Assessing habitat suitability for karure | kakaruia | Chatham Island black robin (*Petroica traversi*): Integrating invertebrate surveys, DNA metabarcoding, and foraging ecology

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Abstract

The karure | kakaruia | Chatham Island black robin (*Petroica traversi*) is one of New Zealand's most remarkable conservation achievements, recovering from a mere five birds in 1980 to around 330 today. However, the species remains Nationally Critical and restricted to two small islands, making establishment of additional populations essential for long-term prosperity. A previous translocation attempt to Rangiauria | Rangiaotea |Pitt Island failed, with inadequate food resources hypothesised as a contributing factor, yet black robin dietary requirements and prey availability at potential translocation sites remain poorly understood. This study integrated invertebrate community surveys, DNA metabarcoding of faecal samples, and behavioural observations to characterise black robin diet, foraging behaviour and food availability, aiming to assess habitat suitability across the Chatham Islands.

In Chapter Two I examined invertebrate communities across four forested sites across the Chatham Island archipelago; the currently inhabited Woolshed Bush and Top Bush on Hokorereoro | Rangatira | Southeast Island, previously failed translocation site Elizabeth Ellen Preece Conservation Covenant | Caravan Bush on Rangiauria | Rangiaotea | Pitt Island, and potential future translocation site Chudleigh Conservation Area on Rēkohu | Wharekauri | Chatham Island. Analyses revealed that predator free sites (Woolshed Bush and Top Bush) supported significantly higher ground-active invertebrate biomass. This difference was driven by large-bodied cave wētā and ground beetles, which were abundant on Rangatira Island but absent from Caravan Bush and Chudleigh Conservation Area. Surprisingly, Woolshed Bush and Top Bush showed similar invertebrate communities despite different black robin densities, indicating that prey availability alone does not determine habitat quality.

DNA metabarcoding of faecal samples in Chapter Three revealed that black robin are generalist insectivores, with Coleoptera, Diptera, and Orthoptera comprising the majority of their diet. Dietary composition showed no significant differences between sites, indicating consistent resource use across Woolshed Bush and Top Bush. Foraging observations confirmed strong ground-level preferences, with 82.2% of foraging events occurring at ground level, emphasising the importance of intact forest floor environments for future translocation sites.

This research demonstrates that black robin persistence depends on multiple interacting factors. Future translocation sites should include abundant large-bodied prey, intact forest floors with deep leaf litter supporting ground foraging, effective predator control or predator-free status, and mature forest structure. DNA metabarcoding proved essential for revealing dietary composition that would be impossible to detect through observation alone by characterising consumption of cryptic prey taxa. While food availability is necessary for translocation success, it is not a sole determining factor; other habitat features such as nest site availability and predator presence must also be considered. The methods I have established here provide a repeatable framework for evidence-based translocation planning.

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A note on naming conventions in this thesis:

Rēkohu | Wharekauri | Chatham Islands have a rich cultural and ecological history involving both Moriori and Māori peoples. This is reflected in the multiple names given to the islands, their flora, and fauna. Throughout this thesis, I have sought to respectfully use ta re Moriori, te reo Māori, and English names on first mention wherever possible, recognising the connections of both Moriori and Māori to these islands and their miheke | taonga (treasures). I acknowledge that my understanding and use of these names may not be perfect, and I remain committed to honouring the Indigenous heritage of Rēkohu | Wharekauri and the mana whenua status of Hokotehi Moriori Trust and Ngāti Mutunga o Wharekauri.

Table of Contents

List of Figures

List of Tables

Chapter 1: General Introduction

1.1 The Role of Translocations in Conservation

We are living in an era of accelerated biodiversity loss, where the variety of life, from plants and animals to entire ecosystems are vanishing at rates far beyond what would be expected under natural background conditions (De Vos et al., 2015; Faurby et al., 2022; Rogers, 2025). According to the International Union for Conservation of Nature (IUCN), 28% of assessed species are currently threatened with extinction, a figure that continues to rise at alarming rates (IUCN, 2025). These losses not only represent the disappearance of individual species, but also the breakdown of ecological processes, interactions, and services that underpin the functioning of ecosystems worldwide (Rogers, 2025; Valiente-Banuet et al., 2015).

Much of this rapid biodiversity loss can be attributed to human activity (Prakash & Verma, 2022; Rogers, 2025). Habitat destruction and fragmentation reduce the space available for species to survive and reproduce, while overexploitation, and the introduction of invasive pest species place further pressure on natural populations (Datta et al., 2025; Yuan et al., 2024). Climate change compounds these effects by changing local environmental conditions more rapidly than many species can adapt, thus disrupting long-established ecological relationships, further decreasing species distributions (Forister et al., 2010; Kissel et al., 2019). Together, these factors create a complex and rapidly changing landscape where many organisms struggle to persist, highlighting the urgent need for proactive conservation strategies.

Addressing these threats requires comprehensive conservation strategies. While habitat preservation remains essential, it is often insufficient on its own to counter such rapid and complex pressures (Simkins et al., 2025). Conservation strategies now increasingly rely on direct hands-on interventions to safeguard vulnerable species and strengthen population survival (Simkins et al., 2025). These hands-on interventions, such as conservation translocations, predator control, and captive breeding, aim to prevent species loss and rebuild populations (Heinen et al., 2020; Marino et al., 2024; Taggart et al., 2023).

One of the most widely used strategies are conservation translocations (hereinafter translocation), defined as the intentional movement of organisms from one location to another for release (IUCN, 2013; Marino et al., 2024). Translocations serve multiple purposes, including re-establishing populations to their former ranges, reinforcing small or declining populations, and establishing new populations in areas free from threats (Gaywood et al., 2022; Marino et al., 2024). Around the world, these goals have been pursued through the reintroduction of mammals such as the plains bison (*Bison bison*), reinforcement of the Gran Canaria blue chaffinch (*Fringilla polatzeki*), recovery programmes for the Telfair's skink (*Leiolopisma telfairii*), and the establishment of the Heldreich's pine (*Pinus heldreichii*) (D'Agostino et al., 2024; Delgado et al., 2024; Wilkins et al., 2019; Young et al., 2025).

While translocations have been widely adopted across the globe, Aotearoa | New Zealand (hereinafter Aotearoa) has been at the forefront of their application. The country's long isolation has resulted in ecosystems dominated by endemic, evolutionary unique species, many of which have evolved in the absence of predators commonly seen in other countries (Wallis & Buckley, 2024; Williams et al., 2007). Following human arrival, the introduction of invasive mammals and widespread habitat clearing has resulted in severe biodiversity loss, with many species surviving in small, fragmented populations (Clarkson, 2022; Wallis & Buckley, 2024). This impact has been significant, with approximately 50% of all native bird and frog species driven to extinction (Holdaway, 1989; Parker et al., 2020) In response, translocation has emerged not only as a supplementary measure, but as a central pillar of Aotearoa's conservation strategy, reflecting both ecological necessity and the responsibilities of kaitiakitanga (guardianship) (Bennett et al., 2021; Parker et al., 2020).

Over the past decades, translocations have been used to re-establish populations on offshore islands, and more recently, within mainland predator-free sanctuaries (Parker et al., 2020). These efforts have been applied to a diverse range of taxa, including reptiles such as the Fiordland skink (*Oligosoma acrinasum*) translocated to Hawea Island (Romijn & Hartley, 2016), invertebrates like the Cook Strait giant wētā (*Deinacrida rugosa*) established on Maud Island (Watts & Thornburrow, 2009), and numerous plant species. However, native bird species have been of the focus of many translocations, reflecting both their vulnerability to predation and their cultural and ecological importance (Armstong & McLean, 1995). Among the most notable successes are the sheer number of successful translocations of kiwi (*Apteryx* spp.), (Jahn et al., 2022), the establishment of tīeke | saddlebacks (P*hilesturnus carunculatus*) on offshore islands (Taylor et al., 2005), and the extraordinary recovery of the karure | kakaruia | Chatham Island Chatham Island black robin (*Petrocia traversi*) (Merton, 1992; Parlato et al., 2025). These examples not only highlight the future potential of translocation but also provide valuable lessons about the challenges and success factors unique to avian translocations.

1.2 Lessons from Avian Translocations

While translocations have proven critical for restoring vulnerable bird populations, their success are highly variable, and depends on a interplay of ecological, behavioural, and management factors (Berger-Tal et al., 2020; Sol et al., 2005). One of the most fundamental drivers of translocation success is habitat quality at the release site (Stadtmann & Seddon, 2020). High quality habitats not only provide the structural features required for nesting or shelter, but also a diverse range of food capable of supporting self-sustaining populations (Stadtmann &

Seddon, 2020). In this sense, “habitat quality” is not defined by a single variable, but rather the condition of the entire ecosystem as a whole, including vegetation composition, resource availability, and the size of the habitat patch (Parker et al., 2020; Stadtmann & Seddon, 2020). Translocations into small or degraded habitats may fail to support long-term persistence, underscoring the importance of restoring ecosystem functions. This point is highlighted by the failed translocation of Dunes Sagebrush Lizard (*Sceloporus arenicolus*) in Crane County, Texas, USA (Bellis et al., 2019; Parker et al., 2023). Restoring ecosystem functions can be achieved through the reintroduction of keystone species, such as top predators or ecosystem engineers, whose activities modify habitats and create conditions that allow other species to thrive (Pettorelli et al., 2019).

Alongside the quality of the potential habitat, species specific traits and behaviours strongly shape translocation outcomes (Sol et al., 2005; Wu et al., 2024). Behavioural flexibility, habitat selection, foraging strategies, and social interactions are therefore key determinants of establishment success (Stamps & Swaisgood, 2007; Wu et al., 2024). In Aotearoa, such traits have played a pivotal role in shaping translocation outcomes. For instance, the tīeke | saddleback (*Philesturnus carunculatus*) has been one of the most frequently translocated bird species, with its flocking behaviour facilitating pair bonding and its broad habitat requirements, allowing it to occupy habitats ranging from shrubland to mature forests (Lovegrove, 1996; Taylor et al., 2005). In contrast, the kōkako (*Callaeas wilsoni*) have proven more challenging to establish in some locations, partly due to their dependence on complex social interactions and territorial nature that can limit dispersal and breeding success post-release (Bradley et al., 2012; Sinclair et al., 2006). Similarly, species-specific behaviour can also hinder translocation success, as highlighted by kākāpō (*Strigops habroptilus*), with their lek mating system and dependence on irregularly fruiting podocarp trees, like rimu (*Dacrydium cupressinum*), which makes natural population growth slow and difficult, demanding intensive management strategies (Clout & Merton, 1998; Eason & Moorhouse, 2006). Collectively, these examples demonstrate that successful translocations not only require suitable habitats, but also careful consideration of how species-specific traits align with ecological and social conditions at release sites.

1.3 Food Resources and Habitat in Translocations

Despite the growing use of translocation as conservation strategies, questions remain about the factors determining their success (Seddon et al., 2007; Seddon & Redford, 2025; Taylor et al., 2017). One crucial, but often overlooked factor is diet, as mismatches between a species' dietary requirements and the food resources available at release sites can reduce survival and reproductive success (Brown et al., 2021; Dimond & Armstrong, 2007). Adequate resources are not only essential for survival, but also for supporting successful breeding and juvenile recruitment (Dimond & Armstrong, 2007). For example, limited prey abundance may constrain body condition and growth (Øigård et al., 2013), while low prey diversity may reduce resilience to environmental challenges (Adje et al., 2023; Bernhardt et al., 2020). Unlike habitat structure or predator control, food availability and diet are not as frequently assessed during translocation planning (Gooch et al., 2015). This gap is particularly evident for insectivorous species, whose reliance on seasonally available prey makes their dietary requirements far more difficult to evaluate compared to other species (Carter et al., 2021; Moorman et al., 2007).

In Aotearoa, evidence of this challenge is limited, aside from a few well-documented examples. Hihi | stitch bird (*Notiomystis cincta*), a nectivorous bird species, have often required supplementary sugar water at release sites to compensate for the lack of resources, particularly during early population establishment (Doerr et al., 2017). In contrast, insectivorous species such as the toutouwai | North Island robin (*Petroica longipes*) depend on abundant and diverse communities of invertebrate prey, which can vary spatially and temporally between release sites, making habitat suitability harder to predict (Boulton et al., 2008). Similarly, kākāpō showcase how dietary constraints can further complicate translocation. Their breeding is tightly linked to rimu masting events, which occur irregular intervals rather than annually (Norton & Kelly, 1988), and limited food availability can greatly restrict reproductive success (Clout & Merton, 1998). Some translocations have started addressing this challenge, for example, the aquatic warbler (*Acrocephalus paludicola*) translocation in Europe successfully hand reared chicks using wild insects captured at the release site (Morkvėnas et al., 2025). However, such approaches remain the exception rather than the norm. Given the critical role of diet and food availability in shaping translocation outcomes, particularly for insectivorous and specialist species, developing methods to assess dietary requirements is a key component for conservation planning (Gooch et al., 2015).

1.3.1 Approaches to Diet Analysis

Historically, avian diets were assessed through stomach content analysis or direct foraging observations (Cezilly & Wallace, 1988; Gaglio et al., 2017; Jordan, 2005; Rosenberg & Cooper, 1990). Techniques such as stomach flushing or examination of gut contents can provide highly detailed taxonomic information on recently consumed prey (Jordan, 2005; Rosenberg & Cooper, 1990). These methods have been particularly valuable for quantifying hard bodied prey items such as beetles or molluscs (Dauvin, 2024). However, they are typically invasive, often lethal, and therefore unsuitable for use for threatened or small populations where individual losses are unacceptable (Provencher et al., 2019). Additionally, these methods only provide a snapshot of the most recent meal and may under-represent soft bodied prey that digest rapidly (Dauvin, 2024).

Foraging observations offer a non-invasive alternative and have long been used to document prey handling, capture rates, and feeding behaviour in the wild (Cezilly & Wallace, 1988; Jordan, 2005; Pompanon et al., 2012; Rosenberg & Cooper, 1990). While useful for understanding behavioural ecology, such observations tend to be biased towards conspicuous prey items or foraging events that are easily visible to researchers (Cezilly & Wallace, 1988; Lee & Hockey, 2001; Pompanon et al., 2012). Small or cryptic prey, such as many arthropods, are often under recorded, and many canopy foraging events may be missed entirely (Lee & Hockey, 2001; Rosenberg & Cooper, 1990). Furthermore, observational studies require extensive field efforts and large sample sizes to capture dietary variation, which can be logistically challenging in remote habitats, or with elusive species (Cezilly & Wallace, 1988; Lee & Hockey, 2001). As a result, recent advances have shifted toward molecular and biochemical approaches that overcome many of these constraints (Pompanon et al., 2012).

An alternative approach that avoids many of the logistical and observational biases seen in earlier diet studies is stable isotope analysis, which uses the ratio of naturally occurring isotopes such as carbon ($\delta^{12}C$ / $\delta^{13}C$) and nitrogen ($\delta^{14}N$ / $\delta^{15}N$) in animal and plant tissues to infer dietary sources (Dauvin, 2024; Prigge et al., 2025). Because “you are what you eat”, the isotope composition reflects what a species consumes, providing a record of diet over weeks to months depending on the tissue type (Dauvin, 2024; Kohn, 1999; Prigge et al., 2025). For example, $\delta^{15}N$ values typically increase with trophic level, allowing broad inferences about whether a species feeds on herbivores, predators, or detritivores (Bearhop et al., 2004; Prigge et al., 2025). In seabirds, $\delta^{15}N$ analysis has been used to distinguish between fish and squid based diets (Cherel et al., 2010), while in fledgling mountain bluebirds (*Sialia currucoides*), isotope analysis has revealed seasonal shifts in invertebrate prey (White & Dawson, 2021). In contrast, $\delta^{13}C$ values can distinguish between plants with different photosynthetic pathways or between marine and terrestrial food webs (Kohn, 1999; Prigge et al., 2025). This makes stable isotope analysis particularly valuable for understanding long-term feeding ecology, niche partitioning, and energy flow in ecosystems (Deschner et al., 2012; Prigge et al., 2025).

However, stable isotope analysis has limitations when applied to conservation. Taxonomic resolution is inherently course, isotopes can indicate general trophic position or habitat of origin of prey items, but cannot easily determine prey species or genus (Inger & Bearhop, 2008; Post, 2002). Interpretation also requires baseline isotope values for local food webs, which may vary seasonally or geographically (Kohn, 1999; Post, 2002; Prigge et al., 2025). Moreover, threatened species often require non-invasive sampling methods (e.g., feathers, faeces), which may integrate diet over different timescales, adding complexity to isotopic interpretation (Ardern et al., 1994; Newsome et al., 2007). Despite these drawbacks, stable isotope analysis remains a powerful complementary tool, particularly when used alongside other more detailed methods such as DNA metabarcoding (hereinafter metabarcoding), where it can validate prey identification (de Sousa et al., 2019; Pompanon et al., 2012).

Metabarcoding has rapidly emerged as one of the most powerful tools for understanding diet in conservation biology (Ando et al., 2020; Pompanon et al., 2012; Rytkönen et al., 2019). This approach allows the simultaneous identification of multiple species from heterogeneous biological samples by combining high-throughput sequencing with universal genetic markers (Pompanon et al., 2012; Rytkönen et al., 2019). In dietary studies, metabarcoding has become especially valuable for non-invasive analysis of faecal, regurgitates, or gut contents, where prey remains are often too degraded or microscopic for traditional morphological identification (Ando et al., 2020; Deagle et al., 2019).

Metabarcoding involves extracting DNA from the sample, amplifying specific gene regions (typically the mitochondrial cytochrome c oxidase I (COI) or 16s for animal prey and the chloroplast trnL or nuclear ITS (internal transcribed space) region for plant material), using certain primers (Deagle et al., 2019; Rennstam Rubbmark et al., 2018; Rytkönen et al., 2019). From this, the amplified regions are then sequenced and compared against a reference database for identification (Ando et al., 2020; Rennstam Rubbmark et al., 2018; Verkuil et al., 2022). Metabarcoding also allows for many samples to be analysed simultaneously, thereby capturing population and individual variation in diet (Deagle et al., 2019; Verkuil et al., 2022).

Metabarcoding has proven effective for assessing the diets of threatened bird species and informing conservation management. For example, metabarcoding has revealed seasonal dietary flexibility in critically endangered grassland birds (*Pedionomus torquatus*) (Nugent et al., 2025a), identifying prey preferences and habitat requirements for declining steppe species (*Tetrax tetrax*) (González del Portillo et al., 2025), and higher biomass availability at migratory stopover sites (Verkuil et al., 2022). Such resolution is valuable in translocation contexts, where assessing dietary flexibility and niches can inform whether release sites contain sufficient and appropriate food sources. For example, metabarcoding has also been used to reveal differences in resource use among reintroduced populations. In Washington State, USA, fishers (*Pekania pennanti*) released into the South and North Cascades exhibited markedly different diets; South Cascade fishers relied heavily on hares and rabbits (*Lepus americanus* and *Sylvilagus floridanus*) with limited prey diversity, whereas North Cascade fishers consumed a much broader range of over 70 taxa (Shively et al., 2025). Such variation highlights the value of dietary studies in assessing whether translocated populations are securing sufficient resources to establish and in guiding management interventions (Berry et al., 2017; Shively et al., 2025).

However, metabarcoding has notable limitations. Polymerase Chain Reaction (PCR), the process used to amplify short fragments of DNA for sequencing, is subject to primer biases, which can skew detection towards certain taxa, underrepresenting others (Ando et al., 2020; Pompanon et al., 2012). Furthermore, incomplete or regionally biased reference databases may restrict taxonomic resolution to family or genus level, limiting ecological interpretation to general groups (Keck et al., 2023). For example, gaps in reference DNA databases can constrain metabarcoding for biodiversity monitoring. In a study of marine macrofauna including sponges, corals, and crustaceans, many species lacked barcodes, meaning sequences could often only be assigned to higher taxonomic levels (Hestetun et al., 2020). This limited the ability to distinguish ecologically important and vulnerable species, reducing the reliability of metabarcoding for conservation assessment and management of sensitive marine ecosystems (Hestetun et al., 2020).

