Chapter 1 – General Introduction

Invasive plants (see glossary for terms) are a major conservation concern and are one of the main factors contributing to environmental degradation. Non-native plants can have serious environmental, economic and social impacts in Australia (AWS 2006). Plant invasions can dramatically alter native habitats by changing the species diversity, trophic structure and function of communities and ecosystems (Walker & Smith 1997; Prieur-Richard 2000). There are several key ways in which plant invaders can alter native species diversity and composition: a) by competing with and displacing native species (e.g. Minchinton *et al.* 2006) b) by facilitating the movement of other invading organisms (Holway 2005) c) by changing fire regimes (e.g Woods 1997) and d) by altering pollination syndromes (Woods 1997; Brown & Mitchell 2001; Levine *et al.* 2003; Moragues & Traveset 2005). These changes can affect organisms at higher trophic levels through the loss of food and shelter (Levine *et al.* 2003). Ecosystem function may be altered through changes in nutrient cycling (Meyerson *et al.* 2000; Walker & Smith 1997) or the hydrological regime (Walker & Smith 1997), which can further influence the rate of community recovery following disturbance (Walker & Smith 1997; Woods 1997).

Over 29,000 plant species have been introduced into Australia, accounting for 15% of the Australian flora (DAFF 2010). Approximately 2700 of these species have become naturalised, establishing self-sustaining populations in the natural environment (DAFF 2011). Around 400 introduced plants in Australia have been declared noxious or 'invasive' and are officially recognised as problem species (AWS 2006). Plants achieve this status when they have established, or have the potential to establish, significant populations with subsequent environmental and socioeconomic impacts (AWS 2006). It is also estimated that on average 10 plant species establish naturalised populations in

Australia each year and that 70% of the naturalised species in Australia are likely to have escaped from private or public gardens (Groves *et al.* 2005). Some non-native plants that have established small naturalised populations but have not yet spread widely, known as 'sleeper weeds', may also have the potential to spread and cause damage if suitable conditions arise (AWS 2006). Some introduced species, however, may never establish invasive populations. These non-invasive species may exploit under-utilised resources, or occupy empty ecological niches within a disturbed community with few consequences for the native components of the ecosystem (Elton 1958; Woods 1997). Alternatively, some plant introductions can have positive effects on native species (reviewed by Schlaepfer *et al.* 2011). For example non-natives can maintain higher levels of pollinator activity (Woods 1997), act as pioneers for degraded land (Ewel & Putz 2004), and provide favourable habitat for rare species (e.g. *Lantana* in Australia and *Tamarix* in the United States as a habitat for rare birds; Schlaepfer *et al.* 2001; DEC 2005; NSW Scientific Committee 2008). Not all non-native plants, therefore, may require management.

Plants that become invasive can have major economic impacts, which in Australia amounts to over \$4 billion annually in lost agricultural productivity and costs associated with control (Sinden *et al.* 2005; AWS 2006; DAFF 2010). Weeds may be detrimental to agriculture by competing with food crops for nutrients and sunlight, increasing production costs of mechanical and chemical control, reducing crop yields, harbouring pest species, contaminating crop seed, reducing foraging areas for livestock and causing stock death or reduction in animal condition (Sinden *et al.* 2005). The cost of weeds to the natural environment is difficult to calculate, but has been estimated as similar or even greater than the estimates for agriculture (AWS 2006; DSEWPC 2010). Other costs associated with plant invasions include those attributed to impacts on human health through allergy. For example, weeds such as parthenium weed, ragweed, rye grass and privet may trigger

12

asthma and other respiratory diseases while others may be toxic or cause skin irritation (AWS 2006). Invasive plants may also interfere with outdoor activities and alter hydrology by choking waterways (AWS 2006).

The significant ecological and economic implications of biological invasions have led to increasing research attention on trying to understand the characteristics of successful invaders (Daehler & Carino 2000). Understanding which biological traits are the best predictors of invasion success may help to identify which species should be the subject of stringent quarantine measures, as well as help to develop more effective management of existing invaders.

Several hypotheses have been proposed to explain why some species become successful invaders (for reviews see Richardson & Pyšek 2006; Pyšek & Richardson 2007; Catford *et al.* 2009) and considerable research has focused on identifying particular biological traits associated with invasion. These traits include life history characteristics, range size, and introduction history (Richardson & Pyšek 2006; Pyšek & Richardson 2007; Catford *et al.* 2009). Despite some progress in identifying the mechanisms and traits associated with invasion success for single species, the complexity of interactions between invaders and recipient communities still makes predicting patterns of invasion difficult (Lodge 1993). The research described in this thesis aims to integrate several hypotheses about determinants of invasion success. In particular, this research focuses on the roles of (1) phylogenetic relationships between the invader and recipient community (2) natural enemies in the invaded community and (3) the time taken for the invertebrate community to adapt to the invader. Each of these roles is discussed below.

Non-native plant invasion in Australia has increased greatly since European settlement (Adair & Groves 1998). Australia has a high degree of endemicity resulting from a long

history of isolation and novel environmental conditions. The distribution of Australian vegetation is largely influenced by high variability in rainfall, topography and infertile soils (Turnbull 1986). The Australian environment provides us with a unique opportunity to research aspects of invasion biology, particularly because many non-native species are likely to be phylogenetically distinct from Australian native species. Biogeographic comparisons of successful non-native species to less successful non-native and native plants further provides us with an opportunity to better understand the mechanisms behind the success of invasive species in novel environments.

Role of phylogeny and natural enemies

The idea that phylogenetic relationships between species may be important in determining the naturalisation and establishment of non-native species was first put forward by Charles Darwin in the "Origin of Species" (Darwin 1859). Now termed Darwin's 'naturalisation' hypothesis (Daehler 2001), this idea proposes that upon introduction, non-native species are less likely to naturalise if there are congeneric native relatives present (Daehler 2001). Unrelated species are less likely to exhibit strong competitive interactions because their environmental requirements may be more dissimilar (Daehler 2001). Unrelated species can therefore exploit under-utilised resources or empty ecological niches in their new environment. Phylogenetically unrelated non-native species may therefore be more successful as invaders than closely related species.

An alternative *mechanism* to the competitive interactions assumption predicted by the naturalisation hypothesis, may be that natural enemy attack would be lower on distantly related species, because host switching by specialised herbivores is mostly observed between closely related non-native and native species (Connor *et al.* 1980; Thomas *et al.* 1987; Keane & Crawley 2002; Carol *et al.* 2005). The Enemy Release Hypothesis (ERH)

suggests that a plant species may spread rapidly due to being liberated from co-evolved herbivores and pathogens (for reviews see Maron & Vila 2001; Colautti *et al.* 2004). This idea is integral to the theory and success of biological control programs (Keane & Crawley 2002). As herbivores can mediate plant competition (Keane & Crawley 2002) by suppressing plant growth and reproduction for example, introduced plants suffering low rates of enemy attack can thereby gain a competitive advantage over native plants. Reduced damage on introduced plants may mean that resources lost to natural enemies or used in defence against herbivores may be reallocated to growth and reproduction. This is likely to be more pronounced in species that are distantly related to the native recipient community.

Darwin's naturalisation hypothesis and the ERH tend to have been tested as separate questions although they are clearly not mutually exclusive. Niche exploitation as part of the naturalisation hypothesis could also include exploitation of enemy-free space. A few recent studies have directly linked the naturalisation hypothesis and the ERH to investigate whether relatedness of non-native plants and their natural enemies may determine invasiveness via interaction with natural enemies such as herbivores and pathogens (Cappuccino & Carpenter 2005; Ricciardi & Ward 2006; Dawson *et al.* 2009). In these studies, the species being compared were in separate genera or families. To date, only two studies that estimate evolutionary divergence have used well-resolved phylogenies to investigate the role of phylogenetic relationships in determining the likelihood of enemy release in non-native plants (Hill & Kotanen 2009; Hill & Kotanen 2010). Several studies have made comparisons between non-native and native congeneric pairs (Schierenbeck *et al.* 1994; Agrawal & Kotanen 2003; Agrawal *et al.* 2005; Cincotta *et al.* 2009; Chun *et al.* 2010). As introduced species within a genus can have a variety of impacts ranging from being relatively innocuous to highly invasive, understanding how important phylogenetic

relationships are at a sub-generic level is essential in underpinning how important release from natural enemies is as a mechanism behind the successful invasion of non-native plants.

In this study I investigate the predictive power of phylogeny to explain the level of damage suffered by invasive species. The first investigation focused on this prediction at the level of genus and above (Chapter 2), and the second investigation examined this question at the level of species within a genus (Chapter 3).

Role of time since establilshment

The formation of a herbivore assemblage on a novel host plants requires a certain amount of time (Strong et al. 1984). As the time since introduction increases, natural enemies such as herbivores are expected to gradually accumulate, with an increasing propoprtion of the assemblage as a whole being specialised; the fitness of non-native plants may thus be reduced over time (Siemann et al. 2006; Hawkes 2007). The rate at which the invertebrate assemblage colonises non-native species may be a result of two main factors: the time since introduction and the phylogenetic relationship between the invader and native species within the invaded community (as noted above). Plant relatedness is important because host choice by insect herbivores is largely driven by plant chemistry. Closely related plant species tend to be more similar in chemistry, thus providing similar cues for feeding and oviposition (Strong et al. 1984; Tallamy 2004). Evidence for phylogenetic-mediated host switching has been found between closely related species (i.e. within genera), but also at higher taxonomic levels (Connor et al. 1980; Thomas et al. 1987; Keane & Crawley 2002; Palmer et al. 2004; Carol et al. 2005). The longer the time since introduction, the more opportunity there exists for invertebrates to adapt to new hosts including, presumably, species that are relatively distantly related to the native plant community. This research

investigates how long it takes for the invertebrate community to adapt to and colonise invaders. Understanding how quickly non-native species are colonised over time may be important in determining whether enemy release is limited to the early stages of invasion.

General aims of thesis

The aim of this research is to examine the role of herbivory and insect assemblages in invasion biology. My research is directed towards identifying traits that may be useful for making generalisations about the success of invasive plants. This thesis consists of three data chapters, described below. Each of these chapters has been written as stand alone papers with each prepared in a form for publication.

Chapter 2 - Australian family ties: does a lack of relatives help invasive plants escape natural enemies?

This paper investigated the importance of phylogenetic relationships for predicting herbivore and pathogen damage on invasive species. The amount and type of damage from herbivores and pathogens was compared among fourteen invasive, non-native species on the east coast of Australia. These species were selected to represent a range of phylogenetic relationships to those of the native Australian plant community and included: (1) invasive plants with native congeners (2) invasive plants that had native species in the same region within the same family (hereafter referred to as con-familial) and (3) invasive species where the family does not naturally occur in Australia (hereafter referred to as nonfamilial). This paper has been accepted for publication in *Biological Invasions*. Chapter 3 - Can phylogenetic relationships within genus indicate the likelihood of enemy release of an invader?

This study extended the analysis of the previous chapter to examine if phylogenetic relationships at the subgeneric level in the genus *Senecio* can predict herbivore and pathogen damage. *Senecio* is an ideal genus to examine the role that insect herbivores play in affecting invasive, non-invasive and native species. The genus has 87 native and ten introduced species present in Australia. Two of the introduced species have been declared noxious in NSW (*S. madagascariensis* Poir., and *Jacobaea vulgaris* Gaertn., formerly *Senecio jacobaea* L.; Pelser *et al.* 2007), while others have become locally or rarely naturalised. The genus has been the focus of recent broad-scale phylogenetic and taxonomic treatments (Thompson 2006; Pelser *et al.* 2007). This study compares damage, and the abundance and richness of the herbivore assemblage across five native and five non-native naturalised *Senecio* species. Four of the non-native species are rarely or locally naturalised (non-invasive), having not been declared as invasive, and one is the invasive species *Senecio madagascariensis* Poir.

Chapter 4 - Does time since introduction influence enemy release of an invasive weed?

The rate of colonisation of exotic plants by native invertebrates (both herbivores and nonherbivores) over time was examined using *Senecio madagascariensis*. This species was first introduced into the Hunter Valley around 1918 and has since spread along the east coast of Australia, extending from south-east Queensland to Victoria (>1000 km). It has been declared a noxious weed in New South Wales, Queensland and the Australian Capital Territory (Parsons & Cuthbertson 1992). Using a space for time substitution, we sampled external and internal invertebrate herbivores and measured leaf damage at multiple sites, encompassing the current latitudinal range of *S. madagascariensis* (~1000 km), including sites to both the north and south of the point of introduction. We also sampled herbivores and measured foliar damage on the closely-related native congener *S. pinnatifolius* var. *pinnatifolius* A. Rich. at the same sites. This species was used as a comparison for evaluating the ERH and also served as a control to investigate other factors that can influence herbivore assemblages, such as climate variation along the latitudinal gradient.

Chapter 5 - Conclusions

The final chapter summarises the major findings, describes future directions and discusses

the implications for management of non-native species.

Glossary

Weed: a native or non-native plant requiring management to reduce its influence on the environment and economy. Weeds can also be known as invasive plants. **Invasive plant:** a plant declared noxious or 'invasive' and officially recognised as a problem species.

Non-native / Exotic: an introduced species that is outside of its known native range often from human mediated transport.

Naturalised: a non-native plant that has established self-sustaining populations in the natural environment.

Sleeper weeds: non-native plants that have established small naturalised populations that have not yet spread widely but have the potential to spread and cause damage if suitable conditions arise.

Non-invasive: an introduced species that has not established invasive populations with few consequences for the native components of the ecosystem.

Darwin's naturalisation hypothesis: Introduced species that are taxonomically distinct from the recipient community may be more successful as invaders because they are less likely to compete with the native community as their environmental requirements may be more dissimilar.

Enemy release: a non-native species that may experience a decrease or loss of the regulation of their natural enemies (consumers, pathogens and parasites) during their invasion into new areas. This can result in an increase of abundance and/or biomass.

Enemy Release Hypothesis: an important mechanism suggested for the success of an invasive species. A plant species may spread rapidly upon its introduction due to a decrease in their regulation by herbivores and pathogens.

Host switching: specialist species attacking a new host.

Specialist: a natural enemy that attacks a single plant species (monophagous) or a few closely related species (oligophagous).

Generalist: a natural enemy that attacks a wide range of species (polyphagous).

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Chapter 2

Australian family ties: does a lack of relatives help invasive plants escape natural enemies?

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Chapter 2: Relatives, insects and invasions

Abstract

Invasive plants may initially be released from natural enemies when introduced to new regions, but once established, natural enemies may accumulate. How closely related invasive species are to species in the native recipient community may drive patterns of herbivore and pathogen damage and therefore, may be important in understanding the success of some invasions. We compared herbivore and pathogen damage across a group of invasive species occurring in natural environments on the east coast of Australia. We examined whether the level of damage experienced by the invasive species was associated with the degree of phylogenetic relatedness between these plants and the native plants within the region. We found that phylogenetic distance to the nearest native relative was a good predictor of herbivore and pathogen damage on the invasive plants, explaining nearly 37% of the variance in leaf damage. Total leaf damage and the variety of damage types declined with increasing phylogenetic distance to the nearest native relative. In addition, as the phylogenetic distance to the nearest native relative increased, invasive species were colonised by fewer functional guilds and the herbivore assemblage was increasingly dominated by generalist species. These results suggest that invasive species that are only distantly related to those in the native invaded community may be released from specialist natural enemies. Our results indicate that the phylogenetic relatedness of invasive plants to species in native communities is a significant predictor of the rate of colonisation by the herbivore and pathogen community, and thus a useful tool to assess invasion potential.

Key words: invasive plants, enemy release hypothesis, naturalisation hypothesis, plantinsect interactions, herbivore and pathogen damage, phylogenetic relationships

Introduction

Invasion by non-native plants is a global threat to the natural environment with major economic consequences (D'Antonio & Meyerson 2002; Culliney 2005). Non-native plants can affect species diversity, trophic structure and the functioning of native communities and ecosystems (Walker & Smith 1997; Vitousek *et al.* 1997; reviewed by Prieur-Richard & Lavorel 2000). Many hypotheses have been proposed to explain the success of biological invasions (for reviews see Richardson & Pyšek 2006; Pyšek & Richardson 2007; Catford *et al.* 2009) and considerable research has focused on identifying particular plant traits associated with invasion success including life history characteristics, range size, and weed and introduction history (Richardson & Pyšek 2006; Pyšek & Richardson 2007; Catford *et al.* 2009); several of these traits are used within weed risk assessments (Weber *et al.* 2009). Despite some progress in identifying the mechanisms and traits associated with invasion success, the complexity of interactions between invaders and recipient communities makes predicting patterns of invasion difficult at a species level (Lodge 1993).

One characteristic that may be associated with invasion success is the degree to which the invader is related to other species in the invaded community. This idea was first put forward by Darwin (1859), who hypothesised that exotic species that are more closely related to native species in a newly colonised region may be less likely to become invasive. This idea, now known as the naturalisation hypothesis (Daehler 2001), is based on the notion that closely related species are less likely to become naturalised because they compete more strongly for similar resources than distantly related species (Daehler 2001). Tests of this hypothesis thus far have been equivocal. Some studies have concluded that introduced species are more successful if surrounded by plant species that were not closely related (Mack 1996; Rejmánek & Richardson 1996; Lockwood *et al.* 2001; Riccarrdi &

Atkinson 2004; Strauss *et al.* 2006), while others have found either no support (Lambdon & Hulme 2006; Ricciardi & Mottiar 2006; Lambdon 2008; Ricotta *et al.* 2010), or marginal support, depending on the introduction history (Diez *et al.* 2008), or the spatial and taxonomic scale assessed (Diez *et al.* 2008; Proches *et al.* 2008). In some communities, higher naturalisation rates in species with native congeners have occurred, suggesting that introduced congeners share some level of pre-adaptation to the conditions of the invaded region (Daehler 2001; Duncan & Williams 2002). In turn, this may outweigh the potential for strong competition between close relatives.

An alternate mechanism by which phylogeny may be important in determining the success of exotic species is through a release from natural enemies. The Enemy Release Hypothesis (ERH) suggests that upon introduction to a new region, a new plant species might spread rapidly because it is liberated from its co-evolved herbivores and pathogens (for reviews see Maron & Vila 2001; Colautti et al. 2004). Most tests of the ERH have either compared damage suffered by exotic plants in their native range to that in their introduced range (biogeographic comparisons), or have been community-based comparisons between invasive species and their native or non-invasive counterparts (for review see Colautti et al. 2004; and meta analysis by Liu & Stiling 2006). The ERH has generally been supported by biogeographic comparisons. In contrast, community-based analyses have yielded mixed results, finding evidence both for and against the ERH, or partial support depending upon seasons and years (e.g. Colautti et al. 2004; Liu & Stiling 2006). As host switching by specialised herbivores has been found between closely related non-native and native species (Connor et al. 1980; Thomas et al. 1987; Keane & Crawley 2002; Carol et al. 2005), the degree of relatedness of non-native species to co-occurring natives may be a contributing factor to whether the non-native species is released from natural enemies.

31

Few studies have directly linked the naturalisation hypothesis and the ERH to investigate whether phylogenetic relatedness, or the taxonomic isolation of invasive plants and their natural enemies, may assist some species to become more invasive than others. The studies that have investigated both hypotheses together have generally quantified the taxonomic isolation of non-native species based on the number of congeneric or confamilial native plants present in the recipient community, finding weak or no support (Cappuccino & Carpenter 2005; Ricciardi & Ward 2006; Dawson et al. 2009). Inconsistent results from different studies may be due to the fact that comparisons have been made across different spatial scales and between plants at varying stages of invasion. Few studies have used a phylogenetic approach that estimates relatedness to the nearest native relative based on their evolutionary divergence rather than taxonomic similarity (Hill & Kotanen 2010). For example, only Hill and Kotanen (2009, 2010) and Pearse and Hipp (2009) have used well-resolved phylogenies to determine whether phylogenetically distinct non-native species suffer less damage from natural enemies than closely related non-native species. Although weak trends, based on distance measures, were found in a common garden experiment (Hill & Kotanen 2009), there is still conflicting evidence as to whether release from natural enemies occurs in non-native taxa that are more phylogenetically distinct from other species in the recipient native community (Hill & Kotanen 2009; Hill & Kotanen 2010).

Interpretation of the naturalisation hypothesis should consider enemy release as a fundamental mechanism by which introduced plants become invasive. This is because closely related plants often present more similar chemical cues than those of unrelated plants, leading to the expectation that specialised herbivores and pathogens may shift onto close relatives of their host more readily than onto distantly or unrelated taxa (Connor *et al.* 1980; Strong *et al.* 1984; Weiblen *et al.* 2006; Gilbert & Webb 2007; Parker & Gilbert

2007). However, the types of damage incurred on non-native taxa closely related to the native community have not been compared to distantly related taxa. Further, the degree to which specialists, compared to generalists, colonise closely and distantly related non-native plants has received little attention. A recent review revealed that loss of fitness in specialist insects is greater than generalist insects and more pronounced with increasing phylogenetic distance from novel hosts (Bertheau *et al.* 2010).

Whether invasive plants may escape their natural enemies if they are distantly related to the plants in the invaded range may also depend on the types of insect herbivores most likely to have a suppressive impact. The success of introduced plants is attributed to escape from specialist natural enemies (Keane & Crawley 2002; Stastny *et al.* 2005), which may include endophagous insect herbivores (miners and gall formers). The invader is therefore more likely to encounter polyphagous (generalist) enemies (Maron & Vila 2001; Keane & Crawley 2002; Stastny *et al.* 2005) that are expected to have a relatively low impact and not impede growth (Stastny *et al.* 2005). While polyphagous herbivores are often the first to colonise introduced plant species, with ectophagous species being more common than endophagous (Strong *et al.* 1984; Liu & Stiling 2006), rarely do comparative studies examine the diversity, impact and type of functional damage by herbivores and pathogens (e.g. grazers, chewers, skeletonizers, sap-suckers, miners, seed feeders, gallers). To our knowledge, no previous studies have quantified both the impact and identity of the herbivore feeding guilds on introduced plants based on their level of relatedness to the recipient native community.

In this study, we compared herbivore and pathogen damage on several species of invasive plants in Australia, based on their level of relatedness to sympatric Australian native plant species. The extent of exotic plant invasion in Australia has increased greatly since European settlement, especially in areas of agricultural and urban development and

33

disturbance (Adair & Groves 1998). Australia's long history of isolation has resulted in a high incidence of endemism, and novel environmental conditions for non-native species. These conditions include relatively infertile soils, aridity, high evaporative water loss, and ecosystem dynamics largely driven by episodic events (Steffen *et al.* 2009). The Australian environment provides a unique opportunity to determine whether (i) invasive plants with closely related native plants suffer more damage than those with more distant relatives; (ii) the composition of damage types found on non-native species is associated with their phylogenetic relationships to Australian natives; and (iii) non-native species more closely related to the native community have a greater variety of damage types than distantly related species.

Methods

Study species

For the purpose of this study, non-native plant species were considered invasive if they have been classified as 'noxious' in one or more council divisions of New South Wales, Australia (AWC 2007). To obtain a broad spread of non-native plants for sampling, three categories of exotic plants were initially defined, based on their degree of relatedness to the native plants of Australia: (1) invasive plants with native congeners (2) invasive plants that had native species in the same region within the same family (hereafter referred to as confamilial) and (3) invasive species with no family members or congeners in Australia (hereafter referred to as non-familial) (Table 1). A total of 14 species were selected. Species chosen were predominantly distributed along the east coast of Australia and include a variety of growth forms (herbs, shrubs and vines). All introduced species chosen are known to have been present in Australia for at least 40 years according to published literature and herbarium records. Selection of species based on these broad taxonomic

groupings was then refined further by reference to published phylogenies obtained from the Angiosperm Phylogeny website (Stevens 2006) which contains regularly updated information on plant phylogenetics.

Once the choice of the 14 invasive species and their general phylogenetic relationship to Australian natives was finalised, we selected a native relative for each species that occurred sympatrically. The absolute nearest native relative was chosen based on having a similar coastal distribution to the non-native species of interest and potentially occurring in a similar habitat (Comparison 1, see Table 1). For six of the 14 species, the native partner chosen in this way was of a different growth form and/or occurred in a different habitat. For these cases we chose a second native species for comparison using criteria that included similar habitat and growth form (Comparison 2, see Table 1). Thus an invasive species that was a climber occurring in rainforest, for example, was paired with the phylogenetically closest native climber in a similar habitat. Several of the native species chosen for the first analysis are the same as for the second analysis. All plant species including non-native and native are represented in one phylogenetic tree with each comparison identified but grouped separately for analysis (Figure 1).

As genera can differ in divergence times, a phylogenetic tree was constructed using Phylomatic software to remove the assumption of equal degrees of divergence between genera and families (Webb & Donoghue 2005). The list of 14 species, including family and genus names, was submitted to the online phylogenetic query tool, which returned a phylogenetic hypothesis for the relationships among the taxa (Webb & Donoghue 2005). Species were matched to the online 'mega-tree', which is a phylogenetic tree containing all angiosperm families of the world, based on the consensus tree from Davies *et al.* (2004). Because the mega-tree is largely incomplete below the level of family, the relationships among genera within each family are returned as a polytomy ('comb' phylogeny).

35

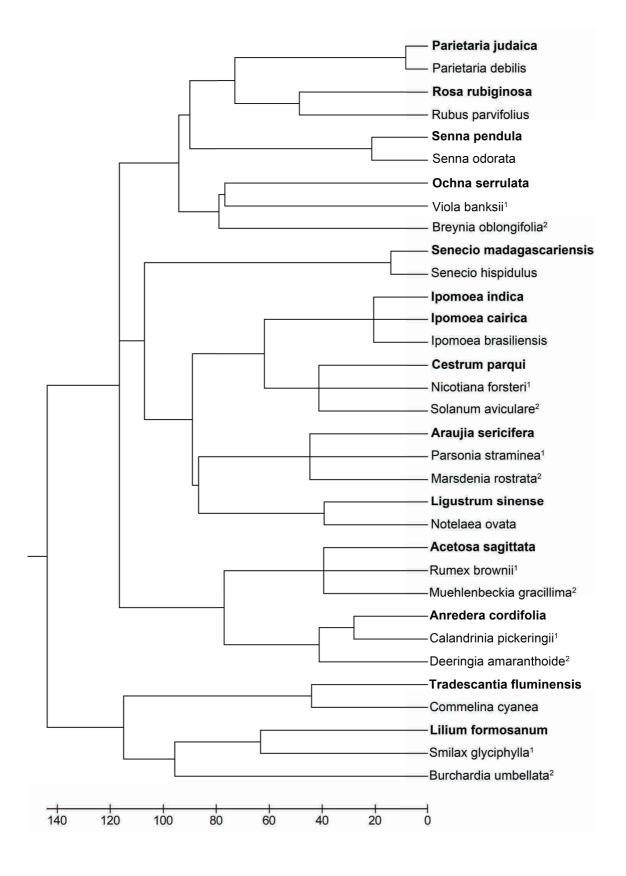
Similarly, species are returned as polytomies within genera. Branch lengths for the tree were estimated using the 'BLADJ' function in Phylomatic (Version 4.0.1) (Webb *et al.* 2009). This function fixes the root node at a specified age, and fixes other angiosperm nodes aged from Wikstrom *et al.* (2001) to the tree. Undated nodes are then placed evenly between nodes of known ages (Webb *et al.* 2009). This allows approximate estimates of distances between taxa. For the purpose of this study approximate evolutionary distances are sound so long as non-native species can be accurately ranked from being closely related to a native plant of Australia, to more distantly-related, based on the approximate divergence time of each non-native species to their closest native relative.

Study Sites

Sampling was conducted throughout spring (September-November) 2007 within disturbed bushland sites on the east coast of Australia. Three broad sampling regions were selected, spanning the geographic ranges of the non-native plants sampled: (1) Sydney Basin: southern region with sites included within the Wollondilly Shire, Shoalhaven and Illawarra districts (2) Sydney Basin: central and western region with sites included within several Sydney suburbs and surrounds, South Eastern Highlands, Lithgow shire and (3) North Coast: with sites included in the Grafton shire, Southeast Queensland including Brisbane suburbs, and Warwick in the Brigalow Belt (Table 1). Each invasive species was sampled at one location within each of the three regions. Table 1. Sampling design for the comparison of damage on invasive plants with native congeners¹, native con-familials² and those where the family does not naturally occur in Australia (non-familial³) across three sampling regions. Invasive plant species used in the study were compared with the nearest Australian relative (comparison 1) and nearest relative with a similar distribution, growth form and habitat (comparison 2).

