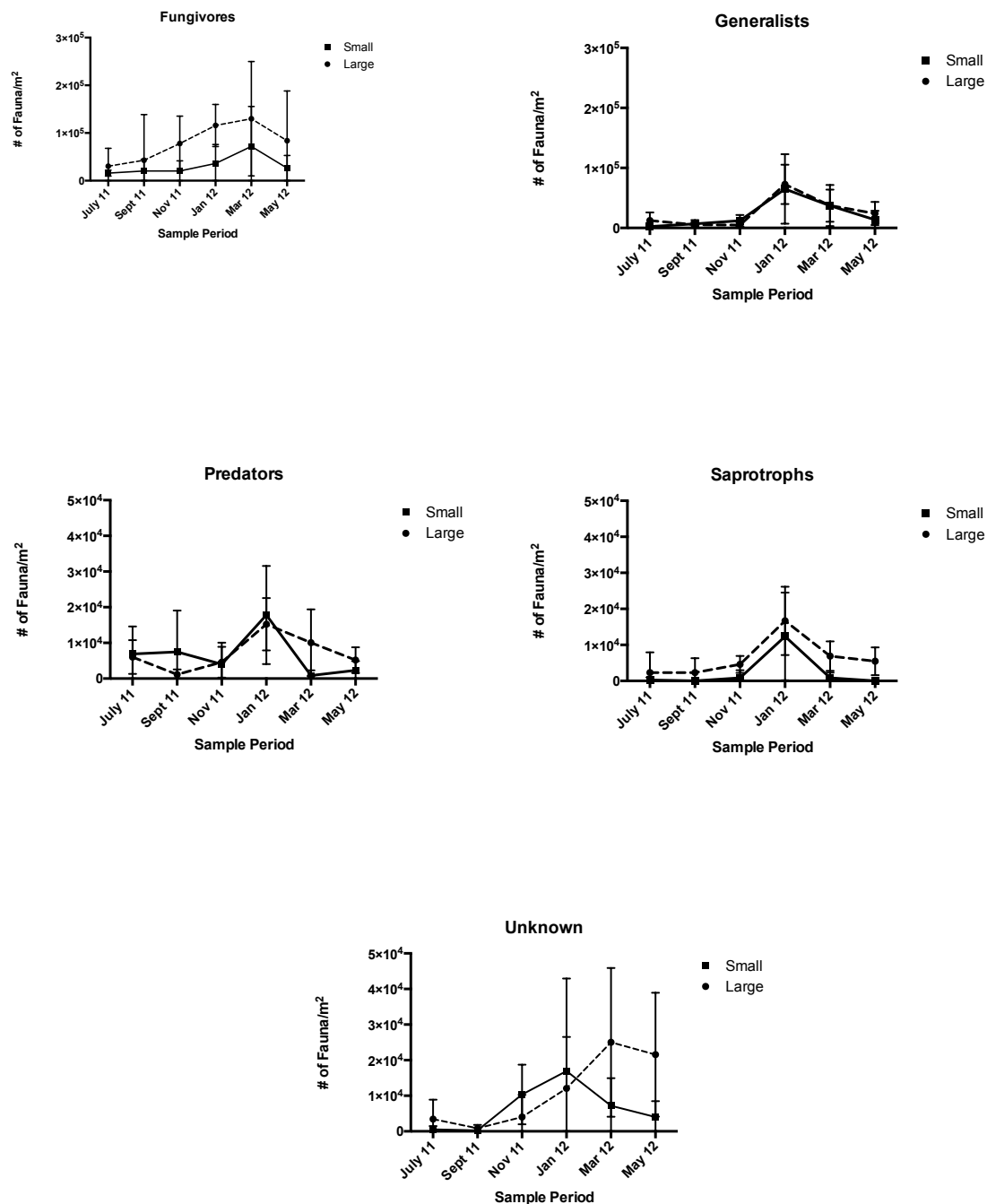


Figure 1.2: Bi-monthly population densities microarthropod functional groups in relation to island area (bars represent means \pm SE).

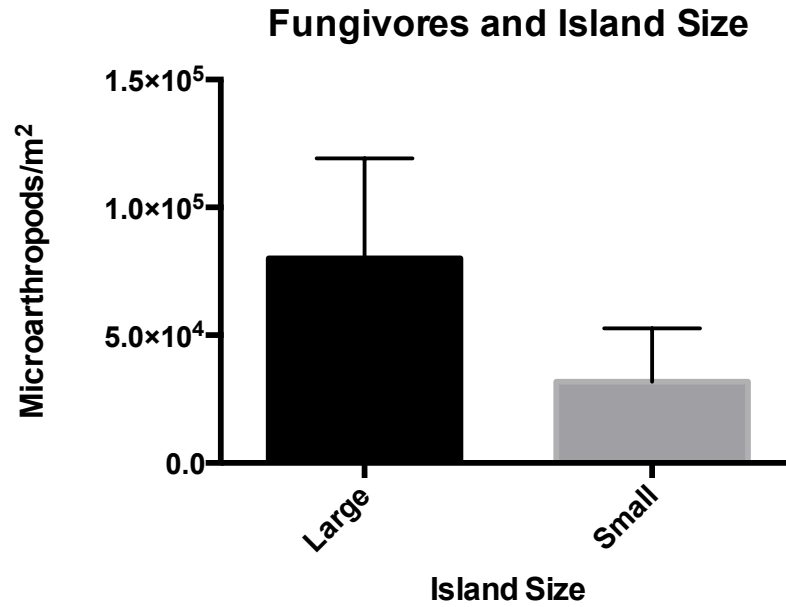


Figure 1.3: Effect of island size on the population density of fungivorous mites over all sampling events. Population densities were significantly higher in large island habitats ($P = 0.0027$, $F = 9.780$).

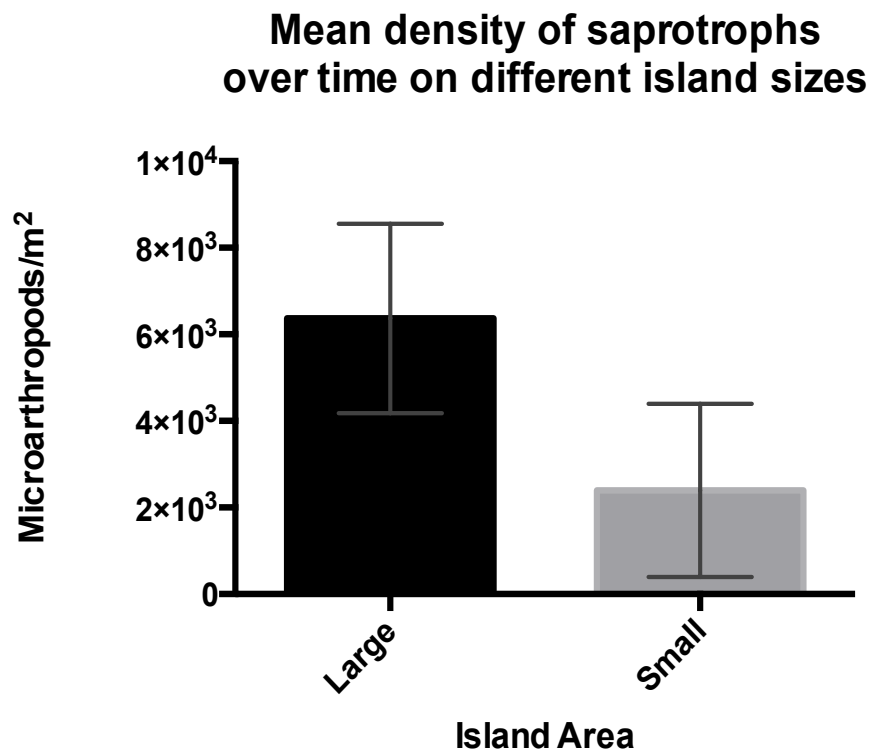


Figure1.4: Comparison of mean saprotrophic faunal density between small and large islands. Results of two-way ANOVA revealed that there was a significant difference

between the population densities of Saprotrophic mites on large and small islands. Large islands harbored significantly more mites ($P = 0.0021$, $F = 10.35$).

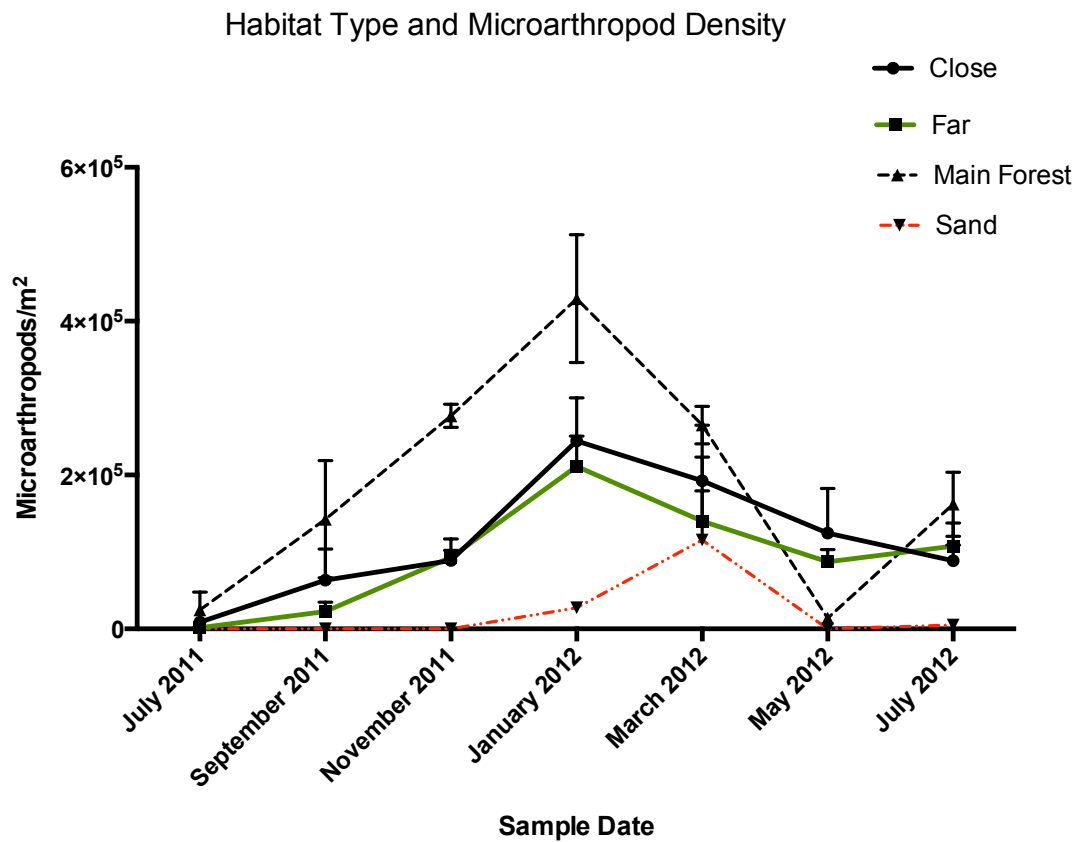


Figure 1.5: Effect of habitat type on microarthropod density. Results of a two-way ANOVA comparing mean microarthropod densities by island distance and sample date showed that there were significantly higher abundances of fauna in the mainland and significantly lower populations in the sand ($P < 0.0001$; $F = 14.68$). There was not a significant difference between close and far islands and the mean microarthropod density on regrowth islands ($P = 0.2880$, $F = 1.146$). There was significant difference in mean microarthropod density and sample date ($P < 0.0001$; $F = 8.032$).

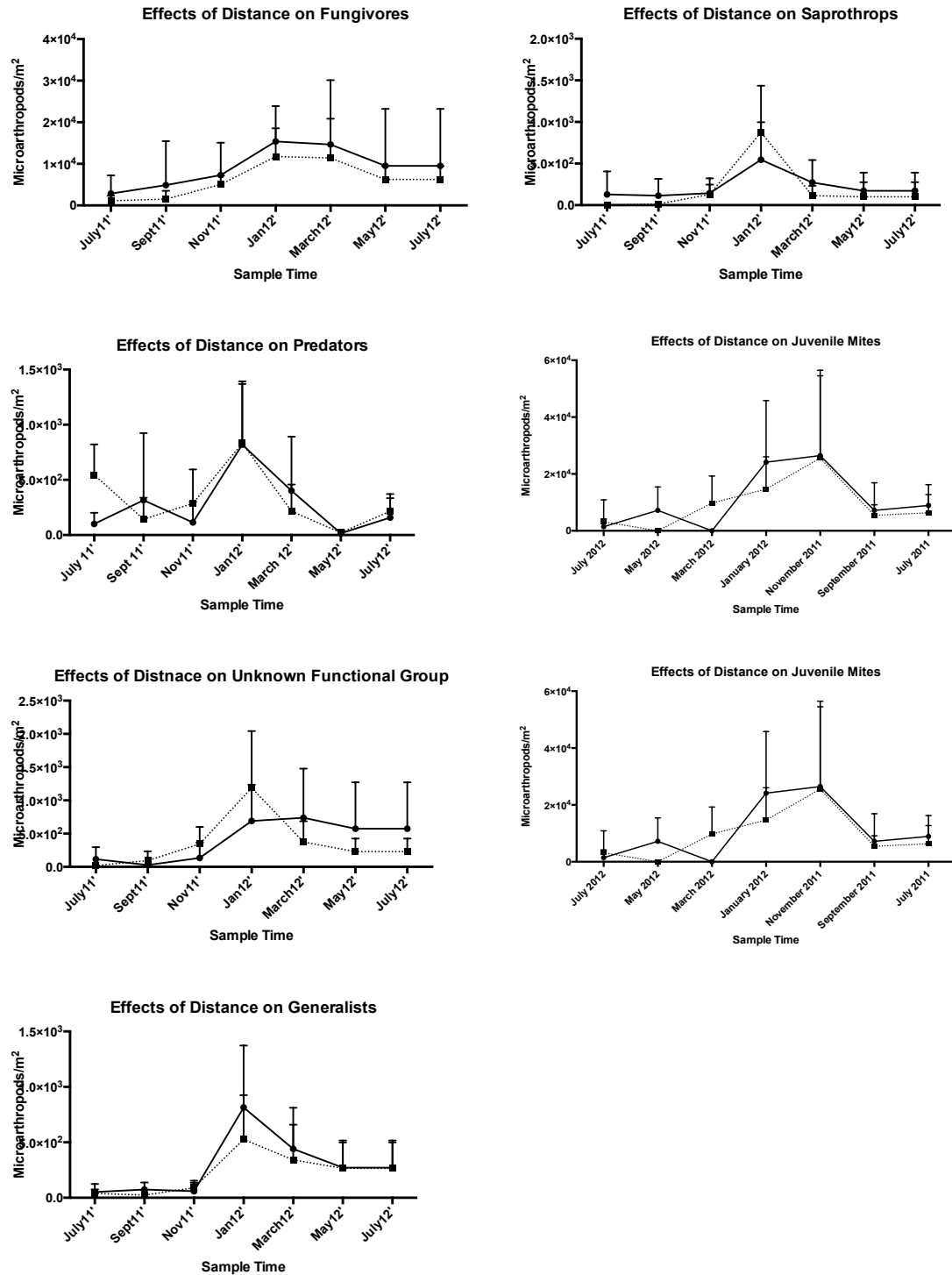


Figure 1.6: Effects of island distance on microarthropods associated with different functional groups. The dotted line represents islands that are furthest away from the main forest. The solid line represents islands that are closest to the main forest.