Interpretation of sequence read abundance requires careful consideration. While read counts do not directly reflect how much biomass was consumed, they can still provide useful information about diet when interpreted with caution (Deagle et al., 2019). Researchers can analyse this data in two ways. The first is by using relative read abundance, which considers how many sequences were detected for each prey item. The second is by using simple occurrence, which records whether a prey item was present or absent. Relative read abundance can reveal which prey are more important in a species or individual's diet, but some prey items are more easily detected that others, which can skew results (Deagle et al., 2019). Occurrence data avoids this problem but may give too much weight to rarely eaten prey or contaminants (Deagle et al., 2019). The best approach depends on the study, and researchers should acknowledge the limitations of whichever method they choose. That said, metabarcoding represents a significant advancement in dietary ecology, particularly for conservation management (Arazmi et al., 2025). By allowing detailed, non-invasive assessment of diet, metabarcoding provides insights into food availability, prey preference, and potential sources of bottlenecks in translocated populations (Arazmi et al., 2025; Gooch et al., 2015).

1.3.2 Habitat Analysis

In addition to dietary analysis, accurately evaluating habitat quality is fundamental to the success of translocations, as the suitability of a release site often determines whether translocated populations persist in the long term (Batson et al., 2015; Bubac et al., 2019; Stone et al., 2025). Habitat assessment typically incorporates multiple factors, including vegetation structure, predator presence, and the availability of crucial resources such as breeding sites and food resources (Armstrong & Seddon, 2008; Box, 2003; Bubac et al., 2019). Among these, food availability is particularly important, since mismatches between a species dietary requirements and prey abundance can decrease survival, growth, and reproduction (Armstrong & Seddon, 2008; Brown et al., 2021; Gooch et al., 2015). For species that rely heavily on invertebrates as a primary food source, understanding the diversity, abundance, and distributions of invertebrate communities is essential.

Invertebrate communities not only form the foundation of many translocated bird species' diets, but are also useful indicators of ecosystem health (Gerlach et al., 2013; Nyffeler et al., 2018a). Their abundance and richness reflect underlying habitat quality, while their population dynamics can reveal the capacity of translocation sites to sustain higher trophic levels (Brose, 2003; Lu et al., 2025). To assess different components of an invertebrate community, researchers employ a range of sampling techniques. Pitfall traps are widely used for ground dwelling species (Oberprieler et al., 2019), while emergence traps target invertebrates transitioning from soil-dwelling stages to winged forms (Watts et al., 2008). Leaf litter extraction methods such as

Winkler funnels, allow sampling of invertebrates inhabiting the soil and leaf litter layer of the forest floor (Agosti et al., 2000). Suction sampling provides access to invertebrates inhabiting low-lying vegetation (Brook et al., 2008), and light traps are effective for capturing nocturnal invertebrates that are otherwise difficult to sample (Kammar et al., 2020). Although no single sampling method captures an entire community, combining multiple techniques can provide a more comprehensive picture of prey availability and community structure across habitats (Borges & Brown, 2003).

Integrating invertebrate surveys with dietary studies, particularly molecular techniques such as metabarcoding, can strengthen conservation assessments by linking what species consume to what is available in the environment (Watts et al., 2019). Metabarcoding provides detailed analysis of diet, while invertebrate samples ground these findings within the prey community found at current or potential future release sites (Watts et al., 2019). For example, a study of the critically endangered plains-wanderer (*Pedionomus torquatus*) combined metabarcoding of faecal samples with GPS tracking and habitat surveys to assess food availability and habitat choice, revealing seasonal dietary flexibility and that birds actively selected grassland patches with higher invertebrate seed abundances (Nugent et al., 2025). Similarly, a study on the little bustard (*Tetrax tetrax*) combined metabarcoding with invertebrate surveys (pitfall traps and sweep netting) to identify prey preferences by combining diet composition with locally available prey (González del Portillo et al., 2025). This approach revealed that little bustards actively selected certain arthropod orders (Orthoptera, Lepidoptera, and Hemiptera) while avoiding others (Hymenoptera), informing habitat management recommendations for natural grassland and cultivated areas (González del Portillo et al., 2025).

These examples demonstrate how combining dietary and habitat analyses can determine whether observed dietary preferences can be supported by local prey populations and can highlight potential resource limitations as translocation sites. This integrated approach can allow conservation managers to make better informed decisions about translocation planning, reducing the risk of mismatches and supporting successful establishment and long-term persistence of translocated populations. One area that may benefit from similar methods is the Chatham Island archipelago, which faces many conservation challenges.

1.4 Conservation on the Chatham Islands

1.4.1 The Chatham Island archipelago

The Chatham Islands are an isolated archipelago located approximately 800km east of mainland Aotearoa. The group comprises around ten islands, the largest being Rēkohu | Wharekauri | Chatham Island (hereinafter Chatham Island) and Rangiauria | Rangiaotea | Pitt Island (hereinafter Pitt island) (Dieffenbach, 1841; Falla, 1950). Smaller islands include Hokorerero | Rangatira | Southeast island (hereinafter Rangatira island), Maung' Rē | Mangere (hereinafter Mangere Island), Tapuaenuku | Little Mangere | The Fort (hereinafter Little Mangere), along with various smaller islets (Dieffenbach, 1841).

Each island and islet hold significant cultural and ecological importance, including by providing breeding sites for seabirds such as the Chatham petrel (*Pterodroma axillaris*) and broad-billed prion (*Pachyptila vittata*) (Sullivan & Wilson, 2001). They also support rare and endemic invertebrates, including *Hadramphus spinipennis* weevils (Schöps et al., 1999) and the Rangatira spider (*Dolomedes schauinslandi*) (Vink & Dupérré, 2010), while also harbouring unique endemic plant species such as Chatham Island akeake (*Olearia traversiorum*) and Chatham Island forget-me-not (*Myosotidium hortensia*) (Heenan et al., 2010). However, their isolation, limited land area, and human impact have also rendered these ecosystems highly vulnerable, placing the Chatham Islands at the centre of some of Aotearoa's most intensive conservation efforts (Aikman & Miskelly, 2004; Merton, 1992; Stilwell & Mays, 2020).

1.4.2 Historical Human Influence and Ecological Change

Human settlement has greatly shaped the ecological trajectory of the Chatham Islands. The Moriori, descendants of Polynesian settlers who arrived around the 15th century, practiced sustainable harvest of marine resources, supplemented by limited horticulture and birding. These practices placed relatively low pressure on terrestrial ecosystems (Shand, 1894; Solomon & Thorpe, 2012; Sutton, 1980). The arrival of Ngāti Mutunga and Ngāti Tama Māori from Aotearoa in 1835 marked a shift toward more intensive land use (King, 2017). This balance was further disrupted following European arrival in the late 18th century (Solomon & Thorpe, 2012). Sealers whalers, and later settlers cleared large areas of forest for grazing, introduced livestock such as sheep and cattle, and brought with them invasive mammals including cats (*Felis catus*) and rats (*Rattus rattus* and *R. norvegicus*) (Aikman & Miskelly, 2004; Sutton, 1980). These changes contributed to major biodiversity loss, with several species becoming extinct, including the mātirakahu | Chatham Island rail (*Cabalus modestus*), mehonui | Hawkin's rail (*Diaphorapteryx hawkinsi*), and Chatham Island coot (*Fulica chathamensis*), while many others were pushed to the brink of extinction (Aikman & Miskelly, 2004).

By the mid-20th century, the Chatham archipelago had become a focal point for island conservation in Aotearoa (Aikman & Miskelly, 2004; Merton, 1992). Predator-free sanctuaries were established on offshore islands such as Mangere and Rangatira, where intensive habitat restoration and species recovery programmes were trialled (Aikman & Miskelly, 2004; Mansfield & Towns, 1997; Merton, 1992; Roberts et al., 2007). These initiatives not only laid the groundwork for saving species such as the ranguru | Chatham Island petrel (*Pterodroma axillaris*) and tchūriwat | tūturuatu | shore plover (*Thinornis novaeseelandiae*), but also paved the way for the rescue of the karure | kakaruia | Chatham Island black robin (*Petroica traversi*) – a conservation story that would come to define the Chatham Islands' global reputation (Aikman & Miskelly, 2004; Merton, 1992).

1.5 The Karure | Kakaruia | Chatham Island Black Robin:

1.5.1 History of robin recovery

The karure | kakaruia | Chatham Island black robin (hereinafter black robin), represents one of the most extraordinary conservation success stories in Aotearoa and globally. Once widespread across the Chatham Islands, the species experienced catastrophic decline following the arrival of humans, habitat destruction, and the introduction of mammalian predators (Aikman & Miskelly, 2004; Kennedy, 2009; Parlato et al., 2025). By the early 1980s, the population had plummeted to just five individuals on Little Mangere Island, with a single surviving breeding female, "Old Blue," forming the genetic foundation for all living black robins today (Butler & Merton, 1992; Kennedy, 2009; Merton, 1992). This severe population bottleneck created a genetic legacy that continues to shape conservation management of the species.

In their natural environment, the black robin typically prefers to breed in cavities within hollow trees or long stumps buried in vine tangles, with nests constructed from various plant fibres and lined with feathers from other birds (Kennedy, 2009; Lawrence et al., 2017). Females are responsible for nest building, incubation, and brooding, while the male attends her with food and song (Aikman & Miskelly, 2004; Kennedy, 2009; Robertson, 1985). Incubation lasts between 17 and 19 days, with fledging occurring 20 to 23 days after hatching (Kennedy, 2009). Most clutches consist of one to three ovoid, creamy-white eggs specked with purplish-brown dots and splotches, usually laid between October and November (Aikman & Miskelly, 2004; Kennedy, 2009). Thanks to targeted conservation programmes, fledging success rates significantly improved with the use of artificial nesting boxes and cross-fostering with murumuru | miromiro | Chatham Island tomtit (*Petroica macrocephala chathamensis*) (Butler & Merton, 1992; Merton, 1993). These interventions were essential in preventing extinction during the early stages of recovery.

The black robin's recovery was made possible by the pioneering work of Don Merton and his team at the New Zealand Wildlife Service, who trialled and refined intensive management techniques and ultimately initiated an intensive recovery programme (Butler & Merton, 1992; Merton, 1993). The decision to translocate the last surviving black robins from Little Mangere to nearby Mangere Island provided access to more suitable habitats, with continued predator control and monitoring of individuals ensured their survival (Butler & Merton, 1992; Merton, 1993). Through these measures, the species was gradually lifted from the brink of extinction, and today numbers have grown to over 300 individuals, with ~300 individuals on Rangatira Island, and ~30 on Mangere Island (Parlato et al., 2025). The black robin's recovery remains one of the most intensive and successful conservation programmes ever undertaken in Aotearoa, cementing its status as a global conservation icon (Parker et al., 2023).

1.5.2 Conservation Challenges

Despite their historic recovery, setbacks and challenges have persisted for the black robin. The extreme genetic bottleneck has resulted in low genetic diversity, raising concerns about the long-term adaptability, inbreeding depression, and disease susceptibility (Forsdick et al., 2017; Kennedy et al., 2014; Parker, Patterson, et al., 2023). Moreover, the population on Mangere Island has been declining and remains at critically low numbers (~30), presenting an ongoing concern and focus for management efforts (Parlato et al., 2025). Currently, only the Rangatira Island population is thriving (~300), highlighting the fragile nature of recovery even for species that have been "saved from extinction" (Merton, 1993; Parlato et al., 2025). Efforts to establish new populations beyond these two islands have also encountered significant challenges. Between 2002 and 2005 translocations to Pitt Island achieved initial success, but the population soon failed to persist with little explanation as to why (Kennedy, 2009; Parlato et al., 2025). The lack of knowledge surrounding key ecological requirements, such as diet composition, prey availability, and habitat suitability, have been identified as a crucial barrier to successful translocations including for the black robin (Kevin Parker personal communication; Stone et al., 2025). Without such information, translocations remain vulnerable to unforeseen failures, highlighting the urgent need for studies that directly examine the relationship between resource availability and black robin behaviour and diet.

1.6 Knowledge Gaps and the Need for This Study

While the recovery of the black robin has been hailed as one of the most successful conservation stories, critical aspects of its ecology remain poorly understood. Past research has focused primarily on population genetics, habitat restoration, and intensive management methods (Forsdick et al., 2017; Lawrence et al., 2017; Parker, Patterson, et al., 2023; Parlato et al., 2025). By contrast, little attention has been given to the species' diet and foraging ecology, despite these being fundamental to survival and reproductive success (Seddon & Redford, 2025; Wu et al., 2024). Existing knowledge of the black robin foraging behaviour and diet is limited to anecdotal observations of invertebrate feeding (Kennedy, 2009; Robertson, 1985). Equally important, our understanding of the invertebrate communities that comprise potential prey resources remain incomplete (Emberson, et al., 1996). No systematic studies have yet quantified or compared invertebrate communities across the different islands and reserves of the Chatham Islands (Emberson, 1998; Emberson, et al., 1996). Previous invertebrate surveys have revealed that the

Chatham Islands support a distinctive fauna characterised by high endemism and flightlessness (Emberson, 1998). Of the 286 beetle species documented, a substantial proportion are endemic to the archipelago, with many larger flightless species now restricted to small predator-free outer islands like Rangatira and Mangere (Emberson, 1998). Together, these gaps in our knowledge of both black robin diet and invertebrate communities that support them leave conservation managers without the detailed information required to evaluate habitat quality or to accurately predict success at novel sites.

These gaps are particularly problematic in the context of black robin translocations. As demonstrated by the failed Pitt Island attempt, uncertainty around food resources and prey availability may directly constrain establishment, as evidenced by the reliance on supplementary feeding following translocation (Kennedy, 2009; Merton, 1993; Parker, Patterson, et al., 2023). In the absence of detailed knowledge about dietary composition, prey availability at potential release sites, and how foraging behaviour responds to resource variation, future translocations remain at risk of repeating past failures.

1.7 Research Aims and Objectives

The karure | kakaruia | Chatham Island black robin is one of the world's most intensively managed and critically endangered bird species and understanding the availability and use of food resources is central to its ongoing conservation. The overarching aim of this study is to investigate the composition and distribution of invertebrate communities within black robin habitats, alongside the diet and foraging ecology of black robins, across both current and potential future sites. By integrating invertebrate community assessments with dietary analysis, this study will inform conservation management practices, particularly translocation site selection and habitat quality assessment.

Specifically, this study addresses the following objectives:

1. **Quantify and compare the invertebrate community across multiple habitats** of varying quality on three different islands, including Top Bush and Woolshed Bush on Rangatira Island, Ellen Elizabeth Preece Conservation Covenant (hereinafter Caravan Bush) on Pitt Island, and Chudleigh Conservation Area on Chatham Island, using standardized sampling methods (Chapter 2). These comparisons of the invertebrate community provide insights into prey availability by contrasting currently occupied habitats (Rangatira), previously abandoned sites (Caravan Bush), and potential translocation areas (Chudleigh Conservation Area and a reintroduction to Caravan Bush).
2. **Characterise the diet of black robin** found on Rangatira Island in high- and low-quality habitats through DNA metabarcoding of faecal samples (Chapter 3) to identify key prey taxa and highlight potential differences in resource use between habitat types.
3. **Characterise foraging behaviour and habitat use of black robins** to identify the specific forest strata where they actively forage and assess how foraging patterns relate to prey availability across habitats (Chapter 3).
4. **Compare diet composition with prey availability** to evaluate whether potential habitats would provide sufficient and suitable food resources to support black robin populations (Chapter 3).
5. **Provide evidence-based information for conservation management**, particularly in the context of translocations, by identifying habitat features and prey communities most strongly associated with black robin foraging and diet (Chapter 4).

Chapter 2: Invertebrate Community Structure on the Chatham Islands: Implications for Black Robin (*Petroica traversi*) Conservation

2.1 Abstract

Invertebrate prey availability represents a critical bottom-up constraint on insectivorous bird populations but is often overlooked in conservation planning. This study characterized invertebrate communities across potential translocation sites for the critically endangered karure | kakaruia | Chatham Island black robin (*Petroica traversi*), whose entire population (~330 individuals) is restricted to two islands. I sampled four forest sites spanning a habitat condition gradient: currently (black robin) inhabited mature forests on predator-free Rangatira Island (Woolshed Bush and Top Bush), a previously failed translocation site with mice and cats present (Caravan Bush on Pitt Island), and a potential future site with multiple invasive predators (Chudleigh Conservation Area on Chatham Island). Using emergence traps, pitfall traps, and suction sampling over several nights per site, I collected 2,455 invertebrates representing 14 orders and 27 families. Ground-active communities showed the strongest site differentiation, with predator-free sites supporting significantly higher biomass than predator-present sites. This was driven by large-bodied cave wētā (181–205 mg) and ground beetles (112–244 mg), which were abundant at Woolshed Bush and Top Bush but largely absent at Caravan Bush and Chudleigh Conservation Area where mammalian predators occur. Body mass distributions at predator-free sites extended to 742 mg, while predator-present sites were dominated by invertebrates <50 mg. However, Woolshed Bush and Top Bush showed similar invertebrate communities despite differing black robin densities, suggesting prey availability alone does not explain habitat quality. Chudleigh Conservation Area exhibited high within-site variability, reflecting habitat heterogeneity that may challenge black robin establishment but indicates restoration potential. These findings highlight the need for integrated habitat assessment considering prey availability, predator presence, forest maturity, and vegetation structure, rather than relying on single factors when selecting translocation sites.

2.2 Introduction

Invertebrates are among the most diverse and functionally important groups of organisms in terrestrial ecosystems (Kellert, 1993; Kitching et al., 2020; Prather et al., 2013). They regulate ecological processes through decomposition, nutrient cycling, pollination, predation and herbivory, while forming the primary prey base for many vertebrates (Eisenhauer & Hines, 2021; Kitching et al., 2020; Prather et al., 2013). The structure of terrestrial food webs is shaped by the diversity, abundance, and biomass of invertebrate communities, which constrain the populations of vertebrate consumers at higher trophic levels through bottom-up effects (Barnes et al., 2017; Prather et al., 2013).

For insectivorous birds, these bottom-up constraints are directly reflected through prey availability, which influences their energetic balance, reproductive timing, and population dynamics (Nyffeler et al., 2018; Stone et al., 2019). Large bodied invertebrates such as some beetles (Coleoptera), spiders (Araneae), and crickets (Orthoptera), provide high protein and fat content, making them valuable prey for meeting their energetic demands (Razeng & Watson, 2015a). When such prey become scarce, or when invertebrate communities shift toward smaller or less energetically rewarding taxa, insectivorous species face a mismatch between energy expenditure and intake (Senécal et al., 2021). Consequences of such shifts are well documented: studies of insectivorous passerines have shown delayed egg laying, reduced nestling provisioning rates, and lower fledgling success when invertebrate availability decreases (Schlesselmann et al., 2023; Stone et al., 2019; Tallamy & Shriver, 2021).

Despite this evidence, conservation efforts to manage threatened insectivorous birds in Aotearoa | New Zealand (hereinafter Aotearoa) have been largely focused on top-down pressures through intensive predator control programs (Norbury, 2017; Parker et al., 2020). Pest management strategies predominantly target introduced mammalian predators such as stoats (*Mustela erminea*), rats (*Rattus* spp.), and possums (*Trichosurus vulpecula*), which directly predate birds, their eggs, and nestlings (Innes et al., 2010). Control methods include trapping regimes, aerial applications of toxins targeting pest species such as sodium fluoroacetate (commonly known as 1080), and predator-proof fencing to create mainland islands (Goldson et al., 2015). While invasive predator management remains critical and has dramatically improved breeding success for many species, this focus has meant that prey availability and invertebrate community dynamics are often overlooked as factors that drive population success (Sherry, 2021). Understanding bottom-up limitations may be particularly important in degraded or fragmented habitats where remaining food resources must support higher insectivorous bird population densities, potentially intensifying competition and constraining reproductive success even when predator pressure is reduced (Norris, 2004).

Island ecosystems provide an ideal context for investigating how invertebrate prey availability affects insectivorous bird populations. With simplified food webs, fewer species and clear boundaries between habitats, islands provide natural systems for investigating how invertebrate prey availability influence predators (Holt, 1996; Massol et al., 2017). The Chatham Islands, 800km east of Aotearoa, provide a valuable system for studying how prey availability influences threatened insectivorous bird populations, particularly in the context of translocation planning. Forest habitats across the archipelago vary in vegetation structure and composition, disturbance history, and the presence and abundance of introduced mammalian and avian predators creating spatial variation in invertebrate communities that may drive variation in insectivorous bird distribution and success (Parlato et al., 2025). These factors make the Chatham Islands an important case study for understanding prey-predator dynamics.