Invasive plant species	Sampling location	Comparison 1: Invasive species with nearest native relative	Comparison 2: Invasive species with nearest native relative, similar distribution, growth form and habitat
Parietaria judaica ¹	34°26'15.61"S 150°53'39.56"E	Parietaria debilis	Parietaria debilis
	33°47'21.96"S 151°09'53.05"E		
Senna pendula ¹	27°26'47.35"S 152°56'45.57"E	Senna odorata	Senna odorata
	33°48'40.15"S 151°08'24.64"E		
	34°26'00.66"S 150°52'44.52"E		
Senecio madagascariensis ¹	29°44'44.72"S 152°57'11.46"E	Senecio hispidulus	Senecio hispidulus
	33°50'08.26"S 150°51'15.20"E		
	34°07'21.49"S 150°41'52.91"E		
Ipomoea indica ¹	27°30'46.58"S 152°56'03.34"E	Ipomoea brasiliensis	Ipomoea brasiliensis
	33°48'40.15"S 151°08'24.64"E		
	34°26'01.70"S 150°52'28.92"E		
Ipomoea cairica ¹	27°56'27.94"S 153°10'49.35"E	Ipomoea brasiliensis	Ipomoea brasiliensis
	33°40'49.00"S 151°18'44.03"E		
	34°35'53.20"S 150°53'54.44"E		
Acetosa sagittata ²	27°56'27.94"S 153°10'49.35"E	Rumex brownii	Muehlenbeckia grasillima
	33°40'49.00"S 151°18'44.03"E		
	34°26'01.70"S 150°52'28.92"E		
Tradescantia fluminensis ²	27°26'47.35"S 152°56'45.57"E	Commelina cyanea	Commelina cyanea
	33°47'21.96"S 151°09'53.05"E		
	34°26'01.70"S 150°52'28.92"E		
Cestrum parqui ²	27°31'05.91"S 153°00'33.08"E	Nicotiana forsteri	Solanum aviculare
	33°48'40.15"S 151°08'24.64"E		
	34°31'49.44"S 150°52'21.81"E		
Araujia sericifera ²	27°56'27.94"S 153°10'49.35"E	Parsonia straminea	Marsdenia rostrata
	33°39'56.70"S 151°18'04.79"E		
	34°35'53.20"S 150°53'54.44"E		
Ligustrum sinense ²	27°50'04.88"S 153°16'24.01"E	Notelaea ovata	Notelaea ovata
	33°48'40.15"S 151°08'24.64"E		
	34°26'00.66"S 150°52'44.52"E		
Rosa rubiginosa ²	27°58'32.36"S 153°18'08.04"E	Rubus parvifolius	Rubus parvifolius
	33°33'36.56"S 149°55'41.07"E		
	34°07'21.49"S 150°41'52.91"E		
Ochna serrulata ³	27°26'47.35"S 152°56'45.57"E	Viola banksii	Breynia oblongifolia
	33°47'42.64"S 151°09'05.93"E		
	34°31'49.44"S 150°52'21.81"E		
Anredera cordifolia ³	27°26'47.35"S 152°56'45.57"E	Calandrinia pickeringii Deeringia amar	Deeringia amaranthoide
	33°48'40.15"S 151°08'24.64"E		
	34°31'49.44"S 150°52'21.81"E		
Lilium formosanum ³	27°56'27.94"S 153°10'49.35"E	Smilax glyciphylla	Burchardia umbellata
	33°48'40.15"S 151°08'24.64"E		
	35°01'07.60"S 150°39'52.49"E		

Figure 1. Phylogenetic tree from Phylomatic (Webb *et al.* 2009), displaying node labels representing divergence (million of years ago) of invasive species (in bold) from their nearest native relatives, based on their most recent common ancestors (comparison 1) and most recent common ancestor with similar distribution, habitat and morphology (comparison 2). Native species with no superscripts were used for both comparison 1 and 2. Phylocom (Webb *et al.* 2009) has complete familial representation but uses angiosperm nodes aged from Wickstrom *et al.* (2001) by running a program called 'BLADJ' to estimate aged distance at the genus and species level.



Herbivory Measurements

Damage by invertebrate herbivores and pathogens was assessed on 15 individual plants for each invasive species per sampling region. Five haphazardly selected mature leaves from each plant, totalling 75 leaves per region per species, were collected. This method of sampling provides a quick easy estimate of herbivory but underestimates total herbivory from leaves or other parts of the plant that are wholly eaten (Lowman 1984). Leaves were scanned within a week of collection using a Canoscan LiDe 20 Image Scanner in grayscale and color. Senescing leaves were not collected because distinguishing decay from herbivore damage is not possible (Lowman 1984).

Types of damage

Herbivore damage (grazing, chewing, skeletonising, sap-sucking, galling, mining) and any sign of pathogen damage (from fungus and bacteria such as leaf spotting and rust) were identified, and the area missing due to the particular damage type, relative to the total leaf area, was assessed using Image J software (Rasband 2003). Grazing, chewing and skeletonising damage result from external feeding by invertebrates with chewing mouthparts, such as caterpillars, beetles and grasshoppers. Grazing damage was identified as leaf necrosis where the scraping of the leaf surface occurred without the complete loss of photosynthetic material. The material slowly decays and in turn can cause holes within the leaf. Chewing damage was identified as holes that occurred from leaf edge surfaces and likely involved insects with cutting mouthparts such as caterpillars and grasshoppers. Direct loss of photosynthetic material and removal of the full depth of leaf lamina occurs. For leaves with damage along the edge, approximate areas were drawn relying on the symmetry of the leaf to estimate area lost (Carpenter & Cappuccino 2005). Any known

mechanical or physiological damage was removed from analysis. Any damage from unknown sources that showed signs of necrosis was included in the analysis.

The probable cause of all herbivore and pathogen damage was broadly identified using texts (Hockings 1980; McMaugh *et al.* 1985; McCarthy 1985; Jones & Elliot 1986; APPS 1997; Agrios 2004) and assistance from entomological and phytopathological experts at the Australian Museum in Sydney and the National Herbarium of NSW.

Statistical analysis

We compared (i) total foliar damage (ii) types of damage and (iii) number of damage types among the 14 invasive species.

(1) Relationship of total leaf damage and phylogenetic distance to Australian natives

Data from different sites within each species range were pooled prior to analysis because between-site variability was not the prime focus of this study. We used linear least-squares regression to test for an association between total damage and phylogenetic relatedness to the closest nearest native (Data Desk[®] 6.1). Total damage was transformed to the natural logarithm before analysis to satisfy the assumption of normality.

(2) Damage type, species identity and phylogenetic distance to Australian natives

To determine if composition of damage types is associated with species identity and their evolutionary distance to the nearest native relative, two steps were used. Firstly, the association between species identity and composition of damage types was tested by multivariate analysis, performed by the PERMANOVA+ add-on package for PRIMER *v*6 using Euclidean distances on data transformed to the arcsine of their square roots with 15 replicates per species (Clarke & Gorley 2006; Anderson 2001; McArdle & Anderson

2001). Second, replicates were averaged and DISTLM, which is a non-parametric, permutation procedure for multivariate multiple regression, was used to test for an association between damage type across species and phylogenetic distance to the nearest native relative (Anderson 2001; McArdle & Anderson 2001). Damage of each type for each species was standardised as a proportion of the mean total damage. Differences in damage types across non-native species were visually represented using pie charts. For visual simplicity, where distinct boundaries in evolutionary distances to the nearest native relative occurred, distances and damage types for these species were averaged.

(3) Number of damage types and phylogeny

To investigate the relationship between plant phylogeny and variety of damage types, the phylogenetic distance to the nearest native relative was plotted against the total number of damage types. The boundary test in EcoSim was then used to determine if there was a limit to the diversity of damage types found on non-native species with distantly related native plant species (Gotelli & Entsminger 2000). From the plot, an asymmetric upper right boundary was determined from the maximum and medium points of the x variable (phylogenetic distance) and y variable (number of damage types). EcoSim then evaluated the number of points that fell outside the selected boundary through randomisation of the x and y variable (Gotelli & Entsminger 2000). Ten thousand random permutations were generated using values within the minimum and maximum range of the data set. An observed and simulated test statistic was then calculated to determine if the observed number of points outside the boundary was significantly smaller than the number found for the simulated data sets. A significant boundary test would indicate that non-native species with distant native relatives are limited in the maximum number of damage types than closely related species. Distantly related species with few types of damage types than

likely to be colonised by specialist herbivores at a slower rate than more closely related species.

Results

Relationship of total leaf damage and phylogenetic distance to Australian natives

Leaf damage on invasive plants was generally low, ranging from an average per species of 0.41% of the total leaf area (*Lilium formosanum*) to 4.5% (*Senecio madagascariensis*). Leaf damage on invasive plants declined with greater phylogenetic distance to the nearest native relative (Fig. 2 a, b). When phylogenetic distance was estimated between invasive plants and their nearest native relative (comparison 1), 31% of variation in damage on invasive plants was explained by phylogenetic distance (F = 5.42, d.f = 1, 12, P = 0.0383) (Fig. 2 a). When phylogenetic distance was estimated between invasive species and their nearest native relative with similar habitat and growth form (comparison 2), phylogenetic distance explained 37% of the variation in damage on invasive plants (F = 7.01, d.f = 1, 12, P = 0.0213) (Fig. 2 b).

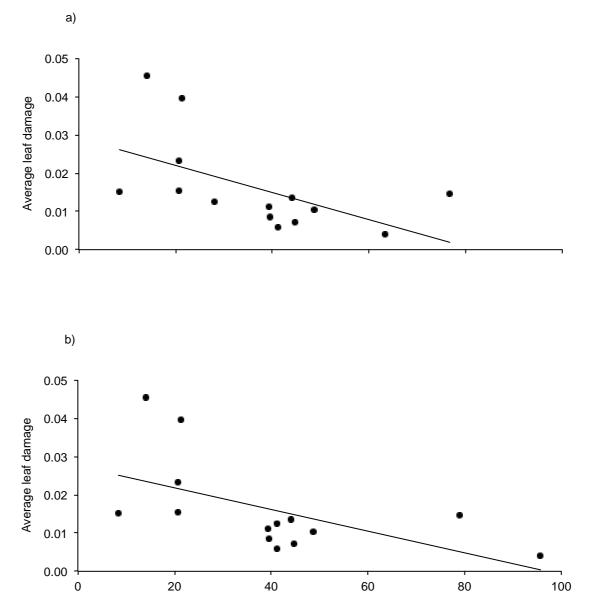
Damage type, species identity and phylogenetic distance to Australian natives

Composition of damage type was strongly associated with species identity (PERMANOVA: $F_{13, 196} = 14.315$, P = 0.0001). However, the relative proportion of damage types among invasive plants was not explained by phylogenetic distance to the nearest native relative (DISTLM: F = 0.585, P = 0.633; Fig. 3). In general, endophagous insect damage (mining and galling) across invasive plant species was minimal and contributed 0.5% of the mean total damage. Damage by ectophagous insects (grazing, chewing, skeletonising and sap-sucking) contributed 86% of the mean total damage. Ectophagous damage was dominated by the impacts of grazing and chewing generalists. Pathogenesis and unknown necrotic damage contributed minimally (12.5% and 1%) to the remainder of the mean total damage (Fig. 3).

Number of damage types and phylogenetic distance to Australian natives

There was a limit to the number of damage types invasive species with distant native relatives can have. Invasive species with a near native relative had a wider range of damage types than those with distant native relatives, as indicated by the absence of points in the top right corner of Figure 4 (observed = 0, simulated = 3.681, p = 0.012 EcoSim Fig. 4).

Figure 2. Relationship of leaf damage on invasive plants with the phylogenetic distance (a) to the nearest native relative and (b) to the nearest native relative with similar distribution, growth form, and habitat.



Phylogenetic distance of invasive species to native relative (divergence time (mya))

Figure 3. External (ectophagous) and internal (endophagous) damage across species that are closely related to native co-occurring species with an average divergence time of (a) 17 mya, to more distantly related to native species (b) 43 mya and with minimal to no relationship to native species (87 mya). N = the number of non-native species averaged.

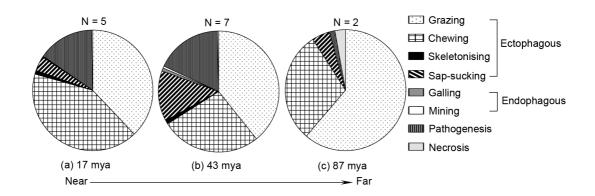
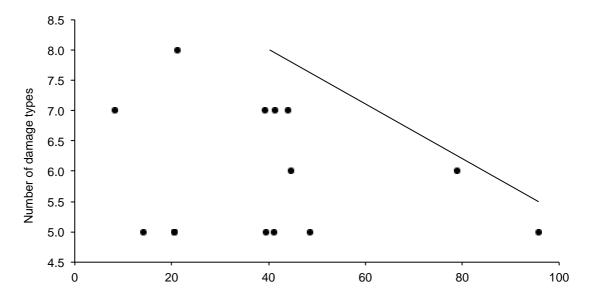


Figure 4. Relationship between the number of damage types occurring on non-native plants and the phylogenetic distance to the nearest native relative with similar distribution, habitat and morphology. The line indicates the asymetric boundary of damage types generated by EcoSim.



Phylogenetic distance of invasive species to nearest sympatrically occurring native species with similar distribution, growth form and habitat (divergence time (mya)). Asymmetric boundaries generated by EcoSim

Discussion

We have demonstrated that phylogenetic relatedness to sympatric plant species is a significant predictor of herbivore and pathogen damage to plant foliage on non-native plants, explaining over 30% of damage variation. Invasive species with closer phylogenetic relationships to Australian natives in the recipient community suffered more total damage, as well as being potentially exposed to a wider variety of damage types, than invasive species more distantly related to local species. These results were consistent whether we estimated phylogenetic distance based on the absolute nearest native relative of an invasive species, or the distance to the nearest relative with similar habitat and growth form. Differences in damage types were found between species, but due to the dominance of chewing and grazing herbivores on all plants, the types of damage was not significantly related to phylogenetic distance to the nearest native relative.

In general, our results support the hypothesis that herbivory is related to the taxonomic isolation of non-native species with respect to the native community. If natural enemies are important for limiting the invasion success of non-natives, our results provide support for a mechanism behind Darwin's naturalisation hypothesis, in that an invasive plant may be more successful if surrounded by plants that are not closely related (Mack 1996; Lockwood *et al.* 2001; Riccarrdi & Atkinson 2004; Strauss *et al.* 2006). Our results are consistent with findings of a common garden experiment in which non-native plants suffered less herbivory with increasing phylogenetic distance from native con-familials (Hill & Kotanen 2009). However, unlike Hill & Kotanen (2009) who did not find a relationship with phylogentic distance and damage in natural communities, we found that phylogenetic relationships within natural communities provide a useful indication of the rate of herbivore and pathogen damage that non-native plants may experience. Our results are also consistent with the finding that introduced oak species closely related to a native

50

oak received more herbivore damage by chewers and miners than more distantly related oaks (Pearse & Hipp 2009).

Determining the types of damage by herbivores and pathogens likely to have a suppressive impact is a crucial step for understanding whether distantly or unrelated non-native plants may be released from specialist natural enemies or share some level of pre-adaptation to natural enemies of the invaded region. In this study, not only did phylogenetically distant invasive species experience less total damage, they were subject to attack from fewer types of herbivores than those more closely related to the native community. Generalist or polyphagous feeding behaviour by grazers and chewers dominated damage on more distantly related or unrelated taxa. In contrast, invasive species that were closely related to the native community were potentially subject to a full suite of damage types by generalists and specialists that included endophagous damage by gallers and miners. Other studies have demonstrated that ectophagous species are more commonly associated with introduced species (Strong et al. 1984; Liu & Stiling 2006). Our finding, that chewing and grazing were the dominant feeding guilds that drove patterns of herbivore and pathogen damage across all invasive species in this study, is consistent with this idea. Although the composition of damage type was associated with species identity, dominance by chewing and grazing damage meant that no phylogenetic signal between damage type and species was found.

Our overall results indicate that taxonomically distinct exotic species are more likely to be susceptible to a wide range of generalist herbivores compared to exotic species that are more closely related to plants in their invaded community (Ricciardi & Ward 2006). This is because generalist herbivores are not as responsive to chemical defences, which are often shared between closely related plants and are important in determining the smell, taste and palatability of leaves for specialist herbivores (Tallamy 2004). However, having

51

found such low proportions of endophagous damage across all species in this study, our results imply that non-native species may be largely released from specialist natural enemies. Other factors, such as time since colonisation of the invader, may therefore be important for determining the accumulation of specialist herbivores (Strong *et al.* 1984; Brändle *et al.* 2008) and warrants further investigation.

The invasive potential of a plant species introduced to new environments is generally assessed by considering whether it (or its close relatives) have a history of becoming invasive elsewhere (DAFF 2010). The results of our study indicate that the phylogenetic relatedness of invasive plants to native species in the new environment may provide an additional tool for understanding and managing this global problem. Promising areas of future research could include an assessment of herbivory and the herbivore community composition at finer taxonomic scales to investigate the influence of phylogenetic relationships on functional herbivore guilds.

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Chapter 3

Can phylogenetic relationships within genus indicate the likelihood of enemy release of an invader?

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Abstract

Invasive plants have become a global environmental and economic problem. Understanding the mechanisms behind invasion is integral for management solutions. The enemy release hypothesis (ERH) is often invoked to explain the success of non-native plant species. The ERH suggests that upon introduction to a new region, a novel plant species may spread rapidly because it is liberated from co-evolved herbivores and pathogens. The phylogenetic relationship between a non-native plant and the native recipient community may be important in understanding the success of some non-native plants because host switching by native herbivores is more likely to occur between closely related rather than distantly related species. In this study, we tested the ERH by comparing leaf damage and herbivorous insect assemblages on the invasive species Senecio madagascariesis Poir. to nine congeneric species, of which five are native to the invasion sites, and four are non-native but considered non-invasive. As the closeness of the phylogenetic relationship between invasive species and other species in the recipient community has been found to play a role in determining invasiveness, we also investigated the relationship of the insect assemblage to the level of relatedness of the host plants. We found that while non-native species had less leaf damage than natives overall, there were no significant differences in the abundance, richness and diversity of herbivores among native and non-native Senecio L. species. The composition of the herbivore assemblages and percentage abundance of herbivore guilds differed between all Senecio species, but patterns were not related to whether the species was native or not. Species level differences suggested that Senecio madagascariensis may have a greater proportion of generalist insect damage (represented by phytophagous leaf chewers) than all other Senecio species. Our results indicate that predictions based on phylogenetic relationships for the success of invasive species within genus are not supported: Senecio

63

madagascariensis was not distantly related to other non-invasive or native *Senecio* species, and there was no correlation between the phylogenetic distance of *Senecio* species and the dissimilarity of herbivore assemblages. Within a plant genus, variation in escape from natural enemies does not appear to support the ERH as a mechanism for why some non-native *Senecio* species are more invasive than others. Predictions based on phylogeny of invasive behaviour through enemy release are likely to be only viable at broad phylogenetic scales.

Key words: invasive plants, enemy release hypothesis, naturalisation hypothesis, plant-insect interactions, congeners, non-invasive plants.

Introduction

Invasive plants pose one of the most serious threats to the environment with major economic consequences. Negative impacts include: displacement of native species, land degradation, reduction in farm and forest productivity, alteration of ecosystem properties, and the disruption of ecosystem function (Adair & Groves 1998; Sinden *et al.* 2005). While our understanding of the impacts of non-native plants on native communities has grown considerably, the reasons why only some introduced plants become invasive still appear to be context dependent.

There is some evidence to suggest that introduced plants are more likely to become invasive in the absence of closely related species in the recipient native community (Mack 1996; Rejmánek & Richardson1996, Lockwood *et al.* 2001; Riccarrdi & Atkinson 2004; Strauss *et al.* 2006; Schaefer *et al.* 2011). This is generally referred to as the naturalisation hypothesis (Darwin 1859; Daehler 2001) and rests partly on the idea that closely related species are likely to compete more strongly for similar resources. However, some studies have shown that higher naturalisation rates of non-native species with congeneric native relatives have occurred, suggesting that competition is outweighed by the importance of sharing similar environmental conditions to which non-natives may be pre-adapted to (Daehler 2001; Duncan & Williams 2002).

Phylogenetic relationships between a potential invader and co-occurring native species may also be important in relation to the impact of natural enemies. If a plant species is introduced to an area where the natural enemies from its native region are not present, the probability of successful establishment may be increased. This is termed the Enemy Release Hypothesis (ERH) (for reviews see Maron & Vila 2001; Colautti *et al.* 2004). The enemy release of non-natives may be more pronounced in species that are distantly related to the recipient native plant community. Plants that are closely related tend to share more natural enemies than those that are distantly related (Connor *et al.* 1980; Frenzel & Brandl 2003; Ødegaard *et al.* 2005), due to sharing similar physical and chemical characteristics (Strong *et al.* 1984; Jones & Lawton 1991; Tallamy 2004). Harvey *et al.* (in press) demonstrated that with increasing phylogenetic distance from native relatives, leaf damage on invasive species declined. Similarly, a common garden experiment demonstrated that with increased phylogenetic distance from native con-familials, non-native plants suffered less herbivory (Hill & Kotanen 2009). Neither of these studies however, investigated the comparative levels of herbivory below the level of genus. The impacts of established nonnative plants within a genus can range from innocuous to invasive, so understanding phylogenetic relationships at a sub-generic level in relation to levels of herbivory is necessary for predicting if release from natural enemies could be a mechanism behind successful invasion.

Several tests of the ERH have attempted to control for phylogenetic signals by comparing herbivore damage and herbivore communities between congeneric native and non-native pairs in the invaded region. Results for the ERH vary between studies (reviewed by Colautti *et al.* 2004; meta-analysis by Chun *et al.* 2010), with some showing that damage may be greater on native species compared to non-natives as predicted by the ERH (Schierenbeck *et al.* 1994; Siemann & Rogers 2003; Cincotta *et al.* 2009), while others demonstrate that non-natives can receive greater damage than native congeners (Keane & Crawley 2002 and references therein; Agrawal & Kotanen. 2003), but that this can also vary with space and over time (Agrawal *et al.* 2005). If release from natural enemies is an important mechanism behind the success of some non-native plants, we would expect that invasive species are more likely to escape natural enemies than non-invasive or innocuous non-invasive species (Liu *et al.* 2006). Therefore, tests to determine the importance of

enemy release in the success of invasive species should ideally include comparisons with non-native non-invasive congeners. The few studies that have performed such comparisons have found that less invasive or non-invasive species suffered greater herbivory than invasive species (Cappuccino & Carpenter 2005; Carpenter and Cappuccino 2005) and have accumulated more pathogens (Mitchell & Power 2003). Only a handful of studies have included three-way comparisons among congeners of native plants and introduced non-invasive and invasive plants (Carpenter & Cappuccino 2005; Liu *et al.* 2006; Liu *et al.* 2007). In two separate studies, similar levels of herbivore damage (Liu *et al.* 2007) and richness (Liu *et al.* 2006) between introduced invasive and non-invasive *Eugenia* species were recorded but herbivore damage and richness were both lower than on their native counterparts (Liu *et al.* 2006; Liu *et al.* 2007). Without including the non-invasive species, the authors would have concluded that escape from natural enemies would have been an important driving mechanism for the success of the invasive *Eugenia* species.

Phylogenetic relationships between plants within a community have been shown to be important in the make up of the co-occurring insect community. As the phylogenetic distance between co-occurring host plant species declines, greater similarities are found between the insect communities (Novotony *et al.* 2006; Ødegaard *et al.* 2005; Weiblen *et al.* 2006; Nipperess *et al.* 2012). These differences are most evident at the level of plant family (Nipperess *et al.* 2012) because differences in plant chemistry and architecture are more pronounced between the taxonomic level of family and above. Phylogenetic relationships between native and non-native species may offer important insights into compositional differences of invertebrates between native and non-native species postinvasion. Comparing insect herbivore communities between native, non-invasive and invasive plants within the same genus offers the chance to detect species that may be the main drivers of enemy impact. It further assists in determining whether the community on the invasive species exhibits relatively little variation between plants or recruits a less diverse fauna compared to native and non-invasive species. Comparing herbivore communities allows us to determine if specialist insects are replaced by generalist insect activity in the new range as predicted by the ERH (Keane & Crawley 2002). Endophagous herbivores including miners and gall inducers may be replaced by more generalist ectophagous chewers and sap-suckers (Strong *et al.* 1984; Ando *et al.* 2010). Endophagous herbivores are considered more specialised as they feed internally on plants (Frenzel & Brandl 1998), and research has indicated that the species richness of endophagous herbivores may be lower on introduced plants than on related native plants, whereas ectophagous insects (leaf chewing and sap-sucking herbivores) are more likely to readily colonise introduced species (Jobin *et al.* 1996). To our knowledge no prior studies have considered the phylogeny of host plants in quantifying both the impact and identity of the herbivore community and guilds between native, non-invasive and invasive species within genus.

In this study we compared invertebrate herbivore faunas among native (five species), invasive (one species; *Senecio madagascariensis* Poir.) and naturalised (four species) of *Senecio* L. growing on the east coast of Australia (Plate 1; Table 1). The *Senecio* spp. studied here included perennial shrubs, vines and annual and biannual herbs. If enemy release is important in the success of the invasive *S. madagascariensis*, we predict that:

(1) Herbivore damage will be greater on native species and non-invasive naturalised species than *S. madagascariensis*.

(2) The abundance and richness of herbivores will be greater on the native and noninvasive naturalised *Senecio* species than the invasive species *S. madagascariensis*. (3) The composition of the insect assemblage on *S. madagascariensis* will (a) be significantly different from other native and non-invasive naturalised species (b) have a relatively larger proportion of non-specialised feeding guilds than native *Senecio* species and (c) will exhibit relatively little plant-to-plant variation compared to native and non-invasive *Senecio* species.

If phylogenetic relationships are important in determining the insect assemblage on *Senecio* spp., and explain why *S. madagascariensis* is more invasive than non-invasive naturalised *Senecio* species, we also predict that:

(1) The dissimilarity in the invertebrate herbivore assemblages found on *Senecio* species will be correlated with the evolutionary relatedness of those species.

Methods

Locations and plant species studied

Sampling of plants from the genus *Senecio* L. (Asteraceae) was conducted during spring and summer between November 2008 and February 2009 and repeated in autumn from March 2009 to May 2009 in coastal bushland, wet sclerophyll rangelands and grazing land along the east coast of Australia (Table 1; Plate 1).

Senecio is one of the largest genera of flowering plants and encompasses a wide range of perennial shrubs, vines and biannual and annual herbs (Frodin 2004). The genus is represented with 87 native species and 10 non-native species in Australia (Thompson 2006). With the exceptions of the invasive species *Senecio madagascariensis* Poir. and *Jacobaea vulgaris* Gaertn. (formerly *Senecio jacobaea* L.; Pelser *et al.* 2007), all other non-native species are either locally or rarely naturalised (Parsons & Cuthbertson 1992; Harden 2011; AWC 2011). *Senecio madagascariensis* has been declared a noxious

invasive weed in New South Wales, Queensland and the Australian Capital Territory (Parsons & Cuthbertson 1992). It is an annual or biannual herb that was first recorded in the Hunter Valley (NSW) in 1918. Originating in South Africa, it has since become a widespread and aggressive weed invading cultivated disturbed lands, pastures and roadsides of NSW extending into south-east Queensland (Parsons & Cuthbertson 1992; Holtkamp & Hosking 1993). It is of significant economic concern due to containing pyrrolizidine alkaloid, which if ingested by livestock can affect fitness and even lead to death (Parsons & Cuthbertson 1992; Sindel 2009). The range of species within the genus, in terms of the variability of invasiveness, makes *Senecio* an ideal system to examine the role that insect herbivores play in affecting invasiveness. Further, this genus has been the subject of recent broad-scale phylogenetic and taxonomic treatments (Thompson 2006; Pelser *et al.* 2007) that provide a basis for relating phylogeny to their interaction with natural enemies.

Sampling design

Sampling took place at three sites, spread across the geographic range of *Senecio madagascariensis* (Table 1). All *Senecio* species were located within 100 km of the east coast of Australia (Table 1). We sampled across seasons to ensure that a large portion of the invertebrate biodiversity was sampled and to target plants when flowering. We used within-species analyses to look at variation across sites and between summer and autumn sampling. No significant effects of sites or seasons were detected. Samples across sites and seasons were therefore pooled prior to analysis because site and seasonal variability was not our focus.