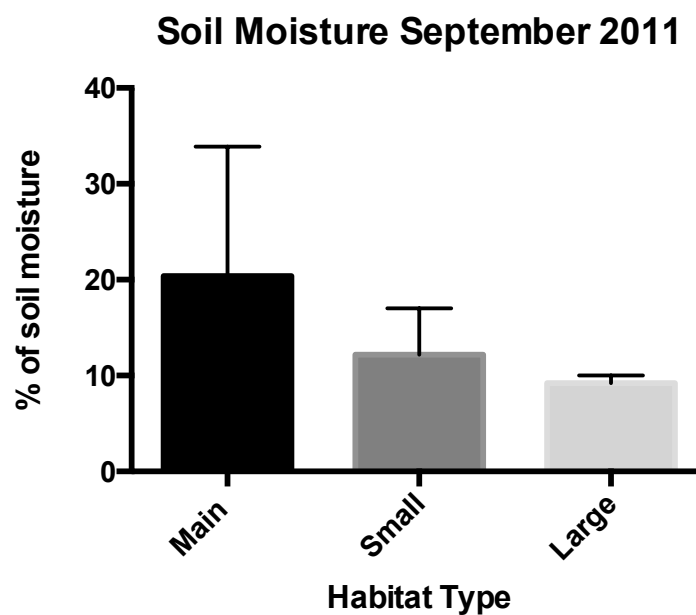
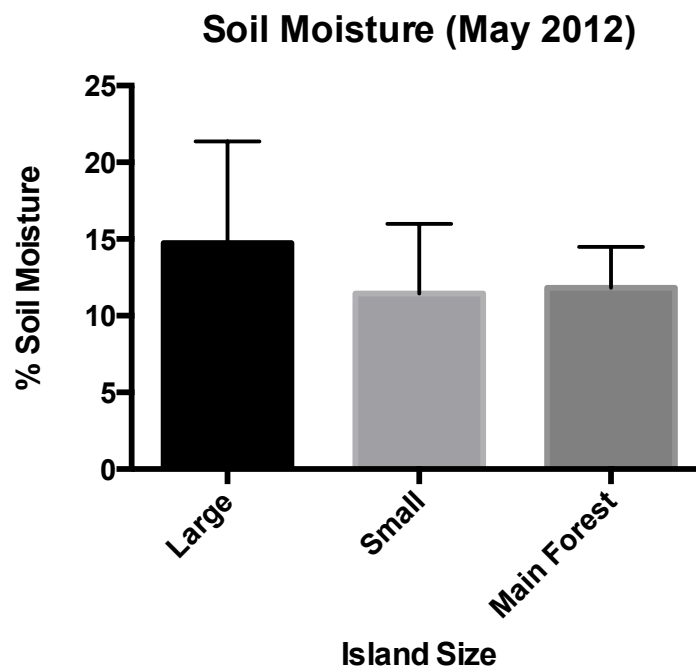


Figure 1.7: Comparison of average soil moisture content between sites. Results of a one-way ANOVA did not reveal a significant difference between soil moisture and habitat type (P 0.0951, F 3.001; P 0.5396, F 0.6506, for each sampling date respectively).

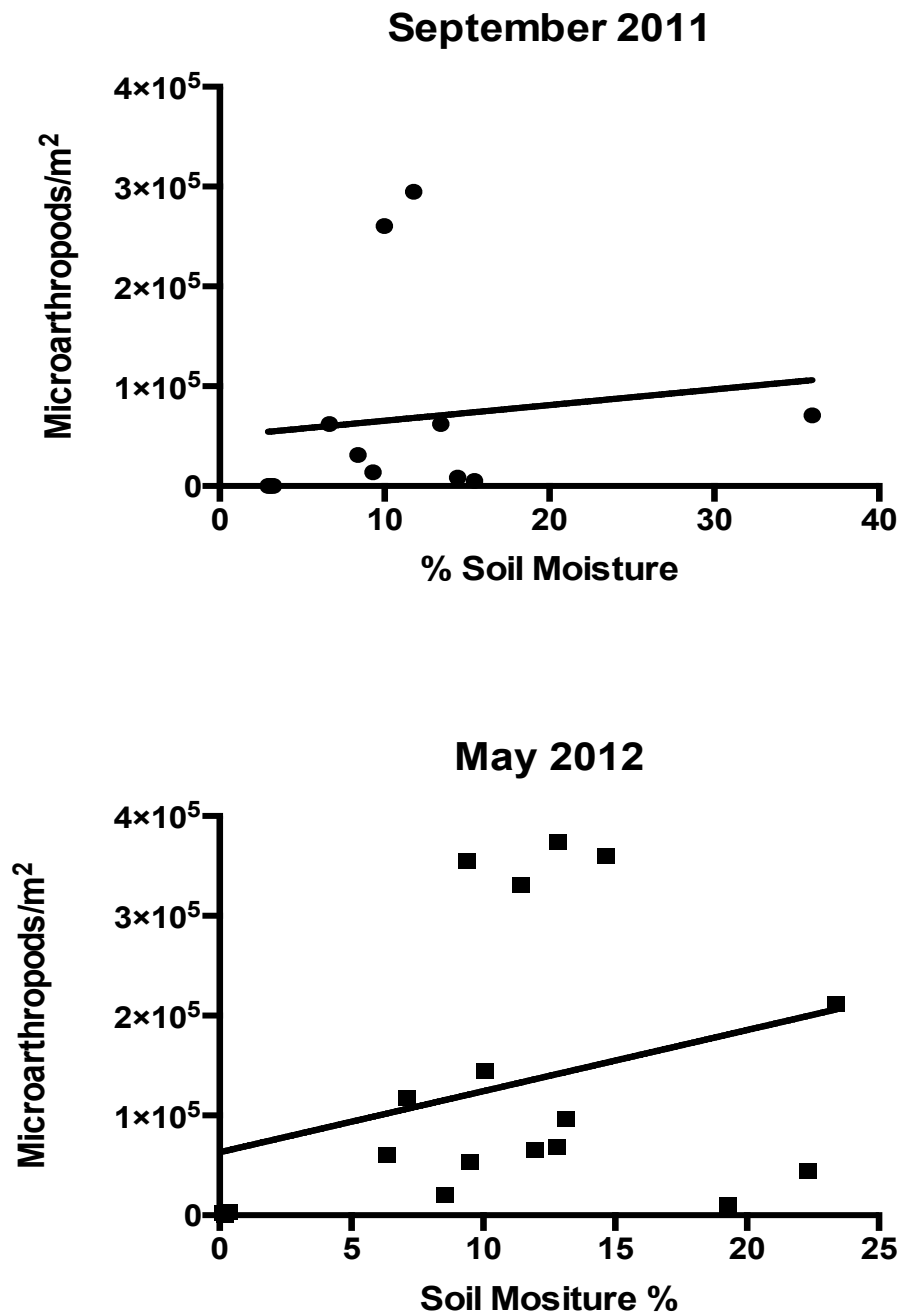


Figure 1.8: Linear regression of mean fauna density of microarthropods for all islands regressed against the % of soil moisture during the September 2011 and May 2012 sample periods (P value 0.6702, F value 0.1925, r^2 0.0188), May 2012 sample period (P value 0.2207, F value 1.624, r^2 0.0921).

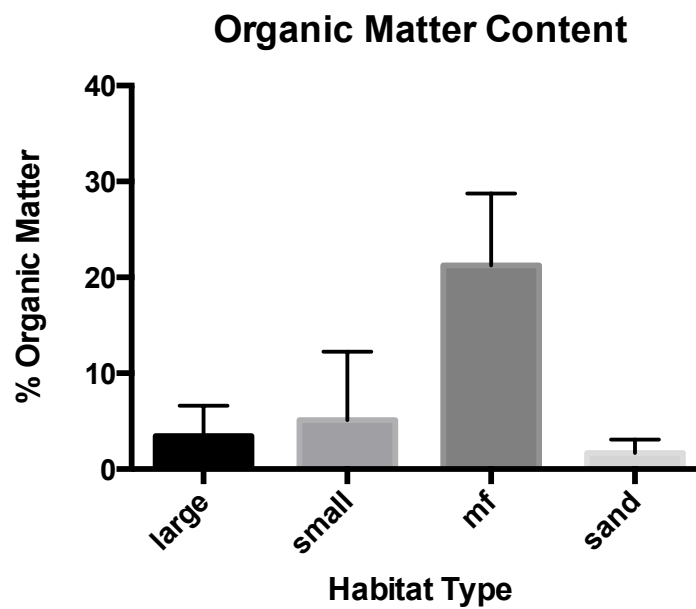


Figure 1.9: Comparison of average soil organic matter content between sites. One-way ANOVA revealed that the main forest had significantly more organic matter content when compare with the other habitat types ($P= 0.0017$, $F= 8.703$).

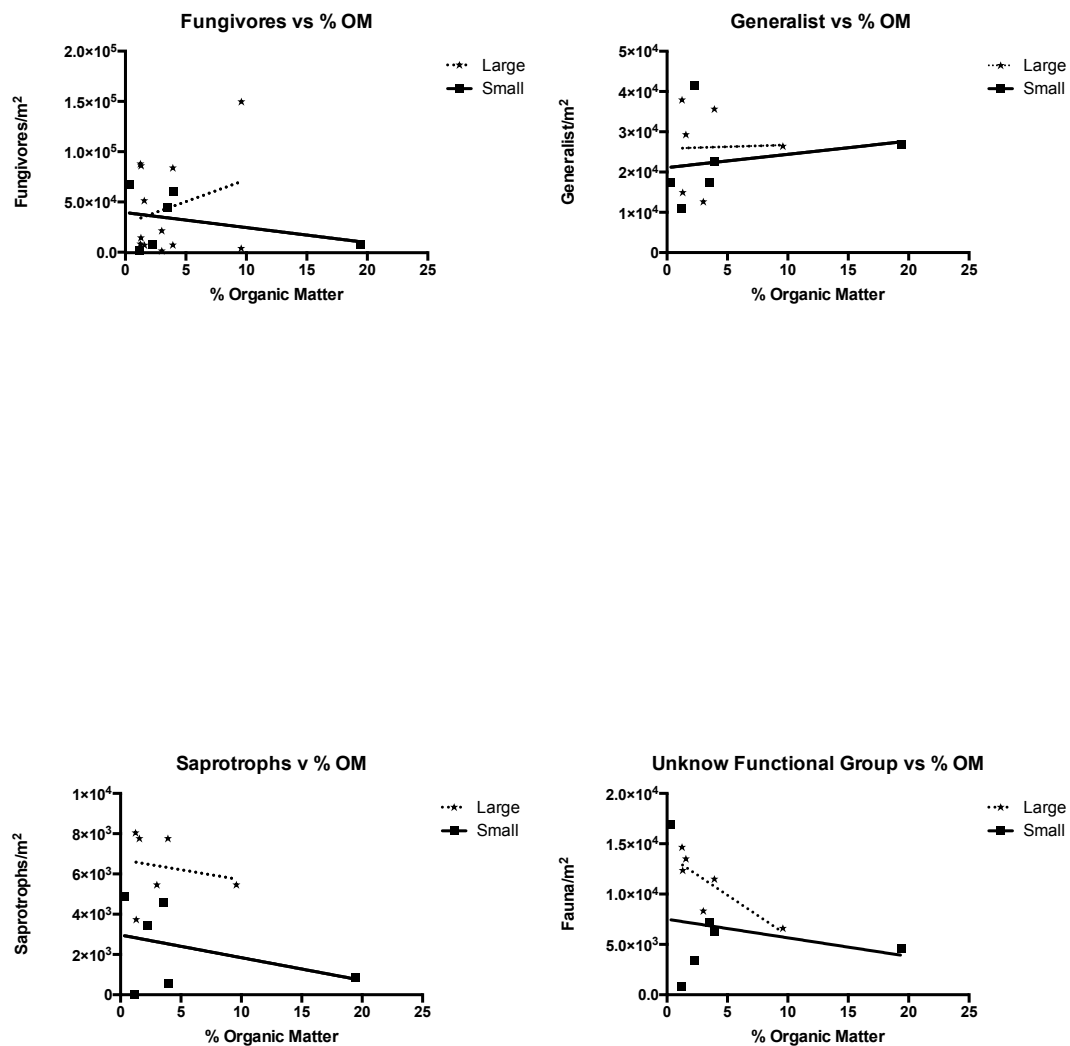


Figure 1.10: Linear regression of the mean density of fauna within each functional group regressed against the % organic matter. Note differences in fauna densities on Y axis, fauna were present at different levels of abundances there standardizing the Y axis would make it difficult to observe small populations.