The karure | kakaruia | Chatham Island black robin (*Petroica traversi*) (hereinafter black robin) provides an ideal focal species for investigating potential bottom-up constraints to bird conservation in the context of how variation in habitat condition shapes invertebrate prey communities and ultimately insectivorous bird populations. As a ground foraging insectivorous bird that hunts primarily on the soil surface, among leaf litter, and in low vegetation, the black robin occupies a trophic niche directly linked to ground-dwelling invertebrate communities (Aikman & Miskelly, 2004; Kennedy, 2009). Because their foraging targets the forest floor and low vegetation, black robin populations are likely strongly influenced by both the structure of these habitat layers and the invertebrate prey available within them. As one of the world's rarest birds (Aikman & Miskelly, 2004; Butler & Merton, 1992), the black robin requires intensive conservation management, including careful assessment of invertebrate prey availability when planning translocations to ensure habitat suitability and long-term population success.

The recovery history of the black robin highlights the importance of understanding potential bottom-up constraints on population recovery. Despite ongoing invasive predator control to reduce top-down pressures, bottom-up constraints through invertebrate prey availability have not yet been assessed. All black robins descend from a single pair on Little Mangere Island and despite intensive management, the population remains restricted to two islands (Butler & Merton, 1992; Parlato et al., 2025). Most individuals (~300) now inhabit Hokorereoro | Rangatira | Southeast Island (hereinafter Rangatira Island), with a smaller population (~30) on Maung' Rē | Mangere Island (hereinafter Mangere Island) (Parlato et al., 2025). Even within Rangatira Island, densities of black robin vary. Woolshed Bush supports high numbers, while Top Bush hosts far fewer (Kennedy et al., 2014; Massaro et al., 2018). Similarly, a translocation between 2002 – 2004 to Elizabeth Ellen Preece Conservation Covenant on Rangiauria | Rangiaotea | Pitt Island (hereinafter Pitt Island) failed to establish a population, with inadequate invertebrate prey availability hypothesised as one factor contributing to this failure (Parker, Parlato, et al., 2023). While Emberson (1998) documented beetle distributions across the Chatham Islands, and Emberson et al (1996) demonstrated differences in ground-dwelling invertebrate faunas between predator-free and predator-present islands, neither study used systematic sampling methods that allow quantitative comparisons across different habitat strata. Consequently, assessments of how invertebrate prey communities vary with habitat condition within individual islands remain lacking.

This study aims to identify ecological factors that may underpin black robin distribution and success by characterising invertebrate prey communities across current habitat and potential translocation sites. To compare variation in invertebrate communities across habitats relevant to black robin conservation, I examined four forest habitats, including currently occupied, previously unsuccessful, and potential future translocation sites across the Chatham Islands. The four habitats investigated in this study span a gradient of habitat and management conditions on the Chatham Islands, ranging from a predator free island to sites with ongoing invasive predator presence with varying degrees of forest clearance and regeneration.

I expect invertebrate communities to vary along this gradient. Specifically, I predict sites free from mammalian predators would support more abundant and diverse invertebrate communities than sites where invasive predators remain present. Mammalian predators can affect invertebrate communities both directly through predation and indirectly through habitat degradation (Gruner, 2004). Predators such as rats degrade habitat through browsing and disturbance to soil and leaf litter, reducing the structural complexity and resource availability needed to support diverse invertebrate communities (Ruscoe et al., 2013; Watts & Thornburrow, 2009). The presence of predators may also limit the recovery of native vegetation, further constraining invertebrate populations. I also expect that forest quality would influence invertebrate availability, with more mature forests supporting greater invertebrate biomass than regenerating habitats. Beyond informing future translocation planning, this work provides baseline data on invertebrate community variation across the archipelago, which will be valuable for evaluating how ongoing conservation interventions (invasive predator control, fencing, and habitat restoration) influence lower trophic levels.

2.3 Materials and Methods

2.3.1 Study Sites

This study was conducted in the Chatham Islands (43.9271° S, 176.4592° W; Figure 2.1), an isolated archipelago situated approximately 800km east of mainland Aotearoa. The islands experience a cool temperate, rapidly changing climate characterised by persistent strong winds, high humidity, and an average annual rainfall of approximately 800-1000 mm (Pearce, 2016). Native coastal broadleaf forest once dominated much of the landscape, but extensive clearance for agriculture and settlement has reduced it to small, scattered remnants (Roberts et al., 2007). Several offshore islands are now free of introduced mammals and form critical refuges for endemic species.

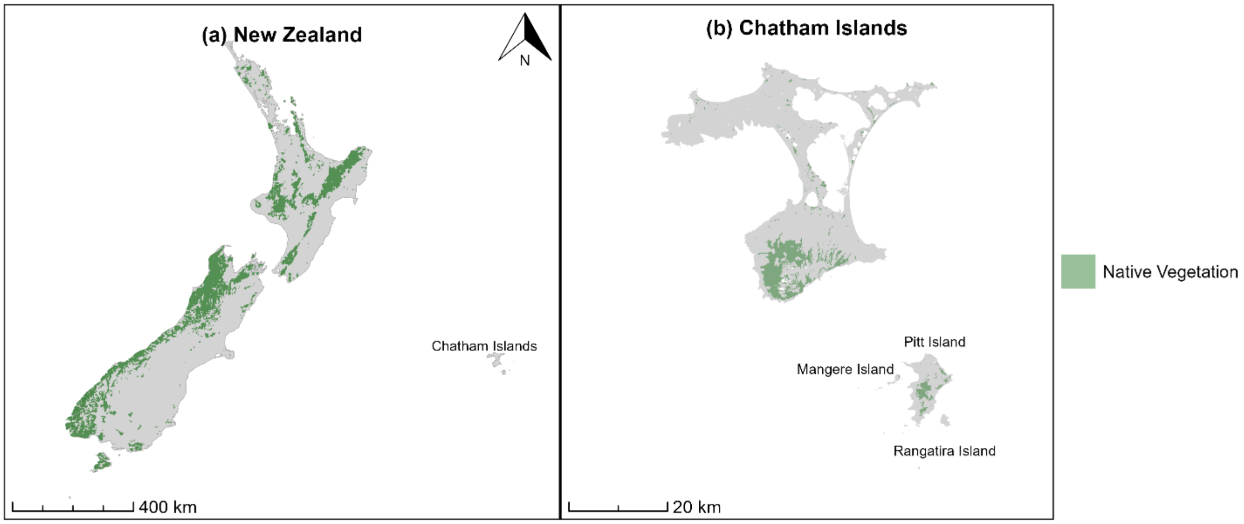

Figure 2.1: Study region location. (a) Aotearoa | New Zealand showing native vegetation (dark green) and the position of the Chatham Islands to the east. (b) The Chatham Islands archipelago showing Hokorereoro | Rangatira | Southeast Island, Rangiauria | Rangiaotea | Pitt Island, Maung' Rē | Mangere Island, and Rēkohu | Wharekauri | Chatham Island (the largest island in the north), with native vegetation coverage indicated in dark green. The north arrow indicates orientation, and scale bars represent 400 km (a) and 20 km (b).

Rēkohu | Wharekauri | Chatham Island (hereinafter Chatham Island) is the largest island in the archipelago (920 km^2) and supports most of the human population (~600 people). Extensive conversion to pastoral farming has left native forest fragmented into small, patchy remnants. Remaining native flora includes hakapiri | akeake (*Olearia traversiorum*), mataira | matipo (*Myrsine chathamica*), and karamu (*Coprosma chathamica*), often found in costal or riparian fragments (Roberts et al., 2007). Conservation efforts are concentrated on such remnants, a few of which provide habitats for threatened flora and fauna. Chudleigh Conservation Area, a 0.42 km^2 nature reserve in northern Chatham Island (43.7253° S, 176.564° W), is one of the few remaining stands of relatively intact forests (Figure 2.2).The site was enclosed by a stock exclusion fence in late 2024, though the fence does not exclude introduced mammalian or avian predators like the brushtail possum (*Trichosurus vulpecula*) or weka (*Gallirallus australis*). Despite this, Chudleigh Conservation Area was assessed and recognised as a potential site for future black robin translocation during a site assessment process in 2023 (Parker, Patterson, et al., 2023).

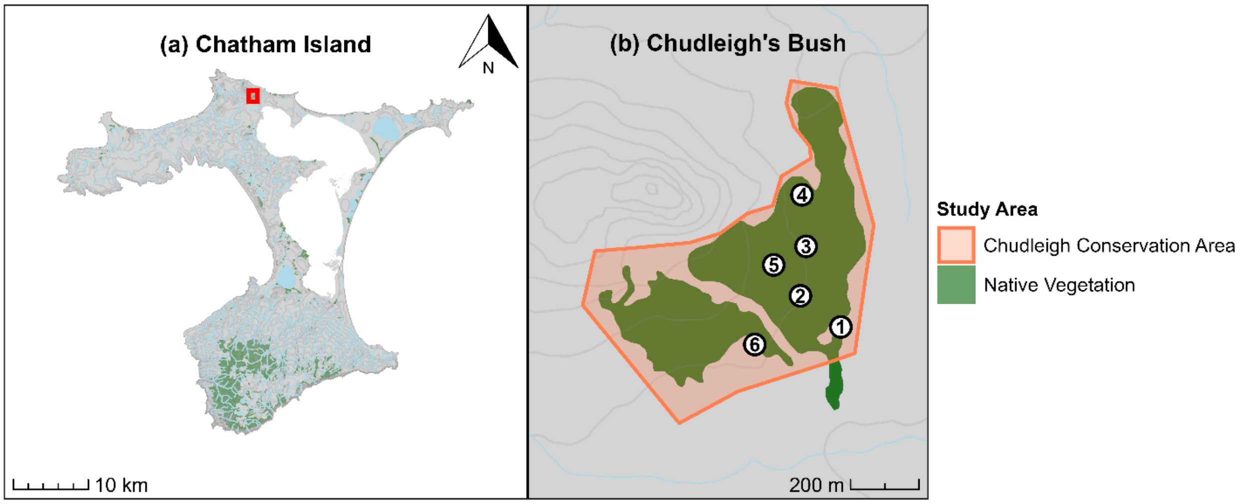

Figure 2.2: Chudleigh Conservation Area study site on Rēkohu | Wharekauri | Chatham Island. Panel (a) Overview of Rēkohu | Wharekauri | Chatham Island showing the location of Chudleigh Conservation Area (red box) with native vegetation in green. Panel (b) shows Chudleigh Conservation Area (Orange) with six study plots (1–6) located within the fenced reserve. Native vegetation is shown in dark green, with topographic contours visible in the background. The north arrow indicates orientation, and scale bars represent 10 km (a) and 200 m (b).

Rangiauria | Rangiaotea | Pitt Island, the second largest island (65 km²), lies 20 km south of Chatham Island (44.2899° S, 176.2260° W; Figure 2.3). It has a smaller human population (~40 people) compared to Chatham Island, but has been similarly affected by agricultural clearance, with only a few forest remnants remaining. The largest forest remnant is Elizabeth Ellen Preece Conservation Covenant | Caravan Bush (hereinafter Caravan Bush) (44.2863° S, 176.187° W), a 0.54 km^2 regenerating patch mostly composed of akeake and hōhō | Chatham Island lancewood

(*Pseudopanax chathamicus*). The site has been partially predator-proof fenced for over 20 years, excluding feral cats (*Felis catus*), weka, and pigs (*Sus scrofa*), but does not exclude mice (*Mus musculus*) (Parker, Patterson, et al., 2023). Pitt Island harbours these introduced predators but, unlike Chatham Island, is free of introduced rats (*Rattus rattus*) and brushtail possums. Although small and isolated, Caravan Bush is ecologically significant, supporting populations of endemic species including the Chatham Island tomtit (*Petroica macrocephala chathamensis*), Chatham Island tui (*Prosthemadera novaeseelandiae chathamensis*), and ranguru | Chatham petrel (*Pterodroma axillaris*). The site also hosted black robin translocation attempts in the early 2000's. While efforts were unsuccessful, the site remains of interest for restoration and as a target for another black robin translocation in future (Parker et al., 2023).

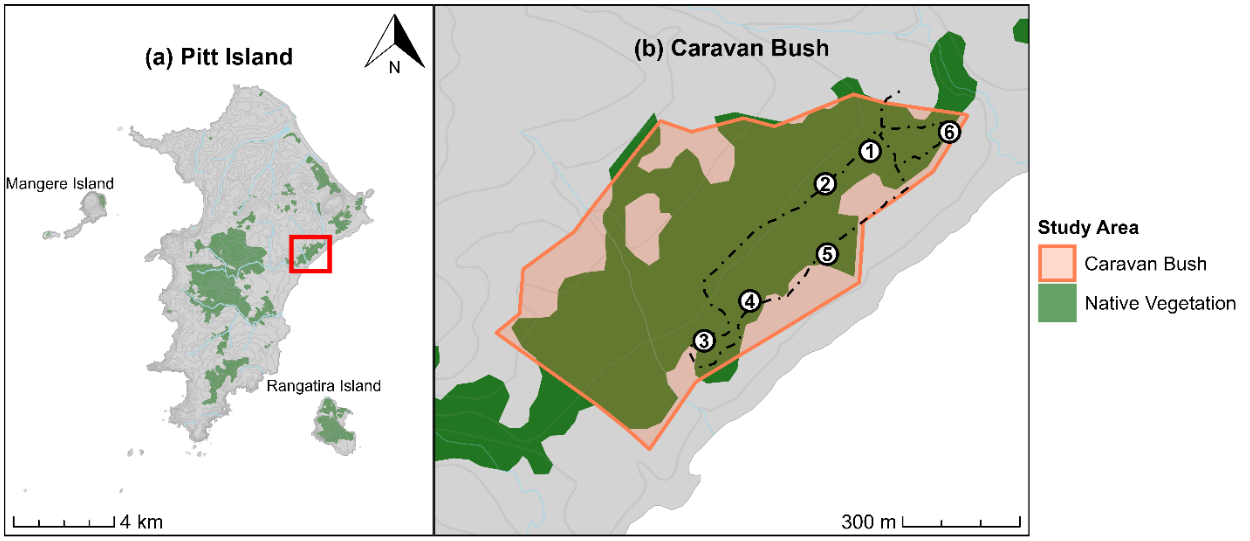

Figure 2.3: Location of study sites on Rangiauria | Rangiaotea | Pitt Island. Panel (a) shows a map of Pitt Island with Caravan Bush (red square) in relation to Mangere and Rangatira Island. Panel (b) details a map of Caravan Bush overlaid on native vegetation (green). Numbered points indicate sampling locations within Caravan Bush. The north arrow indicates orientation, and scale bars represent 4 km (a) and 300 m (b).

Rangatira Island is a 2.18 km^2 nature reserve located south-east of Pitt Island (44.3471° S, 176.1726° W; Figure 2.4). This island has been free from introduced mammals since their eradication when livestock were removed in the 1960s and is now largely covered in dense regenerating forest. Dominant canopy species include akeake and mānatu | Chatham Island ribbonwood (*Plagianthus chathamicus*), influenced by seabird burrowing activity (Roberts et al., 2007). For this study I focussed on two locations on Rangatira Island: (1) Woolshed Bush, which has dense forest with abundant leaf litter and a relatively high abundance of black robins, and (2) Top Bush, which is more open with tall canopy with less leaf litter (Roberts et al., 2007) and relatively fewer black robins.

Rangatira Island hosts the larger of the two populations (~300) of black robins and supports exceptional biodiversity, including the nationally critical Chatham petrel, the nationally critical shore plover (*Thinornis novaeseelandiae*), and endemic invertebrates such as the Rangatira spider (*Dolomedes schauinslandi*) and coxella weevil (*Hadramphus spinipennis*). Invertebrate surveys have documented thriving communities on Rangatira Island, with pitfall trapping studies recording exceptionally high abundance and activity. Chinn & Kennedy (2021) collected over 2000 specimens from 77 recognisable taxonomic units during a ten-day survey, with catch rates and densities (up to 29.5 individuals per m^2 per night) at least 4.5 times greater than comparable pitfall studies on mainland Aotearoa in Otago, a difference potentially attributed to the absence of mammalian predators and high organic production on Rangatira Island. Combined with the contrasting habitat structure between Woolshed Bush and Top Bush, Rangatira Island provides an ideal reference system for examining how invertebrate communities vary across habitats, potentially influencing black robin distribution.

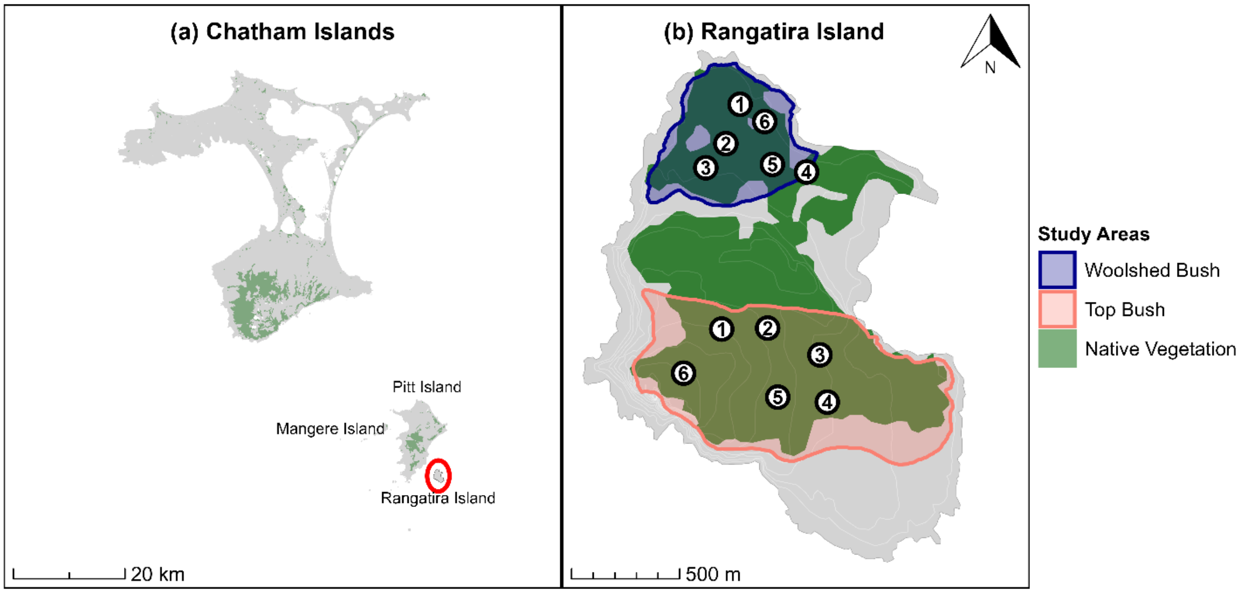

Figure 2.4: Location of study sites on Hokorereoro | Rangatira | Southeast Island. Panel (a) shows a map of the Chatham Islands with Hokorereoro | Rangatira | Southeast Island (red circle) in relation to Maung' Rē | Mangere and Rangiauria | Rangiaotea | Pitt Islands. Panel (b) Rangatira Island showing the two study areas: Woolshed Bush (blue) and Top Bush (pink), overlaid on native vegetation (green). Numbered points indicate sampling locations within each study area. The north arrow indicates orientation, and scale bars represent 20 km (a) and 500 m (b)

2.3.2 *Invertebrate Sampling*

I conducted invertebrate sampling at four sites spanning three islands to assess prey availability across currently inhabited (Woolshed Bush and Top Bush on Rangatira Island), previously failed (Caravan Bush on Pitt Island), and potential future (Chudleigh Conservation Area on Chatham Island) black robin locations. Sampling was carried out on Rangatira Island during two time periods: between the 13th – 18th of November 2024 and 13th – 19th of February 2025. Sampling on Pitt Island occurred from the 21st to the 27th of February 2025, while Chatham Island sampling was conducted between the 1st and 6th of March 2025.

I employed three complementary sampling methods to capture ground and low-vegetation dwelling invertebrates relevant to black robin foraging behaviour (see Chapter 3): emergence traps, pitfall traps, and suction sampling. I randomly deployed six emergence traps (Bug dorm BT2005) covering 1 m^2 at each site to capture invertebrates emerging from leaf litter and soil (Figure 2.5A). I then placed pitfall traps, consisting of plastic 500 ml cups filled with ~100 ml of 70% ethanol, within the centre of each emergence trap to capture ground-dwelling invertebrates (Figure 2.5B). Emergence and pitfall traps were deployed for six nights at Woolshed Bush, Top Bush, and Caravan Bush, but only five nights at Chudleigh Conservation Area due to logistical constraints. Lastly, I conducted suction sampling every second day, for a total of three sessions per plot during the sampling period using a STIHL SHA 56 leaf mulcher fitted with a mesh collection bag. At each plot within a site, samples were taken within a 2.5 m radius around and above the emergence traps, with each suction session lasting two minutes. Each plot consisted of one emergence trap paired with one pitfall trap and associated suction samples, replicated 6 times at each study site for a total of 36 plots (including November and February sampling at Woolshed and Top Bush). All collected invertebrates were preserved in ~70% ethanol and bought back to the University of Waikato for identification.