Herbivore and pathogen damage was estimated on 20 randomly chosen leaves from 10 plants for each species at each site; leaves were collected at the same time as the

invertebrate collections. Leaf damage or necrosis was scored visually on a scale of 0-100% (0 = necrosis, 100 = total necrosis). This method of sampling provides a quick easy estimate of herbivory but underestimates total herbivory from leaves or other parts of the plant that are wholly eaten (Lowman 1984).

At each site where damage levels were scored, the invertebrate assemblage was sampled on five, randomly selected plants, including flower heads, stems and leaves and roots. For larger plants including perennial shrubs, one middle branch of the plant similar in volume to *S. madagascariensis* was collected, in addition to a portion of the roots. Each plant sample collected was separated by at least 2 m for all species.

Plants were sampled using two techniques that targeted: 1) Herbivores that feed externally, such as leaf chewers and phloem feeders, which were collected by bagging whole plants; and 2) Herbivores that feed internally, and those hatching from eggs and immature stages, which were reared from the flowers, stems and leaves and the roots. Species accumulation curves were constructed to determine the number of samples that was needed to collect a representative sample of the richness of invertebrate herbivores (Colwell & Coddington 1994). The accumulation curves indicated that the sampling effort was sufficient to make comparisons across species.

Plate 1. Range of *Senecio* species architectures compared in study. Non-native species denoted by *.



S. madagascariensis*



S. amygdalifolius



S. pinnatifolius var. pinnatifolius



S. angulatus



S. linearifolius var. arachnoideus



S. glastifolius*



S. pterophorus

Latitude	Longitude	Dates collected	Location	Habitat
S. madagascarie	nsis*			
34°46'29.91"S	150°40'11.14"E	10.01.2009 23.04.2009	Schofields Lane, Berry	Farmland
32°42'58.34"S	151°32'50.34"E	05.02.2009 28.05.2009	Walka Water Works, end of Waterworks Rd., Maitland	Disturbed bushland
31°28'32.55"S	152°56'12.85"E	18.12.2009 18.05.2009	Tacking Point Lighthouse, Port Macquarie	Disturbed bushland
S. pterophorus*				
33°46'53.08"S	151° 8'14.79"E	02.12.2009	Lane Cove National Park	Disturbed bushland
33°45'44.87"S	150°53'6.24"E	10.01.2009 25.05.2009	Reserve cnr. of Clarence & McCulloch Road, Doonside	Disturbed bushland
32°51'28.24"S	151°37'5.28"E	05.02.2009	Pambalong Nature Reserve	Disturbed bushland
33°52'38.47"S	150°50'27.37"E	27.05.2009 25.05.2009	Walgrove Rd, Cecil Pk.	Disturbed bushland
<u>S. angulatus*</u>				
33°46'37.00"S	150°59'48.77"E	10.01.2009 25.05.2009	Model Farm Reserve Northmead	Disturbed bushland
33°59'3.73"S	151°14'30.09"E	26.11.2008 18.03.2009	Jennifer St., Little Bay	Disturbed bushland
32°56'14.00"S	151°46'26.77"E	05.02.2009 01.04.2009	Nesca Park, Newcastle	Disturbed bushland
<u>S. glastifolius*</u>				
34° 5'14.43"8	151° 9'29.19"E	24.11.2008 17.03.2009	Fire break near Eric St. Royal National Park, Bundeena	Disturbed bushland
S. macroglossus ²	*			
<u>32°47'14.07"S</u>	152° 6'47.61"E	14.12.2008 28.05.2009	Ocean Pde., Boat Harbour	Disturbed bushland
28°19'39.71"S	153°33'55.84"E	16.05.2009	Cabarita Beach northern end of Grevillea Ave., Cabarita Beach	Disturbed bushland
36° 3'0.29"S	150° 8'23.48"E	22.04.2009	Tuross Head	Hind dunes
S. pinnatifolius v	ar. pinnatifolius			
32°10'2.50"S	152°30'16.87"E	15.12.2008 02.05.2009	Tuncurry	Hind dunes
31°28'32.55"S	152°56'12.85"E	18.12.2009 18.05.2009	Tacking Point Lighthouse, Port Macquarie	Headland
34° 2'21.13"S	151°12'58.53"E	24.11.2008 17.03.2009	400m East S end Sir Joseph Banks Drive, Kurnell	Headland

Table 1. Locations and dates of plant species sampled. Non-native species denoted by *.

Latitude	Longitude	Dates collected	Location	Habitat
S. linearifolius va	r. arachnoideus			
34°24'7.37"S	150°49'39.80"E	15.11.2008 17.03.2009	Harry Graham Drive, Mount Keira	Roadside wet sclerophyll forest escarpment ranges
31°32'51.5"S	151°47'30.6"E	19.01.2009 01.05.2009	Nowendoc Rd, 7.1km E. Nowendoc	Roadside wet sclerophyll forest escarpment ranges
S. amygdalifolius				
31°22'17.64"S	152° 4'10.20"E	16.12.2008 19.05.2009	NSW: Tobins Rd. off Oxley Hwy., Cotton-Bimbang National Park	Roadside wet sclerophyll forest escarpment ranges
31°33'05.6"S	151°48'27.9"E	19.01.2009 01.05.2009	Nowendoc Rd, 9km E. Nowendoc	Roadside wet sclerophyll forest escarpment ranges
31°54'04.0"S	151°37'23.1"E	20.01.2009 02.05.2009	Cobark Lookout, Barrington Tops	Roadside wet sclerophyll forest escarpment ranges
S. minimus				1 6
31°21'55.56"S	152° 2'29.94"E	16.12.2008 19.05.2009	Track off Oxley Hwy. 15km from Gingers Creek.	Roadside wet sclerophyll forest escarpment ranges
31°53'50.2"S	151°36'01.4"E	20.01.2009	Cobark Park, Barrington Tops	Roadside wet sclerophyll forest
33°42'9.56"S	151° 4'47.98"E	26.11.2008	Ginger Meggs Park, Hornsby.	escarpment ranges Disturbed bushland
S hinningtiscotur				
<u>S. bippinatisectus</u> 31°21'56.51"S	152° 2'43.76"E	16.12.2008	Roadside, 15km from Gingers Creek, Oxley Hwy.	Roadside wet sclerophyll forest escarpment ranges
31°59'59.6"S	151°49'23.0"E	20.01.2009 02.05.2009	Scone Rd, Copland Tops State Forest.	Roadside wet sclerophyll forest escarpment ranges
33°42'36.52"S	151° 4'27.71"E	26.11.2008 15.04.2009	Reserve near Westleigh Fire Station, Westleigh	Bushland

Each plant, including the roots (or a similar volume for shrubs and climbers based on the average plant size of S. madagascariensis) was collected into a bag and refrigerated for at least 2 hours before invertebrate removal. Invertebrates found externally on the stems and flowers of plants were then removed. Flower heads, stems and leaves and roots were separated and stored in clear plastic containers (1L and 1.25L) with a covering of polyester organza (Plate 2). The containers were stored in a glasshouse and checked regularly for emerging invertebrates over a four-month period. Immature stages of externally feeding invertebrates that could not be readily identified at time of collection and could not be reared on decaying vegetation were reared to adults on plants of the same species grown in a glasshouse (Plate 2). The stems and leaves, flowers and roots for each individual were then dried separately at 70°C for 12 hours and biomass recorded. Herbivores were identified to family level and then morphospecies based on available taxonomic keys (CSIRO 1973; Rentz 1996; Lawrence et al. 1999; Shattock 1999; Hamiilton et al. 2005; CSIRO 2011) and personal communication with entomologists. Where individual morphospecies dominated species level analyses, genus or species level identification was made where possible (Appendix 2). Voucher specimens of the invertebrates are lodged in the Entomology collection of the Australian Museum in Sydney. Voucher specimens for plant species are lodged in the Downing Herbarium, Macquarie University, Sydney.

Senecio phylogeny

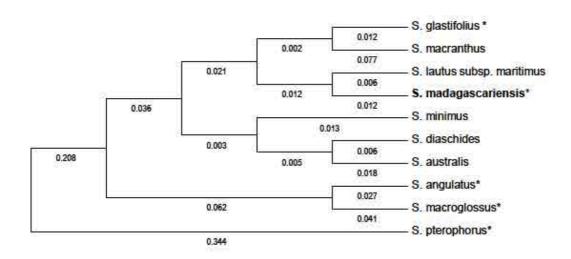
Phylogenetic relationships among *Senecio* species were determined using recent literature (Thompson 2006; Pelser *et al.* 2007) and estimated from internal transcribed spacer 1 (ITS 1) nucleotide gene sequences from a nucleotide database (Pelser *et al.* 2007; National Center for Biotechnology Information (NCBI) database <u>www.ncbi.nlm.nih.gov</u>) (Fig. 1; Appendix 1). All sequences were available for non-native *Senecio* species, but three (*S. linearifolius* var. *arachnoideus*, *S. amygdalifolius* and *S. bippinnatisectus*) of the five native species were not present in the database. For these three species we used information from their taxonomic classification (Thompson 2006; Pelser *et al.* 2007) and substituted available ITS 1 gene sequences of other *Senecio* species as a reasonable indicator of phylogeny. We believe this approach is appropriate because after mapping all *Senecio* species occurring in Australia with available ITS 1 gene sequences, we found that the broad groupings of Australian *Senecio* species as determined by Thompson (2006), matched phylogenetic relationships from ITS 1 nucleotide gene sequences (Pelser *et al.* 2007). An estimate of the phylogeny of *Senecio* was constructed using neighbour joining from maximum composite likelihood and tested using the bootstrap method with 500 replicates. To investigate the association between herbivore assemblages and phylogenetic relationship between *Senecio* species, pairwise genetic distances using Nei's Genetic Distance (Nei & Kumar 2000) from the *Senecio* phylogeny were calculated. All phylogenetic analyses were performed using the software package, Molecular Evolutionary Genetics Analysis (MEGA 5; Tamura *et al.* 2011). Plate 2. Immature stages of externally feeding invertebrates that were reared on adults of the same species grown in a glasshouse because they could not be identified at time of collection and could not be reared on decaying vegetation (a); Invertebrates reared from containers (b) and stored in a glasshouse (c).







Figure 1. Phylogenetic relationships and branch lengths within *Senecio* from nucleotide Internal transcribed spacer 1 gene sequences obtained from NCBI database <u>http://www.ncbi.nlm.nih.gov/nucleotide/</u>. Non-native species are denoted by asterisks. The invasive species *S. madagascariensis* is shown in bold.



Sampling variables

Invertebrate herbivores collected from each species were combined, pooling collections from the two sampling techniques, and from each location and season. The following parameters were calculated: (1) abundance (2) morphospecies richness, and (3) evenness (Shannon diversity index; $(H' = -\sum (p_i \ln p_i))$ where p_i is the proportional abundance of the *i*th morphospecies). Herbivores were assigned to four trophic guilds: leaf chewers, sapsuckers, miners and gall inducers. These groupings were based on the published biology of the invertebrates at family level (CSIRO 1973; Rentz 1996; Lawrence *et al.* 1999; Shattock 1999; Hamilton *et al.* 2005; CSIRO 2011) and personal communications with entomologists.

Statistical analyses

Univariate analyses

To compare leaf damage and herbivore guilds (leaf chewers, sap-suckers, miners and gall inducers) across all the *Senecio* species we used a two factor nested Analysis of Variance (ANOVA) with category (native, non-native) and species (n=10) nested within category. All variables were considered fixed factors. Leaf damage data was transformed to $\log x + 1$ and comparisons for each herbivore guild were transformed to the arcsine of their square roots before the analysis to homogenise the variances and meet the assumption of normality.

To compare herbivore assemblages among native and non-native *Senecio* species, we used a two factor nested Analysis of Covariance (ANCOVA) with category (native or nonnative), and species nested within category. To account for variation in plant sizes between species and across populations and differences in structural complexity between species, plant biomass was fitted as a covariate. All variables were considered fixed factors. Biomass, herbivore abundance and species richness were transformed to the log (x+1) to homogenise variances and meet assumptions of normality.

Multivariate analyses

Multivariate analyses of the invertebrate herbivore assemblage were also performed using the PERMANOVA add-on statistical package (Anderson 2001; McArdle & Anderson 2001) within PRIMER (Clarke 1993; Clarke & Gorley 2006). To compare the herbivore assemblage between native and non-native *Senecio* species we used a two factor nested PERMANOVA with category (native, non-native) and species (n=10) nested within category and biomass (log x+1) for each plant as a covariate. Category and species were both considered fixed factors. We used the Bray-Curtis measure of dissimilarity on log x+1 transformed data with 9999 permutations of residuals under a reduced model and Type 1 sum of squares. Samples without herbivores present were removed prior to analysis. Differences between native and non-native *Senecio* species were also compared using nonmetric, multidimensional scaling (Clarke 1993) based on Bray-Curtis dissimilarity.

Where there were clear patterns of difference in herbivore assemblages between native and non-native *Senecio* species, dominant invertebrate taxa contributing most to differences between plant species (with a cumulative cut-off of approximately 90%) were identified by SIMPER (Clarke 1993; Clarke & Gorley 2006). Dominant taxa collected from *S. madagascariensis* were also separately identified (SIMPER). Similarity Percentage analysis (SIMPER) calculates the average Bray-Curtis dissimilarity between all pairs of inter-group samples and expresses these differences in terms of the average contribution from each species (Clarke 1993).

Comparison of beta-diversity of invertebrate communities between native, non-native Senecio spp.

We used the PERMDISP function in PERMANOVA add-on statistical package (Anderson 2001; McArdle & Anderson 2001; Anderson *et al.* 2006) within PRIMER (Clarke 1993; Clarke & Gorley 2006) to compare the beta-diversity (that is, variation in composition between individual plants within a species) of herbivore communities collected from the invasive *S. madagascariensis* to that of the other *Senecio* species. PERMDISP tests for differences multivariate dispersion among groups by calculating the distances from observations to their centroids and comparing these average distances among groups (Anderson 2006). We ran PERMDISP on log x +1 herbivore abundances to find the mean deviation from the centroid across *Senecio* species with 9999 permutations using Bray-Curtis dissimilarity as the distance measure.

Phylogeny of Senecio and herbivore dissimilarity

The Bray-Curtis dissimilarity index on log x + 1 transformed data was calculated on the sum of herbivore individuals collected for each plant species. The pairwise genetic distances (Nei's Genetic Distance Nei & Kumar 2000) calculated from the *Senecio* phylogeny were then matched to the dissimilarities of herbivore species using the RELATE function within PRIMER (Clarke 1993; Clarke & Gorley 2006). The RELATE function calculates the Mantel correlation between pairwise dissimilarity (Bray-Curtis) in the herbivore assemblage across *Senecio* species and pairwise genetic distances using Spearman's Rank correlation index.

Results

Leaf damage

Leaf damage from herbivores and pathogens ranged from 6 to 20% across native and nonnative *Senecio* species (Fig. 2). Overall leaf damage, on average, was significantly lower on non-native species compared to native (Table 2; Fig. 2). Leaf damage on the invasive species *S. madagascariensis* was similar to the levels of damage found on other non-native *Senecio* species (Fig. 2).

Patterns of invertebrate abundance, richness and evenness

The total number of invertebrate morphospecies collected across the ten species of *Senecio* was 799 with 26% of these being herbivores. Overall, no significant differences were found in the abundance, morphospecies richness or Shannon diversity of invertebrate herbivores collected on native *Senecio* species compared to non-native species (Table 3; Fig. 3). Across *Senecio* species there were species level differences in invertebrate abundance, richness and Shannon diversity (Table 3; Fig. 3). Differences were to a large extent driven by the invasive species *S. madagascariensis* and the native *S. minimus* that supported a considerably more abundant and diverse fauna than the other *Senecio* species (Fig. 3).

Figure 2. Percentage leaf damage from herbivore and pathogen necrosis (\pm SE) across native and non-native *Senecio* species. The horizontal lines indicate the average leaf damage for native and non-native species collectively.

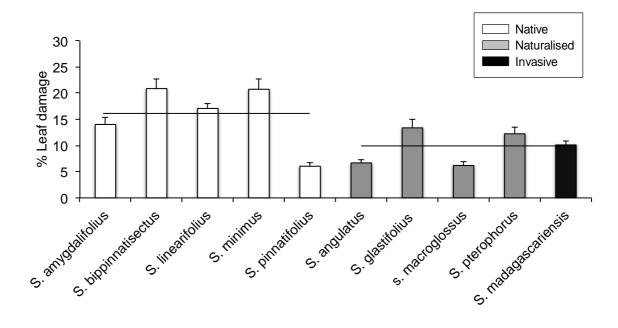


Table 2. Results of a two factor, nested analysis of variance for the effect of category (native, non-native d.f. = 1, 498) and species nested within category (d.f. = 8, 498) on the percentage leaf damage.

	Category		Species (Category)	
Variable	F	Р	F	Р
Percentage leaf damage	58.013	<0.001	24.405	<0.001

Figure 3. Abundance, morphospecies richness, and Shannon diversity of herbivores (±SE) across native and non-native *Senecio* species. Horizontal lines indicate average values for native and non-native species collectively.

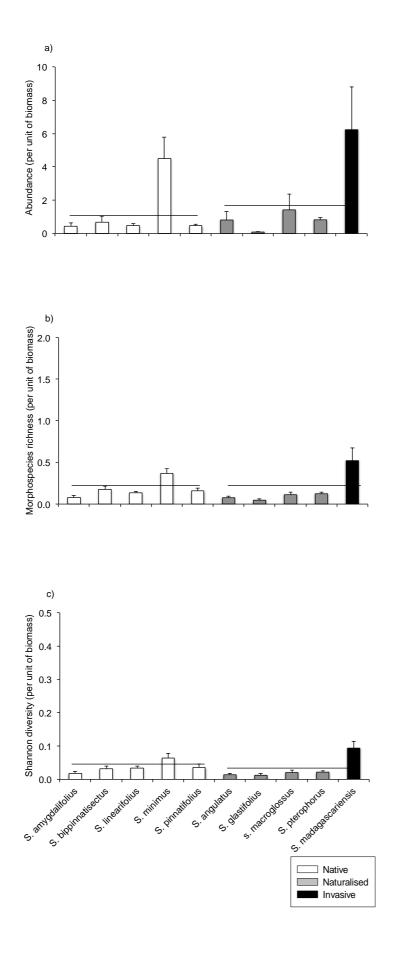


Table 3. Results of a two factor, nested analysis of covariance for the effect of category (native, non-native d.f. = 1, 244) and species nested within category (d.f = 8, 244) on invertebrate herbivore abundance, morphospecies richness and Shannon diversity after accounting for plant biomass (d.f. = 1, 244). Biomass, abundance and richness were transformed to the log (x+1).

	Bio	<u>mass</u>	Cate	egory	Species (<u>Category)</u>
Variable	F	Р	F	Р	F	Р
Abundance	10.477	0.001	0.124	0.726	11.515	<0.001
Morphospecies richness	12.451	<0.001	1.290	0.257	11.907	<0.001
Shannon diversity	8.423	0.004	0.472	0.493	8.640	<0.001

Herbivore guilds

There was no significant difference in the abundance and richness of herbivore guilds between native and non-native *Senecio* species (Table 4; Fig. 4a,b). However, species level differences were found between plant species for the abundance of phytophagous leaf-chewers and sap-sucking invertebrates. Forty per cent of the herbivores collected on the invasive *S. madagascariensis* were leaf-chewing invertebrates and overall, this species had a greater proportion of leaf chewing invertebrates than all other *Senecio* species. The non-native species, *S. macroglossus* DC., had the greatest proportion of sap-sucking herbivores (85%) compared to all other *Senecio* species.

Herbivore species assemblage

There were marked differences in the herbivore species assemblages supported by native and non-native *Senecio* species (Fig. 5, Pseudo F = 5.874, d.f. = 1, 209, p < 0.001), with an average between-group species assemblage dissimilarity of 94.81% (SIMPER). Within each category (native and non-native), herbivore assemblages on individual species were also significantly different (Fig. 5, Pseudo F = 3.406, d.f. = 8, 209, p < 0.001), with an average between-group community dissimilarity of 93.49% (native) and 91.72 % (nonnative).

SIMPER analyses indicated that most of the variation between assemblages was due to 10 herbivore species: two morphospecies of sap-sucking hemipterans (Aphididae Ap. 18, Ap. 27) predominately collected on the non-native *Senecio* species, four morphospecies of sap-sucking Hemipterans dominant on native *Senecio* species (morphospecies Het. 1 Hemiptera: Lygaeoidea; Het. 3 Hemiptera: Orsillidae: *Nysius clevelandensis* (Evans) and Au. 5 Hemiptera: Cicadellidae) and a heteropteran (Het. 2 Hemiptera: Miridae) which was dominant on non-native *Senecio* species. The other morphospecies that contributed

substantial amounts of variation between native and non-native groups all occurred in greater abundance on non-native *Senecio* species and included two leaf chewing herbivores (morphospecies L. 2 Lepidoptera: Pyraloidea and L. 20 Lepidoptera Arctiidae: *Nyctemera* sp. (Hübner)), a sap-sucking mite (morphospecies Ac. 44 Acari: Trombidiformes: Tenuipalpidae) and thrips (morphospecies T. 2 Thysanoptera: Thripidae: *Pseudanaphothrips achaetus* (Bagnall)) (Appendix 2).

Six herbivore species made up 90% of the assemblage collected on *S. madagascariensis*. This group included several of the above mentioned herbivores including the leaf chewing generalist herbivore (morphospecies L. 2 Lepidoptera: Pyraloidea) that contributed to 63% of the total abundance of herbivores collected on this host plant, sap-sucking thrips that contributed 14.5% (T. 2 Thysanoptera: Thripidae: *Pseudanaphothrips achaetus* (Bagnall)), three unknown morphospecies of aphids (morphospecies Ap. 18, Ap. 26 and Ap. 27. Hemiptera: Aphididae) and a sap-sucking heteropteran (morphospecies Het. 1 Hemiptera: Lygaeoidea) (Appendix 2).

Variation in herbivore communities between native and non-native Senecio species

Herbivore communities on non-native *Senecio* species exhibited similar among-plant variation in composition to that of the native species (PERMDISP F = 2.372, d.f = 1, 218, p (perm) = 0.145). However, significant differences between *Senecio* species were found (PERMDISP F = 7.36, d.f = 9, 210, p (perm) < 0.001). With the exception of *S. minimus*, *S. madagascariensis* on average recruited a less diverse fauna overall compared to all other native *Senecio* species, but among-plant variation on *S. madagascariensis* is similar to levels of other non-native *Senecio* species (Table 5; Fig. 6).

Phylogeny and community composition

Senecio madagascariensis is not phylogenetically isolated from the other species sampled, (Fig. 1). There was no correlation between phylogenetic distance between hosts and the dissimilarity of the herbivore assemblage collected (Fig. 7, RELATE Spearman rank correlation Rho = 0.104, p = 0.325). Overall, phylogeny does not appear to have any influence on differences in community composition between *Senecio* species.

Figure 4. Percentage abundance (a) and richness (b) $(\pm SE)$ of herbivore guilds (leaf chewers, sap-suckers, miners and gall inducers) collected on *Senecio* species.

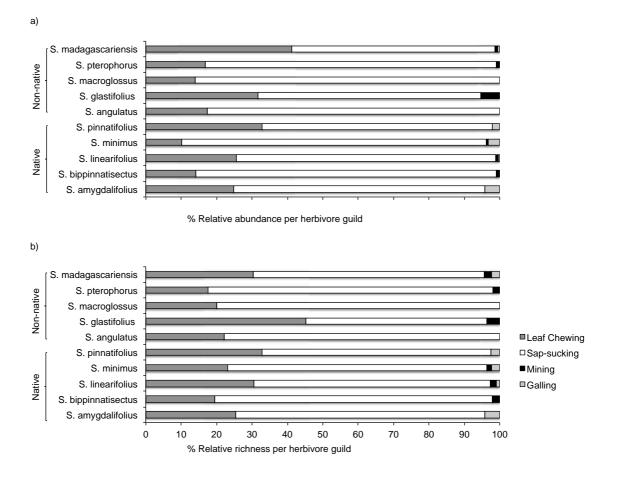


Table 4. Results of a two factor analysis of variance for the relative abundance and richness of herbivore guilds (leaf chewers, sap-suckers, miners and gall inducers) across *Senecio* species with effect of category (native, non-native d.f. = 1, 210) and species nested within category (d.f. = 8, 210).

	Cate	gory	Species (Category)
Variable	F	Р	F	Р
Abundance				
Chewers	0.391	0.533	4.068	0.020
Sap-suckers	0.137	0.711	2.362	0.019
Mining	0.166	0.200	1.597	0.127
Galling	2.157	0.143	0.601	0.777
Morphospecies richness				
Chewers	0.035	0.851	1.255	0.269
Sap-suckers	0.002	0.963	1.482	0.165
Mining	0.568	0.452	1.410	0.194
Galling	1.484	0.225	0.618	0.762

Figure 5. Non-metric, multidimensional scaling plot of herbivore assemblages from replicate samples (one point per plant for each species) of native and non-native *Senecio* species.

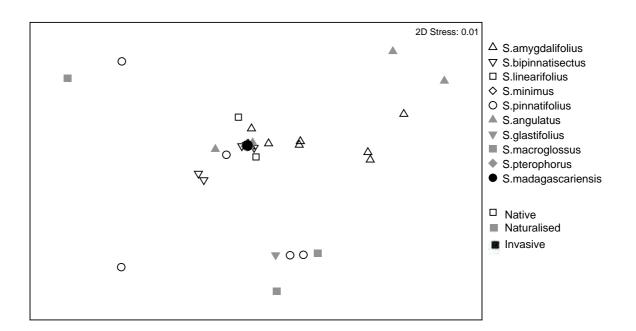


Figure 6. Average distance (±SE) for distance-based multivariate dispersion among native and non-native *Senecio* species.

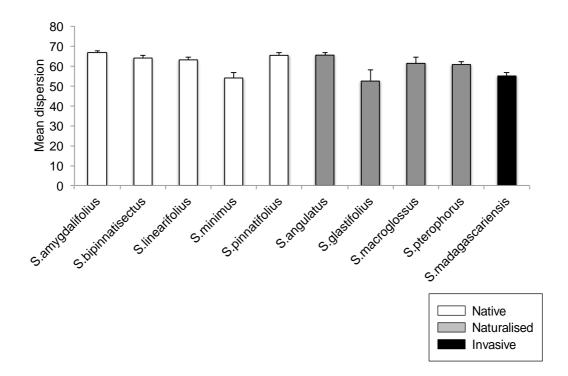
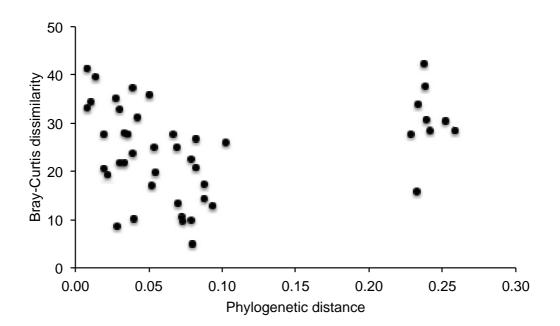


Table 5. Results of PERMDISP for differences in dispersion for *S. madagascariensis* compared to native and non-native *Senecio* species. Non-native *Senecio* species denoted by asterisks.

		Pairwise comparisons		
Variable		t	р	
S. madagascariensi	is			
	S. pterophorus*	2.330	0.033	
	S. glastifolius*	0.558	0.640	
	S. angulatus*	4.402	<0.001	
	S. macroglossus*	1.780	0.136	
	S. amygdalifolius	5.422	<0.001	
	S. bipinnatisectus	3.575	0.002	
	S. linearifolius var. arachnoideus	3.450	0.002	
	S. pinnatifolius var. pinnatifolius	4.536	<0.001	
	S. minimus	0.334	0.761	

Figure 7. Scatter plot of Bray-Curtis dissimilarity of herbivore composition with phylogenetic distance between native and non-native *Senecio* species.