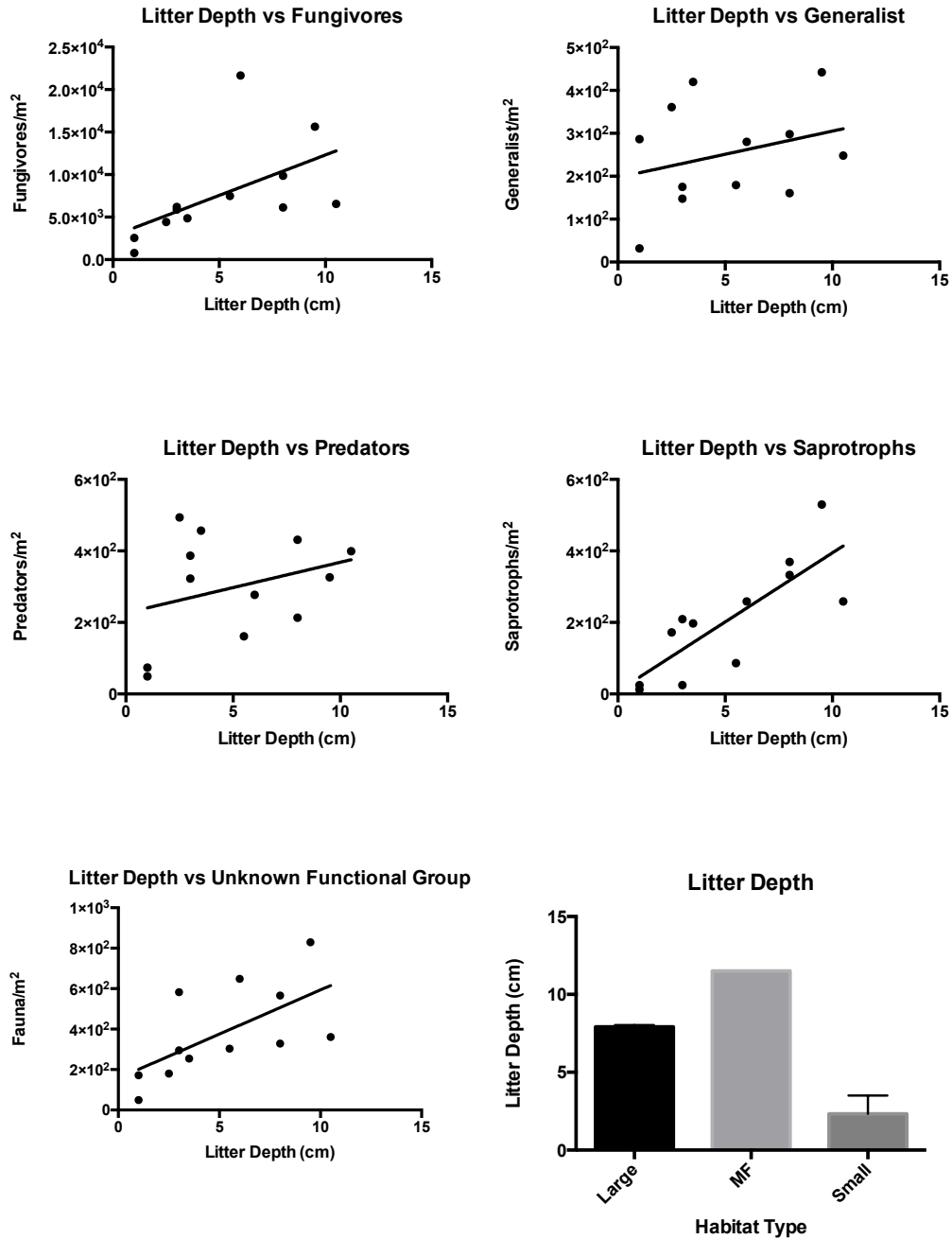


Figure 1.11: Linear regressions of litter depth and the mean number fauna in each group: Fungivores/m² ($P = 0.0692$, $F = 4.143$, $r^2 = 0.2929$). Generalist/m² ($P = 0.2539$, $F = 0.9452$, $r^2 = 0.08636$). Predators/m² ($P = 0.3189$, $F = 1.100$, $r^2 = 0.0911$). Saprotophs ($P = 0.0016$, $F = 18.43$, $r^2 = 0.6483$). Unknown: $P = 0.0293$, $F = 6.454$, $r^2 = 0.3922$). One-way ANOVA of Habitat type and litter depth ($P < 0.0004$, $F = 37.01$)

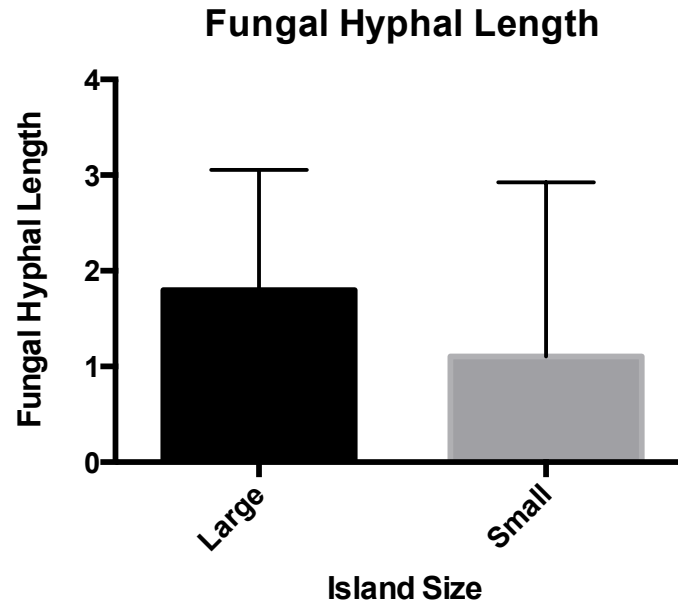


Figure 1.12: Mean fungal hyphal length (units) in soil in relation to island size, there was not a significant difference observed between island size and fungal hyphal length ($P = 0.4608$, $F = 2.102$).

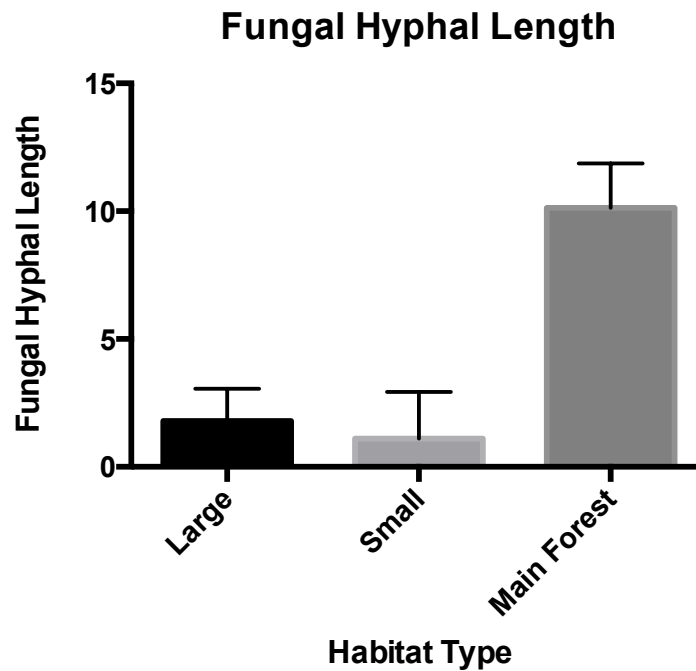


Figure 1.13: Comparison of mean fungal hyphal length in soil between sites. Results from a one-way ANOVA showed that there was a significantly higher lengths of fungal hyphae in the main forest compared to both large and small islands ($P < 0.001$, $F = 35.87$).

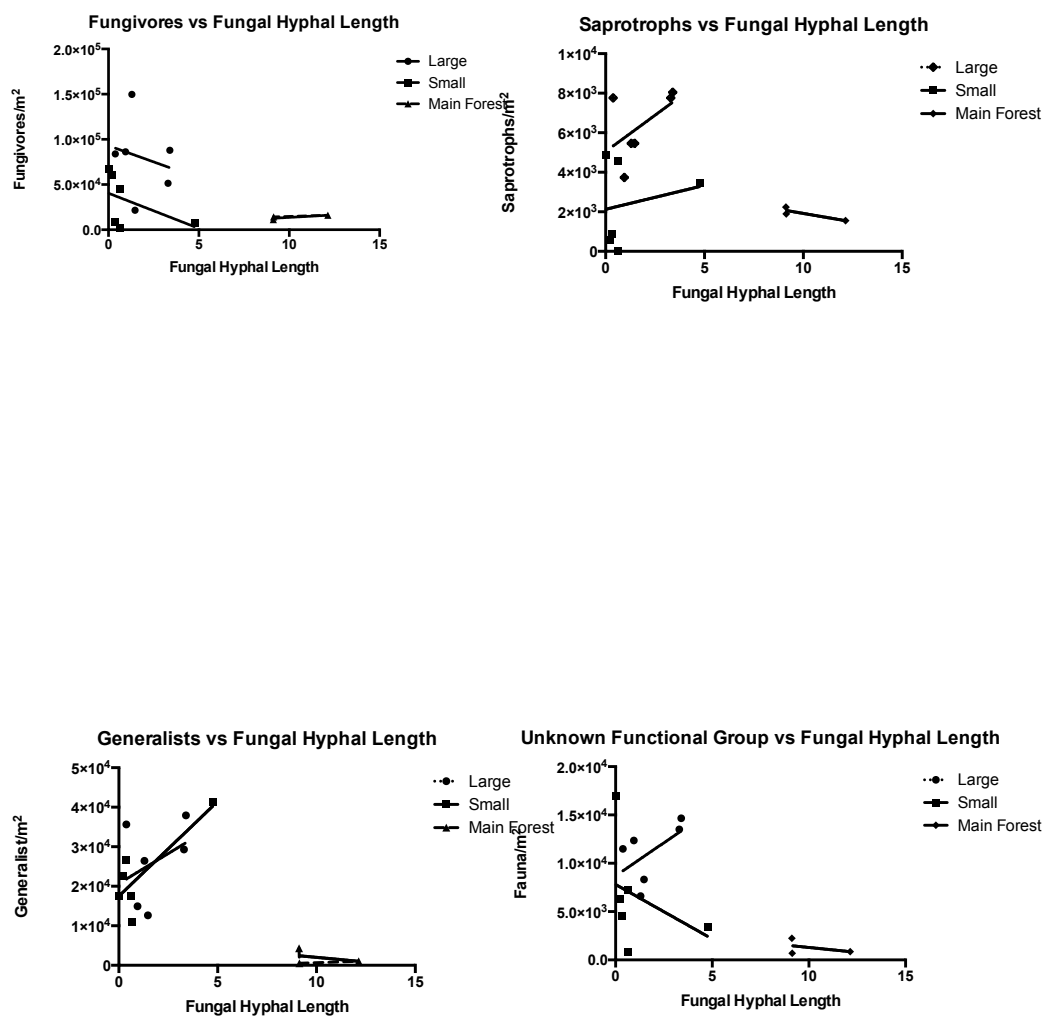


Figure 1.14: Linear regression of the fungal hyphal length (units) on large and small islands versus the mean number of fauna found in each of the functional groups analyzed.