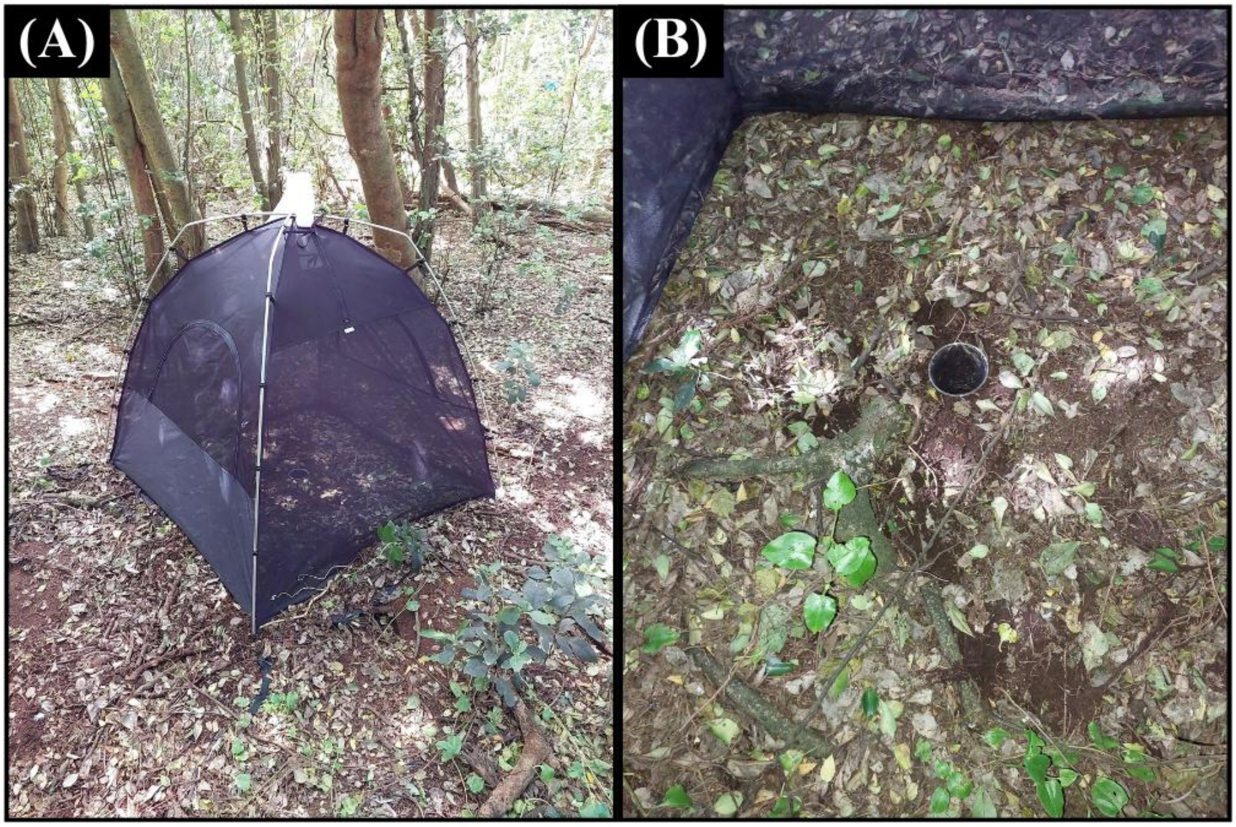

Figure 2.5: (A) Soil emergence trap installed on Hokorereoro | Rangatira | Southeast Island habitat to capture emerging invertebrates from the leaf litter and soil surface. (B) Inside of the emergence trap showing the pitfall trap positioned at the centre, to collect ground-dwelling invertebrates from within the known area of the emergence trap.

2.3.3 Invertebrate Identification

All invertebrate samples were sorted and identified using a dissection microscope (Olympus SZ61) fitted with a graticule (WHSZ10x-H/22). Taxonomic identifications were made using identification keys from Massey University (199.310 Entomology) and Lincoln University (ENTO304 Insect Ecology and Diversity). Invertebrates from suction and emergence traps were identified to order, whereas pitfall traps were identified to family to provide greater taxonomic resolution of ground-dwelling invertebrates. Identifying all samples to family would have been preferable but was not possible due to time constraints. Greater taxonomic resolution was focused on pitfall trap samples because black robins are known to forage predominantly on ground level (McLean et al. (1994) (see also Chapter 3). For each individual invertebrate over 3 mm in body length from all trapping types, I measured length and width (mm) using the graticule. I used a 3 mm threshold (rather than the typical 2 mm macrofauna cutoff) to focus on prey sizes relevant to black robins and to ensure accurate measurements. Length was measured from the anterior tip of the head to the posterior tip of the abdomen, excluding appendages such as antennae and cerci. Width was measured at the widest point of the body, typically across the thorax or abdomen depending on the invertebrate's body shape.

I then estimated individual invertebrate body mass (mg) based on measured body length and width in mm, using an allometric equation (Sohlström et al., 2018):

$$\log_{10}(\text{mass}) = -0.340 + 1.070 \times \log_{10}(\text{length}) + 1.643 \times \log_{10}(\text{width})$$

Plot-level total invertebrate biomass and mean body mass was obtained by calculating, respectively, the sum and the mean of the estimated body masses of all individuals captured within each plot.

2.3.4 Statistical Analysis

I conducted all statistical analyses and visualisations in R version 4.5.0 (R Core Team, 2025). Given that I only collected samples in November 2024 from Woolshed Bush and Top Bush on Rangatira Island and these were collected in a different season than all other samples, I excluded them from the cross-site comparison analyses. Data and summary figures from the 2024 Rangatira samples are presented separately in Appendix A.

To assess variation in invertebrate community composition across sites, I used non-metric multidimensional scaling (NMDS) ordination based on Bray-Curtis dissimilarity for each sampling method using the ‘metaMDS’ function in the ‘vegan’ package (Oksanen et al., 2025). I used permutational multivariate analysis of variance (PERMANOVA) to test for significant differences in community composition among sites. To distinguish whether significant PERMANOVA results reflected true compositional differences or differences in multivariate dispersion, I tested homogeneity of dispersions using the ‘betadisper’ function in the vegan package (Oksanen et al., 2025).

I assessed the effects of site (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area), sampling method (emergence, suction, and pitfall), and their interaction on total abundance, mean body mass, and total biomass through separate two-way analyses of variance (ANOVA). Model assumptions were checked through visual inspection of diagnostic plots (Q-Q plots and residuals vs. fitted values). Mean body mass and total biomass were log-transformed to meet the assumptions of normality and homogeneity of variance, while total abundance met assumptions without transformation. Tukey's Honest Significant Difference (HSD) post-hoc tests were used to identify specific pairwise differences between sites and sampling methods for all three response variables.

To describe how body masses are distributed among individuals at each site, I estimated individual size distributions (ISD) for each site using maximum likelihood estimation through the ‘SizeSpectra’ package in R (Edwards, 2020). The ISD slope (λ) describes the power-law relationship between body mass and abundance. More negative λ values indicate communities dominated by smaller bodied individuals with relatively fewer large individuals, while less negative (i.e. more positive) λ values suggest a higher proportion of larger bodied individuals found in the community. Lambda values closer to zero indicate a more even distribution of large and small bodied individuals. For each location, invertebrates from all three sampling methods were pooled to obtain sufficient sample sizes for robust ISD estimation, as pooled samples contain the full range of body sizes across different habitat strata. Sample sizes and 95% confidence intervals were calculated for λ estimates at each location.

Important note on sampling effort:

Chudleigh Conservation Area was sampled for five nights with emergence and pitfall traps, while all other sites were sampled six nights. This difference in sampling effort means that the total abundance comparisons between Chudleigh Conservation Area and other sites should be interpreted cautiously, as sites with more trapping nights have had longer opportunities to accumulate more invertebrates. This is particularly important for rare or large-bodied taxa that may require longer trapping periods for capture. Suction sampling effort was consistent across all sites (three sampling events each), so comparisons on canopy invertebrates are not affected by this limitation.

2.4 Results

Across the four study sites, I collected a total of 2455 invertebrates in 2025 representing 14 orders (Table 2.1). Invertebrate communities varied substantially across the four locations, with Woolshed Bush supporting the highest total abundance and greatest taxonomic diversity. Each site supported distinct communities that differed in taxonomic composition, abundance, and body mass distributions. The three sampling methods targeted different habitat strata: pitfall traps sampled the soil surface, emergence traps sampled the leaf litter layer, and suction sampling targeted the canopy layer.

Table 2.1: Total invertebrate abundance and taxonomic richness across four sites representing different black robin habitats: Woolshed Bush (current high quality habitat) and Top Bush (current lower quality habitat), Caravan Bush (previously failed translocation site), and Chudleigh Conservation Area (potential future translocation site). Individuals per-night values calculated by dividing total individuals from pitfall and emergence traps by number of trapping nights (5 nights for Chudleigh Conservation Area, 6 nights for all other sites). Suction sampling (3 events at all sites) is not included in per-night calculations.

Site	Total Individuals	Trapping Nights	Individuals Per Night	Total Orders (all methods)	Total Families (pitfall traps only)
Woolshed Bush	783	6	121.0	12	19
Top Bush	541	6	83.7	10	12
Caravan Bush	623	6	89.8	11	11
Chudleigh Conservation Area	508	5	93.6	11	8
Total	**2455**				

2.4.1 Community Composition

Non-metric multidimensional scaling (NMDS) ordination based on Bray-Curtis dissimilarity revealed differences in invertebrate community composition at order level among sites, with the amount of separation varying by habitat strata (Figure 2.6). PERMANOVA analysis detected significant differences in invertebrate community composition among sites across all three habitat strata (Table B1). Soil surface (pitfall traps) communities showed the strongest site differentiation ($P < 0.05$), with site accounting for 40.1% of the variation in community dissimilarity.

The pitfall ordination displayed the clearest differences among sites in community composition (Figure 2.6). The current black robin habitat sites (Woolshed Bush and Top Bush) showed substantial overlap in invertebrate community composition in ordination space. Invertebrate communities at Caravan Bush (previously failed habitat) and Chudleigh Conservation Area (potential future habitat) also showed considerable overlap in ordination space, both relative to each other and to the current habitat sites. Soil surface communities exhibited similar within-site variability across all sites ($P = 0.347$), indicating consistent dispersion of ground-dwelling invertebrate assemblages despite differences in mean community composition among sites (Table B2).

Understory (suction sampling) communities also showed significant site differences ($P < 0.05$), with site explaining 29.1% of variation (Table B1). The NMDS ordination showed moderate separation among sites, with Caravan Bush plots forming a relatively tight cluster, while the other three sites (Top Bush, Woolshed Bush and Chudleigh Conservation Area) showed similar levels of dispersion (Figure 2.6). A marginally non-significant trend suggests differences in within-site variability among sites ($P = 0.057$; Table B2), with Chudleigh Conservation Area and Top Bush showing greater spread in ordination space compared to the tighter clustering observed at Caravan Bush.

Emerging invertebrate communities revealed the weakest, but still significant, site differences ($P < 0.05$), with site explaining 24.3% of variation in community composition (Table B1). The emergence trap ordination showed substantial overlap among all four sites (Figure 2.6). A marginally non-significant trend for differences in dispersion was also observed ($P = 0.068$; Table B2), with Chudleigh Conservation Area and Caravan Bush displaying larger ellipses, suggesting greater within-site variability.

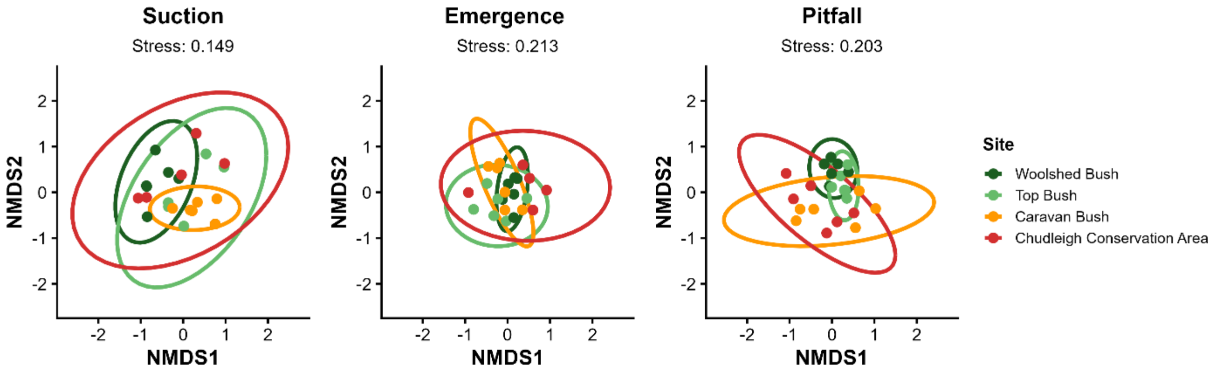

Figure 2.6: Non-metric multidimensional scaling (NMDS) ordination of invertebrate community composition across four sites (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area) using three habitat strata (suction sampling, pitfall traps, and emergence traps). Ordinations are based on Bray-Curtis dissimilarity calculated from order level abundance data. Each point represents a sampling plot (n = 6 per location). Solid ellipses represent 95% confidence intervals around location centroids. Stress values indicate fit for the two-dimensional representation.

2.4.2 Invertebrate Abundance

A two-way ANOVA revealed significant differences in log-transformed total invertebrate abundance among sites and habitat strata, with a significant interaction indicating that site differences depend on the strata measured (Figure 2.7; Table 2.2). Invertebrate abundance in pitfall traps varied significantly among sites, whereas no significant site differences were detected for emergence traps or suction sampling (Table B3).

Total pitfall captures were higher at Woolshed Bush and Top Bush (current black robin habitat) than at Caravan Bush and Chudleigh Conservation Area, with no significant differences within either group of sites. However, Chudleigh Conservation Area was sampled for five nights compared to six nights at other sites. When accounting for this difference in sampling time, per-night catch rates show Chudleigh Conservation Area (93.6 individuals per night) exceeded both

Top Bush (83.7 per night) and Caravan Bush (89.8 per night), though remained lower than Woolshed Bush (121.0 per night; Table 2.1).

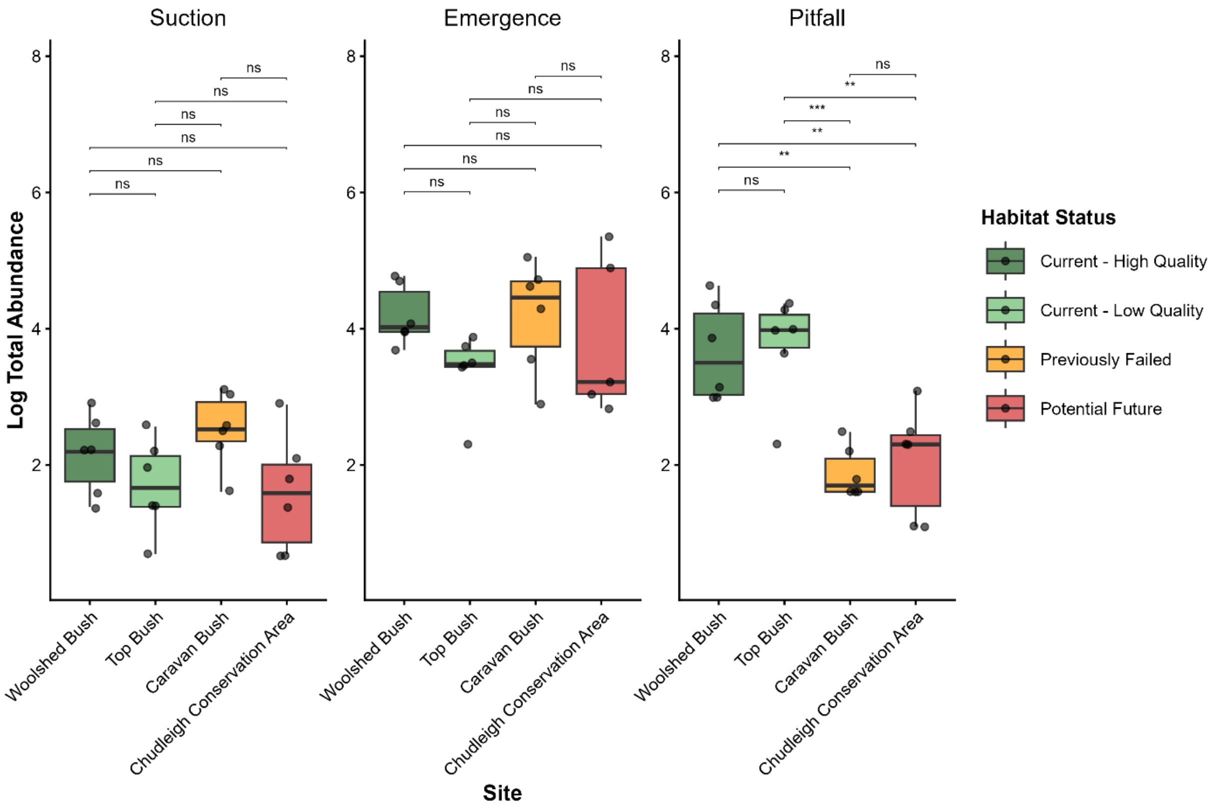

Figure 2.7: Invertebrate abundance across habitat strata at different sites. Log-transformed invertebrate abundance from understory vegetation (suction), belowground (emergence), and soil surface (pitfall) at sites representing current high quality (dark green), current low quality (light green), previously failed (orange), and potential future (red) black robin habitat. Boxes show median and interquartile range; points represent individual plots (n = 6 per site per method). Brackets indicate pairwise comparisons (Tukey post-hoc tests: ** $p < 0.01$, *** $p < 0.001$, ns = not significant).

Table 2.2: Two-way ANOVA results testing the effects of site, sampling method, and their interaction on log-transformed invertebrate abundance. Significant results ($P < 0.05$) are highlighted in bold.

	Df	Sum Sq	Mean Sq	F value	P value
Site	3	7.30	2.43	4.82	**0.005**
Method	2	42.56	21.28	42.17	**<0.001**

Site:Method	6	17.79	2.96	5.88	**<0.001**
Residuals	59	29.77	0.50		

Tukey's HSD post-hoc tests comparing habitat strata within each site revealed distinct differences in invertebrate abundance between the three sampled strata (Table B4). Invertebrates emerging from leaf litter (emergence traps) were significantly more abundant than those in the canopy (suction samples) at all four sites ($P < 0.001$) Comparisons between leaf litter and ground-active invertebrates (pitfall traps) differed among sites. At the two current black robin habitats (Woolshed Bush and Top Bush), leaf litter and ground-active invertebrates showed similar abundances ($P > 0.05$). In contrast, at the previously failed habitat (Caravan Bush) and potential future site (Chudleigh Conservation Area), leaf litter invertebrates were significantly more abundant than ground-active invertebrates. Ground-active invertebrates were significantly more abundant than canopy invertebrates at the current habitat sites (Woolshed Bush and Top Bush), but not at Caravan Bush or Chudleigh Conservation Area.

2.4.3 Total Biomass

Total invertebrate biomass differed significantly among habitat strata and varied between sites, as confirmed by a two-way ANOVA showing a strong main effect of habitat strata ($P < 0.001$) and a significant site-by-method interaction ($P < 0.001$; Table B5; Figure 2.8). No significant main effect of site was detected ($P > 0.05$). At current black robin habitats (Woolshed Bush and Top Bush), soil surface invertebrates had the highest biomass, showing greater median values and variation than Caravan Bush and Chudleigh Conservation Area. In contrast, at previously failed (Caravan Bush) and potential future habitat (Chudleigh Conservation Area), emerging invertebrates dominated biomass contributions, while soil surface contributed comparatively less.