Discussion

This study sought to determine the extent of enemy release and the importance of phylogenetic relationships in predicting invasion success among species within a single genus. As a mechanism of invasion, the enemy release hypothesis (ERH) predicts that non-native species may be successful as invaders due to being released from co-evolved natural enemies. Total damage, abundance, richness and Shannon diversity of herbivores, the proportional abundance and richness of herbivore guilds and the composition of the herbivore assemblage were compared between native, non-invasive and an invasive Senecio species (Senecio madagascariensis Poir.). The results provide very little support for the ERH, with non-native Senecio species receiving less leaf damage than native counterparts, but with similar levels of invertebrate herbivore abundance, richness and Shannon diversity and a similar proportional abundance and richness of feeding guilds compared to native Senecio species. Contrary to predictions, damage levels on the invasive species S. madagascariensis were similar to non-invasive species, and greater than on the closely related native S. pinnatifolius var. pinnatifolius. Overall, S. madagascariensis had a greater abundance and richness of herbivores than all other Senecio species. Herbivore communities were considerably different in composition between native and non-native Senecio species. Senecio madagascariensis did not have a reduced subset of the native herbivore community as indicated by a similar variation in composition among plants to other non-native species, but may be accumulating a more generalist assemblage indicated by a greater abundance of chewing herbivores than all other Senecio species. Phylogenetic distance between Senecio species could not explain the differences in the herbivore assemblages. Further, as the phylogeny of Senecio species does not indicate the phylogenetic isolation of non-natives including S. madagascariensis

(Thompson 2006; Pelser *et al.* 2007), the results overall suggest that enemy release is not an immediate contributing factor to the success of *S. madagascariensis*.

The majority of published studies on herbivore damage and the accumulation of the herbivore community have focused either on herbivory alone, or on herbivore abundance and richness, with few studies considering both. In two separate studies on native, non-invasive and invasive *Eugenia* spp. (Myrtaceae), Liu *et al.* (2006, 2007) found that while herbivore damage was lower on non-native species, non-invasive species sustained similar levels of herbivore damage to the invasive *Eugenia* species. Further, herbivore richness was similar between the native, non-invasive and invasive *Eugenia* species (Liu *et al.* 2007). These studies are consistent with our results. If we did not include the non-invasive *Senecio* species when comparing herbivore damage, we may have concluded that release from the insect herbivores may be an important factor in the success of *S. madagascariensis*.

The enemy release hypothesis further predicts that non-native species are more likely to be released from specialist herbivores in their new range but are more susceptible to generalist insect activity (Keane & Crawley 2002). As internal feeding niches (miners and gall inducers) are often associated with specialised diets (Frenzel and Brandl 1998), non-native plants may be more susceptible to attack by generalist ectophagous herbivores (leaf chewers and sap-sucking herbivores). In this study, we found that the proportion of feeding guilds across *Senecio* species did not vary between native and non-native species. Interestingly, very few endophagous herbivores were collected on *Senecio* species; the assemblages were dominated by leaf chewing and sap-sucking herbivores. Categorising ectophagous insects as generalists in this study, however, is unlikely to be sufficient for determining whether non-natives are released from specialist herbivores and more susceptible to damage by generalist insect activity. While some studies have found

success in categorising ectophagous insects as generalists (Frenzel and Brandl 1998; Liu *et al.* 2007; Frenzel & Brandl 2003), species level identifications are required in our case because it is probable that several of these leaf chewing and sap-sucking herbivores may be specialists. Unfortunately, there is insufficient information on feeding preferences available for the majority of Australian insects to confidently categorise most as eiher specialists or generalists. Further investigation into herbivore feeding rates, host plant choice and the impacts and performance of herbivores across the range of non-native *Senecio* species is required for a greater understanding of whether non-native species may be released from specialist natural enemies.

Contrary to our predictions, *S. madagascariensis* had a greater abundance, richness and Shannon diversity of herbivores than all other *Senecio* species sampled. Other workers have also found high densities of herbivores on non-native species with levels similar to, or greater, than native plants (French & Eardly 1997; Viejo 1999; Hedge & Kriwoken 2000; Petillion *et al.* 2005). Greater density and diversity of herbivores collected from this invasive species compared to native species may not necessarily translate to greater enemy attack, but may be attributed to herbivores using this plant for oviposition sites, nesting and reproduction.

Senecio madagascariensis has rapidly accumulated a generalist herbivore assemblage but may also have developed a specialist assemblage, which may explain why there are greater abundances and richness of herbivores overall collected on this species compared to the other non-native species sampled. A greater density and diversity of herbivores on this species compared to the other non-invasive species may be in part attributed to *S*. *madagascariensis* being present on the east coast of NSW for a longer period of time or having a larger geographical range (species area effect; Connor & McCoy 1979; Southwood 1961) compared to the other non-native species. *Senecio madagascariensis*

was first recorded in the Hunter Valley in 1918 and, according to NSW herbarium records, occurrences for all other non-native species in eastern NSW are no earlier than 1957. Moreover, the species area effect, suggests that plants with large geographical ranges or those that are in larger densities with a greater biomass per unit area have more species of associated insects than those with smaller geographical ranges or smaller densities (Southwood 1961; Strong 1979). Indeed, herbarium records indicate that *S. madagascariensis* has a greater range (in terms of occurrence records) than the other non-native species throughout Australia. Future research focusing on the taxonomy, impacts of herbivores and community development would give insight into how specialised the community has developed over time and the role herbivores play in utilising *S. madagascariensis*.

Although there were some herbivore species in common across *Senecio* species, herbivore communities overall differed markedly among *Senecio* species. Large differences in community composition were particularly evident when the native species as a group were compared to the group of non-native species. Corresponding differences in plant structure or architecture; and/or differences in the nutritional value or chemical composition and biomass per unit area across sites may account for the differences in the herbivore assemblage between *Senecio* species. The *Senecio* species sampled included a variety of herbs, shrubs and vines for both the native and non-native species groups. It is likely that variations in plant architecture (Lawton & Schroeder 1977), that may include differences in the size, growth form and types of aboveground and belowground structures, may provide different microhabitats that influence the colonisation of insect herbivores. Past studies have indicated that differences in microhabitats created by non-native species are associated with variation in the invertebrate assemblage (Hedge & Kriwoken 2000; Petillion *et al.* 2005) through causing variation in light penetration, protection from abiotic

stresses and predators and suitability for resting, feeding, reproduction and nest building (Strong *et al.* 1984). The nutritive value including chemical composition and water content, and other variables such as trichome density and mechanical properties can vary greatly between even closely related species and have been shown to influence host plant selection, palatability and the demography and population dynamics of many insect taxa (Crawley 1983, Strong *et al.* 1984; Agrawal *et al.* 2005). For example, the Richmond birdwing butterfly (*Ornithoptera richmondia*) requires the native plant species of *Aristolochia* and *Pararistolochia* for breeding, but can mistakenly oviposit on the highly invasive Dutchman's Pipe vine - *Aristolochia elegans*, which is highly toxic for the larvae (Braby 2000). *Senecio* species are known to contain pyrrolizidine alkaloids, which can vary within and among species, across their ranges and overall influence herbivore host choice (Hol 2011; Langal *et al.* 2011). By minimizing variation in plant biomass in our sampling and by comparing congeneric species, we have attempted to control for at least some of these potential confounding factors that may contribute to variation in our data.

In summary we did not find evidence to support the hypothesis that enemy release explains the success of the invasive plant *S. madagascariensis*. The results of this study indicate that for closely related species, enemy release may not be important as a mechanism for the success of some invasive species. Areas of future research could include understanding how time may be important for propagules to spread and the populations to increase. Future research focusing on the taxonomy and impacts of herbivores and the development of the community from its point of introduction to its invasion fronts would give insight into the development of a specialist and generalist assemblage on *S. madagascariensis* and give a better indicator of the role of natural enemies in invasion biology over time.

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Chapter 4

Does time since introduction influence enemy release of an invasive weed?

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Abstract

Release from natural enemies is considered to potentially play an important role in the initial establishment and potential success of introduced plants. With time, the species richness of herbivores using non-native plants has been found to increase, providing the community is not already saturated (known as the species-time relationship). During this time herbivores and their hosts may develop closer physiological or co-evolutionary associations. Time since introduction may affect the amount of enemy release experienced by an invader, resulting in its rate of spread being potentially reduced as herbivores adapt to it over time. In this study, we investigated whether the amount of enemy release experienced by an invader may be limited to the early stages of its invasion. Substituting space for time, we sampled invertebrates and measured leaf damage on the invasive species *Senecio madagascariensis* Poir. This species has extensive historical data detailing its known point of introduction and spread on the east coast of Australia. We sampled at multiple sites that encompassed the current latitudinal range of S. madagascariensis (~1000 km) and included sites to both the north and south of the point of introduction. Invertebrate communities were collected from the plants in the field, as well as being reared from collected plant tissue over several months post-collection. Because the sites are located along a latitudinal gradient, and therefore differ in climate as well as in time since introduction, we also sampled invertebrates and estimated damage on the closely related native congener S. pinnatifolius var. pinnatifolius A. Rich. at the same sites. This species therefore served as a control to help account for environmental factors but also as a comparison for evaluating the enemy release hypothesis (ERH). Our results provided no support for the enemy release hypothesis but did provide partial support for the speciestime relationship. Greater damage and herbivore abundances and richness were found on S. madagascariensis than its native congener, S. pinnatifolius, in contrast to predictions of

the enemy release hypothesis. Invertebrates decreased in abundance, richness and Shannon diversity from the point of introduction to the invasion front, supporting the species-time relationship. Leaf damage showed the opposite trend, with highest damage levels at invasion fronts. Greater herbivore abundance, richness and Shannon diversity of reared herbivores (as opposed to external collections) were found on the invasive species at the point of introduction compared with sites further from this region, indicating that closer physiological associations in plant-herbivore interactions may have developed with increasing time since introduction. Our results suggest that there is a complex relationship between the invader and the response of the invertebrate community over time. There is the potential that *S. madagascariensis* may be undergoing rapid changes at its invasion fronts in response to environmental and herbivore pressure, which may in turn be influencing these plant-herbivore interactions.

Key words: species-time relationship, invasive plants, enemy release hypothesis, congeners, plant-insect interactions, evolution of increased compatibility hypothesis.

Introduction

The enemy release hypothesis (ERH) predicts that when non-native plant species are introduced to a new region with few or no co-evolved specialist herbivores from their native habitat, they suffer only minimal damage from generalist polyphagous herbivores and thereby gain a competitive advantage over native plants (e.g. Keane & Crawley 2002). Understanding how rapidly both specialist and generalist insects adapt to and colonise nonnative invasive plants is integral to understanding the basis of the ERH as a mechanism behind successful invasions.

Studies in which the densities and damage by herbivores and pathogens on non-native species within their introduced range compared to that of their native range have generally found support for the enemy release hypothesis (reviewed by Colautti *et al.* 2004; meta-analysis by Liu & Stiling 2006). In contrast, comparisons of non-native species in their introduced range with co-occurring native species have yielded mixed results (reviewed by Colautti *et al.* 2004; meta-analysis by Chun *et al.* 2010), with some cases showing that greater herbivory is found on non-native compared to native species (Agrawal & Kotanen 2003). Although damage levels on non-native species may be generally lower in their country of origin compared to the area of introduction, native herbivores do adapt to and colonise non-native species. The complexity and unpredictability in patterns of damage and densities of herbivores between native and non-native species may be the result of complex interactions between the time since a plant's introduction, the phylogenetic relatedness of the invader and other species within the invaded community, and the influence of a variety of abiotic factors.

The observation that species richness of herbivores on introduced plants accumulates through time was first noted by Preston (1960). This pattern is referred to as the species-

time relationship (STR) and describes how the species richness of a community increases with time, provided the community is not already saturated (*sensu* Preston 1960). This relationship is analogous to the species-area relationship whereby richness increases with the local abundance and area of habitat sampled (Arrhenius 1921; Preston 1960). For non-native species, time since introduction may be an important determinant of herbivore and pathogen accumulation and therefore the potential pressure they may exert on the success of the invader (Strong *et al.* 1984; Siemann *et al.* 2006; Mitchell *et al.* 2010). If herbivores adapt to and colonise the non-native species gradually over time, enemy release may be limited to the early stages of invasion (Siemann *et al.* 2006; Hawkes 2007). Moreover, while time has been suggested to be important for insects and pathogens to adapt to non-native species. Some non-native species have been found to support similar insect communities to natives within a few hundred years (Strong *et al.* 1984), while rapid evolution of specific herbivores to non-native species may occur in as little as 50 years (Carroll *et al.* 2005).

There is conflicting evidence for the importance of time in the success of invasive species (Carpenter & Cappuccino 2005; Siemann *et al.* 2006). It is likely that differences in the extent of species geographic ranges (Strong 1974; Strong 1979; Neuvonen & Niemela 1981), variation in growth forms (Lawton & Schroeder 1977) and the phylogenetic relationships of species with respect to the native community (Conner *et al.* 1980; Lawton & Strong 1981; Strong *et al.* 1984), may mask the role of time in the accumulation of natural enemies on non-native species. Some of these confounding factors can be accounted for by including measures of plant biomass and by comparing herbivory and herbivores on the invader with that of a co-occurring congeneric native species.

Most species of phytophagous insects are specialised to feed on just a few host plant

species (Bernays & Graham 1988). When a non-native plant invades a new habitat, it generally leaves behind its co-evolved herbivores and pathogens (Keane & Crawley 2002). These specialist insects and pathogens are replaced by generalists in the new range (Keane & Crawley 2002). This implies that the longer a plant species has been established within a community, the more specialised the herbivore assemblage it supports (Andow & Imura 1994). Indeed a review of arthropod communities on 24 annual crop species found that the proportion of specialists was greater than generalists on plant species that had been in Japan for longer periods of time (Andow & Imura 1994). This indicates that closer physiological associations may occur between an invader and its natural enemies over time. The overall impact of herbivores and pathogens may thus be determined by the net effect of escaping specialists and acquiring new natural enemies over time.

By comparing rates of herbivore accumulation and damage in newly colonised regions to older sites of invasion, it should be possible to gain insight into the role time plays in adaptation of herbivores to invasive species. In this study, our focus was the invasive species *Senecio madagascariensis* Poir. (Fireweed). This species provides an ideal system to study the process of natural enemy accumulation due to historical data that details its known point of introduction in the Hunter Valley, NSW (1918) and steady spread for over 90 years to the north and south of this region. We investigated how rapidly *S. madagascariensis* has been colonised by invertebrates by comparing the assemblages on *S. madagascariensis* from sites where it was first introduced, to other sites, to both the north and south. Our general aim was to assess whether the relationship between this invasive species and its natural enemies has changed over time. We made the following predictions:

(1) In accordance with the 'Enemy Release Hypothesis' (ERH), the total damage and abundance of invertebrates including non-herbivores would be less on *S. madagascariensis*

than on a closely related congener *S. pinnatifolius* var. *pinnatifolius* A. Rich. at the same sites.

(2) In accordance with the 'Species-Time Relationship' (STR), damage, herbivore abundance, and species richness would decrease on *S. madagascariensis* from its point of introduction to the invasion fronts.

By comparing herbivore accumulation and damage impacts over time, we specifically investigated whether enemy release may be limited to the early stages of its invasion. We further identified herbivores that contributed to differences across the range of *S*. *madagascariensis* to correlate damage with herbivore identity.

Our sampling encompassed both herbivores and the general invertebrate assemblage. Assessing the invertebrate assemblage as a whole assists in investigating whether changes in predator prey interactions, in addition to disturbance by non-herbivorous invertebrates, may contribute to facilitating the establishment and spread of non-native species over time. Therefore, we made the further prediction that:

(3) In accordance with the 'Species-Time Relationship' (STR), the total invertebrate abundance including non-herbivores would decrease on *S. madagascariensis* from its point of introduction to invasion fronts.

We also investigated how the types of herbivores on the plant varied from the introduction point to the invasion fronts. Internal feeders, such as gallers, stem borers and leaf miners and those species that oviposit into the plant tissue, may have developed more specialised associations with the plant than herbivores collected externally. A higher proportion of herbivores reared from internal plant tissues at the introduction point compared to the invasion fronts would indicate that, over time, closer physiological associations may occur between an invader and its natural enemies. Therefore, we further predicted that:

(4) The number of herbivores reared from internal tissues compared to those collected from external sampling of *S. madagascariensis* would increase from its introduction point to the invasion fronts.

For all predictions we compared the damage and invertebrate assemblage on the congeneric native *S. pinnatifolius* var. *pinnatifolius*. This species has a similar distribution to *S. madagascariensis* on the east coast of Australia and they commonly co-occur together. *Senecio pinnatifolius* var. *pinnatifolius* was used as a community based comparison of the ERH, in addition to serving as a control to account for the invertebrate community being influenced by other factors including latitude (Rosenzweig 1995; reviewed by Moles *et al.* 2011).

Methods

Plant species

Senecio madagascariensis Poir. is an aggressive annual or biennial herbaceous weed that invades pastures and disturbed areas of eastern Australia (Holtkamp & Hosking 1993) and is of significant concern due to its toxicity to domestic livestock (Sindel 1986). The species has been declared a noxious weed in New South Wales, Queensland and the Australian Capital Territory (Parsons & Cuthbertson 1992). It was introduced from the KwaZulu-Natal province on the east coast of South Africa (Radford *et al.* 2000), and was first recorded in the lower Hunter Valley, NSW in 1918 (32°43'0"S, 151°49'60"E) (Fig. 1). It has since become prevalent along the east coast of Australia (Holtkamp & Hosking 1993; Radford & Cousens 2000), extending from south-east Queensland into Victoria, a latitudinal distance of over 1000 km (Parsons & Cuthbertson 1992). Herbarium records indicate a steady invasion front along the coast to the north and south of the introduction point (NSW Collections database, National Herbarium of New South Wales). Recent evidence from nuclear microsatellite data indicates an augmentation of the population in far north-eastern NSW occurred in the mid 1950s (E. Dormontt *pers. comm.* 2011). This introduction was from the same genetic stock as the Hunter Valley region and is likely to have originated from crop seed used in industries such as turf farming (E. Dormontt *pers. comm.* 2011).

The invertebrate community on a single host plant, when sampled at different sites, may be influenced by factors other than time since colonisation, such as latitude (Rosenzweig 1995; reviewed by Moles *et al.* 2011). To control for the potential role of latitude in influencing the assemblage sampled on the invasive species, we also sampled a native senecio species, *S. pinnatifolius* var *pinnatifolius* A. Rich., at the same sites or nearby. *Senecio pinnatifolius* var. *pinnatifolius* is an herbaceous sprawling or prostrate annual or short-lived perennial that has a similar geographic range and appearance to *S. madagascariensis* in eastern Australia. It occurs in scattered populations in dry hills, coastal dunes, forest, woodland and scrubland throughout south-east Queensland, extending south into Victoria (Thompson 2005).

Survey design

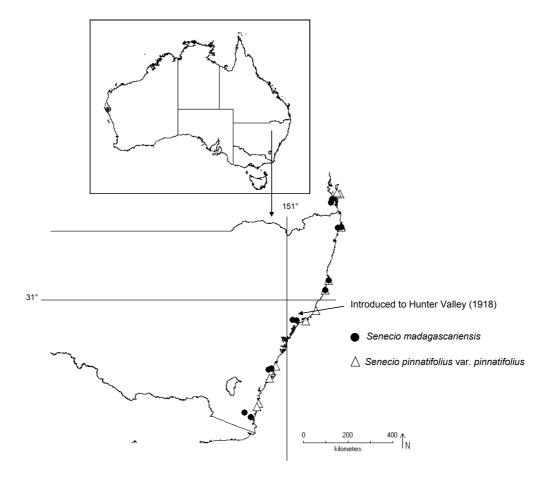
The study was conducted between March and May 2009 in coastal bushland and grazing land along the east coast of Australia extending from south-eastern New South Wales (NSW) to south-eastern Queensland (QLD). Plants were sampled in flowering periods only. Survey sites were divided into six latitudinal bands of 10°, covering the latitudinal distribution of *S. madagascariensis* ((1) 36-37°; (2) 34-36°; (3) 32-34°; (4) 30-32°; (5) 28-30°; (6) 27-28°). The northern-most site sampled was 584 km from the Hunter Valley

introduction region and the southern-most was 484 km south of the introduction region (Fig. 1). The distance between each latitudinal band was approximately 200 km. Sites north and south of the Hunter Valley were then grouped into four bands in terms of the distance from the introduction point to the invasion fronts ignoring latitude (0-100: 101-300: 301-500 and 501-700 in kilometres). Two sampling sites within each of the 6 latitudinal bands were selected in which *S. madagascariensis* and *S. pinnatifolius* var. *pinnatifolius* co-occurred. Where the species did not co-occur, *S. pinnatifolius* var. *pinnatifolius* was sampled at the closest site to where *S. madagascariensis* had invaded (Fig.1). At each site, insect assemblages were sampled once on 5 randomly selected similar sized plants of each plant species. Each plant sampled was separated by at least 2 m from all other plants on the site.

Plants were sampled for invertebrates using two techniques: direct external collections and rearing from plant material. Each plant, including above and belowground biomass was collected and placed into a plastic bag, which was then refrigerated. Invertebrates found externally on the stems, flowers and among the soil from the roots of plants were then removed. Immature stages of externally feeding invertebrates that could not be readily identified at time of collection and could not be reared on decaying vegetation were reared to adults on plants of the same species grown in a glasshouse. The plants were then separated into (1) flowers, (2) stems and leaves and (3) roots, and stored in clear plastic containers with a covering of polyester organza. The containers were stored in a glasshouse and checked regularly for emerging invertebrates over a four-month period. To account for variation in plant sizes between species and across populations, the flowers, stems and leaves, and roots for each individual were dried separately at 70°C for 12 hours and the biomass (expressed per gram of dry plant weight) was recorded.

Invertebrates were identified to family level and then morphospecies, using the published biology of the invertebrates at family level (CSIRO 1973; Rentz 1996; Lawrence *et al.* 1999; Shattock 1999; Hamilton *et al.* 2005) and personal communications with entomologists (Appendix 3). Invertebrate collections are lodged in the entomology collection at the Australian Museum, Sydney and voucher specimens for both plant species collected at each site are lodged in the Downing Herbarium, Macquarie University, Sydney.

Figure 1. Map of the locations of the non-native species *Senecio madagascariensis* and native congener *S. pinnatifolius* var. *pinnatifolius* sampled in this study.



To assess herbivore and pathogen damage, 20 leaves randomly chosen from each of 10 individual plants from both *S. madagascariensis* and *S. pinnatifolius* var. *pinnatifolius* were collected at the same time as the invertebrate collections. Necrosis or leaf damage on each leaf was visually scored on a scale of 0 - 100%. While this method of sampling provides a quick easy estimate of herbivory, it underestimates total herbivory from leaves or other parts of the plant that are wholly eaten (Lowman 1984).

Statistical analysis

Data from the two sampling techniques (external collections plus reared invertebrates) was combined to estimate: (i) abundance of individuals (ii) morphospecies richness and (iii) the Shannon diversity index $(H' = -\sum (p_i \ln p_i))$ where p_i is the proportional abundance of the *i*th morphospecies). These parameters were estimated for the total invertebrate assemblage to gain insight into colonisation of the whole invertebrate community in addition to the herbivores alone. Data from each of the sampling techniques was then separated into external and reared herbivores and the (i) abundance (ii) morphospecies richness and (iii) Shannon diversity was estimated for each.

Two comparisons were made: (1) invertebrate assemblages, leaf damage and external and reared herbivores associated with the invasive *S. madagascariensis* and the native *S. pinnatifolius* var. *pinnatifolius* were compared among sites with increasing distance from the introduction point in the Hunter Valley to the invasion front north and south of this region. Using a space for time substitution, this comparison served to examine how the invertebrate community changes from its point of introduction to invasion fronts while ignoring latitudinal direction; (2) invertebrate assemblages, leaf damage and external and reared feeding herbivores associated with the invasive and native plants were compared among sites across six latitudes. This second comparison served to examine changes in the

invertebrate community over a latitudinal gradient, in particular to examine differences between the point of introduction and invasion fronts. As there was no between site variability for each species, samples from the two sites per species were pooled prior to analysis. Comparisons were made for each of the sampling variables by univariate analyses. Biomass, abundance and richness were transformed to the log (x+1) to improve the homogeneity of variance and to meet assumptions of normality.

For the first comparison, with the exception of leaf damage, a two-factor (plant species, distance) mixed model analysis of covariance (ANCOVA) was used. Plant species (*S. madagascariensis* or *S. pinnatifolius* var. *pinnatifolius*) and distance from the introduction region were considered fixed factors. Plant biomass for each plant was fitted as a covariate. The same analysis was used for the second comparison, but with six latitudinal bands instead of distance. For leaf damage, the same comparisons were made as above except biomass was removed as a covariate and the comparison became a two-factor mixed model analysis of variance (ANOVA). Where there were significant interactions between species and distance or species and latitude for *S. madagascariensis*, results were further analysed using Fisher's Least Significant Difference (LSD) post hoc multiple comparisons tests to determine the location of differences among means.

Multivariate analyses of the invertebrate herbivore assemblage using untransformed individual morphospecies abundance data was also performed using the Similarity Percentage analysis (SIMPER) in the PRIMER statistical package, to determine which taxa contributed most to the differences in the herbivore assemblage. SIMPER calculates the average Bray-Curtis dissimilarity between all pairs of inter-group samples and expresses these differences in terms of the average contribution from each species. A cumulative cut-off of approximately 90% was identified by SIMPER (Clarke 1993; Clarke & Gorley 2006).

Results

Relationship of total leaf damage and number of invertebrates between the native and nonnative invader

Leaf damage was generally low and ranged between ~5 and 15% for both the invasive *S. madagascariensis* and the native *S. pinnatifolius* var. *pinnatifolius* (Fig 2.) Contrary to predictions of the enemy release hypothesis (ERH), damage was significantly greater on the invasive species than the native (Table 1; Fig. 2).

A total of 5,408 invertebrates were collected from *S. madagascariensis*, comprising 309 morphospecies (54% of which were only recorded once) (Appendix 3). The total number of invertebrates collected from *S. pinnatifolius* var. *pinnatifolius* was approximately half that number (2,530) and comprised 215 morphospecies (34% of which were only recorded once). Of the total number of invertebrates collected, *S. madagascariensis* had a greater proportion of herbivores (65%) than the native congener (39%).

Patterns of herbivore damage, abundance, richness, Shannon diversity and composition

Support for the species-time relationship (STR) was found for herbivore loads (abundance, richness & Shannon diversity), which declined on *S. madagascariensis* with increasing distance from the point of introduction, with significant differences apparent for the abundance and Shannon diversity of herbivores from the point introduction to a sampling distance of 300-500 km (Table 2; Fig. 3). No support for the STR was found for leaf damage (Table 1; Fig. 2a). Damage on *S. madagascariensis* did not significantly increase on plants with increasing distance from the introduction region (Table 1; Fig 2a). Damage analyses show that *S. madagascariensis* was not released from natural enemies in its early stage of invasion. Levels of damage on *S. madagascariensis* were significantly lower at

the introduction origin and area of population augmentation in northern NSW compared to invasion fronts at the northern and southern boundary (Table 1; Fig. 2b).

Herbivore loads on S. madagascariensis across latitudes were in contrast to damage analyses, with a significantly greater richness and Shannon diversity of herbivores in the area of introduction compared to the southern-most location and a non significant trend towards an increase in herbivore richness and Shannon diversity in the area of introduction compared to the northern-most location (Table 3; Fig. 3). Although herbivore abundance appears to be greater at the area of introduction compared to the southern most and northern most invasion fronts no significant interaction was found between species and latitude (Table 3; Fig. 3). Northern locations had a significantly greater richness and Shannon diversity of herbivores and a marginally significant increase in abundances compared to the southernmost locations (Table 3; Fig.3). There was a decline in herbivore abundance, richness and Shannon diversity on S. madagascariensis in far north-eastern NSW at the region where augmentation of the population occurred, compared to the introduction origin, but these differences were only significant for Shannon diversity (Table 3; Fig. 3d, e, f). From this point of augmentation, there was a sharp increase in the richness and Shannon diversity of herbivores collected at the Queensland sites in the north but this increase was not significant (Table 3; Fig. 2).

Minimal variation in leaf damage, herbivore abundance, richness and Shannon diversity between latitudes was found for the native control species *S. pinnatifolius* var. *pinnatifolius* (Figs. 2, 3).