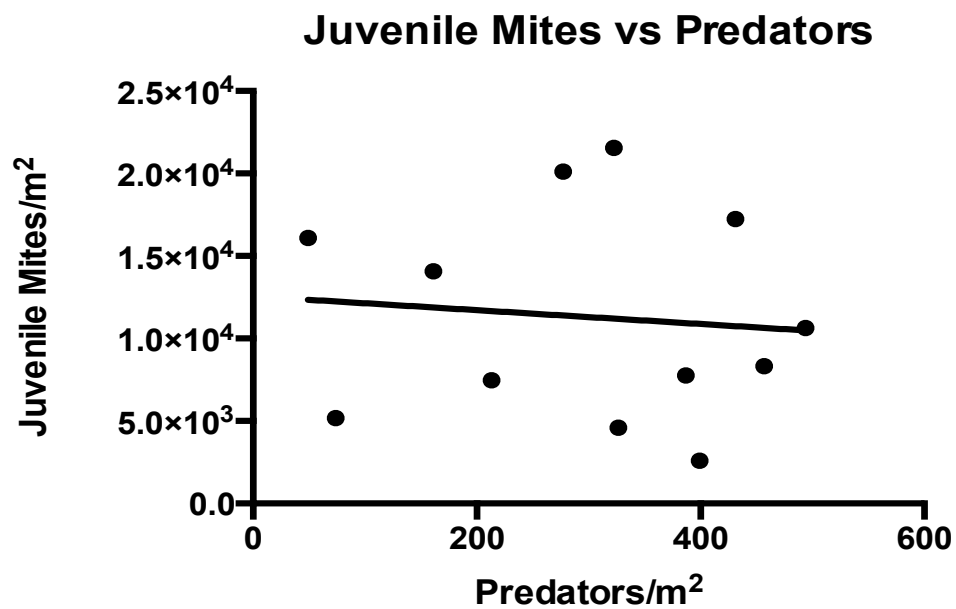
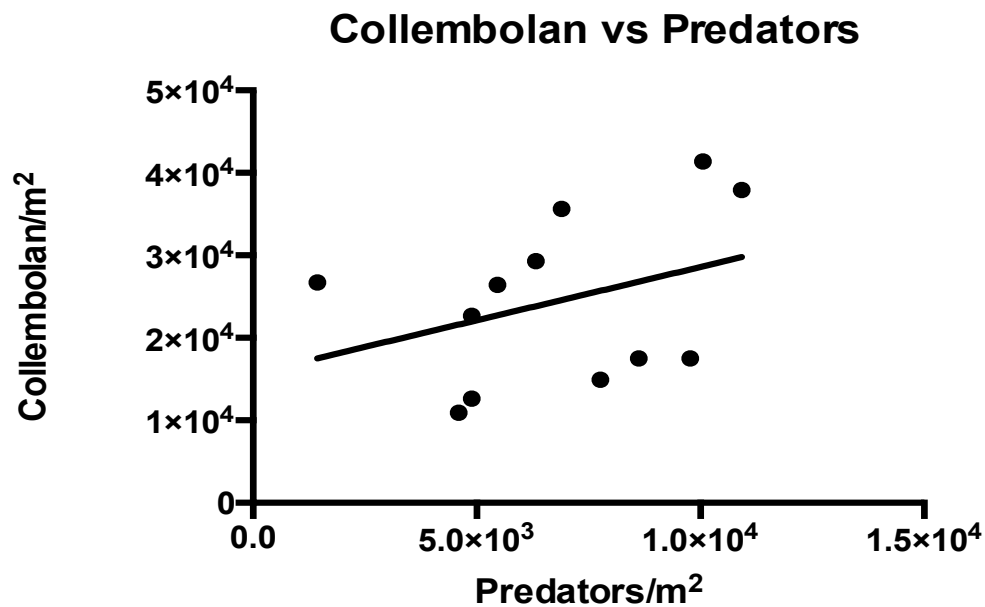


Figure 1.15: Linear regression of prey densities versus predator densities. Collembolan vs.. Predatory mites (P 0.2642 F 1.399 r^2 0.12227), Juvenile Mites vs. Predatory Mites (P 0.7638, F 0.0954, r^2 0.0094).

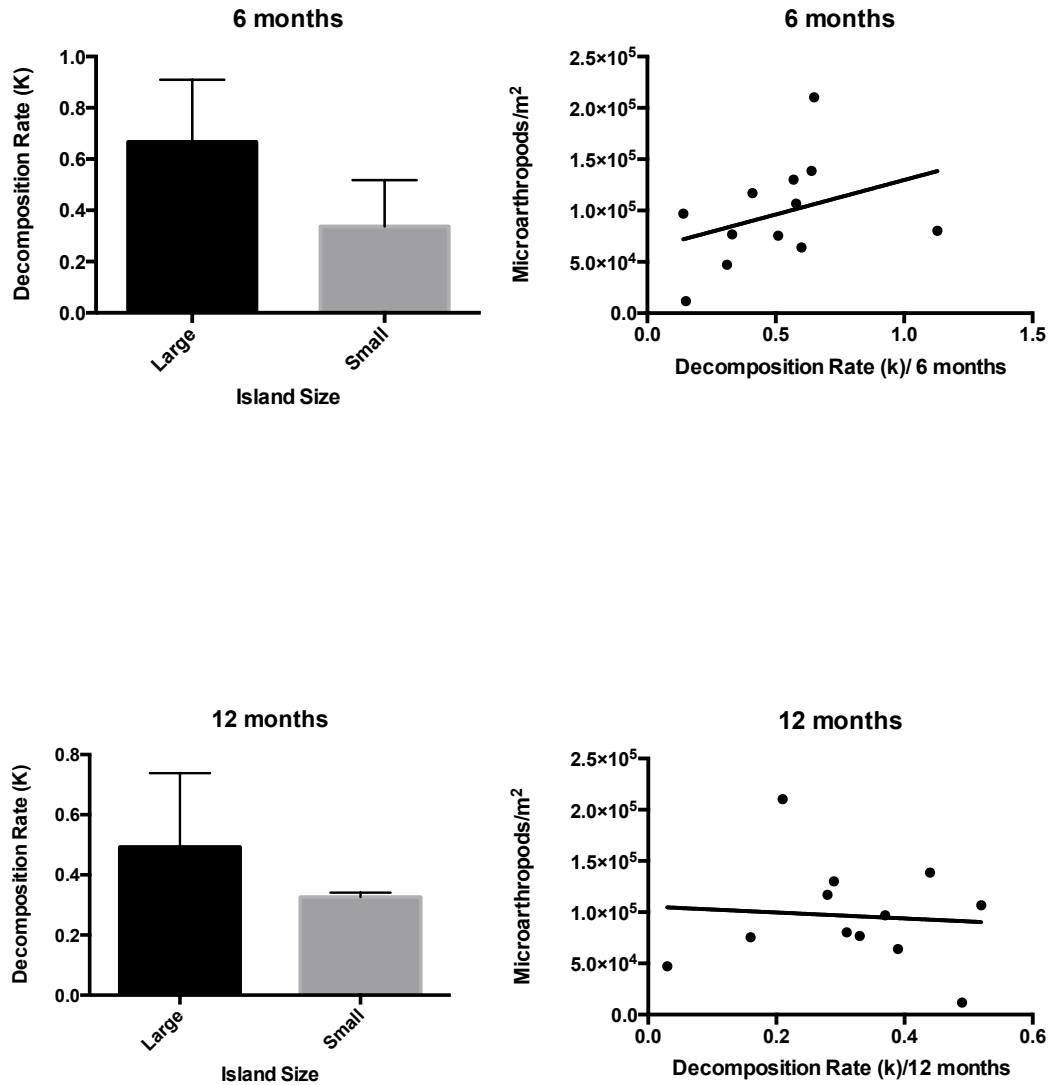


Figure 1.16: Litter decomposition rate for large and small islands at 6 months and 1 year (% mass loss of each litter bag). The results of an unpaired t-test showed rate of decomposition between large and small islands was greater in large islands at the six-month collection ($P=0.0236$, $F=1.806$). Decomposition rate at one-year mark between large and small islands ($P=0.0902$, $F=5.327$). Linear regression of mean number of fauna collected per island against the 6-month and 1 year ($P=0.2572$, $F=1.447$, $r^2=0.1262$; $P=0.8034$, $F=0.0654$, $r^2=0.0064$).

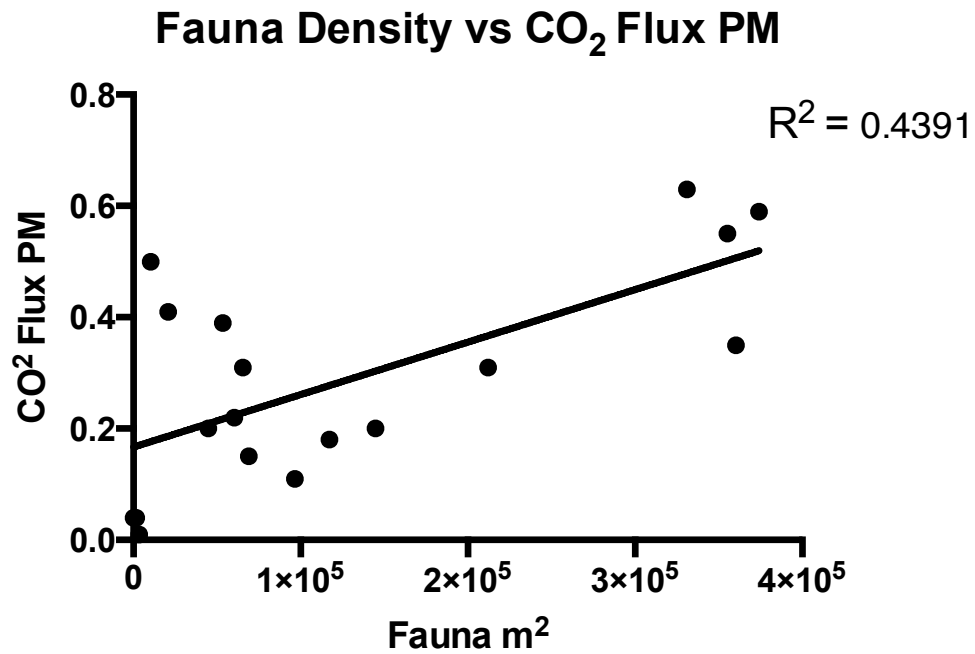
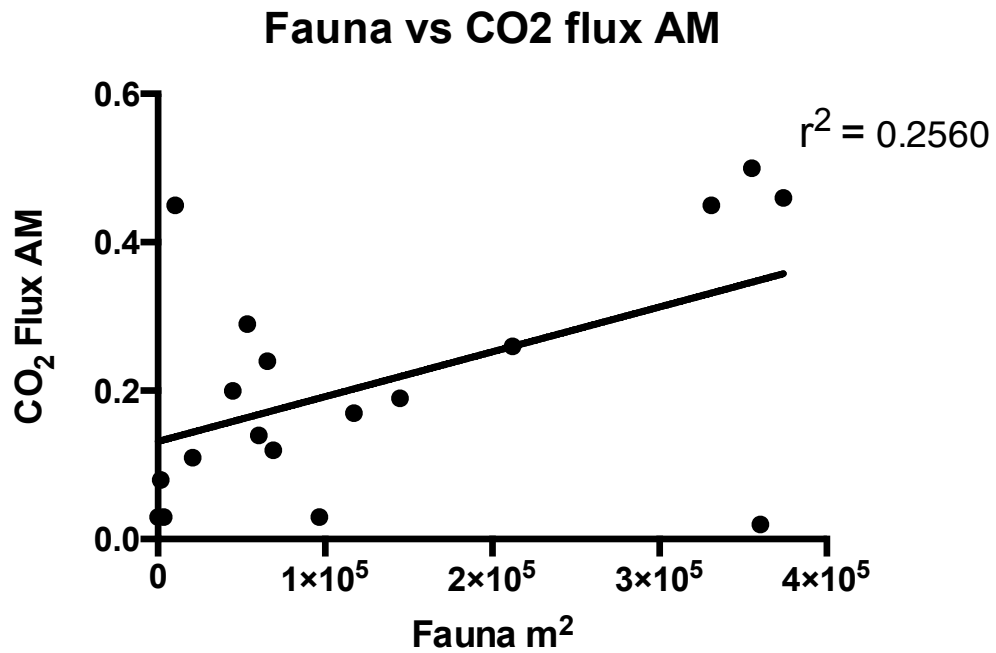


Figure 1.17: CO₂ flux vs. soil fauna density (May 2012) for AM and PM measurements. Linear regression shows a positive correlation between CO₂ respiration and soil fauna densities. AM: (P=0.03, F= 5.51, r^2 0.26) PM: (P=0.003, F= 12.52, r^2 0.44)

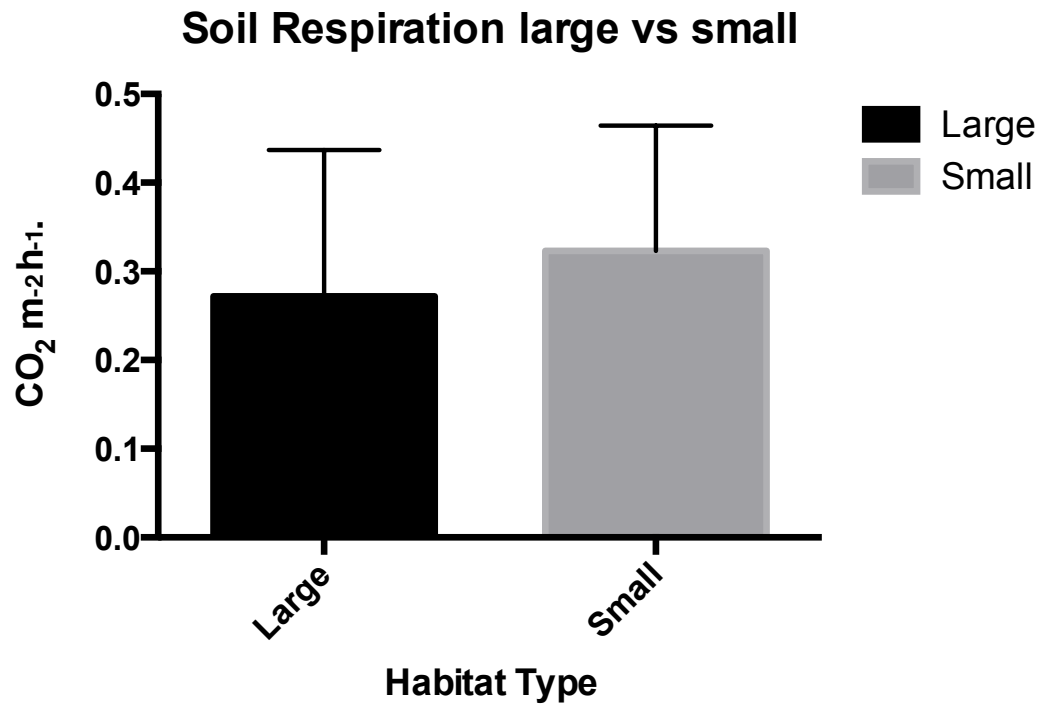


Figure 1.18: Results of an unpaired t-test did not reveal a significant difference between habitat type and soil respiration. (P=0.57; F=1.37)