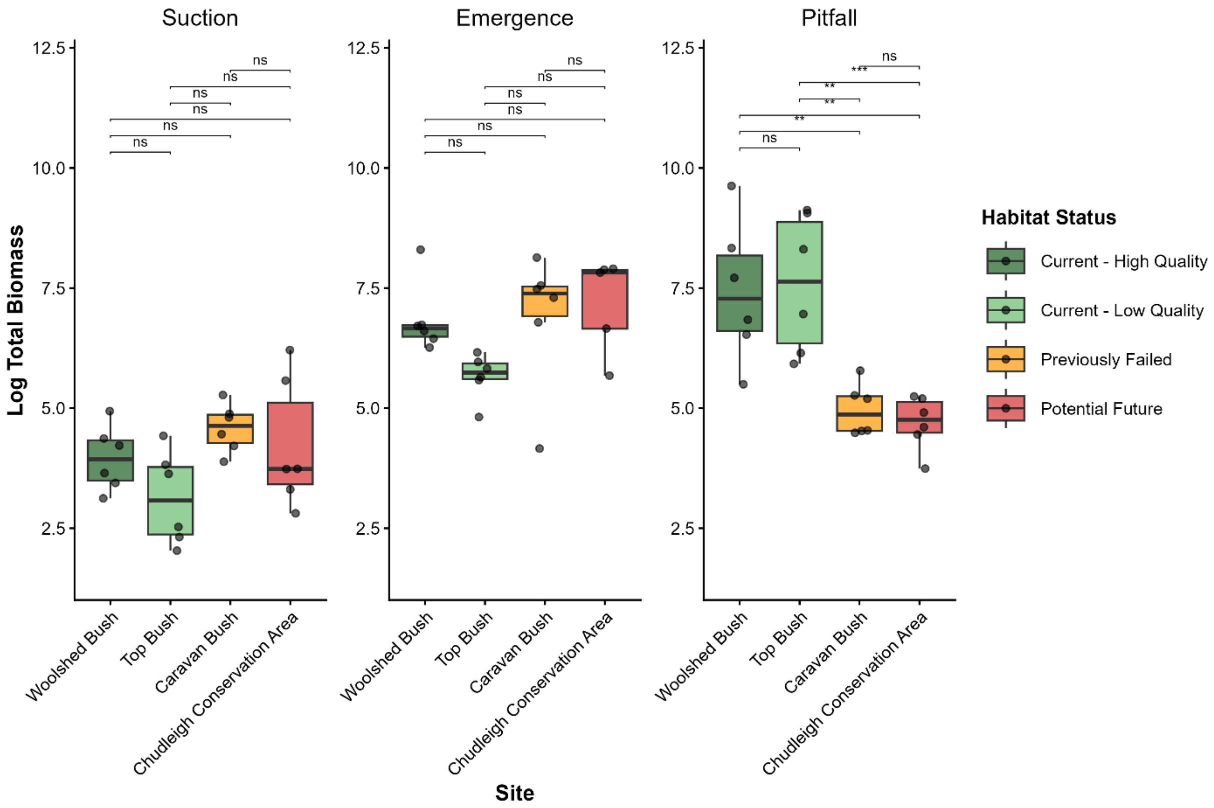

Figure 2.8: Total invertebrate biomass across habitat strata at different sites. Log-transformed invertebrate biomass from understory vegetation (suction), belowground (emergence), and soil surface (pitfall) at sites representing current high quality (dark green), current low quality (light green), previously failed (orange), and potential future (red) black robin habitat. Boxes show median and interquartile range; points represent individual sites (n = 6 per location per method). Brackets indicate pairwise comparisons (Tukey post-hoc tests: ** $p < 0.01$, *** $p < 0.001$, ns = not significant).

Pairwise comparisons among sites for each habitat stratum revealed that significant variation in total biomass only occurred in soil-surface invertebrates sampled by pitfall traps (Table B6). Current black robin sites (Woolshed Bush and Top Bush) had similar soil surface biomass ($P > 0.05$), and both sites showed significantly higher values than previously failed (Caravan Bush) and potential future sites (Chudleigh Conservation Area) ($P < 0.001$). No significant differences in soil surface biomass were detected between Caravan Bush and Chudleigh Conservation Area ($P > 0.05$). Emerging and understory invertebrate biomass showed no significant differences among sites ($P > 0.05$).

Tukey's HSD post-hoc tests revealed specific patterns in biomass from different habitat strata at each site (Table B7). At current black robin sites (Woolshed Bush and Top Bush) both soil surface and emerging invertebrates contributed significantly more biomass than understory vegetation ($P <0.001$), with no significant differences between soil surface and emerging strata ($P > 0.05$). At previously failed and potential future sites (Caravan Bush and Chudleigh Conservation Area), emerging invertebrates had significantly more biomass than both soil surface and understory strata ($P > 0.05$).

2.4.4 Community Body Mass Structure

Individual body mass distributions varied across habitat strata and sites (Figure 2.9), with understory (suction sampling) invertebrate communities at all sites had narrower body size distributions concentrated at smaller to intermediate sizes, with fewer individuals exceeding 50 mg and almost none exceeding 100 mg. The kernel density plots for understory communities showed less spread compared to soil surface invertebrates, indicating a restricted size range (5-10 mg).

In contrast, body mass distributions of emerging invertebrates showed an intermediate pattern between soil surface and understory communities. At currently inhabited sites (Woolshed Bush and Top Bush) body mass distributions of emerging invertebrates were relatively broad, capturing both small and large invertebrates. However, the density of very large individuals (>100 mg) in emerging invertebrates remained lower than in soil dwellers (Figure 2.9).

At current black robin sites (Woolshed Bush and Top Bush), soil surface (pitfall traps) invertebrates showed distributions that included individuals across all size classes, extending to very large body masses (>150 mg). The kernel density plots showed broad, spread-out distributions for soil surface communities at these sites, with relatively even densities of small (~5 mg), intermediate (~10-50 mg), and large (>100 mg) size classes, reflecting high variability in captured body sizes (Figure 2.9). In contrast, soil surface invertebrates at Caravan Bush (previously failed) and Chudleigh Conservation Area (future potential site) showed distinct peaks, with pitfall captures centred around intermediate size classes (<50 mg) and notably lacking larger individuals (>100 mg).

At previously failed (Caravan Bush) and potential future habitats (Chudleigh Conservation Area), body size distributions were generally shifted toward smaller individuals compared to current black robin habitats (Woolshed Bush and Top Bush). Soil surface invertebrates at these sites had fewer large-bodied individuals compared to currently inhabited sites, with distributions more compressed towards smaller invertebrate body masses, showing greater overlap with emerging and understory communities (Figure 2.9). Far fewer large-bodied individuals were captured at Caravan Bush and absent at Chudleigh compared to Woolshed and top Bush. Belowground emerging invertebrates showed contrasting patterns between sites. At Woolshed Bush and Top Bush, emerging communities were made up of smaller individuals, while at Caravan Bush and Chudleigh Conservation Area emerging communities also included larger individuals, like the patterns seen on the soil surface at Woolshed Bush and Top Bush (Figure 2.9).

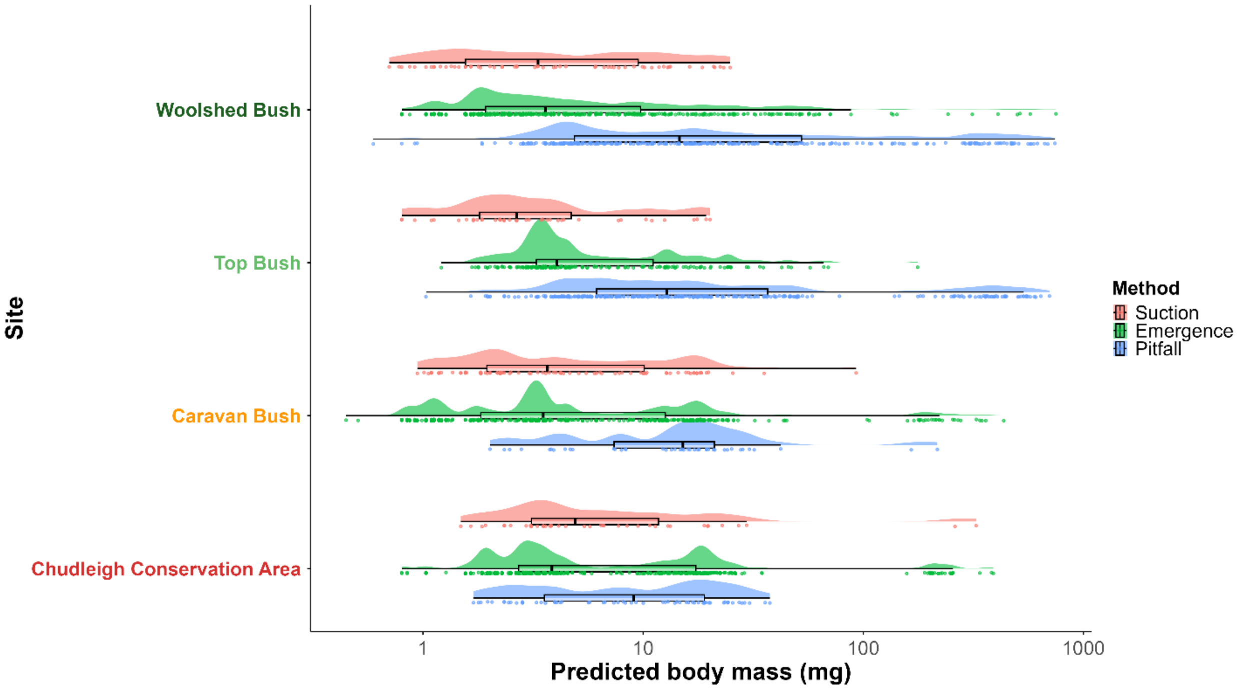

Figure 2.9: Distribution of individual invertebrate body masses (mg) in 2025 from three habitat strata: understory vegetation (suction), belowground (emergence), and soil surface (pitfall) at four sites. Site names are color-coded to indicate habitat quality for black robin translocation: dark green (current high-quality), light green (current low-quality), orange (previously failed), and red (potential future). Plots combine kernel density distributions (half-violins), boxplots (median, interquartile range, and 1.5× IQR whiskers), and individual data points (individual body mass measurements).

To quantify overall differences in body size structure among sites, Individual Size Distribution (ISD) slopes were calculated across all individuals captured at each site. ISD slopes varied among sites, although all the 95% confidence intervals overlap, suggesting the differences in size structure among sites should be interpreted with caution (Figure 2.10, Table B8). Chudleigh Conservation Area showed the most negative slope followed by Caravan Bush, Woolshed Bush and Top Bush. The steeper slopes at Caravan Bush (previously failed habitat) and Chudleigh Conservation Area (potential future habitat) reflect a stronger dominance of small-bodied invertebrates relative to the more even size distribution of invertebrates at Woolshed Bush and Top Bush (current black robin habitat sites), as visualized in the body mass distribution plot (Figure

2.9). Sample size also varied among location, with Woolshed Bush having the largest number of individuals (n = 783) and Chudleigh Conservation Area the smallest (n = 508), which may have influenced slope precision. This difference in sample size is reflected in the confidence interval widths, with smaller sample sizes associated with wider confidence intervals (Table B8). The smaller sample size at Chudleigh Conservation Area partly reflects the shorter sampling duration for pitfall and emergence traps.

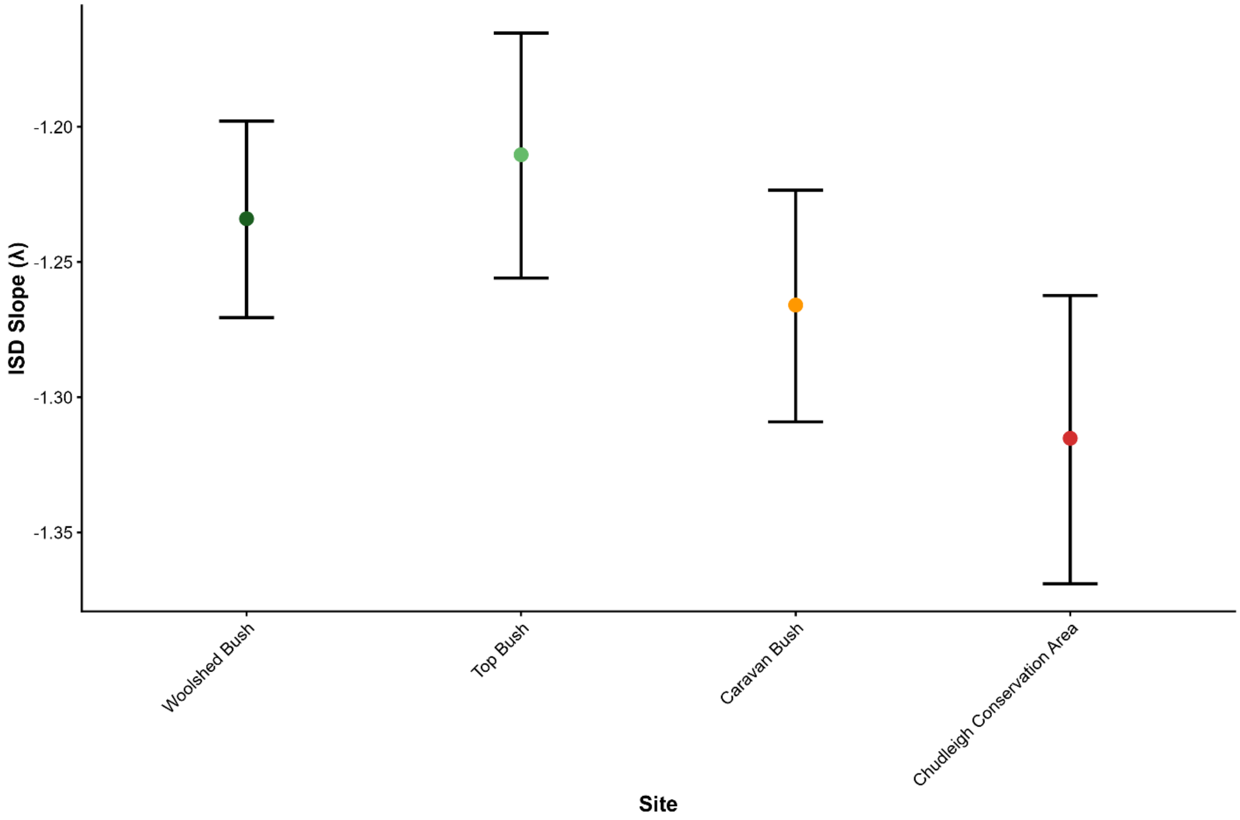

Figure 2.10: Individual size distribution (ISD) slopes across four sites (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area). Each point represents the ISD slope (λ) obtained by maximum likelihood estimation (MLE) for mean invertebrate body mass distributions at each site. Error bars indicate 95% confidence intervals around λ estimates.

Mean invertebrate body mass varied significantly between habitat strata and site (Figure 2.11). A two-way ANOVA revealed significant differences in mean body mass between habitat strata (P < 0.001), as well as a significant site-by-strata interaction (though no main effect of site was detected; Table B9). This interaction indicates that differences in mean invertebrate body size among sites with different habitat status were dependent on the strata (leaf litter, ground surface, and canopy) from which invertebrates were sampled. In other words, habitat status effects on invertebrate body size were not consistent across different habitat strata.

Tukey's HSD post-hoc tests revealed distinct differences in community mean body mass among habitat strata (i.e. trapping types) at different sites (Table B10). At Woolshed Bush and Top Bush (current black robin habitat sites), invertebrates on the soil surface (pitfall traps) were, on average, significantly larger than those emerging from belowground (emergence traps) and occurring in the understory vegetation (suction sampling). In contrast, at Caravan Bush (previously failed habitat) and Chudleigh Conservation Area (potential future habitat), no significant differences in mean body mass were detected among habitat strata (p > 0.05).

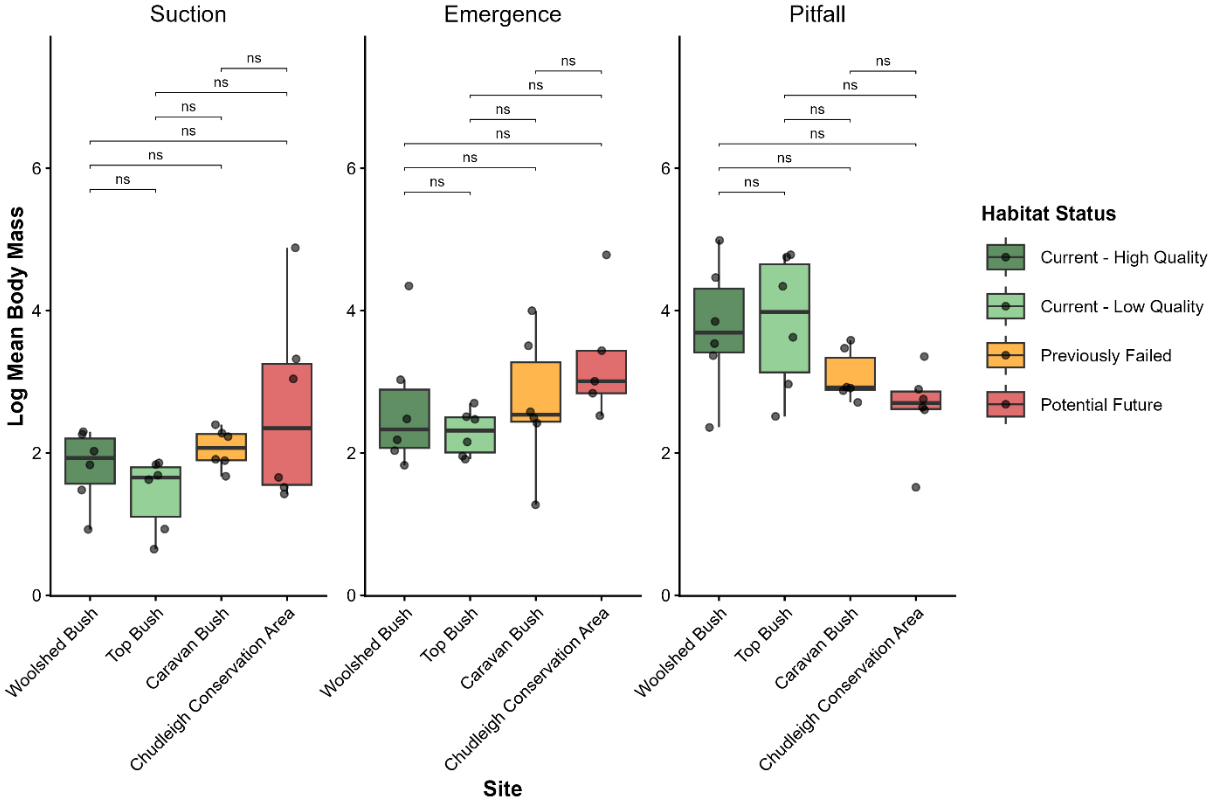

Figure 2.11: Mean invertebrate body mass across habitat strata at different sites. Log-transformed mean body mass of invertebrates from understory vegetation (suction), belowground (emergence), and soil surface (pitfall) at sites representing current high quality (dark green), current low quality (light green), previously failed (orange), and potential future (red) black robin habitat. Boxes show median and interquartile range; points represent individual plots (n = 6 per site per method). Brackets indicate pairwise comparisons (Tukey tests; ns = not significant).

2.4.5 Key Taxonomic Patterns

Despite broad taxonomic resolution, order-level differences revealed some meaningful ecological patterns, with family-level identification providing further insight. Notably, Orthoptera (made up entirely of cave wētā [Rhaphidophoridae]) were abundant at both Woolshed Bush (n = 93) and Top Bush (n = 82) but were not found at Caravan Bush and Chudleigh Conservation Area during my sampling. However, cave wētā are known to occur on both Pitt Island and Chatham Island, including recent sightings of *Talitropsis megatibia* at Caravan Bush and elsewhere on Pitt Island, and *Talitropsis crassicruris* on Chatham Island. Additionally, Chudleigh Conservation Area was sampled for five nights rather than six, which may have reduced detection probability for rare taxa. Therefore, the absence of cave wētā in my samples from Caravan Bush and Chudleigh Conservation Area likely reflects very low population densities at these sites rather than complete absence. These wētā showed very high mean body masses (181–205 mg) with large individual variation, including some of the largest invertebrates recorded in this study (maximum 741.59 mg). Ground beetles (Carabidae) also showed high mean body masses and were well-represented at Woolshed Bush (n = 13, mean 244 mg) and Top Bush (n = 45, mean 112 mg), but were undetected from Caravan Bush and Chudleigh Conservation Area.