Most of the variation among the herbivore assemblages from point of introduction to invasion fronts was due to sap-sucking and chewing herbivores (SIMPER analysis). At sites in the area of introduction, five morphospecies of sap-sucking herbivores from the family Aphididae dominated 88% of the total herbivore assemblage, with a sap-sucker Nysius clevelandensis Evans (Orsillidae) contributing 4% to the herbivore assemblage. At the invasion front in the south, a leaf-feeding moth (Morphospecies L.2, Lepidoptera: Pyraloidea) comprised 88% of the herbivores with a heteropteran (morphospecies Het.2, Heteroptera: Miridae) contributing 8%. At the invasion front to the north, two morphospecies of Aphididae comprised 50% of the assemblage. The same leaf-feeding moth (Lepidoptera: Pyraloidea) that was collected at the invasion front in the south contributed to 7% of the herbivores in the north in addition to leaf-feeding thrips (morphospecies T.3, Thysanoptera: Panchaetothripinae: Bhattithrips sp.), contributing 15% of the herbivores. Other morphospecies of aphids and leaf- and flower-feeding thrips (Thripidae: *Pseudanaphothrips achaetus* Bagnell) contributed the remaining 90%. The herbivore assemblage in the area on the north coast of NSW where S. madagascariensis underwent augmentation in the 1950's was 90% dissimilar to the introduction region. Most of the variation was due to 5 morphospecies of Aphids (65% morphospecies Ap. 18, Ap. 24, Ap26, Ap.27 Ap.28 Aphididae) that were all in greater densities at the introduction origin compared to the region of augmentation, with the exception of Ap. 18. For the region of population augmentation, 39% of the herbivore assemblage was dominated by a sap-sucker (Hemiptera: morphospecies Het. 2, Heteroptera: Miridae) and an Aphid (Ap.18) added 29% of the remaining herbivores (Appendix 3).

Table 1. Results of a two-factor, analysis of variance and Fisher's Least Significant Difference (LSD) post hoc tests for total leaf damage on *S. madagascariensis*, with the effect of (a) plant species (*S. madagascariensis* or *S. pinnatifolius* var. *pinnatifolius*; (d.f. = 1, 228), distance from introduction site of *S. madagascariensis* (d.f = 5, 228) and their interaction (d.f = 5, 228); and (b) plant species (*S. madagascariensis* or *S. pinnatifolius* var. *pinnatifolius*; (d.f. = 1,2 28), latitude (bands 1-6; d.f. = 5, 228) and their interaction (d.f. = 5, 228). Total leaf damage was transformed to the log (x+1).

Leaf damage								
				F		Р		
				(2.001		0.01		
Plant species				62.291	<0	.001		
Distance				7.927 <0.00				
Species × Dis	tance			1.026 0.38				
Plant species				72.399	<0	.001		
Latitude				8.284	<0.001			
Species × Lat	itude			5.484	<0.001			
LSD post hoc	tests - S. mada	gascariensis						
	Lat1	Lat2	Lat3	Lat4	Lat5	Lat6		
Lat1								
Lat2	***							
Lat3	***	ns						
Lat4	ns	**	**					
Lat5	***	ns	ns	***				
Lat6	ns	***	***	ns	***			

ns = not significant; *<0.05; **<0.01; ***<0.001

Note: Latitudes 1-6 (southern most point 1; northern most 6; introduction region 3 and population augmentation 5)

Figure 2. Leaf damage on *S. madagascariensis* and *S. pinnatifolius* var. *pinnitifolius* with a) distance from introduction region to the invasion fronts for *S. madagascariensis* and b) across latitudes 1-6 (southern most point 1; northern most 6; introduction region 3 and population augmentation 5).

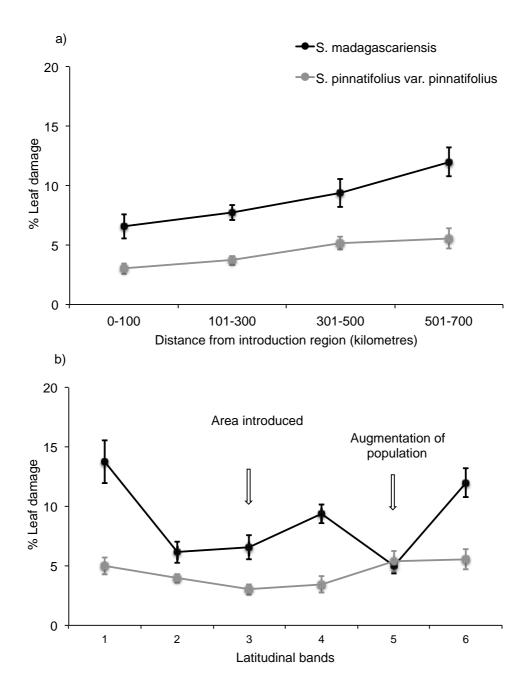


Figure 3. Abundance, morphospecies richness and Shannon diversity of herbivores collected on the non-native species *Senecio madagascariensis* and the native *S. pinnatifolius* var. *pinnatifolius* with distance from where *S. madagascariensis* was first introduced (a,b,c) and across latitudes 1-6 (d,e,f), (southern most point 1; northern most 6; introduction region 3 and population augmentation 5). Response variables are standardised by dividing by the dry weight (biomass) of the individual plants. Data points are means. Error bars are standard errors.

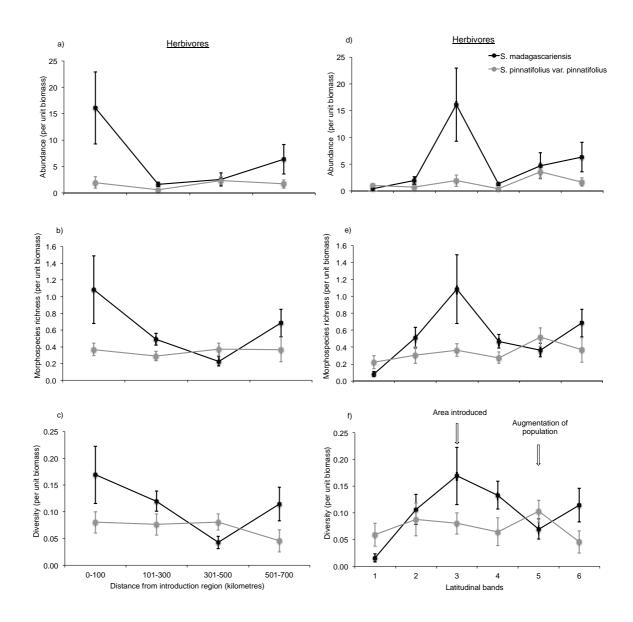


Table 2. Results of a two-factor analysis of covariance and Fisher's Least Significant Difference (LSD) post hoc tests for the effect of plant species (*S. madagascariensis* or *S. pinnatifolius* var. *pinnatifolius*; (d.f. = 1, 111), distance from introduction site of *S. madagascariensis* (0-100; 101-300; 301-500 and 501-700 km; d.f. = 3, 111) and their interaction (d.f. = 3, 111) on the abundance, morphospecies richness and Shannon diversity of invertebrate herbivores and total invertebrates. Dried plant mass (biomass) was fitted as a covariate (d.f = 1, 111). Biomass, abundance and richness were transformed to the log (x+1).

1 <u></u>		Bior	Biomass Plant species			Di	stance	Species	Species × Distance		
Variable		F	Р	F	Р	F	Р	F	Р		
Abundan	ce										
Herbivor	res	0.783	0.378	10.946	0.001	2.297	0.082	2.838	0.041		
Inverteb	Invertebrates 6.18		0.014	8.636	0.004	2.243	0.087	1.803	0.151		
Richness											
Herbivor	res	0.902	0.345	12.149	<0.001	2.191	0.093	5.107	0.002		
Inverteb	rates	6.786	0.010	9.457	0.003	1.635	0.185	3.438	0.019		
Diversity											
Herbivor	res	2.076	0.152	11.631	<0.001	2.264	0.085	5.142	0.002		
Inverteb	rates	3.177	0.077	7.552	0.007	1.626	0.187	3.905	0.011		
LSD post hoc tests - S. madagascariensis											
Herbivor		Abund						ichness			
	0-100	101-300	301-500	501-700) (0-100	101-300	301-500	501-700		
0-100											
101-300 301-500	ns *					18	• •				
501-500 501-700	ns	ns ns	ns				ns ns	ns			
Herbivor		Divers			1	15 1	.15	115			
Incruition	0-100	101-300	301-500	501-700)						
0-100	0 100	101 000	001 000	001 /00							
101-300	ns										
301-500	**	*									
501-700	ns	ns	*								
Invertebrates		Richness				Diversity					
	0-100	101-300	301-500	501-700) ()-100	101-300	301-500	501-700		
0-100											
101-300	ns *	*				15	**				
301-500			20			15		20			
501-700	ns	ns	ns		r	18 1	ns	ns			

ns = not significant; *<0.05; **<0.01; ***<0.001

Note: Distance in kilometres from introduction region

Table 3. Results of a two-factor analysis of covariance and Fisher's Least Significant Difference (LSD) post hoc tests for the effect of plant species (*S. madagascariensis* or *S. pinnatifolius* var. *pinnatifolius*; (d.f. = 1, 107), latitude (bands 1-6; d.f. = 5, 107) and their interaction (d.f. = 5, 107) on the abundance, morphospecies richness and Shannon diversity of invertebrate herbivores and total invertebrates. Dried plant mass (biomass) was fitted as a covariate (d.f = 1, 107). Biomass, abundance and richness were transformed to the log (x+1).

	Biomass		Plant	species_	Latitud	inal ban	<u>d S</u>	Species × Latit				
Variable		F		Р	F	Р	F	Р		F	Р	
Abun	dance											
Herb	oivores		1.600) 0.	.208	8.323	0.005	2.261	0.05	3 1	.926	0.096
Inve	rtebrate	s	7.917	7 O.	.006	6.515	0.012	3.832	0.00	3 2	2.101	0.071
Richn	ess											
Hert	oivores		2.137	0	.147	9.133	0.003	2.694	0.02	5 3	.220	0.010
Inve	rtebrate	s	9.216	5 0 .	.003	8.201	0.005	2.921	0.01	6 2	2.797	0.021
Divers	sity											
Hert	oivores		3.453	3 0 .	.066	8.435	0.004	2.522	0.03	4 3	.268	0.009
Inve	rtebrate	s	4.742	2 0.	.032	5.605	0.020	1.694	0.14	2 2	2.524	0.036
LSD p	ost hoc	tests -	S. mada	gascari	ensis							
Herbivores Richness							Diversity					
	Lat1	Lat2	Lat3	Lat4	Lat5	Lat6	Lat1	Lat2	Lat3	Lat4	Lat5	Lat6
Lat1												
Lat2	**						**					
Lat3	***	ns					***	ns				
Lat4	*	ns	ns				**	ns	ns			
Lat5	*	ns	ns	ns			ns	ns	*	ns		
Lat6	**	ns	ns	ns	ns		**	ns	ns	ns	ns	
Invert	tebrate	s	Ric	hness			Diversity					
	Lat1	Lat2	Lat3	Lat4	Lat5	Lat6	Lat1	Lat2	Lat3	Lat4	Lat5	Lat6
Lat1												
Lat2	***						**					
Lat3	***	ns					*	ns				
Lat4	*	ns	ns				**	ns	ns			
Lat5	**	ns	ns	ns			ns	ns	ns	ns		
Lat6	**	ns	ns	ns	ns		*	ns	ns	ns	ns	

ns = not significant; *<0.05; **<0.01; ***<0.001

Note: Latitudes 1-6 (southern most point 1; northern most 6; introduction region 3 and population augmentation 5)

Patterns of total invertebrate abundance, richness and Shannon diversity

For *S. madagascariensis* the total invertebrate assemblage may be driven by the time in which invertebrates adapt to and colonise the invader, as indicated by the sharp decline in invertebrate abundance, richness and Shannon diversity from the point of introduction to latitudes to the north (580km) and south (480km) of this point (Fig. 4). However, substantial variation in invertebrate abundance among replicate samples within and between latitudes meant that only morphospecies richness and Shannon diversity were found to be significantly affected by an interaction between species and distance from introduction region and between species and latitude (Table 2; Table 3). For the native control *S. pinnatifolius* var. *pinnatifolius* latitude played a minor role in the abundance, richness and Shannon diversity of invertebrates, as indicated by minimal variation in the invertebrate communities across the range (Fig. 4d, e, f). In the region where an augmentation of the population of *S. madagascariensis* occurred, the richness and Shannon diversity was lower than the introduction origin but this trend was not significant (Fig. 4d, e, f).

External herbivore collections and reared herbivores

Overall, the total abundance, richness and Shannon diversity of herbivores reared from *S. madagascariensis* decreased with increasing distance from the point of introduction, with significant differences for richness and Shannon diversity evident at a distance of 301-500km from the point of introduction (Table 4; Fig. 5a, b, c). Although somewhat lower than at the introduction site, levels of reared herbivores increased at the furthest distance from introduction origin, due to higher levels at northern-most locations (Fig. 5,d, e, f). Herbivore richness and Shannon diversity from external collections varied little across distance from the point of introduction whereas external abundances were slightly greater

at the point of introduction (Table 4; Fig. 5a,b,c). At the point of introduction, the richness and Shannon diversity of reared herbivores were greater on *S. madagascariensis* compared to all other latitudes including sites where the population was augmented in the 1950's, with significant differences apparent between the introduction origin and the southernmost latitude (Table 5; Fig. 5). Northern-most sites had a greater richness and Shannon diversity of reared herbivores on *S. madagascariensis* compared to the southern-most sites (Table 5; Fig. 5). Minimal variation in the abundance, richness and Shannon diversity of reared herbivores and external collections occurred in the native *S. pinnatifolius* var. *pinnatifolius* (Fig. 5). Table 4. Results of a two-factor, analysis of covariance and Fisher's Least Significant Difference (LSD) post hoc tests for the effect of plant species (*S. madagascariensis* or *S. pinnatifolius* var. *pinnatifolius*; (d.f. =1, 111), distance from introduction region of *S. madagascariensis* (0-100; 101-300; 301-500 and 501-700 km; d.f. = 3, 111) and their interaction (d.f. = 3, 111) on the abundance, morphospecies richness and Shannon diversity of external collections and reared invertebrate herbivores. Dried plant biomass was fitted as a covariate (d.f = 1, 111). Biomass, abundance and richness were transformed to the log (x+1).

		<u>Biomass</u>		Plant species		Dis	Distance		× Distance
Variable		F	Р	F	Р	F	Р	F	Р
Abundance									
External collections		0.153	0.696	10.903	0.001	6.473	<0.001	3.129	0.029
Reared		0.344	0.559	11.480	0.001	2.946	0.036	2.803	0.043
Richness									
External collections		0.590	0.444	11.082	0.001	2.859	0.040	1.637	0.185
Reared		0.194	0.660	11.011	0.001	2.713	0.048	5.163	0.002
Diversity	Diversity								
External of	External collections		0.089	10.507	0.002	4.495	0.005	1.242	0.298
Reared	Reared		0.264	8.034	0.006	2.550	0.059	5.638	0.001
LSD post	hoc tests - 2	S. madagaso	cariensis						
Reared H	erbivores	A	bundance				R	ichness	
	0-100	101-300	301-500	501-700		0-100	101-300	301-500	501-700
0-100									
101-300	ns					ns			
301-500	ns	ns				*	ns		
501-700	ns	ns	ns			ns	ns	ns	
Reared H	erbivores	Diversity			External Col		ctions Ab	undance	
	0-100	101-300	301-500	501-70	00	0-100	101-300	301-500	501-700
0-100									
101-300 ns						***			
301-500	301-500 *					***	ns		
501-700	501-700 ns		*			*	ns	*	

ns = not significant; *<0.05; **<0.01; ***<0.001

Note: Distance in kilometres from introduction region

Table 5. Results of a two-factor, analysis of covariance and Fisher's Least Significant Difference (LSD) post hoc tests for the effect of plant species (*S. madagascariensis* or *S. pinnatifolius* var. *pinnatifolius*; (d.f. =1, 107), latitude (bands 1-6; d.f. = 5, 107) and their interaction (d.f. = 5, 107) on the abundance, morphospecies richness and Shannon diversity of external collections or reared invertebrate herbivores. Dried plant biomass was fitted as a covariate (d.f = 1, 107). Biomass, abundance and richness were transformed to the log (x+1).

	B	iomass	Plant	species	Latituc	Latitudinal band		pecies >	< Latitude
Variable	F	Р	F	Р	F	Р		F	Р
Abundance									
External collections	0.845	0.360	6.287	0.014	4.352	0.00	1 2	.029	0.080
Reared	0.909	0.343	10.156	0.002	2.524	0.03	4 1.	.844	0.110
Richness									
External collections	2.102	0.150	7.459	0.007	2.546	0.03	2 1.	.202	0.313
Reared	0.605	0.438	10.363	0.002	2.556	0.03	2 3.	.142	0.011
Diversity									
External collections	3.318	0.071	7.708	0.006	2.770	0.02	2 0	.807	0.547
Reared	1.618	0.206	6.795	0.010	2.359	0.04	5 3.	.472	0.006
LSD post hoc tests - S	5. madaga	iscariensis							
Reared Herbivores	Richn	ess		Diversity					
Lat1 Lat2	Lat3	Lat4 Lat5	Lat6	Lat1	Lat2	Lat3	Lat4	Lat5	Lat6
Lat1									
Lat2 *				*					
Lat3 ** ns				**	ns				
Lat4 ns ns	ns			*	ns	ns			
Lat5 ns ns	ns i	ns		ns	ns	ns	ns		
Lat6 * ns	ns	ns ns		*	ns	ns	ns	ns	

ns = not significant; *<0.05; **<0.01; ***<0.001

Note: Latitudes 1-6 (southern most point 1; northern most 6; introduction region 3 and population augmentation 5)

Figure 4. Abundance, morphospecies richness and Shannon diversity of total invertebrates collected on the non-native species *Senecio madagascariensis* and the native *S. pinnatifolius* var. *pinnatifolius* with distance from where *S. madagascariensis* was first introduced (a,b,c) and across latitudes 1-6 (d,e,f), (southern most point 1; northern most 6; introduction region 3 and population augmentation 5). Response variables are standardised by dividing by the dry biomass of the individual plants. Data points are means. Error bars are standard errors.

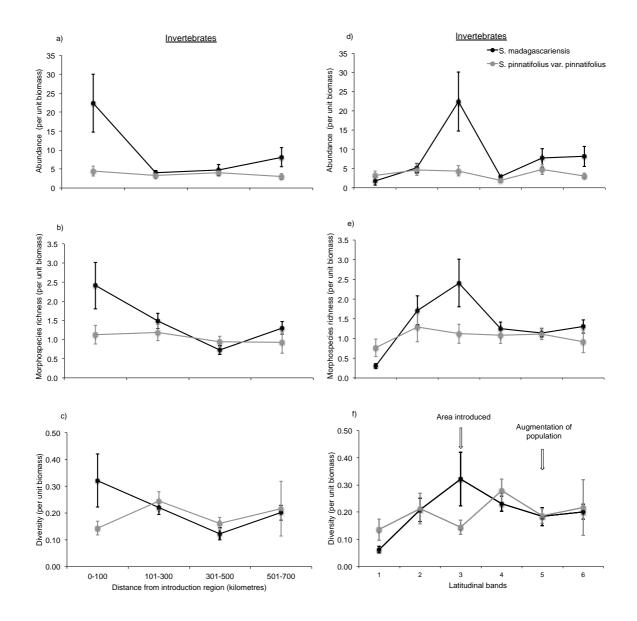
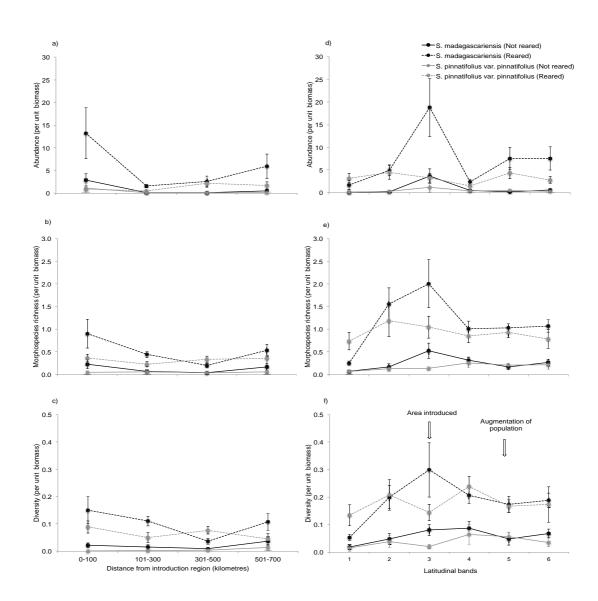


Figure 5. Abundance, morphospecies richness and Shannon diversity of total invertebrates reared versus collected externally from the non-native species *Senecio madagascariensis* and the native *S. pinnatifolius* var. *pinnatifolius* with distance from where *S. madagascariensis* was first introduced (a,b,c) and across latitudes 1-6 (d,e,f), (southern most point 1; northern most 6; introduction region 3 and population augmentation 5). Response varaiables are standardised by dividing by the dry weight (biomass) of the individual plants. Data points are means. Error bars are standard errors.



Discussion

We used a space for time substitution to evaluate the relationship between an invasive species and its natural enemies since establishment. As herbivory is considered to play a potentially important role in the initial success of introduced species via release from natural enemies, we also compared leaf damage as a surrogate for fitness loss to determine whether herbivores may have reduced the fitness of a non-native species. Using *Senecio* madagascariensis Poir. as our focal species, we found the opposite results to what would be predicted from the enemy release hypothesis (ERH) (for reviews see Maron & Vila 2001; Colautti et al. 2004), but partial support for the species-time relationship (STR) (sensu Preston 1960; Strong et al. 1984). Contrary to expectations of the ERH, greater herbivore and invertebrate loads (abundance, richness and Shannon diversity) were found on the invasive species than on the native "control" S. pinnatifolius var. pinnatifolius; this difference was particularly evident in samples collected at sites in the region of introduction. Supporting the STR, herbivore abundance, richness and Shannon diversity declined on S. madagascariensis from its point of introduction in the Hunter Valley NSW, to both its invasion fronts to the north in Queensland and south in southern NSW. The results for the invertebrate assemblages as a whole mirrored that of the herbivores, declining in loads (abundance, richness, Shannon diversity) from the introduction point to the invasion fronts. Also consistent with the STR, there were more herbivores reared from S. madagascariensis at the area of introduction compared to all other locations, indicating that herbivores may be adapting over time and increasing their ability to feed on S. madagascariensis.

In direct contrast to these results, leaf damage on *S. madagascariensis* did not decrease from its point of introduction to the invasion fronts. At the invasion fronts we found high leaf damage on *S. madagascariensis* despite the fact that total herbivore loads were low,

whereas at the point of introduction, damage levels were low and herbivore loads were high. In the region where the population was augmented in the 1950's on the far north coast of NSW, damage levels and herbivore loads were both low compared to the invasion fronts in the north and south. Results from the damage analysis indicated that the potential for enemy release is not limited to the early stages of invasion or presumably linked to the success of this species as an invader. Minimal variation across latitudes in our control species *S. pinnatifolius* var. *pinnatifolius*, confirmed that the patterns observed in our invasive species are not likely to be driven by environmental variation along the latitudinal gradient.

Several studies have shown reduced herbivory on invasive plants, which may have been a contributing factor to their subsequent invasion and spread into native habitats (Vila et al. 2005; Carpenter & Cappuccino 2005). By contrast, our results directly contradict the ERH as greater damage and herbivore loads were found on the invasive species compared to the co-occurring close relative S. pinnatifolius var. pinnatifolius. Our results are consistent with studies that have found greater rates of herbivory on non-native compared to native species (Keane & Crawley 2002 and references therein; Agrawal & Kotanen 2003). Greater rates of damage on non-native plants may be attributed to being closely related to a co-occurring native congener as well as being evolutionarily naive to natural enemies in their new environment. Closely related plants often share similar classes of secondary metabolic compounds that determine their smell, taste and toxicity for phytophagous insects (Tallamy 2004). This may explain some of the similarities in the abundance and richness of the invertebrate assemblage observed, as native insects are more likely to be able to feed on a close relative of the native plant species than on a plant from a different family (Strong et al. 1984; Tallamy 2004). Greater enemy attack on non-native plants may occur because non-natives are unlikely to have developed defences against enemy impact

which is often compounded through invasion bottlenecks (e.g. 'increased susceptibility hypothesis' Colautti *et al.* 2004).

Our results indicate that for Senecio in Australia, there is no simple relationship between the time over which herbivore species can be accumulated on non-native plants and the herbivore community complexity on an invader. In studies by Siemann et al. (2006) and Hawkes (2007) it was demonstrated that the enemy release of a non-native species was limited to the early stages of its invasion. Greater herbivory was found at sites where the Chinese tallow tree (Sapium sebiferum) had been present for longer compared to more recent sites of introduction (Siemann et al. 2006). We found the opposite result - areas where S. madagascareinsis was recently introduced had greater damage than older sites of introduction (i.e. point of introduction and where the population was augmented in the 1950's on the far north coast of NSW). Inconsistent patterns between the relevance of time and herbivore or pathogen community accumulation has emerged across studies, with some demonstrating strong relationships between time and herbivore accumulation or rates of herbivory on non-native species (Birks 1980; Siemann et al. 2006; Brändle et al. 2008) or weak or no relationships (Strong et al. 1977; Carpenter & Cappuccino 2005). Differences among studies may be due to variation in range size, growth form, the taxonomic affiliation of non-native species to the native community, and the interaction of other abiotic and biotic factors (Mitchell et al. 2006). After controlling for at least some of the potential confounding factors, by accounting for differences in biomass and by comparing herbivores and herbivory on a congeneric species, our results also show inconsistent patterns between rates of herbivory and herbivore loads. In this study, some support was found for the STR with respect to herbivore loads (in terms of abundance, richness, Shannon diversity) which declined on S. madagascariensis from its point of introduction to its invasion fronts, but inconsistent for damage levels.

There may be several explanations for the lack of correlation between damage and the number and variety of herbivores. Different herbivore species vary in the relative amount of damage they inflict, due to differences in their size, or feeding mode. Generalist defoliaters such as the moth in the superfamily Pyraloidea found at the invasion fronts may cause considerably more conspicuous and easily measurable damage per plant than more numerous sap-suckers which occurred at the point of introduction. The effects of chewers or defoliaters are often more obvious than those of sap-suckers where damage can be relatively subtle unless damage from sap-sucking insects is exacerbated by them acting as vectors of plant pathogens (Gullan & Cranston 2010). Moreover, surveying for the removal of plant biomass by sap-suckers is often problematic and only possible through controlled experiments.

Greater damage levels at the invasion fronts where low herbivore loads were recorded may not be just a stochastic element or an artefact of the damage inflicted by generalist defoliaters. The net impacts of losing natural enemies from its native range and acquiring a new assemblage in the new range may be influenced by several non-mutually exclusive factors. For example, rates of herbivory may be influenced by evolutionary changes that a plant may undergo in its new environment. Non-native plant species may reallocate resources to growth and reproduction rather than defence due to the release from natural enemies in their new environment, a hypothesis known as the evolution of increased competitive ability (EICA) (Blossey & Notzold 1995). Evidence for the EICA has been demonstrated in *Sapium sebiferum*, which has evolved to be faster growing and less herbivore resistant in its new range (Zou *et al.* 2008).

Alternatively, changes in abiotic and biotic conditions may in turn increase the nutritional value of the plant tissue or bring about other physiological changes that can influence herbivore feeding. For example, natural and human disturbances including changes in

salinity, water stress and patterns of weather, can result in an increase in nutrients such as nitrogen in plant tissues that may in turn lead to an increase in feeding by herbivores (e.g. White 1984). A reduction in plant silicon content from environmental stress, for example, may increase feeding in herbivores. Alternatively, the silicon content may change in response to herbivores whereby the cell wall is reinforced acting as a physical defence against herbivore attack (Epstein 2009; Reynolds *et al.* 2009). Although little is known for herbaceous plants, higher levels of silicon have been found to deter feeding on grasses (Massey *et al.* 2007; Reynolds *et al.* 2009) and subsequently high levels of silicon can reduce the efficiency with which nitrogen can be absorbed by herbivores (Massey & Hartley 2009).