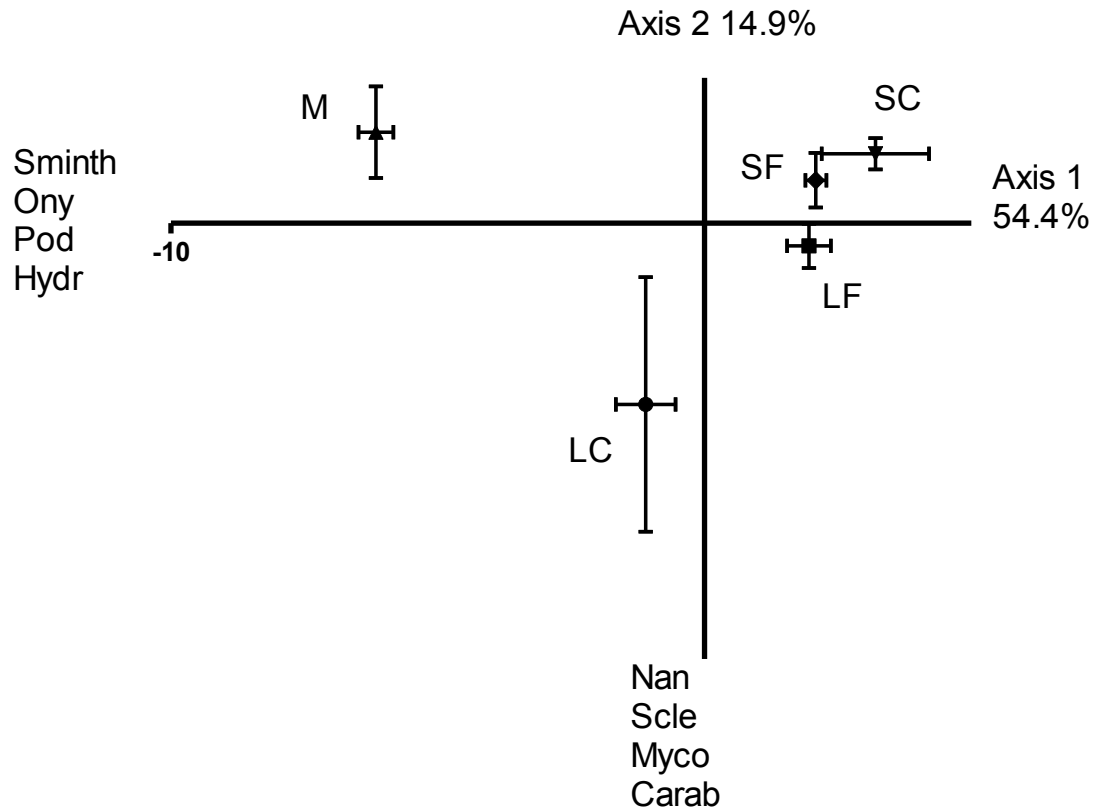


Fig. 1.19. PCA analysis of soil arthropod communities within islands and mainland (M= mainland, LC and LF = large islands close and far respectively, SC and SF = small islands close and far respectively). Faunal genera named on Axis 1 and 2 are those of highest eigenvector loading. The mainland separates significantly from other sites along Axis 1 ($F = 43.93$, $P < 0.0001$), whereas separation along Axis 2 is not statistically significant ($F = 3.06$, $P = 0.07$).

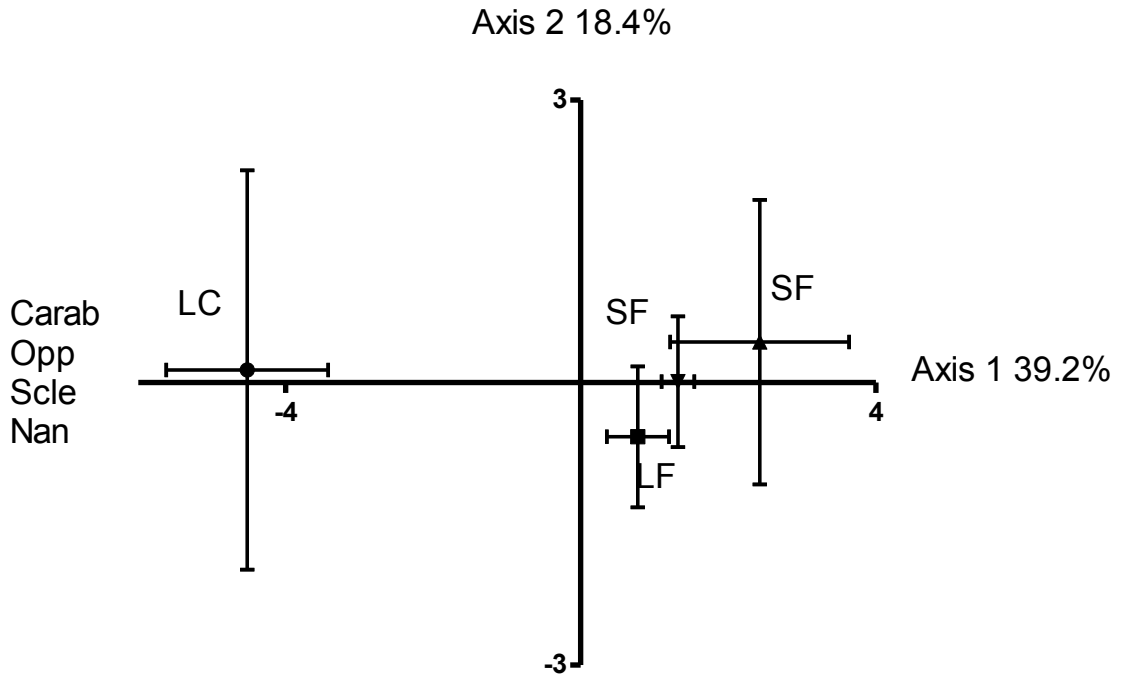


Fig. 1.20. PCA analysis of soil arthropod communities between islands (LC and LF = large islands close and far respectively, SC and SF = small islands close and far respectively. Faunal family named on Axis 1 and 2 are those of highest eigenvector loading. Large-close islands separate significantly from small or large distant islands along Axis 1 ($F = 13.17$, $P = 0.002$), whereas separation along Axis 2 is not statistically significant ($F = 0.09$, $P = 0.96$).

Table 1.1: Summary table of the results of a two-way ANOVA for all microarthropod functional groups comparing island size and sample date.

Two-Way ANOVA	% of total variation	P value	F Value
Fungivores			
Interaction	2.551	0.8288	0.4259
Sample Period	13.86	0.0256	2.817
Island Size	11.72	0.0463	5.17
Generalists			
Interaction	1.059	0.9339	0.2584
Sample Period	49.48	< 0.0001	12.07
Island Size	0.2739	0.5654	0.3342
Predators			
Interaction	8.411	0.1728	1.604
Sample Period	28.58	0.0003	5.451
Island Size	0.08318	0.7792	0.07931
Saprotrophs			
Interaction	1.134	0.9168	0.2899
Sample Period	43.83	< 0.0001*	11.2*
Island Size	8.096	0.0021	10.35
Unknown Guild			
Interaction	12.28	0.0633	2.226
Sample Period	18.78	0.009	3.404
Island Size	2.731	0.1209	2.475

Table 1.2: Effect of island habitat (including mainland and sand) on the mean number of microarthropod results table of two-way ANOVA for Figure 1.5.

Source of Variation	% of total variation	P value	F Value
Interaction	11.53	0.0850	1.56
Sample Period	27.95	< 0.0001	11.36
Habitat Type	18.06	< 0.0001	14.68

Table 1.3: Summary results table of two-way ANOVA comparing the variation in population density of microarthropods for near and close islands Figures 1.6.

Functional Group	Source of Variation	% of total variation	P value	F Value
Fungivores	Interaction	0.13	0.1999	0.01974
	Sample Period	20.78	0.0082	3.173
	Distance	2.699	0.1203	2.473
Generalist	Interaction	2.363	0.8024	0.5052
	Sample Period	42.17	< 0.0001	9.015
	Distance	0.9008	0.2861	1.155
Predators	Interaction	6.228	0.3035	1.226
	Sample Period	34.16	< 0.0001	6.725
	Distance	0.359	0.517	0.4241
Saprotrophs	Interaction	5.585	0.293	1.248
	Sample Period	41.97	< 0.0001	9.376
	Distance	0.2247	0.5849	0.3012
Unknown	Interaction	8.464	0.1642	1.586
	Sample Period	29.01	0.0001	5.435
	Distance	0.257	0.5926	0.2889

Table 1.4: Results from linear regressions in Figure 1.10, soil organic matter content and soil fauna.

Functional Group	Large Island	Small Island
Fungivores		
P value	0.39	0.48
F value	0.82	0.61
R Square	0.08	0.13
Generalist		
P value	0.96	0.67
F value	0.003	0.21
R Square	0.0008	0.05
Saprotrophs		
P value	0.73	0.47
F value	0.14	0.64
R Square	0.03	0.14
Unknown		
P value	0.04	0.65
F value	8.99	0.24
R Square	0.69	0.06

Table 1.5: Results from linear regression of functions group vs. fungal hyphal length.

Functional Group	Large	Small	Main Forest	Slopes Significantly Different
Fungivores				No
R ²	0.44	0.23	0.60	
P	0.69	0.33	0.43	
F	0.18	1.21	1.52	
Generalist				No
R ²	0.13	0.68	0.15	
P	0.48	0.04	0.74	
F	0.62	8.57	0.15	
Saprotrophs				No
R ²	0.28	0.04	0.76	
P	0.28	0.70	0.33	
F	1.6	0.18	0.31	
Unknown				No
R ²	0.31	0.14	0.17	
P	0.25	0.47	0.73	
F	1.78	0.63	0.21	

Figures and Tables: Chapter Two

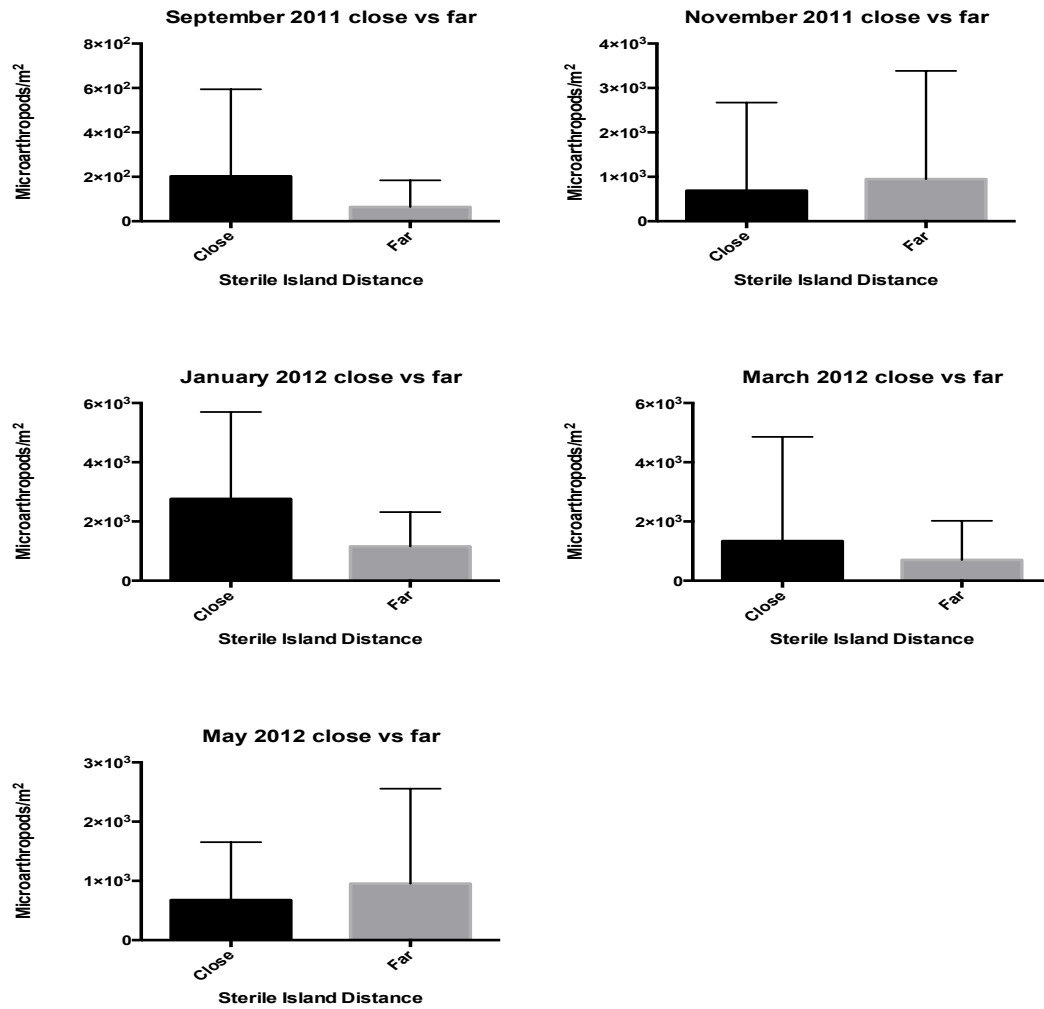


Figure 2.1: Comparison of the mean number of microarthropods extracted from close and far sterile islands for each sample date. Results of an unpaired t-test are found in Table 2.1.

Table 2.1: Results of an unpaired t-test comparing the mean number of fauna found on close and far islands for each sample period.