Conversely, Opiliones (harvestmen) were present at Caravan Bush (n = 4) and Chudleigh Conservation Area (n = 12) but undetected from both predator-free sites. Family-level identification confirmed these were Triaenonychidae. Other taxa showed site-specific patterns:

Dermaptera (earwigs, family Forficulidae) and Julida (millipedes) were recorded only at Woolshed Bush, while Hemiptera in pitfall traps were captured only at Caravan Bush. Amphipoda (landhoppers, family Talitridae) were abundant across all sites but particularly dominant at Top Bush (n = 136 in pitfall traps). These order- and family-level differences likely reflect fundamental habitat differences between sites. Detailed taxonomic summaries for all orders captured by each stratum at each site are provided in Appendix C (Tables C1–C4).

2.5 Discussion

This study characterized invertebrate prey communities across four forest sites spanning a conservation gradient on the Chatham Islands, from a mammalian predator-free island with mature forest (Woolshed Bush and Top Bush) to island sites with ongoing predator presence (Caravan Bush and Chudleigh Conservation Area). The results revealed complex patterns that only partially support initial predictions, indicating that variation in invertebrate communities is likely influenced by a combination of habitat maturity, vegetation structure, and invasive mammalian predator presence, rather than any single factor alone.

2.5.1 Predator Effects on Invertebrate Communities

Contrary to my prediction that predator-free sites would support more abundant and diverse invertebrate communities, invertebrate abundance and taxonomic richness showed no consistent relationship with predator management across sites. Woolshed Bush (predator-free island, mature forest) did support the highest overall abundance and taxonomic diversity (783 individuals, 12 orders, 19 families), but Top Bush (also predator-free with mature forest) showed intermediate values (541 individuals, 10 orders, 12 families) that were lower than Caravan Bush (623 individuals, 11 orders, 11 families), where invasive mammalian predators remain present.

However, Chudleigh Conservation Area (508 individuals, 11 orders, 8 families) was sampled for five nights compared to six nights at other sites, which may have reduced total catch and affected detection of rare taxa. Notably, Woolshed Bush and Top Bush showed similar invertebrate communities despite differences in black robin abundance, suggesting that prey availability alone may not explain habitat quality differences between these sites. This pattern suggests that mammalian predators influence invertebrate communities in more selective ways than simple reductions in overall abundance or taxonomic diversity. The complete absence of large-bodied ground-dwelling taxa such as cave wētā and ground beetles from sites with predators indicates substantial impacts on specific components of the community, even when overall abundance remains similar.

The lack of strong invasive mammalian predator-mediated effects on overall invertebrate abundance in this study aligns with broader patterns observed across invasion ecology, though the evidence is mixed and context-dependent. While some studies have documented significant impacts of invasive mammalian predators on invertebrate communities, particularly mice on beetles, wētā, and other large-bodied invertebrates (Norbury et al., 2023; Watts et al., 2022), the magnitude and direction of these effects vary considerably with invasive predator density, habitat conditions, and the presence of other invasive predators (King, 2023; Ruscoe et al., 2013). In many Aotearoa ecosystems, the most well documented impacts of introduced mammalian predators have been on vertebrate prey, particularly ground-nesting birds, lizards, and frogs (Cowan & Moeed, 1987; King, 2023; Skinner et al., 2026; Woolley et al., 2020), though this may partly reflect research bias toward vertebrate studies. Importantly, invasive predators may have relatively weak direct consumptive effects on many invertebrate taxa, with impacts instead mediated indirectly through top-down trophic cascades by reducing insectivorous vertebrate populations. For this reason, predator presence alone would not necessarily predict overall invertebrate abundance. Instead, predator effects appear more selective, disproportionately affecting certain taxa (particularly large-bodied ground-dwelling species) while having minimal impact on others, with additional indirect effects through habitat degradation and altered trophic interactions.

The patterns of invertebrate biomass and body size distributions provide key insights into how mammalian predators may structure invertebrate communities. While overall abundance and order-level diversity showed limited variation among sites, examination of body size structure revealed striking differences. Body mass distributions showed a clear pattern: predator-free sites (Woolshed Bush and Top Bush) supported numerous individuals exceeding 100 mg, while sites with mammalian predators (Caravan Bush and Chudleigh Conservation Area) showed distributions compressed towards smaller body masses with far fewer large individuals. Ground-active invertebrate biomass was significantly higher at both predator-free sites compared to sites with predators, driven primarily by the presence of large-bodied invertebrates. Cave wētā (Rhaphidophoridae) and ground beetles (Carabidae) were abundant at Woolshed Bush and Top Bush, but largely or completely absent from Caravan Bush and Chudleigh Conservation Area.

This pattern could reflect selective predation on larger, more conspicuous invertebrates by mammalian predators, as these prey items are both vulnerable and energetically valuable (Ruscoe et al., 2013) However, other factors such as differences in habitat quality, forest maturity, and vegetation structure among sites could also contribute to reduced abundances of large-bodied invertebrates at sites with predators. The complete absence of cave wētā and ground beetles from sites with predators, combined with their high abundances at predator-free sites, suggests predation pressure likely plays a role, though separating this from habitat differences would require further investigation.

The reduced abundance of large-bodied invertebrates at Caravan Bush and Chudleigh Conservation Area could result from multiple mechanisms beyond direct predation by mammals. Avian predators, including native insectivorous birds, may play an important role in structuring invertebrate communities, particularly targeting larger, more conspicuous prey (Nyffeler et al., 2018). At sites with mammalian predators, complex trophic interactions could also influence invertebrate communities. For example, the presence of rats may increase predation pressure on large ground-dwelling invertebrates directly, while also altering ecosystem processes such as seed dispersal, litter accumulation, and nutrient cycling, all of which can indirectly affect invertebrate habitat quality and food resources (Notman & Villegas, 2005; Zeng et al., 2024). However, the high variability within sites like Caravan Bush and Chudleigh Conservation Area, combined with the absence of clear predator-related patterns in overall invertebrate abundance, suggests that habitat factors such as forest structure, microclimate, and vegetation composition may more strongly structure invertebrate communities than top-down predation effects alone (Evans et al., 2003; Perry et al., 2018).

2.5.2 Food Availability and Black Robin Habitat Quality

The similarity in invertebrate communities between Woolshed Bush and Top Bush on Rangatira Island is particularly informative for understanding black robin habitat requirements. Despite Woolshed Bush supporting slightly higher abundance and diversity, both predator-free forest sites appear to provide comparable food resources based on broad metrics of invertebrate abundance, biomass, and body size distributions. However, several caveats limit the conclusions that can be drawn about prey availability. First, this study did not identify specific prey items consumed by black robins, so it remains unknown whether key prey species differ in availability between these sites. Second, the coarse taxonomic resolution (primarily order-level identification) means that important prey-specific patterns could be overshadowed by broad taxonomic groups. For example, particular beetle species or wētā populations that black robins preferentially consume may differ between sites despite overall similarity at the order level. With these limitations in mind, the comparable invertebrate community metrics between Woolshed Bush and Top Bush suggest that documented differences in black robin abundances between these sites (Kennedy, 2009) may be influenced by factors beyond overall prey availability, such as nesting site availability, vegetation structure, or territory quality (Huang et al., 2015; Massaro et al., 2013).

The finding that invertebrate communities alone may not fully explain black robin distribution patterns has important implications for future translocation site selection. Identifying sites with sufficient invertebrate prey may be necessary but not enough for successful establishment. An integrated approach should consider the full suite of habitat requirements, including nest site availability, vegetation structure, and prey availability, rather than relying on a single factor. Black robins are cavity nesters with specific requirements (Kennedy, 2009), and changes in cavity abundance or quality between sites could affect carrying capacity regardless of food availability (Catry et al., 2013; Stone et al., 2025).

2.5.3 Habitat Structure and Invertebrate Communities

Forest maturity and structural complexity are also likely to be important drivers of invertebrate community patterns, partially supporting my second prediction. Ground-active invertebrate communities showed the strongest site differentiation, with currently inhabited sites (Woolshed Bush and Top Bush) supporting different community assemblages than previously failed (Caravan Bush) and potential future site (Chudleigh Conservation Area). However, these patterns may also reflect the absence of mammalian predators at Woolshed Bush and Top Bush, particularly given the similarity between these two sites. As such, differences in invertebrate communities among sites may likely be driven by a combination of habitat structure, forest maturity, and predator presence, which cannot be fully determined in this study.

Woolshed Bush and Top Bush, both characterised by mature forest with well-developed canopy and understory layers (Roberts et al., 2007), supported different invertebrate communities compared to regenerating habitats at Chudleigh Conservation Area. Mature forests typically provide greater structural complexity, including diverse habitat strata such as woody debris and well-developed leaf litter layers, which can support specialised invertebrate taxa (Fuchs, 2013; St. Pierre & Kovalenko, 2014). The presence of large-bodied cave wētā and ground beetles exclusively at the mature forest sites suggests that these taxa may depend on specific habitat strata conditions, such as stable microclimates or established litter layers, that are limited or absent in regenerating habitats (Evans et al., 2003; Fitness et al., 2015). However, large-bodied invertebrates are also known to be particularly vulnerable to predation by invasive mammals (Norbury et al., 2023; Watts et al., 2022), and predator absence at Woolshed Bush and Top Bush may therefore be an important, interacting driver of their presence. Together, these patterns suggest that both habitat structure and invasive predator pressure likely influence the presence and abundance of large-bodied invertebrates, although their relative importance cannot be highlighted in this study. This dual constraint of habitat suitability and predation vulnerability may help explain the absence of these taxa from both the regenerating habitat at Chudleigh Conservation Area and the mature forest at Caravan Bush, where mice are present.

The high variation in community composition among plots within Chudleigh Conservation Area reflects the diverse nature of this regenerating habitat. Unlike the forests at Woolshed Bush and Top Bush, Chudleigh consists of a variety of regenerating forest patches with variable canopy cover, understory development, and forest age (Parker, Patterson, et al., 2023). This habitat patchiness likely creates corresponding patchy invertebrate communities based on local habitat strata conditions (Perry et al., 2018).

For black robin translocation, this high within-site variability creates both challenges and opportunities. The inconsistent prey availability may make it difficult for black robin to establish stable territories. However, the variations in invertebrate communities showcase habitats responding to current management and regenerating. Continued habitat management, such as targeted predator control and restoration planting (Parker, Patterson, et al., 2023), could create suitable territories for the black robin. As the forest matures and structure becomes more uniform, invertebrate communities may become more consistent and abundant, potentially increasing the site's future suitability for black robin translocation. However, the dispersal limitations of many invertebrates, particularly large-bodied and flightless taxa (Auger et al., 2024), may constrain natural recolonisation of regenerating sites. This raises the possibility that active invertebrate translocations could be required, not only to support black robin populations but also to facilitate broader ecosystem restoration.

2.5.4 Methodological Considerations and Limitations

Several methodological limitations should be considered when interpreting these results. Most importantly, Chudleigh Conservation Area was sampled for five nights with emergence and pitfall traps, while all other sites were sampled for six nights. This difference in sampling effort means that direct comparisons of total abundance between Chudleigh Conservation Area and other sites should be interpreted cautiously. This limitation is particularly relevant for rare taxa that may require extended trapping periods for detection. For example, cave wētā (*Talitropsis* spp.) are known to occur on both Pitt Island and Chatham Island, yet were not captured at Caravan Bush or

Chudleigh Conservation Area during my sampling, likely reflecting low population densities combined with limited sampling duration at Chudleigh Conservation Area.

When total pitfall catches are standardized to per-night rates, Chudleigh Conservation Area (93.6 individuals per night) shows values exceeding both Top Bush (83.7 per night) and Caravan Bush (89.8 per night), though still lower than Woolshed Bush (121.0 per night). Patterns in total biomass, mean body mass, and individual size distributions are less affected by this limitation because these metrics reflect the composition and size structure of captured individuals rather than total counts. Additionally, suction sampling effort was equal across all sites (three events each), and these data also showed significant differences in community composition among sites. Future studies should ensure equal sampling effort across all sites or employ approaches such as generalized linear models with offset terms to account for differences in sampling duration.

2.5.5 Temporal Variation in Invertebrate Communities

This study captured invertebrate communities at a single point in time (February-March 2025 across all sites), but prey availability likely varies seasonally in response to weather patterns and invertebrate life cycles (Schlesselmann et al., 2023). Black robin breeding success may depend on prey availability during critical periods such as chick-rearing, which occurs from October through January (Kennedy, 2009), so understanding seasonal dynamics across previously failed and potential future sites is important for assessing habitat suitability.

To partially address this limitation, I replicated sampling at Woolshed Bush and Top Bush on Rangatira Island in November 2024 (Appendix A). Notable differences emerged between sampling periods: for example, cave wētā (Orthoptera) abundance in pitfall traps was substantially lower in November compared to February-March, while ground beetles (Coleoptera) showed the opposite pattern with higher November abundance. Variation was also evident across other invertebrate groups, including smaller-bodied taxa, although the magnitude and direction of these changes varied among groups and sites. Total invertebrate abundance at Woolshed Bush remained stable across seasons, but far fewer invertebrates were trapped in November at Top Bush compared to February. These temporal differences, observed at the same sites under identical sampling protocols, highlight the importance of accounting for seasonal variation when assessing habitat quality for black robins. This is particularly relevant given that black robins likely exploit a range of prey sizes, and that both large- and small-bodied invertebrate groups may fluctuate substantially between the breeding season (spring) and late summer.

Importantly, I did the 2025 sampling across the four sites within the smallest timeframe as logistically possible (three weeks in February-March 2025) to minimize temporal effects on the comparative data presented here. This temporal control strengthens our ability to attribute observed differences among sites to habitat and management factors rather than seasonal variation. However, future work incorporating multi-season sampling across all sites, particularly during the October-January breeding period, would provide a more complete picture of prey resource dynamics and their implications for black robin translocation success.

2.5.6 Conclusion

This study provides the first comprehensive and quantitative analysis of invertebrate communities across the Chatham Islands. In particular, I was able to characterise the invertebrate prey among currently inhabited, previously failed, and future potential black robin translocation sites. While Rangatira Island sites (Woolshed Bush and Top Bush) generally supported higher invertebrate biomass and larger-bodied prey, the results broadly supported predictions while highlighting habitat structure as an additional, potentially important influence. The similarity in invertebrate communities between Woolshed Bush and Top Bush, at least at the coarse taxonomic level I was able to analyse for this study, suggests that prey availability alone may not explain differences in black robin habitat quality, pointing to important factors such as nest site availability and vegetation structure. The lower abundance of large-bodied invertebrate prey like cave wētā from Caravan Bush and Chudleigh Conservation Area, combined with high variability in invertebrate composition within Chudleigh Conservation Area itself, highlights both challenges and opportunities for habitat management to enhance future black robin translocation success.

These findings emphasise the need for holistic habitat assessments considering multiple ecological factors beyond prey abundance. While adequate invertebrate prey, particularly large-bodied taxa, is necessary for black robin populations, prey availability may not be the primary limiting factor at all sites. Rather, a broad suite of habitat requirements should be taken into consideration when selecting and managing sites for black robin recovery. As restoration continues across the Chatham Islands, ongoing monitoring of both invertebrate communities and black robin responses will be essential for adaptive management and successful species recovery.

Chapter 3: Black Robin (*Petroica traversi*) Diet and Foraging Behaviour: Evidence from DNA Metabarcoding and Field Observation

3.1 Abstract

Invertebrate prey availability represents a critical constraint on insectivorous bird populations, yet dietary requirements are often poorly understood for threatened species. This study characterised the diet and foraging ecology of the critically endangered Karure | Kakaruia | Chatham Island black robin (*Petroica traversi)* to inform their conservation. COI DNA metabarcoding of faecal samples ($n = 23$) from Rangatira Island revealed that black robins are generalist insectivores, with Coleoptera (28.6%), Diptera (22.9%), and Orthoptera (19.9%) comprising over 70% of diet. All Orthoptera sequences were assigned to cave wētā (Rhaphidophoridae), detected in 95.7% of samples. Dietary composition showed no significant differences between Woolshed Bush and Top Bush sites (PERMANOVA: $R^2 = 0.05$, $P = 0.42$), indicating consistent resource use across sites. Foraging observations ($n = 202$ from 106 individuals) revealed strong preferences for ground-level substrates, with 82.2% of foraging at ground level, including 46.0% on leaf litter and 35.6% on bare ground. Pouncing (43.6%) and gleaning (32.2%) were the dominant foraging behaviours, with minimal use of higher vegetation strata. Comparison with invertebrate communities (from Chapter 2) revealed that diet composition broadly matched prey availability at the order level, though Coleoptera appeared proportionally more abundant in diet, suggesting possible preference or greater catchability. These findings provide the first metabarcoding-based characterisation of black robin diet and emphasise the importance of intact forest floor environments and abundant ground-dwelling prey, particularly large-bodied taxa like cave wētā, for future black robin translocation success.

3.2 Introduction

Diet is a fundamental aspect of an animal's ecology, directly influencing survival, reproduction, and interactions with the surrounding environment (Gaglio et al., 2017; Sih, 1993; Tang et al., 2023). The food resources that an animal can access and exploit not only shape their immediate fitness, but also their distribution, behaviour, and ultimately their evolution (Gaglio et al., 2017; Parsons, 2005).

For threatened species confined to small ranges, understanding their dietary requirements becomes even more critical for effective conservation management, particularly when using conservation translocations (hereinafter translocations) as a recovery tool (Birnie-Gauvin et al., 2017; Tarszisz et al., 2014). Translocations are defined as the intentional movement of organisms from one location to another (IUCN, 2013) and have become a cornerstone of modern conservation techniques (Seddon & Redford, 2025). Yet, the success of translocations hinges on ensuring that the destination provides the necessary conditions for population success and reproduction (Berger-Tal et al., 2020; Sol et al., 2005). Among these conditions, food availability stands as one of the most important factors to the success of translocated populations (Gooch et al., 2015). Therefore, accurate knowledge of what a species eats, the abundance and diversity of its prey, and whether these resources are available at potential translocation sites, can mean the difference between successful population establishment and failure (Parker, Patterson, et al., 2023).

Historically, studies have relied on direct behavioural observation and stomach content analysis to identify an animal's diet (Cezilly & Wallace, 1988; Gaglio et al., 2017; Rosenberg & Cooper, 1990). Direct observations provide a non-invasive method for studying foraging behaviour but is biased towards large prey items and easily identifiable foraging events, often missing small, cryptic prey or canopy foraging (Dauvin, 2024). This approach also requires extensive field work to capture dietary variation, which can be challenging for elusive species in remote habitats (Cezilly & Wallace, 1988; Lee & Hockey, 2001). Stomach flushing and gut content analysis can provide more detailed taxonomic information and have been valuable for quantifying hard bodied prey, but these methods are often invasive or even lethal, making them less viable for threatened populations (Provencher et al., 2019). They also only provide a snapshot of recent meals and may under-represent soft bodied prey that digest rapidly (Dauvin, 2024).

In the 1970s stable isotope analysis emerged as a modern alternative, using isotope ratios in animal tissues (i.e., feathers or fur) to infer dietary sources (Dauvin, 2024; Prigge et al., 2025). However, stable isotope analysis provides coarse taxonomic resolution, indicating general trophic position and basal resource use from the consumer, rather than species, and requires baseline values for local food webs that may vary seasonally (Inger & Bearhop, 2008; Post, 2002).

The recent emergence of DNA metabarcoding has transformed our ability to characterize animal diets. Metabarcoding uses high-throughput sequencing to identify multiple taxa from genetic material in faecal samples (Ando et al., 2020; Pompanon et al., 2012; Rytkönen et al., 2019). This non-invasive approach can allow taxonomic resolution to genus or species level, even when prey items are completely digested, and can detect cryptic prey items often missed through visual observation (Ando et al., 2020; Deagle et al., 2019). For insectivorous species, where prey items are often small, diverse, and difficult to identify morphologically, metabarcoding represents a key advancement in dietary ecology research. For translocation planning, metabarcoding could be valuable for determining dietary requirements, and this knowledge can then be integrated with invertebrate community surveys at potential sites to evaluate habitat suitability and food resource availability.