There is some evidence to suggest that *S. madagascariensis* may be undergoing physiological changes in its new environment, which is likely to influence its interaction with herbivores. *Senecio* species are known to contain pyrrolizidine alkaloids, which can play a role in defence against herbivores (Parsons & Cuthbertson 1992; Sindel 2009). Although changes in chemical defences have not been measured in *S. madagascariensis*, the genes potentially associated with defence against insect herbivores are more switched on in their native range of South Africa than in Australia (Prentis *et al.* 2010). Preliminary research indicates that *S. madagascariensis* may be allocating more resources to reproduction and growth at the range edges as indicated by a larger pappus and moderately larger achene than at non-edges (S. Bonser *pers. comm.*). Higher germination rates, faster growth rates and reproduction at the range edges compared to non-edges have also been found (S. Bonser *pers. comm.*). Greater growth rates and damage has also been found in the invasive *Jacobaea vulgaris* Gaertn. (formerly *Senecio jacobaea* L.; Pelser *et al.* 2007) compared to native populations (Stastny *et al.* 2005), and partial support for increased

dispersal in invasive populations of *S. inaequidens* has also been found (Monty & Mahy 2010).

An extension of the ERH predicts that when a non-native plant is introduced it leaves behind its co-evolved specialist herbivores, which are then replaced by generalist polyphagous herbivores (e.g. Keane & Crawley 2002). Generalists have been found to be replaced by a more specialised assemblage over time (Andow & Imura 1994). Our results may be consistent with this idea, as the herbivores collected on S. madagascariensis may be widening their niche to include this invasive weed, potentially developing a stronger physiological link with the host plant. The proportion of reared herbivores, dominated by aphids, at the area of introduction on S. madagascariensis was greater than all other regions including where the population was augmented in far northern NSW in the 1950's. Aphids are predominately monophagous (Carver 1959; Eastop 1973) and food selection is based on complex behavioural patterns that test for chemical structure, surface properties and nutrients (Niemeyer 1990). Aphids may be developing specialised associations with the plant, by utilising the plant for oviposition and and/or sequestering toxins for defence against parasites. At the invasion fronts, generalist defoliaters, dominated by a moth species in the superfamily Pyraloidea, were the main herbivores present and are likely to be the main drivers of herbivory and damage levels seen in this study.

This study has shown that time since introduction is a factor affecting the composition of the invertebrate assemblage in terms of increasing in density, richness and potential specialisation but these changes in the herbivore community were not associated with the damage suffered by the invading species. Due to high leaf damage at invasion fronts on the invader compared to the native species, the low level of herbivory on this non-native species does not appear to be an important mechanism underlying its apparent invasion success. High damage levels and invertebrate loads on this invader may be due to *S*.

155

madagascariensis being a closely related congener and evolutionary naive in its new range. Further investigation of two possible non-mutually exclusive ideas may explain why we found greater damage at the invasion fronts compared to point of introduction. These include exploring the relationship between herbivores and the damage they inflict on plants. For example, by determining whether the generalist herbivores present at the invasion fronts are doing most of the damage, or whether the damage and herbivore loads observed are unpredictable in time and space. Research is also needed into understanding whether non-natives may become better defended against herbivores over time. For example, a comparison of in defence and growth at the invasion fronts with that at the older sites of introduction could test whether *S. madagascariensis* may be undergoing physiological changes that may increase or decrease its tolerance to herbivory. It is likely that abiotic and biotic interactions may prevail in understanding the success of species that are closely related to the native community. By better understanding the mechanisms behind the plasticity of this species it may be possible to gain clearer insight into the naturalisation and success of other non-native species.

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Chapter 5: Conclusions

Chapter 5 - Conclusions

Invasive plants can have devastating consequences on both natural and agricultural systems via their impact of native species assemblages, disturbance regimes, primary productivity, stability and ecosystem function (Walker & Smith 1997; Prieur-Richard & Lavoral 2000). In Australia, the economic costs of lost agricultural productivity and weed management are estimated to be over \$4 billion per year (Sinden *et al.* 2005; AWS 2006; DAFF 2008); the costs for natural ecosystems are far more difficult to quantify. By understanding which biological traits are characteristic of successful invasive species we can improve quarantine procedures and provide a better basis for management decisions.

Elton (1958) in *The Ecology of Invasions by Animals and Plants* noted that predicting the success of introduced species would be a major aim in ecological research in the future. Since this publication there has considerable research into characteristics associated with successful invasive behaviour (Williamson 1996; Goodwin *et al.* 1999; Rejmánek & Richardson 1996; reviewed by Richardson & Pyšek 2006), with several of these traits used for the risk assessment of weeds (Weber *et al.* 2009). Theory suggests that the success of invasive species may depend upon the evolutionary relationships between the invader and the native community to which it invades. Charles Darwin (1859) was the first to recognise the potential importance of evolutionary relationships in the naturalisation of non-native species. Introduced species that are phylogenetically distinct from the native community are more likely to be successful invaders than closely related species for two main reasons. Firstly, phylogenetically distinct non-native invaders may be relatively free from competition with closely related species and are therefore more likely to exploit under-utilised niches (i.e. Darwin's Naturalisation Hypothesis). Secondly, non-native plants with close native relatives are more likely to suffer more damage from natural

enemies in the native community (i.e. Enemy Release Hypothesis) than species with few co-occurring relatives. This is because host choice in insect herbivores is generally determined by plant relatedness and host switching has been found between closely related non-native and native species. During this process the time taken for the insect herbivore community and the associated assemblage to develop may be important in determining whether an invader is immediately released from natural enemies upon its introduction, or if the herbivore community readily colonises and hinders its spread and invasive ability.

This study investigated patterns of plant-insect interactions on non-native and native plants with the aim of understanding the relative importance of phylogenetic relationships between the invader and the native community with respect to the likelihood of a species becoming colonised and damaged by natural enemies. In a series of field surveys on the east coast of Australia I explored these ideas at a variety of taxonomic levels. Chapter 2 examined the degree and kinds of damage fourteen invasive plants sustained based on how closely related they were to native species. Chapter 3 used Senecio L. as a case study to explore how important phylogenetic relationships are on a finer taxonomic scale. The amount of damage and the herbivore assemblages was compared across native and nonnative, invasive and non-invasive Senecio species. This chapter specifically addressed the likelihood of enemy release being associated with the success of the invasive species Senecio madagascariensis (Poir.). Chapter 4 tested the importance of time since introduction in relation to the accumulation of the herbivore species on *Senecio* madagascariensis Poir. This chapter aimed at determining whether the herbivore community on S. madagascariensis quickly colonised and damaged this host potentially playing a role in reducing its invasive ability.

I found that phylogenetic distance to the nearest native relative at the genus level and higher was a good predictor of herbivore and pathogen damage on the invasive plants, explaining nearly 37% of the variance in leaf damage. As phylogenetic distance to the nearest native relative increased the total leaf damage decreased. These invasive species were colonised by fewer functional herbivore guilds and were dominated by apparent generalist natural enemies. My results suggest that those invasive species that are distantly related to the native community may be released from specialist natural enemies. The results supported expectations generated by both Darwin's Naturalisation and the Enemy Release hypotheses. The phylogenetic relationship between non-native and native communities may therefore be a useful tool for assessing the invasive potential of different species with respect to colonisation by the herbivore and pathogen community.

On a finer taxonomic scale within the genus of *Senecio*, my results indicate that phylogenetic relationships and enemy release may be less important for determining the invasiveness of an introduced species. Damage levels and invertebrate abundance and richness on *S. madagascariensis* were similar to the native and other non-native non-invasive *Senecio* species. There was no correlation between the genetic distance of different *Senecio* species and the herbivore assemblage. *Senecio madagascariensis* does not appear sufficiently phylogenetically distant from native and naturalised non-native *Senecio* species to be released from native herbivore assemblages. At this level there appears to be no support for enemy release in the case of the invasive species *S. madagascariensis*, unless the enemy release relates to specialist herbivores from its native range, which was not investigated in this study.

Over the time since introduction, the invertebrate community on *S. madagascariensis* has increased in abundance and richness and become apparently more specialised, as defined

167

by the number of herbivores reared from plant samples. These herbivores are more likely to have stronger physiological associations with their host plants than do external feeding herbivores, which were more abundant and diverse at the point of introduction than at invasion fronts. Leaf damage showed the opposite trend, with the highest damage levels at the invasion fronts compared to introduction point. Compared to its native congener *S. pinnatifolius* var. *pinnatifolius* A. Rich., *S. madagascariensis* sustained higher levels of herbivore damage, invertebrate abundance and diversity. Due to *S. madagascariensis* having many closely related species in the recipient community to which it has invaded, many herbivores and pathogens appear to be pre-adapted to using it as a source for food and site for reproduction.

Overall these results have significant implications for current research in invasion biology and for how invertebrate communities on non-native species change over time. This research has shown that phylogenetic relationships may play an important role in predictions of invasiveness for non-natives but is dependent on the taxonomic level assessed. Predictions of invasive potential based on non-native species being released from natural enemies for introductions above the level of genus may be successful. At a finer taxonomic scale (within genus), complex biotic interactions between an invader and the recipient native community make predictions of invasion success much more unreliable.

Management implications

Results from the findings of this thesis could be directly applied to the weed risk assessment process used in Australia, or similarly, in other quarantine systems used globally for screening plants for proposed introductions or for detection of high risk accidental introductions including "sleeper weeds". Results can also be applied to

Chapter 5: Conclusions

targeting existing non-native plants for management and control that have been imported prior to the stringent quarantine methods used today.

The Australian Weeds Risk Assessment (WRA) process, developed on a system-based model by Pheloung (1995), is a scientifically-based quarantine risk analysis tool used to identify whether a plant proposed for import may become a serious weed (DAFF 2008). The WRA has been adopted by the Australian Quarantine Inspection Service (AQIS) in 1997 and has since become internationally recognised and modified for use in other countries, including Japan (Kato *et al.* 2006), Hawaii (Daehler & Carino 2000), Florida (Gordon *et al.* 2008), the Czech Republic (Křivánek & Pyšek 2006), and the Pacific Islands (Daehler *et al.* 2004). To evaluate the invasive potential of a plant suggested for import, a part of the WRA utilises a questionnaire that includes information on a plant species biology, climatic preferences, reproductive and dispersal methods and proven weed history of congeneric taxa (Steinke 1999). Each of the 49 questions generates a score and the combined total evaluates the outcome of whether a plant is accepted for importation, rejected or prohibited pending further evaluation (Steinke 1999). A plant unsuitable for importation.

At present the WRA system utilises no known information about a species' phylogenetic relationship to the local environment. With global databases emerging on plant phylogenetics (e.g. Angiosperm phylogeny and Phylomatic (Stevens 2001; Webb & Donaghue 2005; Webb *et al.* 2009) it is now possible to incorporate phylogenetic relationships in weed risk assessments. Generating phylogenetic distances from scratch for weed risk assessments is too time consuming and impractical for use in a questionnaire but incorporating basic knowledge on a plants' taxonomic similarity to the native community will be possible in many cases. Online regional databases such as Flora of Australia

169

Online and the Australian Plants Name Index (APNI) or comparable databases in other countries can supply information on phylogenetic relationships, which in turn could be incorporated into the WRA process. The Flora of Australia and APNI are online databases that give access to taxonomic and biological information on plants, both native and weedy which currently occur in Australia. Simple searches could be conducted to ascertain whether a proposed plant species for import has family members present in the region of introduction or congeners present. Under the assumption that phylogenetically distant plant species are likely to be released from natural enemies, which may contribute to their initial success as invaders, the questionnaire could include a few extra steps that indicate the phylogenetic relationship of the plant in question to existing native plants in Australia. Questions could include: (1) Is the plant family present in Australia? (2) If the plant family is present, are congeneric native species present? If the proposed species has no congeneric native relatives present or no family members present in Australia, a higher score would be given to each, indicating a higher risk of enemy release. If there are native congeners present, my research findings suggest that further evaluation based on other weed risk assessment characteristics such as life history traits are required to determine its invasive potential.

There have been many plants introduced to Australia before stringent quarantine measures were in place, such as those used in the nursery industry. Many weeds start as innocuous "sleeper weeds", with as many as 150 years elapsing between naturalisation and achieving significant weed status (Caley *et al.* 2008). Applying the WRA process to these existing non-native species present in Australia using phylogenetic relationships may enable informed decisions prior to the species becoming a serious pest. For example, *Hieracium aurantiacum* L., which has no native congeners present in Australia, is currently listed as a sleeper weed with the potential to become a serious pest (Groves 1999). Similarly,

Mimosa pigra L. (Fabaceae) (past sleeper weed now currently listed as a 'Weed of National Signficance') is from a family that is represented in Australia but has no native congeners present. It was first recorded in 1891 in the Northern Territory and was naturalised in the Darwin area as a sleeper weed until 1952 when it was relocated and subsequently increased its population size to become a serious invader (Groves 2006). The invasive plant *Anredera cordifolia* from the family Basellaceae, represented in Chapter 2 as one of the declared noxious invasive species, is from a family with no native family representatives in Australia. It was introduced as a garden ornamental from South America and is now widespread and common in all Australian states with the exception of South Australia (Groves *et al.* 2005). It is a serious climbing weed invading margins of rainforests, inland watercourses and bushland. It can smother small trees and shrubs and producers thousands of aerial tubers along its stem (Harden 1990). At present it is still listed as a species available for sale throughout Australia with the exception of some council regions in Queensland and NSW (Groves *et al.* 2005).

Application of a phylogenetic component in weeds risk assessments could also be applied to many of the current species listed as 'Weeds of National Significance' (WONs) in Australia (Table 1). Most of the WONs have family representatives in Australia but 75% of the species are from a novel genus. A further two species *Tamarix aphylla* and *T*. *ramosissima* are from the family Tamaricaceae, which is not represented in Australia by any native relatives (Table 1).

At present, application of the WRA system results in rejection of approximately 90% of known invasive species (Gorden *et al.* 2008) and economic assessment indicates that it only takes a few species to cause significant environmental damage with large associated economic costs (Keller *et al.* 2007). Considering that the WRA has demonstrated

171

considerable bioeconomic benefits within a few years of implementation (Keller *et al.* 2007), any additional tools that improve the WRA may further reduce the risk of plants present in ecosystems from becoming weeds and prevent the importation of potential new weed species.

Closing remarks

The research outlined in this thesis provides evidence that phylogenetic distance between non-natve species and the native recipient community is a useful tool that could be incorporated in weed risk assessment modules. Results suggest that the interaction between non-native and native plants and their natural enemies has a phylogenetic component. This phylogenetic component is only evident at taxonomic scales above the level of genus. Below this level, predictions for invasive potential based on phylogenetic relationships are weak. Incorporating phylogeny into current weeds risk assessments for potential imports or for targeting present non-native species for management has the potential to improve upon our current predictive power for assessing likely invaders. Presently the weeds risk assessment process has been successful in identifying 90% of known invasive weeds. A further 10% of non-native plants potentially slip through quarantine procedures with the risk of becoming serious invasive weeds. Improvements to current weeds risk assessment processes such as the application of a phylogenetic component has significant environmental and economic benefits on a local and global scale. Table 1. Weeds of National Significance (WONs) and their phylogenetic relationship to

Australian natives. Native relative present \checkmark or absent \checkmark

WONS	Family	Novel Family	Novel Genus
Acacia nilotica (L.) Willd. Ex Delile	Fabaceae	×	×
Alternanthera philoxeroides (Mart.) Griseb.	Amaranthaceae	×	×
Annona glabra L.	Annonaceae	×	
Asparagus asparagoides (L.) Druce	Asparagaceae	×	×
Cabomba caroliniana A. Gray	Cabombaceae	×	
Chrysanthemoides monilifera (L.) Norl subsp. monilifera Chrysanthemoides monilifera (DC.) Norl. subsp. Rotundata	Asteraceae	×	
Cryptostegia grandiflora R. Br.	Apocynaceae	×	1
Hymenachne amplexicaulis (Rudge) Nees	Poaceae	×	×
Lantana camara L.	Verbenaceae	×	 ✓
Mimosa pigra L.	Fabaceae	×	 ✓
Nassella neesiana (Trin. & Rupr.) Barkworth	Poaceae	×	
Nassella trichotoma (Nees) Hack. Ex Arechav	Poaceae	×	
Parkinsonia aculeate L.	Fabaceae	×	 ✓
Parthenium hysterophorus L.	Asteraceae	×	
Prosopis L. spp.	Fabaceae	×	 ✓
Rubus fruticosus L. aggregate	Rosaceae	×	×
Salix L. spp. except S. babylonica, S. x calodendron & S. x reichardtiji	Salicaceae	×	
Salvinia molesta D.S. Mitch	Salviniaceae	×	√
Tamarix aphylla (L.) H. Karst. Tamarix ramosissima Ledeb.	Tamaricaceae	✓ ✓	
Ulex europaeus L.	Fabaceae	×	 ✓

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Appendix 1

Species	ITS availability	Replacement species	Where collected	Group	Sequence	Reference
S. madagascariensis	Yes		Australia	Lautusoid	U93198.1	Scott <i>et al.</i> (1998)
S. glastifolius	Yes		New Zealand	Exotic	EF538340.1	Pelser et al. 2007
S. pterophorus	Yes		South Africa	Exotic	AF085188.1	Vincent & Getliffe (1992)
S. macroglossus	Yes		Southern Africa	Exotic	DQ915881.1	Sombra Staeheli <i>et al.</i> unpub.
S. angulatus	Yes		Unknown	Exotic	AF459953.1	Pelser et al. (2002)
S. minimus	Yes		New Zealand	Disciform	EU331119.1	Gardner <i>et al</i> . unpub.
S. lautus subsp. maritimus (synonym of S. pinnatifolius var. pinnatifolius)	Yes		Australia	Lautusoid	U93203.1	Scott <i>et al.</i> (1998)
S. linearifolius var. arachnoideus	No	S. australis	Australia	Odoratus	EF538302.1	Pelser et al. 2007
S. amygdalifolius	No	S. macranthus	Australia	Macranthus	EF538358.1	Pelser et al. 2007
S. bipinnatisectus	No	S. diaschides	Australia	Disciform	EF538328.1	Pelser et al. 2007

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Group	Morphospecies	Family	Species	Guild	Abuno	lances: Na	tive Sened	<i>cio</i> spp.	
-		-	_		pin.	min.	lin.	amy.	bip.
Acarina	Acarina 44	Tenuipalpidae		Sap-sucker	3	0	0	0	0
Coleoptera	Coleoptera 1	Brentidae		Leaf chewer	0	0	0	0	0
-	Coleoptera 9	Chrysomelidae		Leaf chewer	0	0	0	0	0
	Coleoptera 18	Curculionidae		Leaf chewer	0	0	3	0	0
	Coleoptera 20	Curculionidae: Scolyt	inae	Leaf chewer	0	0	0	0	0
	Coleoptera 39	Curculionidae		Leaf chewer	0	0	1	0	0
	Coleoptera 41	Chrysomelidae		Leaf chewer	0	0	2	0	0
	Coleoptera 52	Curculionidae		Leaf chewer	0	0	0	1	0
	Coleoptera 54	Chrysomelidae		Leaf chewer	0	1	0	0	0
	Coleoptera 55	Cerambycidae		Leaf chewer	0	1	0	0	0
	Coleoptera 58	Chrysomelidae		Leaf chewer	0	4	0	0	0
	Coleoptera 61	Chrysomelidae: Crypt	tocephalinae	Leaf chewer	0	1	0	0	0
	Coleoptera 63	Aderidae		Leaf chewer	0	0	0	0	0
	Coleoptera 65	Brentidae		Leaf chewer	0	0	0	1	0
	Coleoptera 66	Brentidae		Leaf chewer	0	0	0	0	1
	Coleoptera 67	Curculionidae		Leaf chewer	0	0	2	0	0
	Larvae 24	Curculionidae		Leaf chewer	3	0	3	0	0
	Larvae 25	Curculionidae		Leaf chewer	6	0	0	0	0
	Larvae 32	Curculionidae		Leaf chewer	0	0	76	0	0
	Lep. Coleoptera 56	Cerambycidae		Leaf chewer	0	0	0	0	0
	Lepidoptera 73	Cerambycidae		Leaf chewer	0	0	0	0	1
	Lep. Coleoptera 80	Curculionidae		Leaf chewer	0	0	0	0	0
Diptera	Diptera 5	Agromyzidae		Miner	0	0	0	0	0
	Diptera 41	Agromyzidae		Miner	0	4	3	0	2
	Col: Auchenorrhyncha 45	Membracidae		Sap-sucker	0	1	0	0	1
Iemiptera	Dip: Sternorrhyncha 82	Coccoidea		Sap-sucker	0	0	0	0	1
	Aphididae 1	Aphididae		Sap-sucker	0	6	0	0	0
	Aphididae 10	Aphididae		Sap-sucker	0	0	0	0	0
	Aphididae 11	Aphididae		Sap-sucker	0	0	0	0	0
	Aphididae 13	Aphididae		Sap-sucker	0	3	0	0	0
	Aphididae 14	Aphididae		Sap-sucker	0	0	0	0	0

Appendix 2: Can phylogenetic relationships within genus indicate the enemy release of an invader?

Note: pin. – Senecio pinnatifolius var. pinnatifolius; min. – S. minimus; lin. – S. linearifolius var. arachnoideus; amy. – S. amygdalifolius; bip. – S. bippinnatisectus.

Group	Morphospecies	Family	Species	Guild	Abundances: Native Senecio spp.					
					pin.	min.	lin.	amy.	bip.	
Hemiptera	Aphididae 18	Aphididae		Sap-sucker	6	110	8	233	58	
cont.	Aphididae 2	Aphididae		Sap-sucker	0	6	0	12	1	
	Aphididae 20	Aphididae		Sap-sucker	0	1	1	3	6	
	Aphididae 21	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 23	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 24	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 25	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 26	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 27	Aphididae		Sap-sucker	0	0	1	0	0	
	Aphididae 28	Aphididae		Sap-sucker	2	2	0	13	0	
	Aphididae 29	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 30	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 31	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 34	Aphididae		Sap-sucker	0	1	0	1	1	
	Aphididae 35	Aphididae		Sap-sucker	0	2	0	0	0	
	Aphididae 36	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 38	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 39	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 40	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 41	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 42	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 43	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 44	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 45	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 46	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 48	Aphididae		Sap-sucker	0	0	0	0	0	
	Aphididae 49	Aphididae		Sap-sucker	0	0	1	0	0	
	Aphididae 50	Aphididae		Sap-sucker	0	0	2	0	0	
	Aphididae 51	Aphididae		Sap-sucker	0	16	1	8	1	
	Aphididae 52	Aphididae		Sap-sucker	0	0	0	3	0	
	Auchenorrhyncha 4	Cicadellidae		Sap-sucker	0	0	0	0	1	
	Auchenorrhyncha 5	Cicadellidae		Sap-sucker	18	4	45	3	1	
	Auchenorrhyncha 7	Cicadellidae		Sap-sucker	1	0	0	0	0	
	Auchenorrhyncha 8	Cicadellidae: Deltocephalinae	Attenuipyga minor	Sap-sucker	0	0	0	0	0	

Group	Morphospecies	Family	Species	Guild	Abundances: Native Senecio spp.					
					pin.	min.	lin.	amy.	bip.	
Hemiptera	Au: Heteroptera 9	Fulgoroidea		Sap-sucker	9	0	1	1	0	
cont.	Auchenorrhyncha 15	Delphacidae		Sap-sucker	1	0	0	0	0	
cont.	Auchenorrhyncha 16	Fulgoroidea		Sap-sucker	2	0	0	0	0	
	Auchenorrhyncha 17	Cicadellidae		Sap-sucker	2	0	2	1	0	
	Auchenorrhyncha 18	Flatidae		Sap-sucker	2	0	0	0	0	
	Auchenorrhyncha 19	Cicadellidae		Sap-sucker	0	0	0	0	8	
	Auchenorrhyncha 20	Cicadellidae		Sap-sucker	0	0	0	0	0	
	Auchenorrhyncha 21	Flatidae		Sap-sucker	0	1	63	2	0	
	Auchenorrhyncha 22	Cicadellidae		Sap-sucker	0	5	37	-	1	
	Auchenorrhyncha 23	Cicadellidae		Sap-sucker	0	0	1	0	0	
	Auchenorrhyncha 24	Cicadellidae		Sap-sucker	0	0	9	0	0	
	Auchenorrhyncha 25	Cicadellidae		Sap-sucker	0	0	1	1	0	
	Auchenorrhyncha 27	Cicadellidae		Sap-sucker	0	0	0	0	1	
	Auchenorrhyncha 28	Cicadellidae		Sap-sucker	0	0	0	Ő	1	
	Auchenorrhyncha 29	Cixiidae		Sap-sucker	0	0	0	1	0	
	Auchenorrhyncha 30	Cicadellidae		Sap-sucker	0	0	0	1	0	
	Auchenorrhyncha 31	Unknown		Sap-sucker	0	0	0	2	2	
	Auchenorrhyncha 32	Ricaniidae	Scolypopa australis	Sap-sucker	0	0	0	1	0	
	Auchenorrhyncha 33	Cicadellidae		Sap-sucker	0	0	0	1	0	
	Auchenorrhyncha 34	Fulgoroidea		Sap-sucker	0	0	0	0	2	
	Auchenorrhyncha 35	Cicadellidae		Sap-sucker	0	0	12	0	0	
	Auchenorrhyncha 36	Cicadellidae		Sap-sucker	0	1	0	0	0	
	Auchenorrhyncha 37	Aphrophoridae		Sap-sucker	0	2	0	0	0	
	Auchenorrhyncha 38	Cicadellidae		Sap-sucker	0	1	0	0	0	
	Auchenorrhyncha 39	Cicadellidae		Sap-sucker	0	3	0	0	0	
	Auchenorrhyncha 40	Cixiidae		Sap-sucker	0	0	0	0	0	
	Auchenorrhyncha 41	Cicadellidae		Sap-sucker	0	1	0	0	0	
	Auchenorrhyncha 42	Cicadellidae		Sap-sucker	0	2	0	0	0	
	Auchenorrhyncha 43	Flatidae		Sap-sucker	0	0	0	0	0	
	Auchenorrhyncha 44	Flatidae		Sap-sucker	0	0	0	0	0	
	Auchenorrhyncha 45	Fulgoroidea		Sap-sucker	0	0	0	0	1	
	Auchenorrhyncha 46	Fulgoroidea		Sap-sucker	0	0	1	0	0	
	Auchenorrhyncha 47	Cicadellidae		Sap-sucker	0	0	2	0	0	
	Auchenorrhyncha 48	Issidae		Sap-sucker	0	0	1	0	0	

Group	Morphospecies	Family	Species	Guild	Abune	dances: Na	tive <i>Senec</i>	<i>io</i> spp.	
_			-		pin.	min.	lin.	amy.	bip.
Hemiptera	Auchenorrhyncha 50	Cixiidae		Sap-sucker	0	1	0	0	0
cont.	Auchenorrhyncha 51	Cicadellidae		Sap-sucker	1	0	0	0	0
	Auchenorrhyncha 52	Cicadellidae		Sap-sucker	0	0	1	0	0
	Heteroptera 1	Lygaeoidea		Sap-sucker	135	994	135	2	97
	Heteroptera 2	Miridae		Sap-sucker	1	14	23	0	0
	Heteroptera 3	Orsillidae	Nysius clevelandensis	Sap-sucker	32	37	22	0	15
	Heteroptera 4	Miridae	Creontiades sp.	Sap-sucker	0	1	1	0	0
	Het: Sternorrhyncha 14	Coccoidea	L	Sap-sucker	2	0	0	0	0
	Heteroptera 16	Miridae		Sap-sucker	0	0	0	0	0
	Het: Sternorrhyncha 17	Coccoidea		Sap-sucker	0	0	0	0	0
	Heteroptera 18	Miridae		Sap-sucker	2	0	0	0	0
	Heteroptera 19	Miridae		Sap-sucker	2	0	0	0	0
	Heteroptera 20	Coreidae		Sap-sucker	2	0	0	0	0
	Heteroptera 21	Pentatomidae		Sap-sucker	1	0	0	0	0
	Heteroptera 24	Pentatomidae		Sap-sucker	0	0	0	0	5
	Heteroptera 26	Rhyparochromidae: Rhypa	rochominae	Sap-sucker	0	0	0	1	0
	Heteroptera 27	Miridae		Sap-sucker	0	0	0	2	0
	Heteroptera 28	Coreidae		Sap-sucker	0	1	0	0	0
	Heteroptera 29	Pentatomidae		Sap-sucker	0	3	0	0	0
	Heteroptera 30	Rhyparochromidae		Sap-sucker	0	2	0	1	0
	Heteroptera 32	Miridae		Sap-sucker	0	0	0	0	0
	Heteroptera 33	Miridae		Sap-sucker	0	1	0	0	0
	Heteroptera 34	Lygaeidae		Sap-sucker	0	2	0	0	0
	Heteroptera 35	Lygaeidae	Nysius vinator	Sap-sucker	0	0	0	0	0
	Heteroptera 36	Miridae		Sap-sucker	0	0	0	0	0
	Heteroptera 38	Aleyrodidae		Sap-sucker	0	0	0	2	0
	Heteroptera 39	Piesmatidae		Sap-sucker	0	0	1	0	0
	Heteroptera 40	Lygaeidae		Sap-sucker	0	0	0	0	0
	Unknown 21	Coccoidea		Sap-sucker	4	0	0	0	0
	Unknown 31	Coccoidea		Sap-sucker	0	0	0	0	0
	Unknown 32	Coccoidea		Sap-sucker	0	0	0	0	0
	Unknown 44	Coccoidea		Sap-sucker	0	0	0	0	0
	Unknown 52	Coccoidea		Sap-sucker	0	0	0	0	0
	Unknown 53	Coccoidea		Sap-sucker	0	0	0	2	0