Date	P	F	Significantly Different
September	0.1065	10.67	No
November	0.6871	1.508	No
January	0.0616	6.391	Yes
March	0.4114	7.092	No
May	0.4704	2.684	No

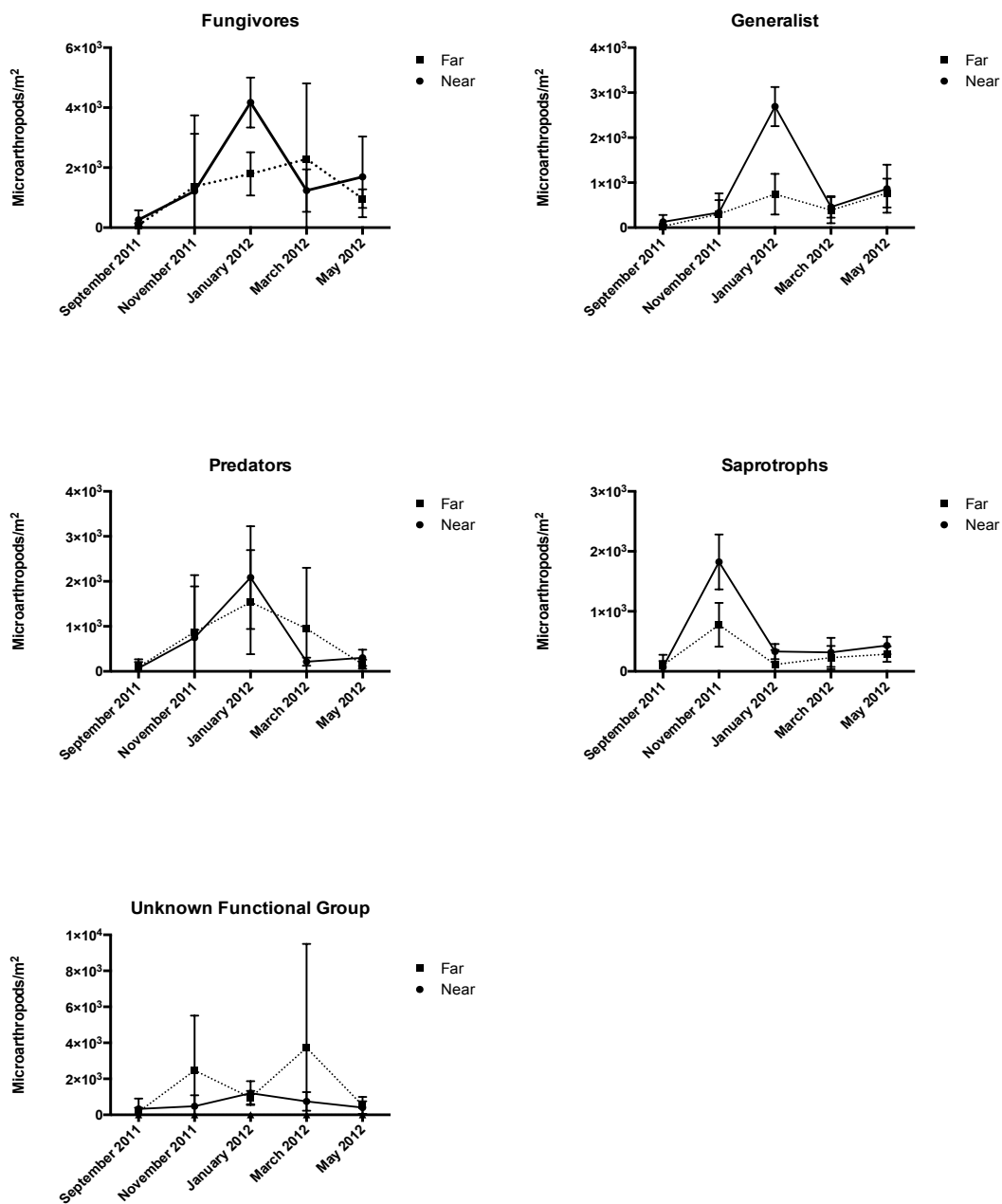


Figure 2.2: Two-way ANOVA of functional groups comparing sample date, island distance and microarthropod density.

Table 2.2: Results of a two-way ANOVA comparing microarthropod densities with sample date and island distance. Results are significant at <. 05% value.

Two-Way ANOVA of Functional Groups vs. Distance vs. Time				
Fungivores				
Source of Variation	% Of total variation	P value	P value summary	F value
Interaction	11.54	0.0545	ns	2.495
Sample date	29.14	0.0003	***	6.302
Distance	1.528	0.2557	ns	1.322
Generalists				
Interaction	22.51	< 0.0001	****	17.20
Sample Time	53.02	< 0.0001	****	40.50
Distance	8.115	< 0.0001	****	24.80
Predators				
Interaction	4.149	0.4934	ns	0.8618
Sample Time	35.63	< 0.0001	****	7.400
Distance	0.03881	0.8582	ns	0.03225
Saprotrophs				
Interaction	12.54	< 0.0001	****	9.441
Sample Time	63.64	< 0.0001	****	47.92
Distance	7.22	< 0.0001	****	21.75
Unknown				
Interaction	9.455	0.6126	ns	0.7914
Sample Time	2.599	0.7827	ns	0.4350
Distance	6.284	0.1326	ns	F (2, 50) = 2.104

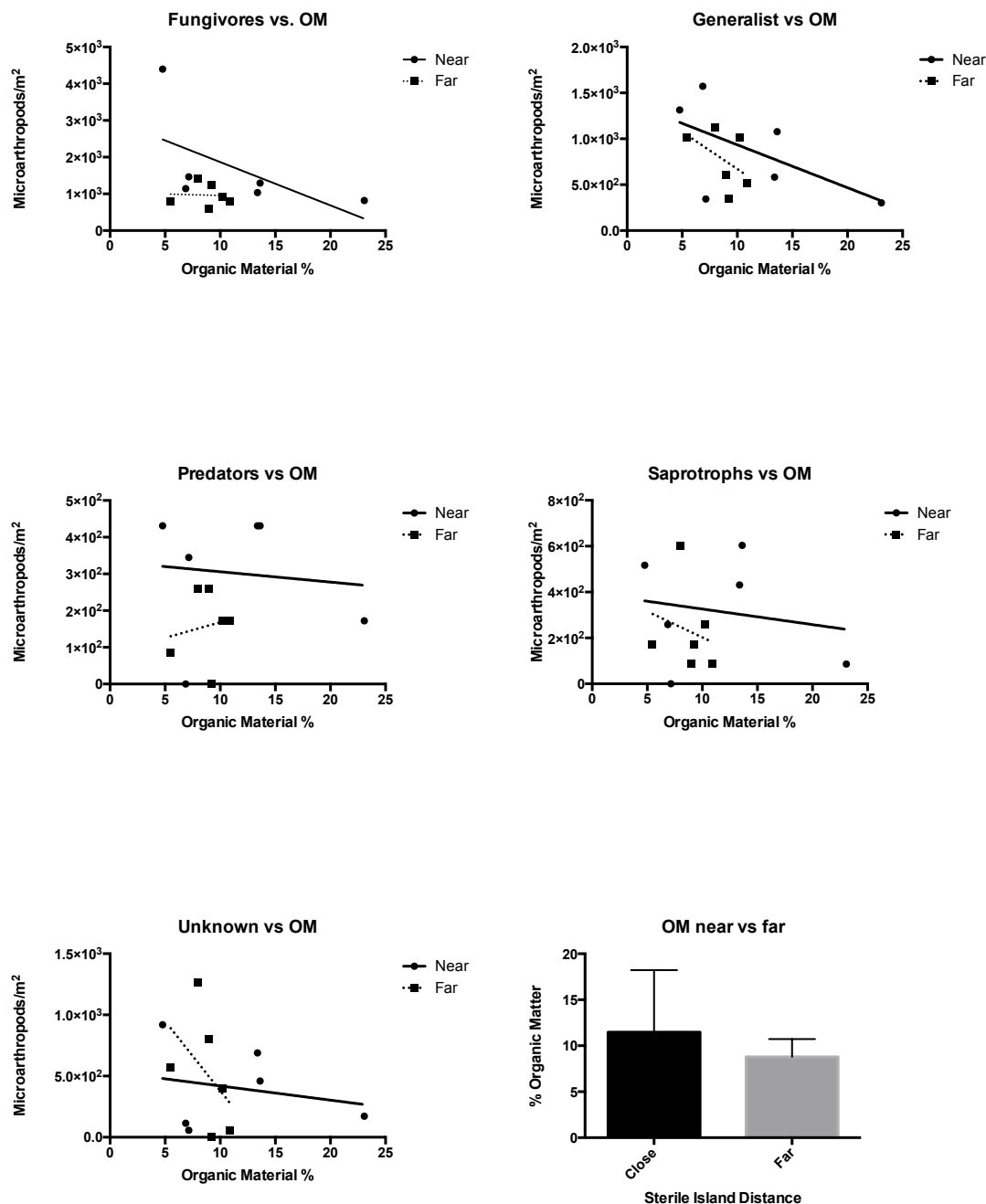


Figure 2.3: Linear regression of organic matter % and functional guild population densities from May 2011 on both near and far islands. Results of an unpaired t-test showed that there was not a significant difference between the organic matter % and island distance ($P = 0.3707$, $F = 12.29$).

Table 2.3: Results from linear regression comparing the % of organic matter in near and far sterile island patches with the mean number of microarthropods collected during May 2011.

Linear Regression Results	Near	Far	Slope Significantly Different
Fungivores			No
P value	0.22	0.92	0.62
F value	2.16	0.01	0.26
R square	0.35	0.003	
Generalists			No
P value	0.22	0.33	0.7356
F value	2.16	1.24	0.12
R square	0.35	0.24	
Predators			No
P value	0.84	0.76	0.78
F value	0.05	0.11	0.085
R square	0.01	0.03	
Saprotrophs			No
P value	0.72	0.67	0.79
F value	0.1489	0.21	0.076
R square	0.03589	0.05	
Unknown			No
P value	0.67	0.36	0.35
F value	0.21	1.07	0.97
R square	0.05	0.21	

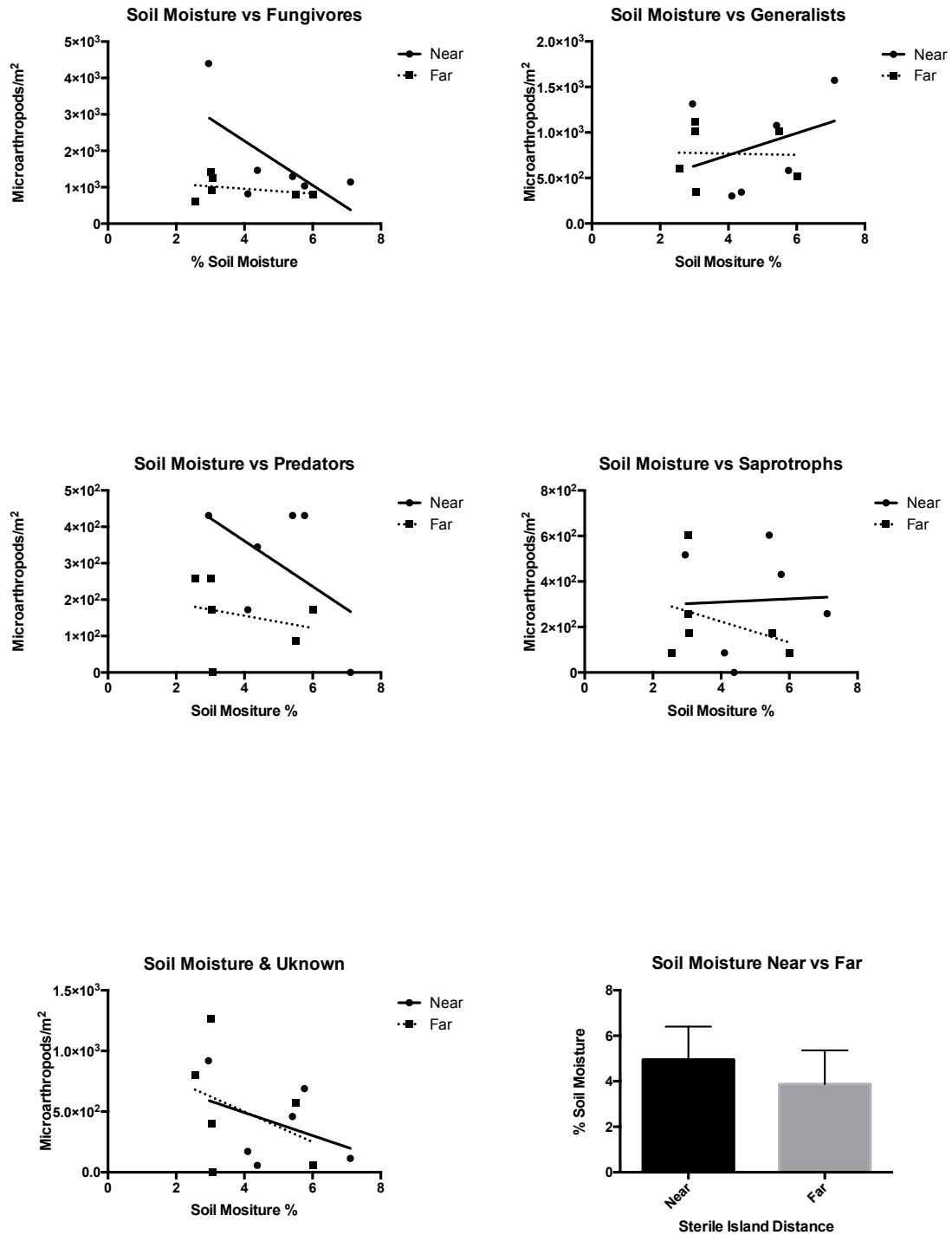


Figure 2.4: Linear regression of soil moisture and soil fauna collected during May 2011. Results of an unpaired t-test did not show that there was not a significant difference between soil moisture and island distance ($P=0.2308$, $F=1.044$).