The application of metabarcoding on threatened species has revealed critical insights for conservation management, particularly in translocation planning. Metabarcoding revealed seasonal dietary shifts in the critically endangered Rhone streber (*Zingel asper*), with the availability of key prey taxa being essential for selecting potential reintroduction sites and guiding river restoration programmes (Villsen et al., 2022). Spatial dietary variation has also been demonstrated in the declining hawfinch (*Coccothraustes coccothraustes*) populations across six sites in Denmark and Germany, with diet differing significantly between countries and suggesting the species can adapt to spatially varying food sources (Stenhouse et al., 2023). Comparative metabarcoding approaches have simultaneously characterized diets across different declining species, with one study examining six farmland birds inhabiting European cereal pseudo-steppes (little and great bustard, Montagu's harrier, pin-tailed sandgrouse, calandra lark) to assess their conservation requirements (Morales et al., 2023). For little bustard (*Tetrax tetrax*), a highly endangered European steppe bird, metabarcoding during the chick-rearing period identified dietary preferences by comparing prey consumed with prey availability in the study area, providing crucial information for developing effective conservation strategies (Morales et al., 2023). These studies demonstrate that metabarcoding can reveal subtle dietary differences between potential translocation sites, identify key prey taxa essential for population establishment, and assess whether release sites contain adequate food sources.

The karure | kakaruia | Chatham Island black robin (hereinafter black robin), showcases the challenges and opportunities in translocations. This small endemic passerine is one of the world's most celebrated conservation success stories, having recovered from just five individuals with one breeding female ("Old Blue") on Little Mangere | Tapuaenuku | The Fort (hereinafter Little Mangere Island) in the Chatham Islands (Butler & Merton, 1992; Merton, 1993). Following translocations to Maung' Rē | Mangere Island (hereinafter Mangere Island) and Hokorerero | Rangatira | Southeast Island (hereinafter Rangatira island) in 1983, along with cross-fostering with murumuru | miromiro | the Chatham Island tomtit (*Petroica macrocephala*), the population has since increased to ~330 individuals, with Rangatira Island supporting the most birds (Butler & Merton, 1992; Parlato et al., 2025).

Despite their remarkable recovery, black robins remain classified as Nationally Critical due to their low overall abundance and restriction to just two island populations. There is ongoing interest in establishing populations on other islands to increase genetic diversity and population size (Parker, Patterson, et al., 2023; Parlato et al., 2025). However, the failure of a previous translocation attempt to Rangiauria | Rangiaotea | Pitt Island (hereinafter Pitt Island) between 2002 and 2005, where birds failed to establish despite being introduced to an apparently suitable habitat, underscores the importance of understanding all ecological requirements before translocation (Parker, Parlato, et al., 2023)

While black robins are known to be insectivorous ground foragers, feeding primarily on invertebrates from leaf litter, low vegetation, and tree trunks (Aikman & Miskelly, 2004; Kennedy, 2009), the specific taxonomic composition of their diet remains limited. This knowledge gap is significant for habitat assessment for potential translocation sites. Assessments of potential black robin translocation sites have focused primarily on vegetation structure and composition as indicators of habitat suitability and the presence / absence of invasive mammalian predators (Parker, Patterson, et al., 2023). However, vegetation structure and invasive predator presence alone may not capture habitat quality for insectivorous birds, as they do not directly measure invertebrate prey abundance (Mott et al., 2023). Sites that appear structurally similar can support vastly different invertebrate communities due to factors such as soil type, habitat strata, plant species composition, predator presence and abundance, and time since restoration or successional stage (Evans et al., 2003; Fuchs, 2013; Ramey & Richardson, 2017). Without identifying what the black robin eats and confirming that their prey species are abundant at potential translocation sites, vegetation-based habitat assessments and predator monitoring alone cannot reliability predict translocation success.

Rangatira Island provides an ideal site to study the dietary ecology of the black robin in relation to habitat condition. The island supports the largest black robin population with a range of habitat condition ranging from dense mature forests to more open vegetation (Kennedy et al., 2014; Massaro et al., 2018). This vegetation gradient allows us to investigate whether dietary composition changes with habitat condition and the current distribution and abundance of birds across the island. In this chapter, I use DNA metabarcoding of black robin faecal samples collected across Rangatira Island, alongside behavioural foraging observations to provide the first comprehensive characterisation of black robin diet. Specifically, this research aims to: (1) identify the invertebrate prey consumed by black robin, (2) examine whether dietary composition differs significantly between high- and low-condition habitats to reveal potential resource-driven differences in habitat use, (3) compare dietary composition with prey availability (see Chapter Two) to assess whether potential translocation sites provide suitable food resources to support black robin populations, and (4) examine foraging behaviour and habitat strata use in the black robin.

3.3 Materials and Methods

3.3.1 Study Site & Sample Collection

This study focuses on Rangatira Island (44.3471° S, 176.1726° W), which is the third largest island in the Chatham Island archipelago. The island covers 218 hectares (2.18 km^2) and supports ~300 black robins, representing the largest of only two populations of this Nationally Critical species (Parlato et al., 2025). The Department of Conservation Te Papa Atawhai (DOC) designated the island as a Nature Reserve in 1953, and it has been free from introduced predators since 1961, allowing for ecosystem recovery (Roberts et al., 2007). The vegetation on the island is dominated by regenerating mareira parakau | Chatham Island ribbonwood (*Plagianthus chathamicus*), with other canopy species including hakapiri | akeake (*Olearia traversiorum*), matipo (*Myrsine chathamica*), and karamū (*Coprosma chathamica*) (Roberts et al., 2007).

I collected four faecal samples between the 1st and 8th of December 2024 for a pilot study to develop and refine the laboratory methodology described below. Unfortunately, during bioinformatic analysis, I found these samples to be highly contaminated by laboratory products, and they were excluded from further analysis. On Rangatira Island, 33 faecal samples from black robins were collected between January and May 2025 (Figure 3.1). Between the 21st of January to 12th of February, faecal samples (collected by Zita Roithmair and me) were obtained opportunistically through direct observation of individual black robins, with individuals being identified using their unique band combinations. Samples were immediately collected using sterilised spatulas to prevent contamination and placed into sterile collection tubes containing 95% ethanol. Between the 28th of April and 6th of May, 9 samples were collected by Tertia Thurley from cloth bags during DOC (Department of Conservation) post-breeding black robin census banding operations, including five samples from Top Bush and four from Trig/Marlesh that were then stored in 95% ethanol. The four samples from locations outside my study area were included in descriptive dietary analyses but excluded from statistical comparisons between Woolshed and Top Bush habitats due to small sample sizes. All samples were labelled with the bird's band combination, location, date, and time of collection, transported to the University of Waikato, and stored in a -18 °C freezer.

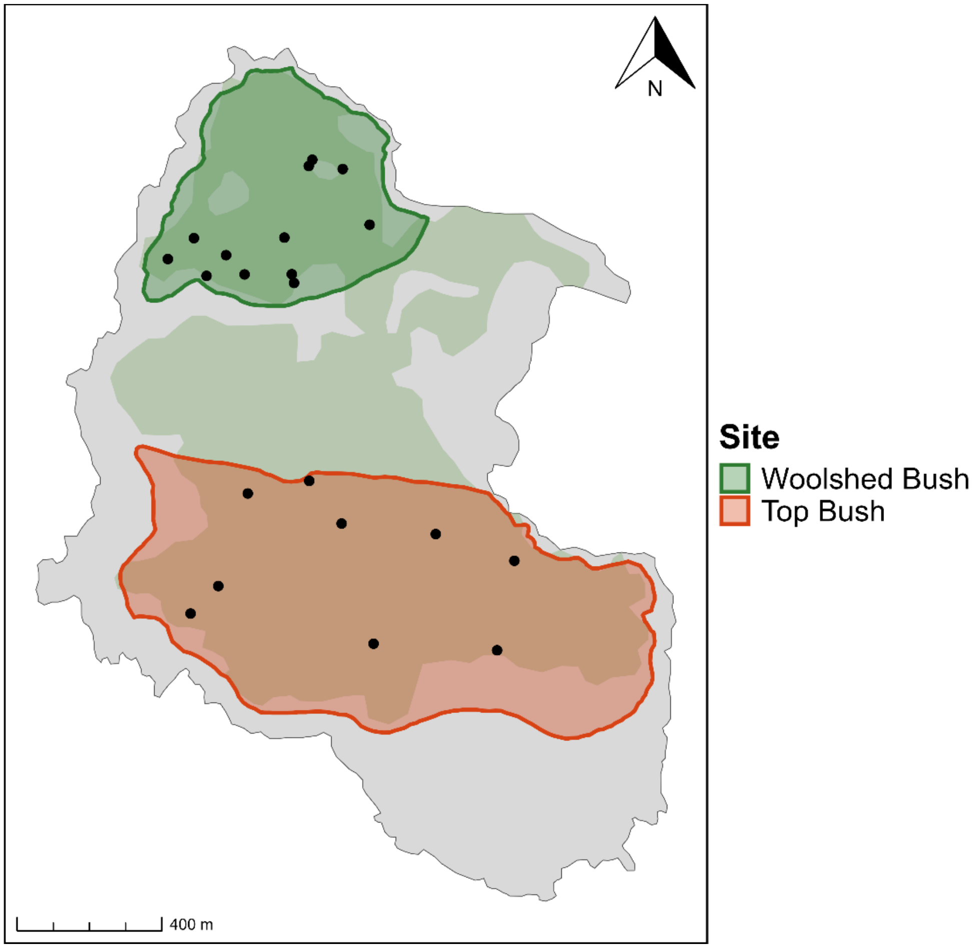

Figure 3.1: Location of faecal samples collected from karure | kakaruia | Chatham Island black robins (*Petroica traversi*) on Hokorereoro | Rangatira | Southeast Island, showing samples with GPS coordinates (n = 21) across Woolshed Bush (green) and Top Bush (orange/red) habitats. Light green areas indicate native vegetation. Samples lacking GPS data are excluded. Scale bar = 400 m.

3.3.2 DNA Extraction

I extracted DNA from the faecal samples collected using the QIamp DNA Stool Mini Kit following the manufactures protocol. I weighed approximately 180-220 mg of the faecal sample into a 2 mL microcentrifuge tube. 1 uL of InhibitEX Buffer was added to each sample, and tubes were vortexed continuously for one minute until homogenised. I then heated the suspension at 70°C, vortexed for 15 seconds, and then centrifuged the sample for one minute at full speed to pellet stool particles.

I added 1.5 uL of Proteinase K was added to a new 1.5 mL microcentrifuge tube, followed by 200 µL of the supernatant from each centrifuged sample. I added 200 µL of Buffer AL and vortexed each mixture for 15 seconds to ensure homogenisation. I incubated each sample at 70°C for 10 minutes, then added 200 µL of ethanol (100%) and mixed by vortexing. I applied the lysate to a QIAamp spin column in 600 µL aliquots, centrifuging for 1 minute between applications until all lysate was loaded. I washed the column with 500 µL Buffer AW1 (centrifuged 1 minute) and 500 µL Buffer AW2 (centrifuged 3 minutes), changing collection tubes between washes. I then transferred the column to a clean 2 mL collection tube and centrifuged for another 3 minutes to remove residual wash buffer.

I eluted DNA by transferring the column to a new, labelled 1.5 mL microcentrifuge tube and applying 200 µL Buffer ATE directly onto the membrane. After incubation for 1 minute at room temperature, I centrifuged each column for 1 minute to collect eluted DNA. I stored extracted DNA at -20°C until PCR amplification.

3.3.3 PCR Amplification

The mitochondrial cytochrome c oxidase subunit I (COI) gene was amplified for metabarcoding analysis to identify invertebrate prey consumed by black robin. I used the primer pair mlCOIintF (forward: 5'-GGWACWGGWTGAACWGTWTAYCCYCC-3') and jgHCO2198 (reverse: 5'-TAIACYTCIGGRTGICCRAARAAYCA-3') which amplifies a ~313 base pair fragment of the COI barcode region for metabarcoding analysis (Leray et al., 2013). PCR reactions were run using 20uL volumes containing 5 μL MyFi Mix, 0.5 μL mlCOIintF primer, 0.5 μL jgHCO2198 primer, 1 μL bovine serum albumin (BSA), 4 μL sample DNA, and 9 μL nuclease-free water.

Thermal cycling conditions were as follows: initial denaturation at 94°C for 10 minutes; 40 cycles of denaturation at 94°C for 20 seconds, annealing at 49°C for 45 seconds, and extension at 72°C for 45 seconds; final extension at 72°C for 5 minutes; and hold at 4°C. Negative controls were included in each PCR run to monitor contamination. PCR products were then visualized on 1.5% agarose gels stained with loading buffer (TrackIt Cyan/Orange) to confirm successful amplification and estimate product size. Successful amplifications showed bands at approximately 313 bp.

3.3.4 Sequencing and Bioinformatics

A total of 36 PCR products showing successful amplification were shipped to Sequench (Nelson, New Zealand) for high-throughput sequencing on an Illumina platform, including 33 black robin faecal samples, two negative extraction controls, and one PCR negative control.

Sequench processed raw FASTQ files through their bioinformatics pipeline. They removed primer sequences using Cutadapt (Martin, 2011) with a 0.1 error rate, minimum 20bp overlap, and discarded reads shorter than 10bp. They then processed sequences in R (R Core Team, 2025) using DADA2 package (Callahan et al., 2016), truncating forward reads to 225 bp and reverse reads to 210 bp. They filtered reads with a maximum expected error (maxEE) of 2, discarding reads not meeting this threshold. They constructed a parametric error matrix, dereplicated and denoised reads using the DADA2 algorithm, merged paired reads with a minimum 10 bp overlap and no mismatches, and removed chimeras using removeBimeraDenovo.

Sequench conducted taxonomic assignment of COI amplicon sequence variants (ASVs) using MEGABLAST against the NCBI nucleotide (nt) database, retrieving up to five top hits per query. They filtered hits for ≥80% query coverage and valid taxonomic assignments. They assigned consensus taxonomy per ASV based on percent identity thresholds: Kingdom ≥71%, Phylum ≥79%, Class ≥81%, Order ≥83%, Family ≥87%, Genus ≥95%, Species ≥97%, retaining the deepest resolved taxonomic level for classification.

Quality control included a contamination subtraction step, where the maximum sequence count detected across negative controls was used as the removal threshold for all samples. Two samples were excluded from downstream analysis: one sample failed to produce sequences, and one sample was removed after subtracting amplicon sequence variants (ASVs) found in negative controls. This resulted in 32 successfully sequenced samples for dietary analysis (15 from Woolshed Bush, 13 from Top Bush, and 4 from Trig/Marlesh).

3.3.5 Metabarcoding Analysis

I conducted all metabarcoding statistical analyses in R Version 4.5.0 (R Core Team, 2025) using the ‘phyloseq’, ‘vegan’, and ‘dplyr’ packages (McMurdie & Holmes, 2013; Oksanen et al., 2025; Wickham et al., 2023). First, I excluded ASVs classified as marine or aquatic taxa (Euphausiacea, Diplostraca, Haplosclerida, Poecilosclerida, Anthoathecata, Leptothecata, Littorinimorpha), which likely represented environmental contamination or sequencing artefacts. I then retained only ASVs classified as terrestrial arthropod classes that constitute potential black robin prey: Insecta (insects), Arachnida (spiders and mites), Collembola (springtails), Chilopoda (centipedes), and Diplopoda (millipedes). This filtering removed sequences from fungi, plants, and other non-prey organisms (such as Rhabditida and Poduromorpha).

Mealworms (*Tenebrio molitor*, family Tenebrionidae) are used to attract black robin during post-breeding census trapping. *Tenebrio* sequences were detected in 7 samples (30% of samples collected during the post-breeding census period) and given that there are no native mealworms in this genus at this site, these detections definitively reflect the feeding of mealworms used as bait. Notably, *Tenebrio* sequences were only detected in samples from the post-breeding census period. However, the majority of Tenebrionidae sequences (88%) could not be identified to genus level and therefore could not be reliably defined as provisioned mealworms versus naturally consumed darkling beetles. Importantly, unidentified Tenebrionidae sequences were detected in samples outside the post-breeding census (n = 3), when no mealworms were provided. As a result, all Tenebrionidae sequences were retained in dietary analyses. This approach may slightly overestimate the natural dietary importance of this family, though native darkling beetles are present on the island.

Following filtering, I rarefied samples to an even sequencing depth of 1,000 reads per sample to account for differences in sequencing coverage. I removed samples with fewer than 1,000 reads prior to rarefaction, retaining 27 samples for subsequent analysis (Woolshed Bush: n = 11, Top Bush: n = 12, and Trig/Marlesh: n = 4). I calculated relative abundance by transforming read count data to proportions, dividing the read count of each taxon by the total number of reads in each sample.

I calculated alpha diversity metrics (observed richness, Chao1 species richness estimator, Shannon diversity index, and Simpson index,) using the phyloseq package. I compared alpha diversity in black robin diet from Woolshed Bush versus Top Bush using independent samples *t*-

tests for observed richness, Chao1 richness estimator, and Shannon diversity index. For the Simpson index, which violated normality assumptions even after log-transformation, I used a Wilcoxon rank-sum test. I present alpha diversity values as means ± standard error. To assess variation in the relative abundance of prey taxa detected in black robin faecal samples, I calculated Bray-Curtis dissimilarity using rarefied data and performed permutational multivariate analysis of variance (PERMANOVA) with 999 permutations to test whether dietary composition differed significantly among sites. I visualized variation in the taxonomic composition of black robin diet using non-metric multidimensional scaling (NMDS) ordination based on Bray-Curtis dissimilarity.

To assess differences in relative abundances of individual prey orders within the faecal samples collected at the two sites, I analysed the top 10 most abundant orders detected in the metabarcoding data. For each Order, I assessed model assumptions through visual inspection of diagnostic plots (Q-Q plots and residuals vs. fitted values). Orders violating these assumptions were log-transformed and re-tested. I used independent t-tests for data meeting parametric assumptions (either originally or after transformation) and Wilcoxon rank-sum tests only when transformation failed to achieve normality. I applied Benjamini-Hochberg correction for multiple comparisons across all order-level tests, such that adjusted p-values < 0.05 were considered statistically significant.

To assess how closely the composition of black robin diet based on faecal analysis reflected available prey on Rangatira Island, I compared the taxonomic composition of prey detected in faecal samples with invertebrate community data collected from Woolshed Bush and Top Bush in 2025. I combined invertebrate data from three sampling methods: pitfall traps, emergence traps, and suction sampling. See Chapter 2 for details on how those invertebrate samples were collected.

For metabarcoding data, I calculated relative abundance at the order level by first transforming sample counts to proportions, then collapsing ASVs to order using taxonomic agglomeration. I identified the top 10 most abundant orders across all faecal samples based on total read abundance and calculated the mean relative abundance of each order at each location (Woolshed Bush, Top Bush, and Trig/Marlesh). For the invertebrate sampling data, I calculated the relative abundance of each order as the proportion of individuals captured at each location across all sampling methods combined. To represent true prey availability, I included all orders detected in the invertebrate samples. This approach allowed assessment of whether black robins selectively consumed prey orders relative to their environmental availability. I visualized the comparison using stacked bar charts showing the top 10 dietary orders alongside the complete invertebrate community composition (all orders) at each site.

3.3.6 Behavioural Sampling

Understanding foraging site preferences is essential for habitat management decisions and assessing habitat suitability for this critically endangered species. I conducted behavioural observations of black robins in November 2024 on Rangatira Island (Figure 3.2) to determine where they forage most frequently across different substrates, heights, and habitat types. Observations were conducted between 8am and 5pm throughout the day.

Observations took place within known territories of the black robin, identified through consultation with DOC staff. Following McLean et al. (1994), I used focal sampling to record foraging behaviour. Once a black robin was located and identified by its unique band combination, I maintained an approximately five-metre distance to minimise disturbance. I began observations only after birds resumed normal foraging activity, indicated by cessation of chirping and the bird actively searching for prey rather than focusing on the observer. After each observation I moved to a different territory to avoid repeated observations of the same individual as much as possible.

During each five-minute observation period, I collected data on foraging location, substrate type, habitat quality, and prey handling. Foraging location was categorised by height above ground: ground (0 m), low (0-4 m), or high (4-6 m). Substrate type was recorded as bare ground, leaves (leaf litter), bark, or air (i.e. they caught prey on the wing) (Figure 3.3). Habitat quality was classified as high (Woolshed Bush) and low (Top Bush). I recorded foraging behaviours using an ethogram adapted from Perera and Kotagama (2013) and descriptions from Kennedy (2009) (Table 3.1), which included behaviours such as gleaning, probing, and hawking. Where possible, for each foraging attempt I noted whether prey was captured and subsequently eaten or carried away.