Group	Morphospecies	Family	Species	Guild	Abundances: Native Senecio spp.					
-					pin.	min.	lin.	amy.	bip.	
Hemiptera	Unknown 58	Coccoidea		Sap-sucker	0	1	0	0	0	
cont.	M.1. Hemiptera 1	Derbidae		Sap-sucker	0	0	0	2	0	
Hymenoptera	Hymenoptera 15	Torymidae: Megastigminae	Megastigmus sp.	Galling	2	9	1	2	0	
Lepidoptera	Larvae 26	Unknown: pupae	megusugnus sp.	Leaf chewer	0	0	0	0	0	
Lepidoptera	Lepidoptera 1	Pyraloidea		Leaf chewer	0	0	0	0	0	
	Lepidoptera 2	Pyraloidea		Leaf chewer	81	7	7	ů 0	2	
	Lepidoptera 5	Pyraloidea		Leaf chewer	0	0	0	Ő	0	
	Lepidoptera 6	i graforada		Leaf chewer	0	0	0	ů 0	0	
	Lepidoptera 13	Arctiidae: Ctenuchinae	Amata sp.	Leaf chewer	0	0	0	ů 0	0	
	Lepidoptera 15	Tortricidae	innara sp.	Leaf chewer	1	0	0	ů 0	0	
	Lepidoptera 20	Arctiidae: Arctiinae	Nyctemera sp.	Leaf chewer	6	7	12	8	1	
	Lepidoptera 24	Arctiidae: Ctenuchinae	Amata sp.	Leaf chewer	0	2	1	4	3	
	Lepidoptera 30	Arctiidae: Arctiinae	Nyctemera sp.	Leaf chewer	1	0	0	0	1	
	Lepidoptera 31	Tortricidae		Leaf chewer	5	0	0	0	0	
	Lepidoptera 32	Pyraloidea		Leaf chewer	1	0	0	0	0	
	Lepidoptera 36	Pyraloidea		Leaf chewer	0	0	1	0	0	
	Lepidoptera 37	Cosmopterigidae	Pyroderces sp.	Leaf chewer	0	0	0	0	0	
	Lepidoptera 38	Gelechiidae	у т	Leaf chewer	0	0	0	0	0	
	Lepidoptera 39	Pyraloidea		Leaf chewer	0	0	0	0	0	
	Lepidoptera 40	Geometridae		Leaf chewer	0	0	11	0	4	
	Lepidoptera 41	Geometridae		Leaf chewer	0	0	5	0	1	
	Lepidoptera 42	Arctiidae: Arctiinae	<i>Nyctemera</i> sp.	Leaf chewer	0	0	0	0	0	
	Lepidoptera 43	Cosmopterigidae	· I	Leaf chewer	0	0	0	0	0	
	Lepidoptera 44	Tortricidae		Leaf chewer	0	0	0	0	2	
	Lepidoptera 46	Tortricidae		Leaf chewer	0	1	0	0	1	
	Lepidoptera 49	Tortricidae		Leaf chewer	0	0	1	1	0	
	Lepidoptera 50	Arctiidae		Leaf chewer	0	0	0	1	0	
	Lepidoptera 52	Gelechioidea		Leaf chewer	0	0	0	1	0	
	Lepidoptera 53	Arctiidae		Leaf chewer	0	0	0	1	0	
	Lepidoptera 54	Geometridae		Leaf chewer	0	1	0	0	0	
	Lepidoptera 55	Pterophoridae		Leaf chewer	0	1	0	0	0	
	Lepidoptera 58	Noctuidae		Leaf chewer	0	1	0	0	0	
	Lepidoptera 59	Gelechioidea		Leaf chewer	0	1	0	0	0	
	Lepidoptera 61	Geometridae	Phrissogonus laticostata	Leaf chewer	0	0	0	0	0	

Group	Morphospecies	Family	Species	Guild	Abune	dances: Na	tive Senec	<i>io</i> spp.	
					pin.	min.	lin.	amy.	bip.
Lepidoptera	Lepidoptera 62	Tortricidae		Leaf chewer	0	0	0	0	0
cont.	Lepidoptera 66	Tortricidae		Leaf chewer	0	0	0	0	0
contr	Lepidoptera 67	Geometridae		Leaf chewer	0	Ő	0	0	0 0
	Lepidoptera 68	Tortricidae		Leaf chewer	Ő	Ő	Ő	Ő	Ő
	Lepidoptera 69	Oecophoridae		Leaf chewer	Ő	Ő	Ő	Ő	0
	Lepidoptera 70	Gelechiidae		Leaf chewer	0	0	3	1	0
	Lepidoptera 72	Tortricidae		Leaf chewer	0	0	0	1	0
	Lepidoptera 74	Geometridae		Leaf chewer	0	0	1	0	0
	Lepidoptera 75	Pyraloidea		Leaf chewer	0	0	1	0	0
	Lepidoptera 76	Geometridae		Leaf chewer	0	1	0	0	0
	Lepidoptera 78	Geometridae		Leaf chewer	0	1	0	0	0
	Lepidoptera 79	Gelechioidea		Leaf chewer	0	1	0	0	0
	Lepidoptera 81	Noctuidae		Leaf chewer	0	0	0	0	0
	Lepidoptera 82	Arctiidae: Ctenuchinae	Amata sp.	Leaf chewer	0	0	0	0	0
	Lepidoptera 83	Gelechioidea	-	Leaf chewer	0	0	0	0	0
	Lepidoptera 84	Gelechioidea		Leaf chewer	2	0	0	0	0
	Lepidoptera 85	Gelechioidea		Leaf chewer	1	0	0	0	0
	Lepidoptera 86	Pyraloidea		Leaf chewer	1	0	0	0	0
	Lepidoptera 87	Pyraloidea		Leaf chewer	1	0	0	0	0
	Lepidoptera 88	Tortricidae		Leaf chewer	0	0	0	0	0
	Lepidoptera 89	Pyralidae		Leaf chewer	0	1	0	0	0
	Lepidoptera 90	Gelechioidea		Leaf chewer	0	1	0	0	0
Orthoptera	Orthoptera 4	Acrididae		Leaf chewer	1	0	0	0	0
	Orthoptera 6	Tettigoniidae		Leaf chewer	0	0	1	0	0
	Orthoptera 9	Tettigoniidae		Leaf chewer	0	1	1	0	1
			Pseudanaphothrips						
Thysanoptera	Thysanoptera 1	Thripidae: Thripinae	achaetus	Sap-sucker	3	0	1	0	0
	Thysanoptera 23	Thripidae: Thripinae	Thrips imaginis Pseudanaphothrips	Sap-sucker	0	0	0	0	0
	Thysanoptera 2	Thripidae: Thripinae	achaetus	Sap-sucker	6	3	3	0	1
	Thysanoptera 3	Panchaetothripinae	Bhattithrips sp.	Sap-sucker	22	1	1	0	1
	Thysanoptera 25	Thripidae	Larvae	Sap-sucker	0	0	4	0	0
	Thysanoptera 35	Thripidae: Thripinae	Thrips sp.	Sap-sucker	1	0	19	0	0
	Thysanoptera 37	Thripidae		Sap-sucker	0	0	0	0	0

Group	Morphospecies	Family	Species	Guild	Abundances: Native Senecio spp.					
					pin.	min.	lin.	amy.	bip.	
Thysanoptera	Thysanoptera 39	Thripidae	Larvae	Sap-sucker	2	0	0	0	0	
cont.	Thysanoptera 47	Thripidae	Larvae	Sap-sucker	0	0	0	0	0	
	Thysanoptera 50	Panchaetothripinae Phlaeothripidae:	Bhattithrips larvae	Sap-sucker	0	0	0	0	0	
	Thysanoptera 51	Phlaeothripinae Phlaeothripidae:	Haplothrips sp.	Sap-sucker	0	0	0	0	1	
	Thysanoptera 52	Phlaeothripinae	Haplothrips sp.	Sap-sucker	0	0	0	0	1	
	Thysanoptera 53	Thripidae: Thripinae	Thrips imaginis & T. tabaci	Sap-sucker	0	0	0	0	1	

Group	Morphospecies	Family	Species	Guild	Abunda	nces: Non	-native Sen	<i>ecio</i> spp.	
					mad.	ang.	ptero.	glast.	macro.
Acarina	Acarina 44	Tenuipalpidae		Sap-sucker	5	9	66	0	116
Coleoptera	Coleoptera 1	Brentidae		Leaf chewer	2	0	0	0	0
-	Coleoptera 9	Chrysomelidae		Leaf chewer	2	0	0	0	0
	Coleoptera 18	Curculionidae		Leaf chewer	0	1	0	1	0
	Coleoptera 20	Curculionidae: Scolytinae		Leaf chewer	0	1	0	0	0
	Coleoptera 39	Curculionidae		Leaf chewer	0	0	0	0	0
	Coleoptera 41	Chrysomelidae		Leaf chewer	0	0	0	0	0
	Coleoptera 52	Curculionidae		Leaf chewer	0	0	0	0	0
	Coleoptera 54	Chrysomelidae		Leaf chewer	0	0	0	0	0
	Coleoptera 55	Cerambycidae		Leaf chewer	0	0	0	0	0
	Coleoptera 58	Chrysomelidae		Leaf chewer	0	0	0	0	0
	Coleoptera 61	Chrysomelidae: Cryptocephal	inae	Leaf chewer	0	0	0	0	0
	Coleoptera 63	Aderidae		Leaf chewer	0	0	1	0	0
	Coleoptera 65	Brentidae		Leaf chewer	0	0	0	0	0
	Coleoptera 66	Brentidae		Leaf chewer	0	0	0	0	0
	Coleoptera 67	Curculionidae		Leaf chewer	0	0	0	0	0
	Larvae 24	Curculionidae		Leaf chewer	1	0	0	0	0
	Larvae 25	Curculionidae		Leaf chewer	0	0	0	0	0
	Larvae 32	Curculionidae		Leaf chewer	0	0	0	0	0
	Lep. Coleoptera 56	Cerambycidae		Leaf chewer	0	0	1	0	0
	Lepidoptera 73	Cerambycidae		Leaf chewer	0	0	0	0	0
	Lep. Coleoptera 80	Curculionidae		Leaf chewer	0	0	0	0	1
Diptera	Diptera 5	Agromyzidae		Miner	1	0	0	0	0
_	Diptera 41	Agromyzidae		Miner	8	0	7	3	0
	Col: Auchenorrhyncha 45	Membracidae		Sap-sucker	0	0	0	0	0
Hemiptera	Dip: Sternorrhyncha 82	Coccoidea		Sap-sucker	0	0	0	0	0
-	Aphididae 1	Aphididae		Sap-sucker	0	0	34	0	0
	Aphididae 10	Aphididae		Sap-sucker	11	0	0	0	0
	Aphididae 11	Aphididae		Sap-sucker	0	0	55	0	0
	Aphididae 13	Aphididae		Sap-sucker	11	0	0	0	0
	Aphididae 14	Aphididae		Sap-sucker	2	0	0	0	0

Appendix 2: Can phylogenetic relationships within genus indicate the enemy release of an invader?

Note: mad. – Senecio madagascariensis; ang. – S.angulatus; ptero. – S. pterophorus; glast. – S. glastifolius; mac. – S. macroglossus.

Group	Morphospecies	Family	Species	Guild	Abunda	nces: Non	-native Ser	<i>ecio</i> spp.	
					mad.	ang.	ptero.	glast.	macro.
Hemiptera	Aphididae 18	Aphididae		Sap-sucker	240	327	439	0	1
cont.	Aphididae 2	Aphididae		Sap-sucker	0	0	12	0	0
	Aphididae 20	Aphididae		Sap-sucker	17	4	34	0	1
	Aphididae 21	Aphididae		Sap-sucker	35	0	0	0	0
	Aphididae 23	Aphididae		Sap-sucker	34	0	0	0	0
	Aphididae 24	Aphididae		Sap-sucker	268	0	2	0	0
	Aphididae 25	Aphididae		Sap-sucker	32	0	0	0	0
	Aphididae 26	Aphididae		Sap-sucker	298	0	0	0	0
	Aphididae 27	Aphididae		Sap-sucker	126	34	98	0	196
	Aphididae 28	Aphididae		Sap-sucker	135	42	37	0	22
	Aphididae 29	Aphididae		Sap-sucker	20	0	0	0	0
	Aphididae 30	Aphididae		Sap-sucker	1	0	0	0	0
	Aphididae 31	Aphididae		Sap-sucker	12	0	0	0	0
	Aphididae 34	Aphididae		Sap-sucker	0	0	5	0	1
	Aphididae 35	Aphididae		Sap-sucker	0	0	0	0	0
	Aphididae 36	Aphididae		Sap-sucker	1	0	0	0	0
	Aphididae 38	Aphididae		Sap-sucker	9	0	0	0	0
	Aphididae 39	Aphididae		Sap-sucker	8	0	0	0	0
	Aphididae 40	Aphididae		Sap-sucker	3	0	0	0	0
	Aphididae 41	Aphididae		Sap-sucker	3	0	0	0	0
	Aphididae 42	Aphididae		Sap-sucker	30	0	0	0	0
	Aphididae 43	Aphididae		Sap-sucker	15	0	0	0	0
	Aphididae 44	Aphididae		Sap-sucker	2	0	0	0	0
	Aphididae 45	Aphididae		Sap-sucker	2	0	0	0	0
	Aphididae 46	Aphididae		Sap-sucker	1	0	0	0	0
	Aphididae 48	Aphididae		Sap-sucker	0	0	9	0	0
	Aphididae 49	Aphididae		Sap-sucker	0	0	2	0	0
	Aphididae 50	Aphididae		Sap-sucker	0	0	0	0	0
	Aphididae 51	Aphididae		Sap-sucker	0	1	2	0	0
	Aphididae 52	Aphididae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 4	Cicadellidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 5	Cicadellidae		Sap-sucker	1	0	0	0	0
	Auchenorrhyncha 7	Cicadellidae		Sap-sucker	1	0	0	0	0
	Auchenorrhyncha 8	Cicadellidae: Deltocephalinae	Attenuipyga minor	Sap-sucker	1	0	0	0	0

Group	Morphospecies	Family	Species	Guild	Abunda	nces: Non-	-native Ser	<i>iecio</i> spp.	
					mad.	ang.	ptero.	glast.	macro.
Hemiptera	Au: Heteroptera 9	Fulgoroidea		Sap-sucker	0	0	0	0	0
cont.	Auchenorrhyncha 15	Delphacidae		Sap-sucker	0	0	0	Ő	Ő
	Auchenorrhyncha 16	Fulgoroidea		Sap-sucker	0	0	0	Ő	0 0
	Auchenorrhyncha 17	Cicadellidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 18	Flatidae		Sap-sucker	0	1	5	0	0
	Auchenorrhyncha 19	Cicadellidae		Sap-sucker	2	0	0	0	0
	Auchenorrhyncha 20	Cicadellidae		Sap-sucker	17	1	0	0	0
	Auchenorrhyncha 21	Flatidae		Sap-sucker	0	0	2	5	0
	Auchenorrhyncha 22	Cicadellidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 23	Cicadellidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 24	Cicadellidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 25	Cicadellidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 27	Cicadellidae		Sap-sucker	0	0	8	0	0
	Auchenorrhyncha 28	Cicadellidae		Sap-sucker	0	1	0	0	0
	Auchenorrhyncha 29	Cixiidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 30	Cicadellidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 31	Unknown		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 32	Ricaniidae	Scolypopa australis	Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 33	Cicadellidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 34	Fulgoroidea		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 35	Cicadellidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 36	Cicadellidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 37	Aphrophoridae		Sap-sucker	0	0	3	0	0
	Auchenorrhyncha 38	Cicadellidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 39	Cicadellidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 40	Cixiidae		Sap-sucker	0	0	1	0	0
	Auchenorrhyncha 41	Cicadellidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 42	Cicadellidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 43	Flatidae		Sap-sucker	0	0	4	0	0
	Auchenorrhyncha 44	Flatidae		Sap-sucker	0	2	0	0	0
	Auchenorrhyncha 45	Fulgoroidea		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 46	Fulgoroidea		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 47	Cicadellidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 48	Issidae		Sap-sucker	0	0	0	0	0

Group	Morphospecies	Family	Species	Guild	Abundances: Non-native Senecio spp.				
					mad.	ang.	ptero.	glast.	macro
Hemiptera	Auchenorrhyncha 50	Cixiidae		Sap-sucker	0	0	0	0	0
cont.	Auchenorrhyncha 51	Cicadellidae		Sap-sucker	0	0	0	0	0
	Auchenorrhyncha 52	Cicadellidae		Sap-sucker	0	0	0	0	0
	Heteroptera 1	Lygaeoidea		Sap-sucker	263	3	13	3	0
	Heteroptera 2	Miridae		Sap-sucker	3	8	106	0	0
	Heteroptera 3	Orsillidae	Nysius clevelandensis	Sap-sucker	4	0	15	15	0
	Heteroptera 4	Miridae	Creontiades sp.	Sap-sucker	0	0	1	0	0
	Het: Sternorrhyncha 14	Coccoidea	•	Sap-sucker	0	0	0	0	0
	Heteroptera 16	Miridae		Sap-sucker	1	0	0	0	0
	Het: Sternorrhyncha 17	Coccoidea		Sap-sucker	0	1	0	0	0
	Heteroptera 18	Miridae		Sap-sucker	7	0	1	0	0
	Heteroptera 19	Miridae		Sap-sucker	4	0	0	0	0
	Heteroptera 20	Coreidae		Sap-sucker	0	0	0	0	0
	Heteroptera 21	Pentatomidae		Sap-sucker	0	0	0	0	0
	Heteroptera 24	Pentatomidae		Sap-sucker	0	0	0	0	0
	Heteroptera 26	Rhyparochromidae: Rhyparochominae		Sap-sucker	0	0	0	0	0
	Heteroptera 27	Miridae		Sap-sucker	0	0	8	0	0
	Heteroptera 28	Coreidae		Sap-sucker	0	0	0	0	0
	Heteroptera 29	Pentatomidae		Sap-sucker	0	0	0	0	0
	Heteroptera 30	Rhyparochromidae		Sap-sucker	0	0	0	0	0
	Heteroptera 32	Miridae		Sap-sucker	0	0	2	0	0
	Heteroptera 33	Miridae		Sap-sucker	0	0	1	0	0
	Heteroptera 34	Lygaeidae		Sap-sucker	0	0	0	0	6
	Heteroptera 35	Lygaeidae	Nysius vinator	Sap-sucker	0	0	1	0	0
	Heteroptera 36	Miridae	-	Sap-sucker	0	0	1	0	0
	Heteroptera 38	Aleyrodidae		Sap-sucker	0	0	0	0	0
	Heteroptera 39	Piesmatidae		Sap-sucker	0	0	0	0	0
	Heteroptera 40	Lygaeidae		Sap-sucker	0	0	0	0	1
	Unknown 21	Coccoidea		Sap-sucker	0	0	0	1	0
	Unknown 31	Coccoidea		Sap-sucker	0	0	0	0	1
	Unknown 32	Coccoidea		Sap-sucker	0	0	0	0	1
	Unknown 44	Coccoidea		Sap-sucker	0	0	4	0	19
	Unknown 52	Coccoidea		Sap-sucker	0	97	1	0	0
	Unknown 53	Coccoidea		Sap-sucker	0	0	0	0	0

Group	Morphospecies	Family	Species	Guild	Abundances: Non-native Senecio spp.				
					mad.	ang.	ptero.	glast.	macro.
Hemiptera	Unknown 58	Coccoidea		Sap-sucker	0	0	0	0	0
cont.	M.1. Hemiptera 1	Derbidae		Sap-sucker	0	0	0	0	0
Hymenoptera	Hymenoptera 15	Torymidae: Megastigminae	Megastigmus sp.	Galling	4	0	0	0	0
Lepidoptera	Larvae 26	Unknown: pupae		Leaf chewer	1	0	0	0	0
	Lepidoptera 1	Pyraloidea		Leaf chewer	0	1	1	0	0
	Lepidoptera 2	Pyraloidea		Leaf chewer	221	1	12	2	2
	Lepidoptera 5	Pyraloidea		Leaf chewer	2	0	0	0	0
	Lepidoptera 6			Leaf chewer	0	0	1	0	0
	Lepidoptera 13	Arctiidae: Ctenuchinae	Amata sp.	Leaf chewer	1	0	0	0	0
	Lepidoptera 15	Tortricidae		Leaf chewer	0	0	0	0	0
	Lepidoptera 20	Arctiidae: Arctiinae	<i>Nyctemera</i> sp.	Leaf chewer	17	0	77	1	0
	Lepidoptera 24	Arctiidae: Ctenuchinae	Amata sp.	Leaf chewer	0	0	0	0	0
	Lepidoptera 30	Arctiidae: Arctiinae	Nyctemera sp.	Leaf chewer	0	0	0	3	0
	Lepidoptera 31	Tortricidae		Leaf chewer	1	0	0	0	0
	Lepidoptera 32	Pyraloidea		Leaf chewer	0	0	0	0	0
	Lepidoptera 36	Pyraloidea		Leaf chewer	1	0	0	0	0
	Lepidoptera 37	Cosmopterigidae	Pyroderces sp.	Leaf chewer	1	0	0	0	0
	Lepidoptera 38	Gelechiidae		Leaf chewer	0	0	0	3	0
	Lepidoptera 39	Pyraloidea		Leaf chewer	0	0	0	1	0
	Lepidoptera 40	Geometridae		Leaf chewer	0	0	0	0	0
	Lepidoptera 41	Geometridae		Leaf chewer	0	0	0	0	0
	Lepidoptera 42	Arctiidae: Arctiinae	Nyctemera sp.	Leaf chewer	0	0	0	0	2
	Lepidoptera 43	Cosmopterigidae		Leaf chewer	0	0	0	0	1
	Lepidoptera 44	Tortricidae		Leaf chewer	0	0	0	0	0
	Lepidoptera 46	Tortricidae		Leaf chewer	0	1	0	0	0
	Lepidoptera 49	Tortricidae		Leaf chewer	0	0	0	0	0
	Lepidoptera 50	Arctiidae		Leaf chewer	0	0	0	0	0
	Lepidoptera 52	Gelechioidea		Leaf chewer	0	0	0	0	0
	Lepidoptera 53	Arctiidae		Leaf chewer	0	0	0	0	0
	Lepidoptera 54	Geometridae		Leaf chewer	0	0	0	0	0
	Lepidoptera 55	Pterophoridae		Leaf chewer	0	0	0	0	0
	Lepidoptera 58	Noctuidae		Leaf chewer	0	0	0	0	0
	Lepidoptera 59	Gelechioidea		Leaf chewer	0	0	0	0	0
	Lepidoptera 61	Geometridae	Phrissogonus laticostata	Leaf chewer	0	0	4	0	0

Group	Morphospecies	Family	Species	Guild	Abundances: Non-native Senecio spp.				
					mad.	ang.	ptero.	glast.	macro.
Lepidoptera	Lepidoptera 62	Tortricidae		Leaf chewer	0	0	1	0	0
cont.	Lepidoptera 66	Tortricidae		Leaf chewer	0	1	0	0	0
	Lepidoptera 67	Geometridae		Leaf chewer	0	1	0	0	0
	Lepidoptera 68	Tortricidae		Leaf chewer	0	1	0	0	0
	Lepidoptera 69	Oecophoridae		Leaf chewer	0	1	0	0	0
	Lepidoptera 70	Gelechiidae		Leaf chewer	0	0	0	0	0
	Lepidoptera 72	Tortricidae		Leaf chewer	0	0	0	0	0
	Lepidoptera 74	Geometridae		Leaf chewer	0	0	0	0	0
	Lepidoptera 75	Pyraloidea		Leaf chewer	0	0	0	0	0
	Lepidoptera 76	Geometridae		Leaf chewer	0	0	0	0	0
	Lepidoptera 78	Geometridae		Leaf chewer	0	0	0	0	0
	Lepidoptera 79	Gelechioidea		Leaf chewer	0	0	0	0	0
	Lepidoptera 81	Noctuidae		Leaf chewer	0	0	0	0	1
	Lepidoptera 82	Arctiidae: Ctenuchinae	Amata sp.	Leaf chewer	0	0	0	0	1
	Lepidoptera 83	Gelechioidea	*	Leaf chewer	0	0	0	0	1
	Lepidoptera 84	Gelechioidea		Leaf chewer	0	0	0	0	0
	Lepidoptera 85	Gelechioidea		Leaf chewer	0	0	0	0	0
	Lepidoptera 86	Pyraloidea		Leaf chewer	0	0	0	0	0
	Lepidoptera 87	Pyraloidea		Leaf chewer	0	0	0	0	0
	Lepidoptera 88	Tortricidae		Leaf chewer	0	0	1	0	0
	Lepidoptera 89	Pyralidae		Leaf chewer	1	0	0	0	0
	Lepidoptera 90	Gelechioidea		Leaf chewer	0	0	0	0	0
Orthoptera	Orthoptera 4	Acrididae		Leaf chewer	0	0	0	0	0
	Orthoptera 6	Tettigoniidae		Leaf chewer	0	0	0	0	0
	Orthoptera 9	Tettigoniidae		Leaf chewer	0	1	0	0	0
Thysanoptera	Thysanoptera 1	Thripidae: Thripinae	Pseudanaphothrips achaetus	Sap-sucker	7	0	4	0	0
	Thysanoptera 23	Thripidae: Thripinae	Thrips imaginis	Sap-sucker	0	1	0	0	0
	Thysanoptera 2	Thripidae: Thripinae	Pseudanaphothrips achaetus	Sap-sucker	31	12	8	0	3
	Thysanoptera 3	Panchaetothripinae	Bhattithrips sp.	Sap-sucker	7	0	0	0	0
	Thysanoptera 25	Thripidae	Larvae	Sap-sucker	2	0	0	0	0
	Thysanoptera 35	Thripidae: Thripinae	Thrips sp.	Sap-sucker	0	8	10	0	1
	Thysanoptera 37	Thripidae		Sap-sucker	0	3	0	0	0
	Thysanoptera 39	Thripidae	Larvae	Sap-sucker	24	0	0	0	0
	Thysanoptera 47	Thripidae	Larvae	Sap-sucker	32	0	0	0	0

Group	Morphospecies	Family	Species	Guild	Abundances: Non-native Senecio spp.				
					mad.	ang.	ptero.	glast.	macro.
Thysanoptera	Thysanoptera 50	Panchaetothripinae Phlaeothripidae:	Bhattithrips larvae	Sap-sucker	0	0	0	0	1
cont.	Thysanoptera 51	Phlaeothripinae Phlaeothripidae:	Haplothrips sp.	Sap-sucker	0	0	0	0	0
	Thysanoptera 52 Thysanoptera 53	Phlaeothripinae Thripidae: Thripinae	Haplothrips sp. Thrips imaginis & T. tabaci	Sap-sucker Sap-sucker	0	0	2 20	0	0

Group	Morphospecies	Family	Species	Guild	Abdundance		
					S. madagascariensis	S. pinnatifolius	
Acarina	Acarina 1			Unknown	1	0	
	Acarina 10			Fungivore	268	0	
	Acarina 11	Ascidae and Histiostomatidae mix		Unknown	9	1	
	Acarina 12			Unknown	1	0	
	Acarina 13			Unknown	6	18	
	Acarina 2	Ascidae		Fungivore	2	0	
	Acarina 3			Fungivore	12	23	
	Acarina 4			Unknown	1	0	
	Acarina 5			Unknown	1	4	
	Acarina 6	Acaridae and other Oribatida mix	Acaridae: Tyrophagus sp.	Unknown	1	8	
	Acarina 7			Unknown	89	54	
	Acarina 8	Erythraeidae		Predator	1	0	
	Acarina 9			Fungivore	2	15	
	Acarina 14			Unknown	1	0	
	Acarina 15	Ologamasidae		Predator	34	10	
	Acarina 16	Phthiracaridae		Detritivore	6	2	
	Acarina 17			Unknown	5	0	
	Acarina 18			Unknown	1	0	
	Acarina 19			Fungivore	14	1	
	Acarina 20			Unknown	1	0	
	Acarina 21	Acaridae	Tyrophagus sp.	Fungivore	8	2	
	Acarina 22			Predator	2	5	
	Acarina 24	Acaridae	Tyrophagus putrescentiae	Fungivore	9	99	
	Acarina 25	Bdellidae		Predator	1	1	
	Acarina 26			Unknown	1	1	

Appendix 3: Does time since colonisation influence enemy release of an invasive weed?