Table 2.4: Summary results of linear regression in Figure 2.4 analyzing the relationship between the mean number of soil fauna collected during May 2011 and soil moisture percentage.

Linear Regression of Soil Moisture % and soil fauna	Near	Far	Slopes Significantly Different
Fungivores			No
P value	0.1543	0.5322	0.1684
F value	3.076	0.4664	2.293
R square	0.4347	0.1044	
Generalists			No
P value	0.5242	0.9489	0.546
F value	0.4859	0.0046	0.3974
R square	0.1083	0.0012	
Predators			No
P value	0.3033	0.6345	0.4832
F value	1.393	0.264	0.5406
R square	0.2583	0.0619	
Saprotrophs			No
P value	0.9366	0.4958	0.6215
F value	0.0072	0.5602	0.2637
R square	0.0018	0.1229	
Unknown			No
P value	0.4371	0.4436	0.8732
F value	0.7436	0.721	0.0272
R square	0.1568	0.1527	

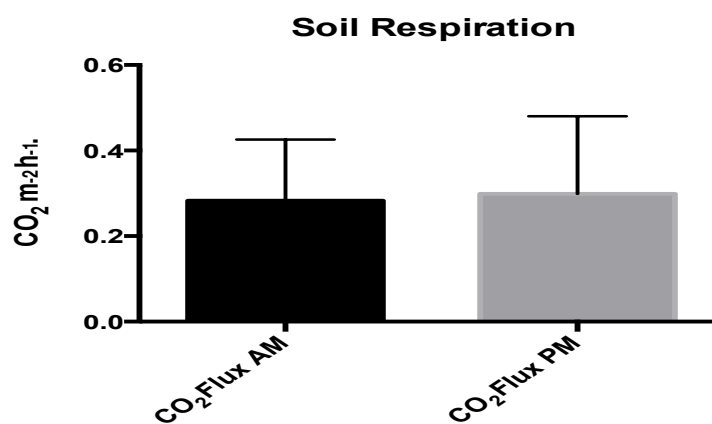
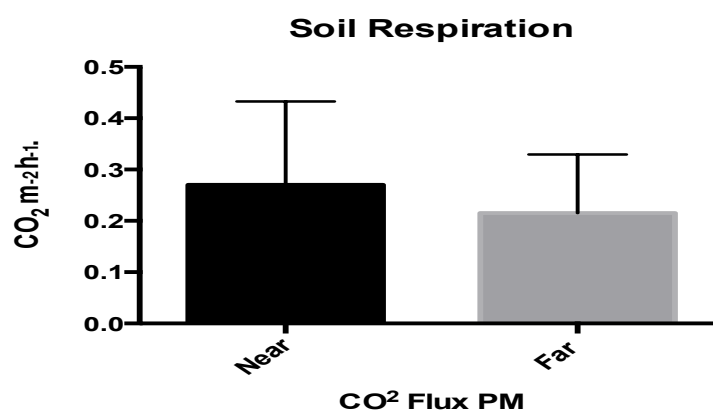
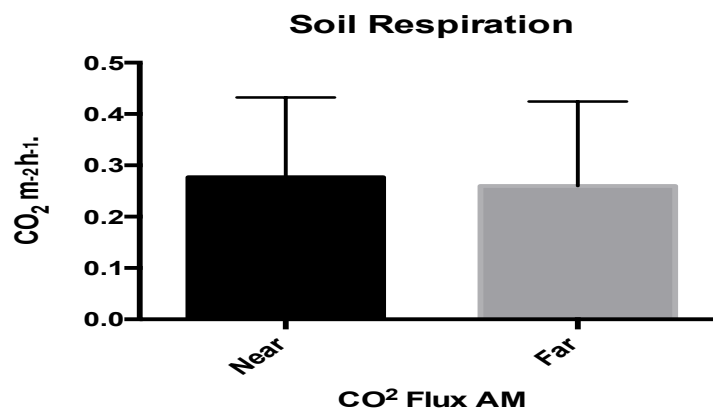


Figure 2.5: Comparison of CO₂ efflux in near and far patches during AM and PM measurements: CO₂ AM sample round (P=0.5135, F=2.017); CO₂ PM near vs. far (P=0.8602, F=1.611); CO₂ efflux AM vs. PM (P=0.8605, F=1.611).

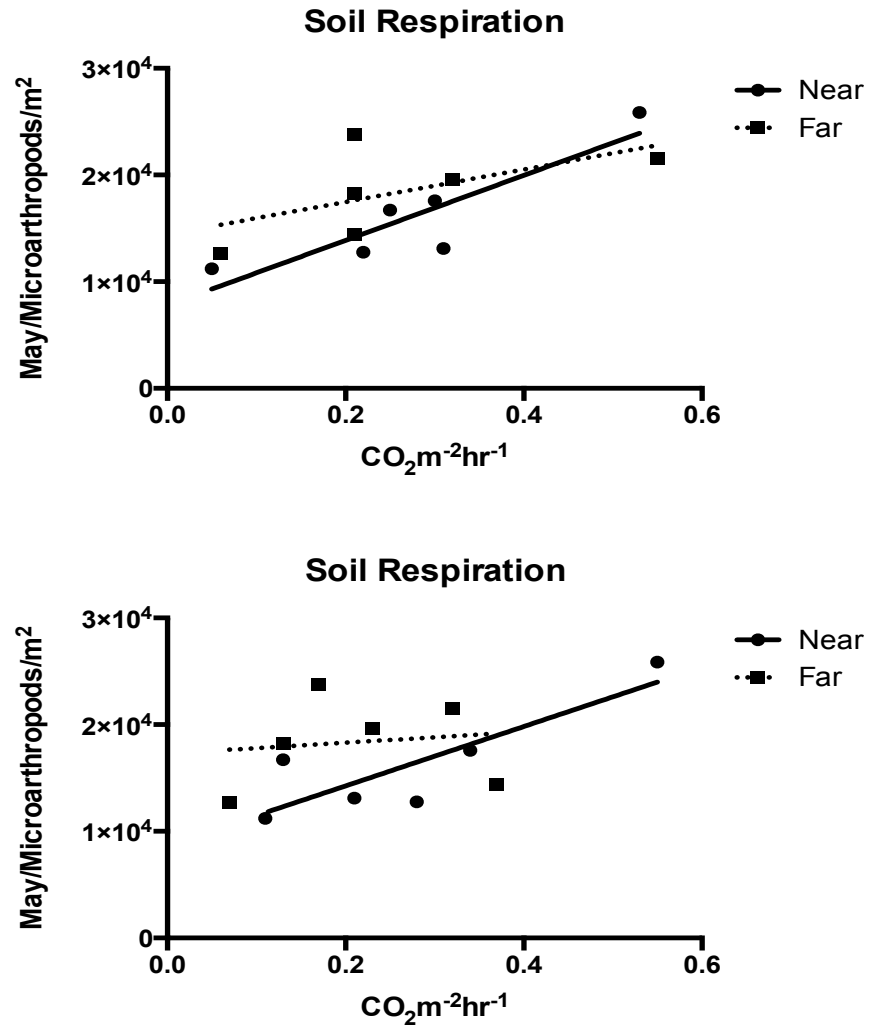


Figure 2.6: CO₂ respiration regressed against the mean number of soil fauna collected during May 2012 on near and far islands.

Table 2.5: Linear regression results comparing the mean number of microarthropods on near and far island to CO₂ respiration measurements.

Linear Regression of soil respiration	Near	Far	Slopes Significantly Different
AM			No
P	0.0175	0.2138	0.2754
F	15.22	2.181	1.371
R	0.7919	0.3528	
PM			No
P	0.0323	0.7947	0.2648
F	10.37	0.07739	1.4381
R	0.7216	0.01898	

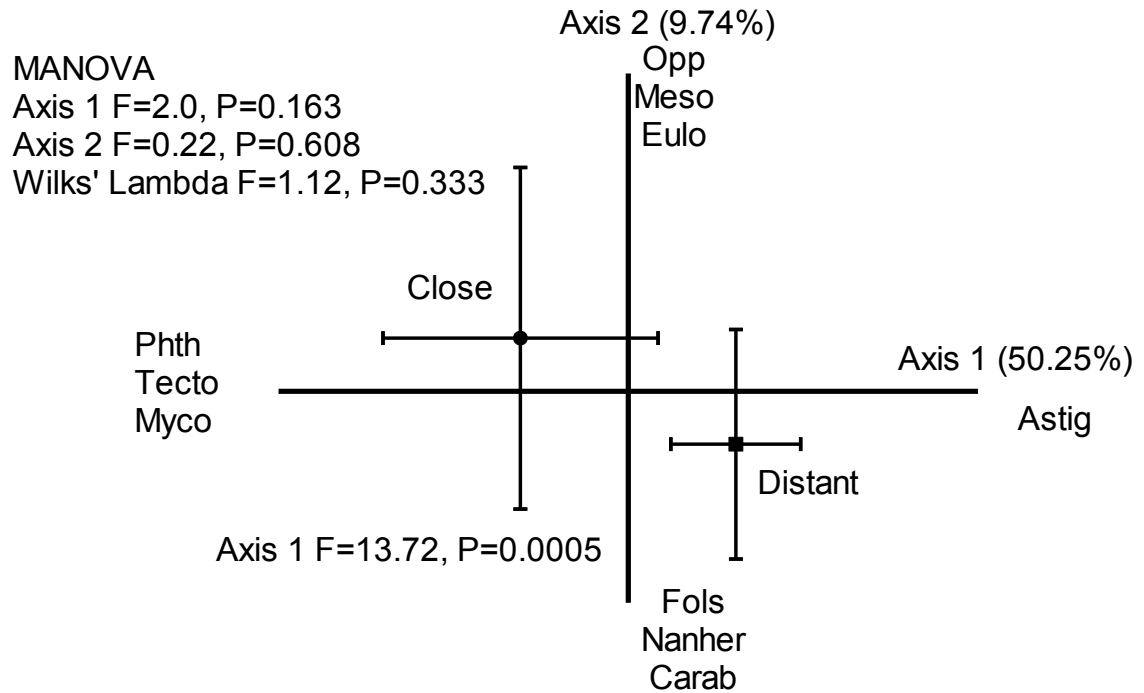


Figure 2.7: Looking at the effect of time on the community, there was significant difference in community composition. A MANOVA showed this separation, primarily along Axis 1 of the PCA, and separate ANOVA of coordinate scores for Axis 1 with Tukey *post hoc* means separation showed the separation on Axis 1 as depicted by the ovals.

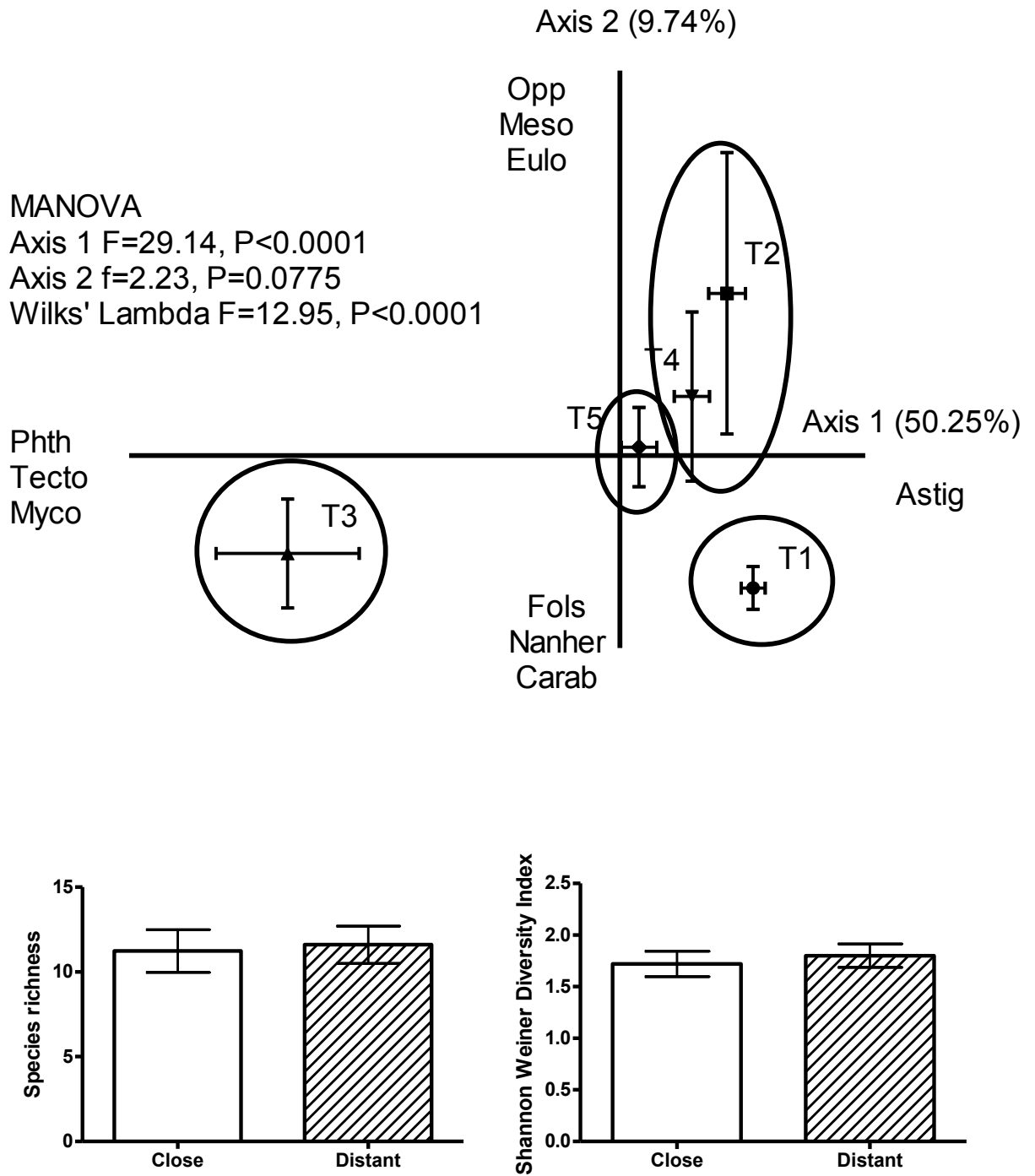


Figure 2.8: Community development over time showed some differences between close and distant islands in terms of species richness (total number of taxonomic groups) and diversity (Shannon Wiener Diversity Index). There is no significant difference in richness or diversity with distance from the mainland

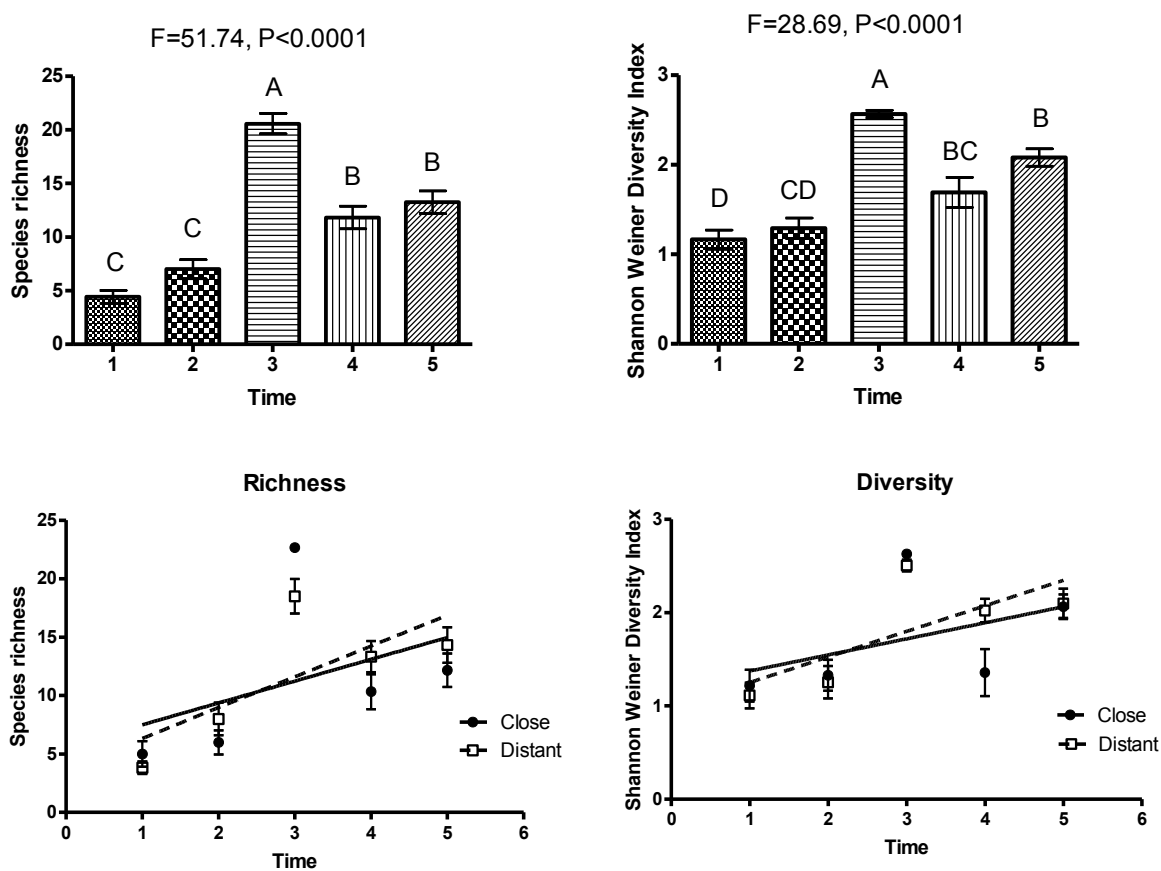


Figure 2.9: Richness and diversity increase with time and regression analysis suggests that species accumulation and diversity increases more rapidly in distant islands than close islands.

Appendix 1: Parker Preserve Experiment

Preliminary data of ongoing experimental plots in the Franklin Parker Preserve. Forest plots 20x20m had treatments of thinned and thinned and plowed. Soil microarthropods were sampled seasonally from the first 5 cm of the soil profile and extracted using a high gradient extractor. Soil fauna were classified as mite or collembolan for the preliminary data. The preliminary data suggests that mites dominate the plots more so than collembolan. Treatment appears to have little effect on the density of mite or collembolan when comparing the treatments, further investigation may yield differences between families.

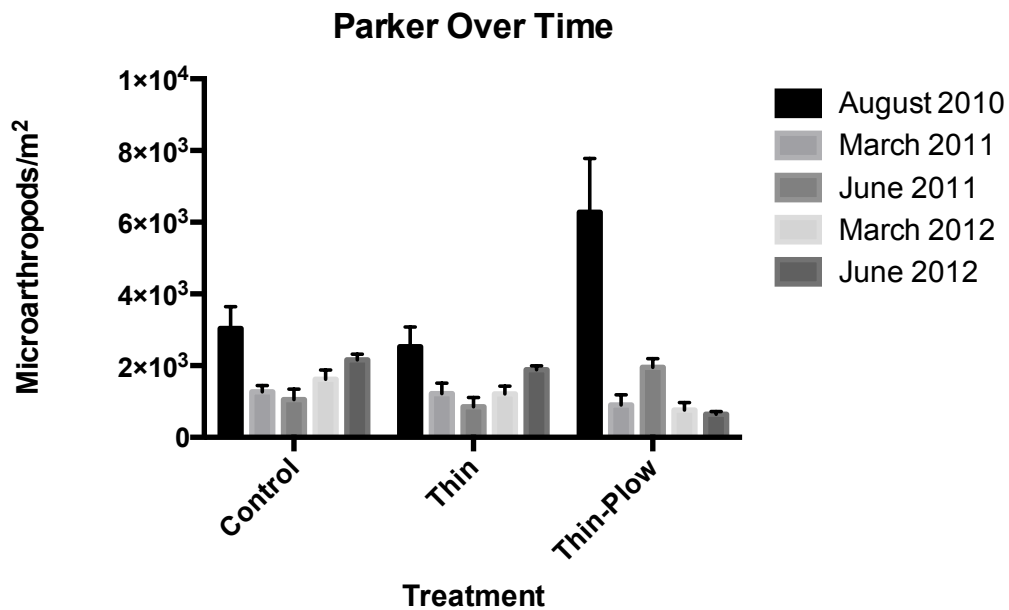


Figure 3.0: Results of a two-way ANOVA of treatment vs. date did not reveal any significant differences in microarthropod density between treatments ($P=0.18$; $F=1.71$). There was a significant difference between sample dates ($P<0.0001$; $F=18.36$)

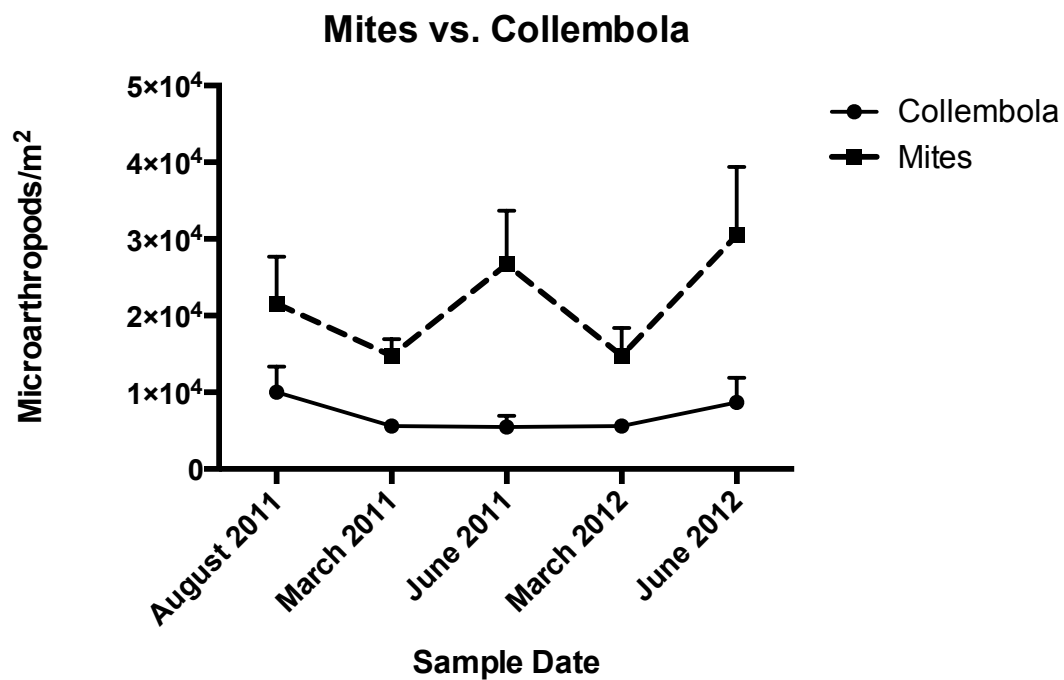


Figure 3.1: Results of a two-way ANOVA comparing fauna type and sample date, revealed that there were significantly higher abundances of mites than collembolan ($P < 0.0001$, $F = 25.42$) collected during the survey.

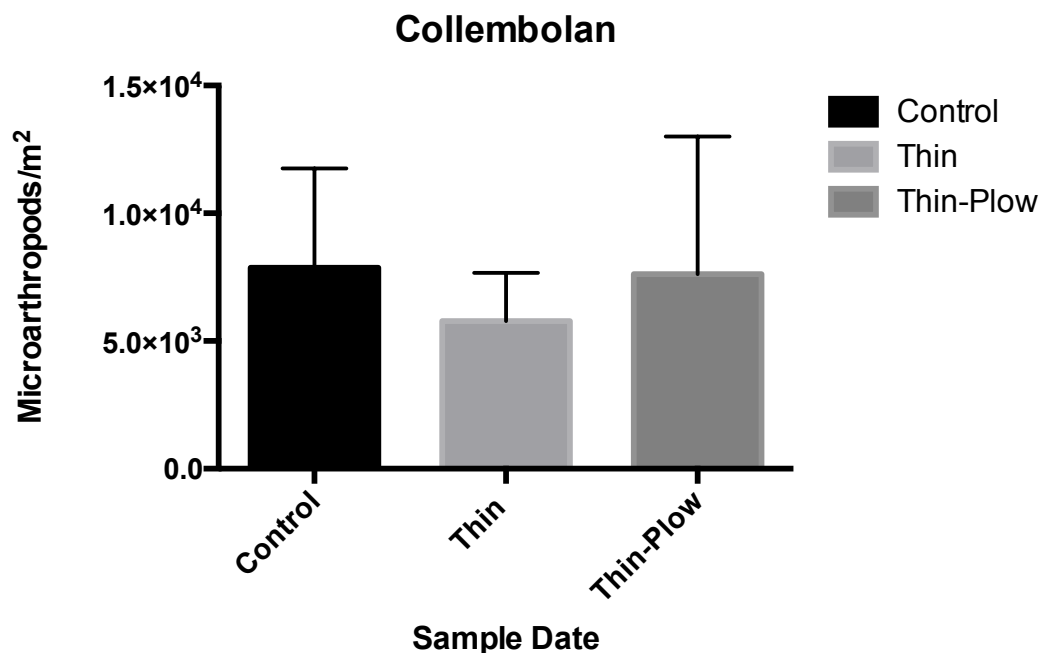


Figure 3.2: Results of a one-way ANOVA did not show a difference in the average number of collembolan collected from each treatment ($P=0.60$; $F=0.38$).

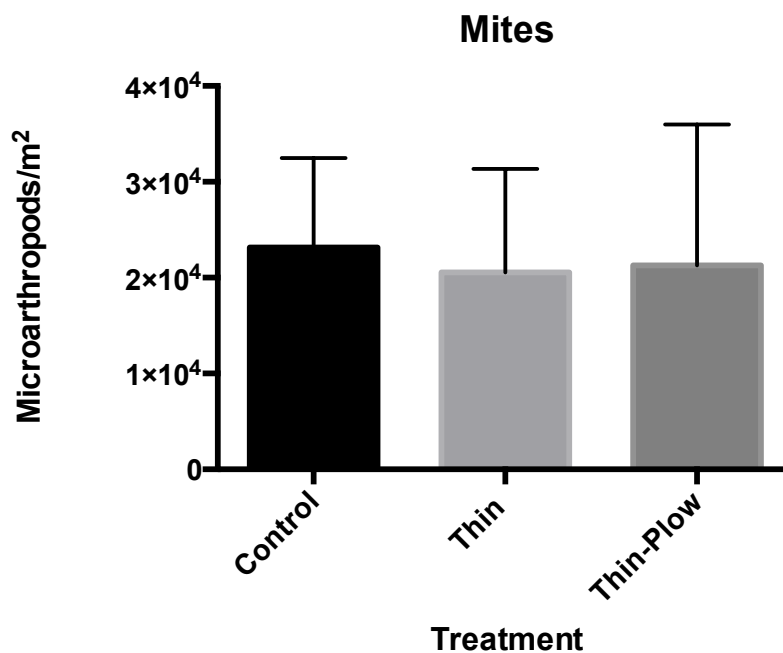


Figure 3.3: Results of a one-way ANOVA did no reveal a significant difference in the mean number of mites collected based on treatment ($P=0.82$; $F=0.07$).

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