Group	Morphospecies	Family	Species	Guild	Abdund	ance
					S. madagascariensis	S. pinnatifoliu
Acarina cont.	Acarina 27			Unknown	5	0
	Acarina 28			Unknown	1	0
	Acarina 29			Unknown	2	0
	Acarina 30			Unknown	1	0
	Acarina 31	Anystidae	Anystis baccarum	Predator	1	4
	Acarina 32			Unknown	2	1
	Acarina 33			Unknown	3	0
	Acarina 35			Unknown	1	0
	Acarina 36			Fungivore	18	138
	Acarina 37			Fungivore	5	7
	Acarina 38			Unknown	1	0
	Acarina 39	Bdellidae		Predator	2	3
	Acarina 40			Unknown	1	0
	Acarina 41			Unknown	1	0
	Acarina 42			Fungivore	5	4
	Acarina 43			Unknown	1	0
	Acarina 44	Tenuipalpidae		Herbivore	1	3
	Acarina 45			Unknown	2	0
	Acarina 46			Unknown	1	0
	Acarina 47			Unknown	1	0
	Acarina 48	Ascidae	Proctolaelaps sp.	Fungivore	1	1
	Acarina 49			Unknown	1	0
	Acarina 50			Unknown	0	2
	Acarina 51			Unknown	0	2
	Acarina 52			Unknown	0	16
	Acarina 53			Unknown	0	1
	Acarina 54			Unknown	0	1

Group	Morphospecies	Family	Species	Guild	Abdundance		
					S. madagascariensis	S. pinnatifoliu	
Acarina cont.	Acarina 55			Unknown	0	1	
	Acarina 56			Unknown	0	1	
	Acarina 57	Ologamasidae		Predator	0	2	
	Acarina 58			Unknown	0	2	
	Acarina 59			Unknown	0	3	
	Acarina 60			Unknown	0	1	
	Acarina 61	Neoliodidae		Fungivore	0	1	
	Acarina 62			Unknown	0	7	
	Acarina 63			Predator	0	1	
	Acarina 64			Fungivore	0	1	
	Acarina 65			Unknown	0	1	
	Acarina 66			Unknown	0	1	
Araneida	Araneida 1	Araneidae		Predator	1	0	
	Araneida 2	Araneidae		Predator	2	0	
	Araneida 3	Araneidae		Predator	1	0	
	Araneida 4	Araneidae		Predator	1	7	
	Araneida 5	Araneidae		Predator	1	0	
	Araneida 6	Araneidae		Predator	1	0	
	Araneida 7	Araneidae		Predator	1	0	
	Araneida 8	Araneidae		Predator	1	0	
	Araneida 9	Araneidae		Predator	1	0	
	Araneida 10	Araneidae		Predator	1	0	
	Araneida 11	Araneidae		Predator	1	0	
	Araneida 12	Araneidae		Predator	1	0	
	Araneida 13	Araneidae		Predator	1	0	
	Araneida 14	Araneidae		Predator	1	0	
	Araneida 15	Araneidae		Predator	0	1	

Group	Morphospecies	Family	Species	Guild	Abdund	ance
					S. madagascariensis	S. pinnatifolius
Araneida cont.	Araneida 16	Araneidae		Predator	0	1
	Araneida 17	Araneidae		Predator	0	2
	Araneida 18	Araneidae		Predator	0	1
	Araneida 19	Araneidae		Predator	0	1
Pseudoscorpiones	Pseudoscorpiones 1			Predator	2	0
Amphipoda	Amphipoda 1	Talitridae		Unknown	1	0
	Amphipoda 2	Talitridae		Unknown	0	41
Annelida	Unknown 24			Unknown	3	3
Blattaria	Blattaria 1			Omnivore	1	0
Coleoptera	Coleoptera 1	Brentidae		Herbivore	1	0
	Coleoptera 2	Corylophidae		Fungivore	18	19
	Coleoptera 3	Carabidae		Detritivore	3	0
	Coleoptera 4	Corylophidae		Fungivore	5	1
	Coleoptera 5	Curculionidae		Herbivore	1	0
	Coleoptera 6	Coccinellidae		Predator	1	3
	Coleoptera 7	Latridiidae		Fungivore	1	11
	Coleoptera 9	Chrysomelidae		Herbivore	2	0
	Coleoptera 10	Staphylinidae		Unknown	1	0
	Coleoptera 11	Corylophidae		Fungivore	1	3
	Coleoptera 12	Latridiidae		Fungivore	0	18
	Coleoptera 13	Staphylinidae		Unknown	0	2
	Coleoptera 14	Curculionidae		Herbivore	0	1
	Coleoptera 15	Tenebrionidae		Scavenger	0	1
	Coleoptera 16	Tenebrionidae		Scavenger	0	1
	Coleoptera 17	Scarabidae: Aphodiinae		Dung	0	2
	Coleoptera 18	Curculionidae		Herbivore	0	1
	Coleoptera 19	Curculionidae		Herbivore	0	1

Group	Morphospecies	Family	Species	Guild	Abdund	ance
				S. m.	adagascariensis	S. pinnatifolius
Coleoptera cont.	Coleoptera 20	Curculionidae: Scolytinae		Wood boorers	0	3
	Coleoptera 72	Latridiidae		Fungivore	0	1
	Larvae 1	Curculionidae		Herbivore	1	0
	Larvae 24	Curculionidae		Herbivore	0	6
	Larvae 25	Curculionidae		Herbivore	0	20
	L.7: Coleoptera 72			Unknown	2	5
	L.8: Coleoptera 73	Staphylinidae		Unknown	1	0
	L.10: Coleoptera 74			Unknown	1	0
	L.18: Coleoptera 75			Unknown	0	1
	L.21: Coleoptera 76	Chrysomelidae		Herbivore	0	54
	L.28: Coleoptera 77			Unknown	0	1
	L.57: Coleoptera 78			Unknown	0	1
	Unknown 10			Unknown	1	0
	Unknown 12			Unknown	1	8
	Unknown 14	Corylophidae		Fungivore	6	6
	Unknown 20	Melyridae	Pupae	Predator	2	4
	Unknown 25			Unknown	2	22
	Unknown 27	Carabidae/Staphylidae		Predator	0	1
Collembola	Collembola 1			Detritivore	2	1
	Collembola 2			Detritivore	1	0
	Collembola 3			Detritivore	1	0
	Collembola 4			Detritivore	10	0
	Collembola 5			Detritivore	1	0
	Collembola 6			Detritivore	1	2
•	Collembola 7			Detritivore	1	0
	Collembola 8			Detritivore	1	0
	Collembola 9			Detritivore	2	0

Group	Morphospecies	Family	Species	Guild	Abdundance		
					S. madagascariensis	S. pinnatifolius	
Colombola cont	Collembola 10			Detritivore	2	0	
	Collembola 11			Detritivore	0	1	
	Collembola 12			Detritivore	0	1	
	Larvae 19			Detritivore	0	3	
	Unknown 7			Detritivore	1	0	
	Unknown 9			Detritivore	1	0	
	Unknown 23			Detritivore	1	0	
Diplura	Unknown 8	Diplura		Predator	1	0	
	Unknown 11	Diplura		Predator	1	13	
Diptera	Diptera 2	Psychodidae		Non-feeding	1	0	
	Diptera 1	Lauxaniidae		Unknown	1	0	
	Diptera 10	Chloropidae		Unknown	1	0	
	Diptera 11	Tephritidae		Unknown	4	13	
	Diptera 12			Unknown	1	0	
	Diptera 14	Phoridae		Detritivore	1	0	
	Diptera 4	Cecidomyiidae		Unknown	11	3	
	Diptera 5	Agromyzidae		Herbivore	1	0	
	Diptera 6	Tephritidae		Herbivore	1	0	
	Diptera 7	Phoridae		Detritivore	1	0	
	Diptera 8	Cecidomyiidae		Unknown	4	0	
	Diptera 9	Cecidomyiidae		Unknown	1	1	
	Diptera 13	Lauxaniidae		Unknown	1	0	
	Diptera 15			Unknown	1	0	
	Diptera 16	Cecidomyiidae		Unknown	1	0	
	Diptera 17	Sciaridae		Detritivore	1	0	
	Diptera 18	Chironomidae		Unknown	1	0	
	Diptera 19	Psychodidae		Non-feeding	4	0	

Group	Morphospecies	Family	Species	Guild	Abdundance		
					S. madagascariensis	S. pinnatifolius	
Diptera cont.	Diptera 20	Cecidomyiidae		Unknown	3	0	
	Diptera 21	Lauxaniidae		Unknown	1	13	
	Diptera 22	Chloropidae		Unknown	1	38	
	Diptera 23	Cecidomyiidae		Unknown	7	2	
	Diptera 24	Chironomidae		Unknown	2	1	
	Diptera 25	Phoridae		Detritivore	1	0	
	Diptera 26	Milichiidae		Unknown	0	10	
	Diptera 27	Chloropidae		Unknown	0	14	
	Diptera 28	Chloropidae		Unknown	0	2	
	Diptera 29	Lauxaniidae		Unknown	0	3	
	Diptera 30	Empididae		Unknown	0	1	
	Larvae 2	Cecidomyiidae		Unknown	4	3	
	Larvae 3	Cecidomyiidae		Unknown	417	44	
	Larvae 4	Cecidomyiidae		Unknown	431	41	
	Larvae 6	Cecidomyiidae		Unknown	15	0	
	Larvae 7	Cecidomyiidae		Unknown	1	0	
	Larvae 8			Unknown	1	0	
	Larvae 10	Cecidomyiidae		Bacteria	1	0	
	Larvae 13	Syrphidae		Unknown	2	0	
	Larvae 14			Unknown	1	0	
	Larvae 15			Unknown	0	1	
	Larvae 16	Cecidomyiidae		Unknown	0	3	
	Larvae 17	Stratiomydiae		Unknown	0	73	
	Larvae 23	Syrphidae		Predator	0	1	
	Diptera 31	Nematocera		Unknown	2	0	
	Unknown 18	Cecidomyiidae		Unknown	20	0	
Gastropoda	Gastropoda 1			Unknown	5	5	

Group	Morphospecies	Family	Species	Guild	Abdundance		
					S. madagascariensis	S. pinnatifolius	
Gastropoda cont.	Gastropoda 2			Unknown	5	2	
	Gastropoda 3			Unknown	0	50	
	Gastropoda 4			Unknown	0	1	
Hemiptera	Aphididae 1	Aphididae		Herbivore	5	109	
	Aphididae 10	Aphididae		Herbivore	18	0	
	Aphididae 11	Aphididae		Herbivore	2	0	
	Aphididae 12	Aphididae		Herbivore	1	0	
	Aphididae 13	Aphididae		Herbivore	16	66	
	Aphididae 14	Aphididae		Herbivore	3	0	
	Aphididae 15	Aphididae		Herbivore	2	1	
	Aphididae 16	Aphididae		Herbivore	1	0	
	Aphididae 17	Aphididae		Herbivore	2	1	
	Aphididae 18	Aphididae		Herbivore	704	72	
	Aphididae 19	Aphididae		Herbivore	32	0	
	Aphididae 2	Aphididae		Herbivore	4	0	
	Aphididae 20	Aphididae		Herbivore	32	1	
	Aphididae 21	Aphididae		Herbivore	108	15	
	Aphididae 22	Aphididae		Herbivore	1	0	
	Aphididae 23	Aphididae		Herbivore	37	0	
	Aphididae 24	Aphididae		Herbivore	269	10	
	Aphididae 25	Aphididae		Herbivore	249	1	
	Aphididae 26	Aphididae		Herbivore	676	25	
	Aphididae 27	Aphididae		Herbivore	334	36	
	Aphididae 28	Aphididae		Herbivore	307	23	
	Aphididae 29	Aphididae		Herbivore	22	0	
	Aphididae 3	Aphididae		Herbivore	2	0	
	Aphididae 30	Aphididae		Herbivore	12	6	

Group	Morphospecies	Family	Species	Guild	Abdund	ance
					S. madagascariensis	S. pinnatifoliu
Hemiptera cont.	Aphididae 31	Aphididae		Herbivore	18	8
	Aphididae 32	Aphididae		Herbivore	2	0
	Aphididae 33	Aphididae		Herbivore	2	19
	Aphididae 34	Aphididae		Herbivore	1	0
	Aphididae 35	Aphididae		Herbivore	16	2
	Aphididae 36	Aphididae		Herbivore	2	0
	Aphididae 37	Aphididae		Herbivore	1	7
	Aphididae 38	Aphididae		Herbivore	14	0
	Aphididae 41	Aphididae		Herbivore	14	4
	Aphididae 47	Aphididae		Herbivore	0	9
	Aphididae 4	Aphididae		Herbivore	1	0
	Aphididae 5	Aphididae		Herbivore	1	0
	Aphididae 6	Aphididae		Herbivore	17	0
	Aphididae 7	Aphididae		Herbivore	16	0
	Aphididae 8	Aphididae		Herbivore	1	0
	Aphididae 9	Aphididae		Herbivore	1	0
	Aphididae 39	Aphididae		Herbivore	12	0
	Aphididae 40	Aphididae		Herbivore	12	0
	Aphididae 42	Aphididae		Herbivore	48	0
	Aphididae 43	Aphididae		Herbivore	15	0
	Aphididae 44	Aphididae		Herbivore	2	0
	Aphididae 45	Aphididae		Herbivore	2	0
	Aphididae 46	Aphididae		Herbivore	1	0
	Au: Heteroptera 1	Tropiduchidae		Herbivore	1	0
	Auchenorrhyncha 2	Cicadellidae		Herbivore	1	0
	Auchenorrhyncha 3	Cicadellidae		Herbivore	1	0
	Auchenorrhyncha 4	Cicadellidae		Herbivore	2	0

Group	Morphospecies	Family Species	Guild	Abdundance		
					S. madagascariensis	S. pinnatifoliu
Hemiptera cont.	Auchenorrhyncha 5	Cicadellidae		Herbivore	4	3
	Au: Heteroptera 9	Fulgoroidea		Herbivore	1	4
	Au: Heteroptera 10	Flatidae		Herbivore	0	2
	Au: Heteroptera 11	Flatidae		Herbivore	0	1
	Au: Heteroptera 12	Fulgoroidea		Herbivore	0	2
	Au: Heteroptera 7	Delphacidae		Herbivore	1	7
	Auchenorrhyncha 8	Cicadellidae		Herbivore	1	11
	Heteroptera 1	Lygaeoidea		Herbivore	106	88
	Heteroptera 2	Miridae		Herbivore	87	5
	Heteroptera 3	Orsillidae	Nysius clevelandensis	Herbivore	6	0
	Heteroptera 4	Miridae	Creontiades sp.	Herbivore	1	0
	Heteroptera 5	Miridae		Herbivore	2	0
	Heteroptera 8	Reduviidae		Generalist	1	0
	Heteroptera 10	Thaumastocoridae		Tourist	1	0
	Het: Sternorrhyncha 12	Coccoidea		Herbivore	0	1
	Het: Sternorrhyncha 14	Coccoidea		Herbivore	0	7
	Heteroptera 15	Reduviidae		Predator	0	1
	Heteroptera 16	Miridae		Herbivore	0	2
	Het: Sternorrhyncha 17	Coccoidea		Herbivore	0	1
	Hy. Hemiptera 37	Psyllidae		Herbivore	0	1
	Unknown 1	Aphididae		Herbivore	1	0
	Unknown 13	Cicadellidae		Herbivore	3	5
	Unknown 15			Herbivore	1	8
	Unknown 17			Unknown	4	0
	Unknown 21			Herbivore	1	5
	Unknown 30			Herbivore	0	2
	Unknown 31			Herbivore	0	1

Group	Morphospecies	Iorphospecies Family Species	Species	Guild	Abdundance	
				S. madagascariensis	S. pinnatifolius	
Unknown cont.	Unknown 32			Herbivore	0	1
Hymenoptera	Hymenoptera D.3	Braconidae		Parasite	0	1
	Hymenoptera 1	Eulophidae		Unknown	1	0
	Hymenoptera 2	Braconidae		Parasite	4	0
	Hymenoptera 3	Mymaridae		Parasite	2	0
	Hymenoptera 5	Scelionidae		Parasite	1	0
	Hymenoptera 6	Braconidae		Parasite	1	0
	Hymenoptera 7	Pteromalidae		Parasite	2	0
	Hymenoptera 8	Platygasteridae		Parasite	2	3
	Hymenoptera 9	Eurytomidae		Unknown	6	1
	Hymenoptera 11	Mymaridae		Parasite	1	0
	Hymenoptera 12	Braconidae		Parasite	1	0
	Hymenoptera 13	Braconidae		Parasite	1	0
	Hymenoptera 14	Diapriidae		Parasite	2	0
	Hymenoptera 15	Torymidae: Megastigminae	Megastigmus sp.	Herbivore	3	0
	Hymenoptera 16	Braconidae		Parasite	3	1
	Hymenoptera 17	Eulophidae		Parasite	1	0
	Hymenoptera 18	Eulophidae		Unknown	1	0
	Hymenoptera 19	Eulophidae		Unknown	1	0
	Hymenoptera 20	Mymaridae		Parasite	1	0
	Hymenoptera 21	Eulophidae		Unknown	1	0
	Hymenoptera 23	Platygastridae		Parasite	2	0
	Hymenoptera 24	Braconidae		Parasite	1	0
	Hymenoptera 25	Mymaridae		Parasite	1	0
	Hymenoptera 26	Mymaridae	Mymar sp.	Parasite	1	0
	Hymenoptera 27	Figitidae		Parasite	1	0
	Hymenoptera 28	Braconidae		Parasite	6	0

Group	Morphospecies	phospecies Family	Species	Guild	Abdundance	
					S. madagascariensis	S. pinnatifolius
Iymenoptera	Hymenoptera 29	Braconidae		Parasite	1	0
cont.	Hymenoptera 30	Aphelinidae		Parasite	1	0
	Hymenoptera 32	Pteromalidae		Parasite	1	0
	Hymenoptera 33	Pteromalidae		Parasite	1	1
	Hymenoptera 34	Braconidae		Parasite	1	1
	Hymenoptera 35	Eulophidae		Unknown	2	0
	Hymenoptera 36	Eupelmidae		Parasite	0	1
	Hymenoptera 38	Encyrtidae		Parasite	0	2
	Hymenoptera 39	Pteromalidae		Parasite	0	3
	Hymenoptera 40	Scelionidae		Parasite	0	1
	Hymenoptera 41	Scelionidae		Parasite	0	3
	Hymenoptera 42	Mymaridae		Parasite	0	2
	Hymenoptera 43	Platygasteridae		Parasite	0	2
	Hymenoptera 44	Eulophidae		Unknown	0	19
	Hymenoptera 59	Ichneumonidae		Parasite	1	0
	Hymenoptera 106	Encyrtidae		Parasite	1	0
	Formicidae 1	Myrmicinae	Solenopsis sp.	Omnivore	1	16
	Formicidae 2	Ponerinae	Rhytidoponera sp.	Omnivore	1	0
	Formicidae 3	Myrmicinae	Pheidole sp.	Omnivore	1	0
	Formicidae 4	Dolichoderinae	Ochetellus sp.	Predator	2	24
	Formicidae 5	Formicinae	Paratrechina sp.	Generalist	3	0
	Formicidae 6	Dolichoderinae	Ochetellus sp.	Predator	1	6
	Formicidae 7	Dolichoderinae	Ochetellus sp.	Predator	1	1
	Formicidae 8	Ponerinae	Rhytidoponera sp.	Omnivore	2	0
	Formicidae 9	Myrmicinae	Pheidole sp.	Omnivore	1	1
	Formicidae 10	Myrmicinae	Pheidole sp.	Omnivore	0	1
	Formicidae 11	Myrmicinae	Pheidole sp.	Omnivore	0	1

Group	Morphospecies	forphospecies Family	Species	Guild	Abdundance	
					S. madagascariensis	S. pinnatifolius
Hymenoptera	Formicidae 12	Myrmicinae	Crematogaster sp.	Predator	0	1
cont.	Formicidae 13	Myrmicinae	Metanoplus sp.	Scavenger	0	2
	Formicidae 14	Myrmicinae	Monomorium sp.	Omnivore	0	2
	Formicidae 15	Dolichoderinae	Tapinoma sp.	Scavenger	0	1
	Formicidae 16	Dolichoderinae	Tapinoma sp.	Scavenger	0	1
	Formicidae 17	Myrmicinae	Pheidole sp.	Omnivore	0	3
	Larvae 5	Pupae		Unknown	1	0
	Larvae 9	Scelionidae		Parasite	2	0
	Larvae 11	Hymenoptera		Unknown	1	0
	Larvae 12	Hymenoptera		Parasite	2	0
	Larvae 21	Scelionidae		Parasite	0	3
	Larvae 38	Braconidae		Parasite	0	0
	Unknown 28			Parasite	0	1
lsopoda	Isopoda 1	Isopoda:Oniscidea		Detritivore	6	1
	Isopoda 2	Isopoda:Oniscidea		Detritivore	5	0
	Isopoda 3	Isopoda:Oniscidea		Detritivore	3	0
lsopoda cont.	Isopoda 4	Isopoda:Oniscidea		Detritivore	0	28
Lepidoptera	Lepidoptera 1	Pyraloidea		Herbivore	1	47
	Lepidoptera 2	Pyraloidea		Herbivore	145	73
	Lepidoptera 3	Arctiidae: Arctiinae	Nyctemera sp.	Herbivore	1	1
	Lepidoptera 4	Arctiidae: Ctenuchinae	Amata sp.	Herbivore	2	0
	Lepidoptera 5	Pyraloidea		Herbivore	1	0
	Lepidoptera 6	Lepidoptera		Herbivore	1	0
	Lepidoptera 13	Arctiidae: Ctenuchinae	Amata sp.	Herbivore	1	0
	Lepidoptera 14	Noctuidae		Herbivore	1	0
	Lepidoptera 15	Tortricidae		Herbivore	1	0
	Lepidoptera 16	Tortricidae		Herbivore	1	0

Group	Morphospecies	ecies Family	Species	Guild	Abdundance	
					S. madagascariensis	S. pinnatifolius
Lepidoptera cont.	Lepidoptera 17	Arctiidae: Arctiinae	Nyctemera sp.	Herbivore	0	1
	Lepidoptera 20	Arctiidae: Arctiinae	Nyctemera sp.	Herbivore	0	20
	Lepidoptera 22	Pyraloidea		Herbivore	0	6
	Lepidoptera 23	Tortricidae		Herbivore	0	1
	Lepidoptera 24	Arctiidae: Ctenuchinae	Amata sp.	Herbivore	0	12
	Lepidoptera 26	Pyralidae: Phycitinae		Herbivore	0	2
	Unknown 19		Pupae	Herbivore	1	0
Myriopoda	L.12: Myriapoda 1	Myriapoda		Unknown	1	0
	L.25: Myriapoda 2	Diplopoda		Detritivore	0	3
	Larvae 22	Diplopoda		Detritivore	0	1
Neuroptera	C: Neuroptera 8	Neuroptera		Predator	1	0
	Unknown 2	Hemerobiidae		Predator	1	0
	Unknown 3	Hemerobiidae		Predator	1	0
Orthoptera	Orthoptera 1	Acrididae:Catantopinae		Herbivore	2	0
	Orthoptera 2	Gryllacrididae		Omnivore	1	0
Pscoptera	Pscoptera 1			Detritivore	1	3
	Pscoptera 2			Detritivore	1	4
	Pscoptera 3			Detritivore	2	4
	Pscoptera 4			Detritivore	0	11
	Unknown 5			Detritivore	3	0
	Unknown 6			Detritivore	3	0
	Unknown 29			Detritivore	0	2
Thysanoptera	Thysanoptera 1	Thripidae: Thripinae	Pseudanaphothrips achaetus	Herbivore	13	10
	Thysanoptera 10		Neso larvae	Unknown	1	31
	Thysanoptera 11		Neso larvae	Unknown	100	296
	Thysanoptera 12	Thripidae: Thripinae	Psudonathothrips sp.	Herbivore	1	0
	Thysanoptera 13			Unknown	3	0

Group	Morphospecies	Morphospecies	Family Species	Guild	Abdundance	
					S. madagascariensis	S. pinnatifoliu
Thysanoptera	Thysanoptera 14	Phlaeothripidae: Idolothripinae	Nesothrips sp.	Fungivore	1	0
cont.	Thysanoptera 15			Unknown	1	0
	Thysanoptera 16			Unknown	3	0
	Thysanoptera 17		Neso larvae	Unknown	2	5
	Thysanoptera 18		Neso larvae	Unknown	14	25
	Thysanoptera 19	Phlaeothripidae: Phlaeothripinae		Fungivore	1	0
	Thysanoptera 20			Unknown	1	0
	Thysanoptera 21			Unknown	2	0
	Thysanoptera 22	Phlaeothripidae: Idolothripinae:N	esothrips	Fungivore	1	4
	Thysanoptera 23	Thripidae: Thripinae	Thrips imaginis	Herbivore	2	11
	Thysanoptera 2	Thripidae: Thripinae	Pseudanaphothrips achaetus	Herbivore	57	116
	Thysanoptera 3	Panchaetothripinae	Bhattithrips sp.	Herbivore	29	8
	Thysanoptera 4			Unknown	1	0
	Thysanoptera 5			Unknown	8	0
	Thysanoptera 6	Thripidae	Larvae	Unknown	3	0
	Thysanoptera 7			Unknown	2	0
	Thysanoptera 8			Unknown	9	0
	Thysanoptera 9		Neso larvae	Unknown	12	0
	Thysanoptera 24			Unknown	1	0
	Thysanoptera 25	Thripidae	Larvae	Herbivore	2	0
	Thysanoptera 26			Unknown	2	0
	Thysanoptera 27			Unknown	1	0
	Thysanoptera 28			Unknown	3	0
	Thysanoptera 29			Unknown	1	0
	Thysanoptera 30			Unknown	1	0
	Thysanoptera 31			Unknown	1	0
	Thysanoptera 32	Phlaeothripidae: Idolothripinae	Nesothrips sp.	Fungivore	5	9

Group	Morphospecies	Family	Species	Guild	Abdundance	
					S. madagascariensis	S. pinnatifolius
Thysanoptera	Thysanoptera 33	Thripidae	Pupae	Unknown	1	1
cont.	Thysanoptera 34		Neso larvae	Unknown	0	7
	Thysanoptera 35	Thripidae: Thripinae	Thrips sp.	Herbivore	0	7
	Thysanoptera 36	Phlaeothripidae: Idolothripinae	Nesothrips sp.	Fungivore	0	10
	Thysanoptera 37	Thripidae		Herbivore	0	3
	Thysanoptera 38	Phlaeothripidae: Idolothripinae	Nesothrips sp.	Fungivore	0	18
	Thysanoptera 39	Thripidae	Larvae	Herbivore	0	3
	Thysanoptera 40			Unknown	0	2
	Thysanoptera 41			Unknown	0	2
	Thysanoptera 42	Panchaetothripinae	Bhattithrips sp. Larvae late instar	Herbivore	0	4
	Thysanoptera 43			Unknown	0	2
	Unknown 16			Unknown	1	9
U nknown	Heteroptera 7	Unknown		Unknown	1	0
	L.9: Unknown 33	Unknown		Unknown	4	0