For each observation, I recorded the GPS location and environmental conditions to characterize foraging habitat. Canopy cover was estimated visually as percentage cover directly overhead. Light conditions were categorized as full sun, dappled shade, or full shade. Wind speed was estimated using a five-point scale (0-5). Daily temperature data was obtained from a thermometer located outside the DOC hut on Rangatira Island. Litter depth was measured at one point within a 2m radius around each observation.

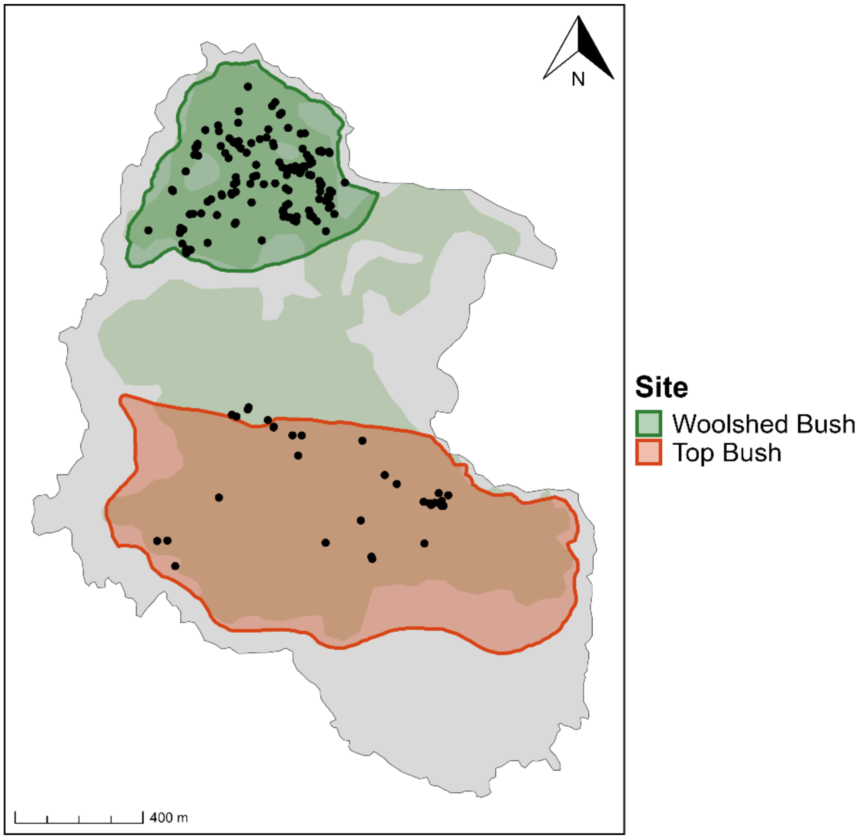

Figure 3.2: Location of foraging behaviour observations for karure | kakaruia | Chatham Island black robins (*Petroica traversi*) on Hokorereoro | Rangatira | Southeast Island. Each point represents a GPS-recorded behavioural observation across Woolshed Bush (green, n = 168) and Top Bush (orange/red, n = 34) habitats. Light green areas indicate native vegetation. Scale bar = 400 m.

Table 3.1: Ethogram defining karure | kakaruia | Chatham Island black robin (*Petroica traversi*) feeding behaviours used during behavioural observations. Definitions were applied consistently to classify foraging actions observed in the field.

Behaviour	**Description**
Gleaning	Removing insects or small invertebrates directly from leaves, twigs, bark, or other surfaces while perched or moving slowly through vegetation.

Hawking	Capturing insects in sustained flight without an immediate return to a perch.
Pouncing	Dropping from a perch or flying a short distance to capture prey on the ground.
Probing	Using the beak to dig into soft substrates (like soil or leaf litter) to extract hidden invertebrates.
Sallying	Flying out from a perch to capture an airborne insect and immediately returning to the same or a nearby perch.
Pecking	Delivering a single, rapid strike with the bill at prey located on the ground or on exposed surfaces, without substrate manipulation.
Hover-gleaning	Hovering briefly near foliage, bark, or other surfaces to remove insects from otherwise inaccessible locations.
Flicking	Flipping leaves, small twigs, or debris on the ground to expose hidden insects.
Courtship Feed	Receiving food from another black robin, typically during pair bonding or breeding contexts.

Figure 3.3: Karure | kakaruia | Chatham Island black robins (*Petroica traversi*) showing typical (A) ground foraging on leaf litter, (B) perching on branch substrate at mid-height, (C) bark gleaning behaviour on tree trunk, and (D) low-height perching with distinctive leg bands visible for individual identification. These images illustrate the range of foraging heights (ground to 4-6m) and substrate types (leaf litter, bark, branches) recorded during behavioural observations.

3.3.7 Statistical Analysis of Foraging Observations

I calculated the frequency and proportion of foraging observations for substrate type, foraging height, and foraging behaviour at each study site (Top Bush and Woolshed Bush). Rare substrate categories (Courtship Feed and Grass, n = 6) were combined as 'Other' for analysis. To test whether foraging patterns differed between sites, I used a series of multinomial logistic regressions with site as the fixed effect for three response variables: (1) substrate type (ground, leaves, bark, other), (2) foraging height (ground 0 m, low 0-2 m, mid 2-4 m), and (3) foraging behaviour (gleaning, pouncing, probing, etc.). Model significance was assessed using likelihood ratio tests. Although 46% of individuals were observed multiple times (mean = 1.9 observations per bird), I used standard multinomial regression rather than mixed models because the nnet::multinom function does not support random effects and alternative multinomial GLMM packages have significant convergence issues. Given the low number of repeat observations per individual, any bias from non-independence likely has minimal effects.

Sex was not included as a predictor due to insufficient data (83% of all observations were from birds of unknown sex). Environmental variables (canopy cover, litter depth, wind) were compared between sites using *t*-tests. Statistical significance was assessed at $\alpha = 0.05$. Analyses were conducted in R 4.5.0 using nnet (Venables & Ripley, 2002).

3.4 Results

3.4.1 Dietary Composition

Metabarcoding of black robin faecal samples yielded 1,303,472 total sequences, of which 84.4% could be classified to order level, 64.8% to family level, and 32.2% to genus level. While genus-level resolution was limited by the representation of Chatham Island invertebrates in global sequencing databases, family-level classification (64.8%) provided sufficient taxonomic detail to identify key dietary components beyond order level (Figure 3.5). All subsequent dietary analyses were conducted primarily at order level to maximize sample coverage while maintaining taxonomic resolution.

Metabarcoding analysis revealed that the black robin diet was dominated by three orders: Coleoptera (beetles), Diptera (flies), and Orthoptera. On Rangatira Island, all Orthoptera are wētā, represented exclusively by the family Rhaphidophoridae (cave wētā), with two genera detected: *Talitropsis* (primarily *T. megatibia*) and *Novoplectron* (*N. serratum*) at both high quality

(Woolshed Bush) and low quality (Top Bush) habitats (Figure 3.4, Table 3.2). These three orders comprised over 70% of black robin diet and were detected in more than 90% of samples. Lepidoptera (moths and butterflies), Hymenoptera (ants and parasitoid wasps), Hemiptera (true bugs), and Scolopendromorpha (centipedes) contributed smaller but consistent proportions to their dietary makeup. The remaining three orders Sarcoptiformes (mites), Poduromorpha (springtails), and Araneae (spiders) each comprised less than 1% of the diet and occurred in fewer than half of the samples analysed.

Family-level analysis revealed substantial taxonomic diversity within the dominant orders at Woolshed and Top Bush (Figure 3.5). Within Coleoptera, the most abundant families were Curculionidae (weevils), Tenebrionidae (darkling beetles), and Staphylinidae (rove beetles). Diptera families included Tachinidae (parasitoid flies), Heleomyzidae Chloropidae (grass flies), Calliphoridae (blow flies), and Agromyzidae (leaf-miner flies). Lepidoptera sequences included Oecophoridae, Noctuidae, and Nepticulidae. Hemiptera was represented by Cicadidae and Meenoplidae. As noted above, Orthoptera sequences were exclusively assigned to Rhaphidophoridae (cave wētā), with no representation of other orthopteran families. Within Hymenoptera, sequences were dominated by ants (Formicidae, primarily the endemic *Chelaner antarcticus*), with parasitoid wasps (Ichneumonidae, Braconidae) also detected; no bee sequences (Apidae) were found.

Several notable taxa were identified at high taxonomic resolution. Cicadas (Cicadidae, primarily *Kikihia longula*) comprised 0.79% of the overall diet but were detected in 82.6% of samples, suggesting consistent opportunistic consumption when available. Two additional *Kikihia* species were identified: *K. paxillulae* and *K. nelsonensis*. Samples collected from Trig/Marlesh (n = 4) showed Coleoptera, Diptera, and Orthoptera as dominant orders, but with proportionally more

Hemiptera and Scolopendromorpha and relatively fewer Diptera and Orthoptera compared to Woolshed and Top Bush (Figure 3.4), though the small sample size warrants caution with interpretation.

Comparison of the dietary composition of faecal samples to the invertebrate communities quantified in Chapter 2 revealed that while the three dominant orders in the diet (Coleoptera, Diptera, and Orthoptera) broadly align with some of the most abundant orders available, there were notable differences suggesting selective foraging. Black robins consumed proportionally more Coleoptera and Orthoptera (particularly cave wētā) relative to their availability in pitfall traps, while Diptera appeared to be consumed far less than expected given their abundance in invertebrate surveys. Hymenoptera (primarily ants) comprised a substantial portion of the diet at Woolshed Bush despite their apparent low capture in the invertebrate community. Notably, amphipods, a dominant proportion of the invertebrate fauna especially at Top Bush, were largely absent from the diet, suggesting black robins avoid these taxa despite their availability.

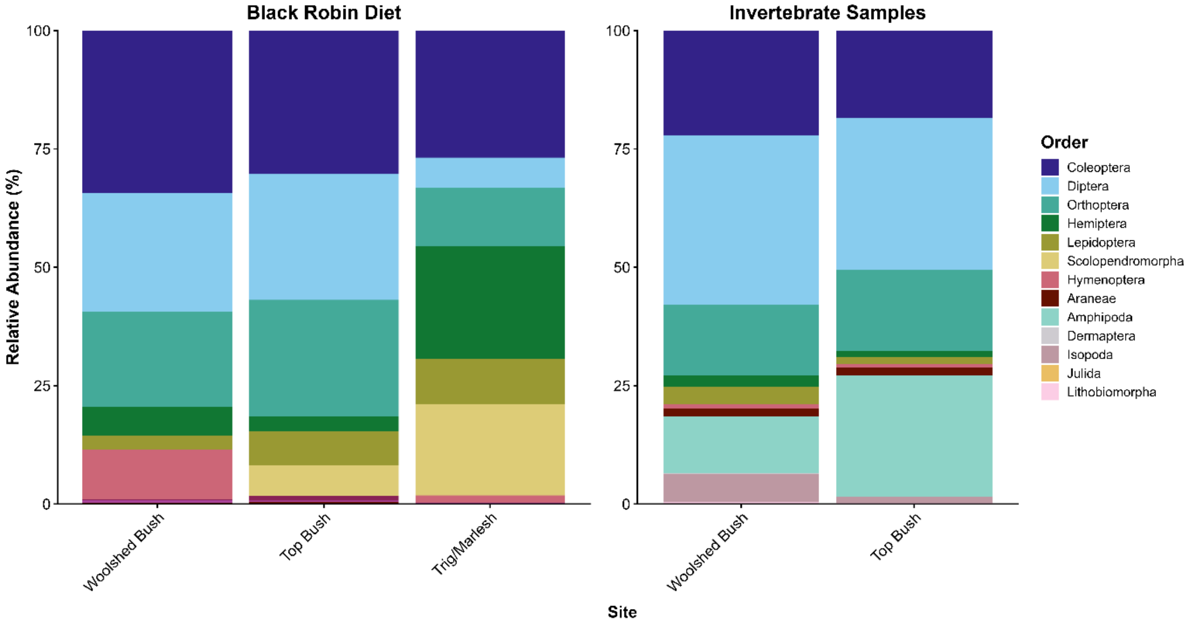

Figure 3.4: Relative abundance (%) of invertebrate orders detected via metabarcoding of black robin faecal samples and invertebrate sampling (emergence traps, suction sampling, and pitfall traps). Left panel shows relative abundance of the top 10 orders detected in faecal samples via

metabarcoding from Woolshed Bush (n = 11 samples), Top Bush (n = 12), and Trig/Marlesh (n = 4). Right panel shows all orders captured through invertebrate sampling at Woolshed Bush and Top Bush, representing complete prey availability.

Table 3.2: Mean relative abundance and frequency of occurrence of invertebrate orders detected in black robin faecal samples through metabarcoding (n = 23 samples). Frequency represents the percentage of faecal samples in which each order was detected. Only the top 10 most abundant orders are shown.

Order	Mean Abundance (%)	SE	Frequency (%)
Coleoptera	27.7	6.4	96.3
Diptera	20.5	5.3	92.6
Orthoptera	18.3	4.7	92.6
Hemiptera	6.4	3.0	74.1
Scolopendromorpha	5.0	3.2	11.1
Lepidoptera	4.9	1.3	92.6
Hymenoptera	4.0	3.5	29.6
Sarcoptiformes	0.4	0.3	25.9
Poduromorpha	0.3	0.2	22.2
Araneae	0.3	0.2	25.9

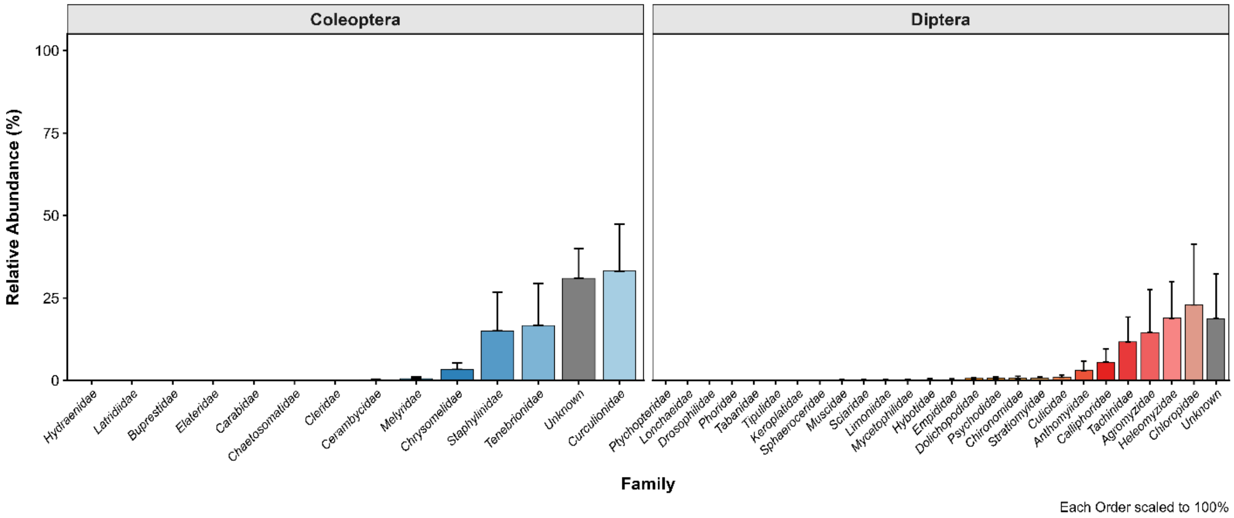

Figure 3.5: Family-level composition within the two dominant orders in black robin diet. Bars represent the proportion of each family within its order (scaled to 100% per order), with error bars showing standard error. Data are from Woolshed Bush, Top Bush, and Trig/Marlesh (n = 27 samples). "Unknown" categories represent specimens identified only to order level.

3.4.2 Diversity Analysis

Alpha diversity metrics showed no significant differences between Woolshed Bush and Top Bush (Figure 3.6, Table 3.3). Observed richness was similar between sites, as was the Chao1 richness estimator. Shannon diversity, which accounts for both richness and evenness, also did not differ significantly between sites. Similarly, there was no significant difference in Simpson diversity between sites. These results indicate that black robin diets at both sites contain similar numbers of invertebrate orders with comparable evenness in their distribution. Samples from Trig/Marlesh (n = 4) were excluded from statistical comparisons due to small sample size but are shown in Figure 3.6 for visual comparison.

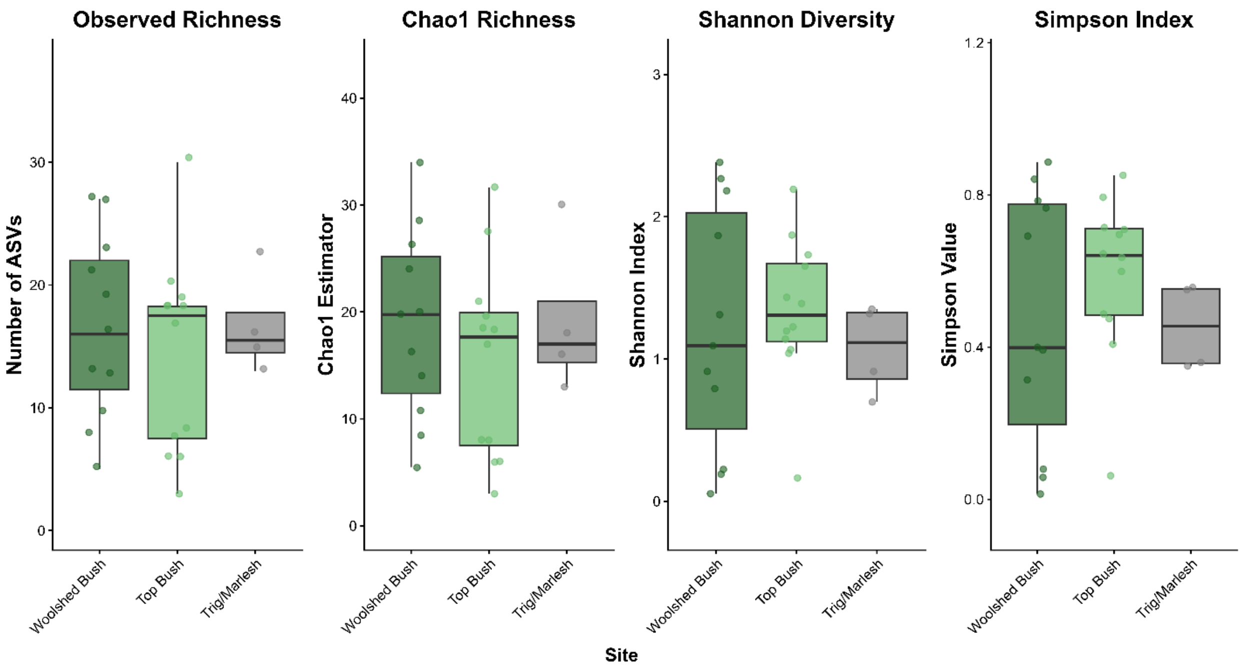

Figure 3.6: Alpha diversity metrics across three sites on Rangatira Island. Boxplots show the distribution of (A) observed richness, (B) Chao1 richness estimator, (C) Shannon diversity index, and (D) Simpson diversity index for black robin diet composition sampled at Woolshed Bush (dark green, n = 11), Top Bush (light green, n = 12), and Trig/Marlesh (grey, n = 4). Each panel displays the median (horizontal line), interquartile range (box), range (whiskers), and individual samples (jittered points).

Table 3.3: Alpha diversity metrics (mean ± SE) and statistical comparisons between Woolshed Bush (n = 11) and Top Bush (n = 12) sites. Independent samples *t*-tests were used for Observed Richness, Chao1, and Shannon Diversity; Wilcoxon rank-sum test (W) was used for Simpson Index.

Metric	Woolshed Bush (SE)	Top Bush (SE)	Test Statistic	p-value
Observed Richness	16.5 ± 2.3	14.2 ± 2.3	t = 0.71	0.485
Chao1 Richness	18.9 ± 2.7	15.4 ± 2.6	t = 0.93	0.364
Shannon Diversity	1.21 ± 0.26	1.34 ± 0.15	t = -0.46	0.651
Simpson Index	0.48 ± 0.10	0.59 ± 0.06	W = 54.0	0.487

3.4.3 Diet Community Composition

NMDS ordination of order-level prey composition revealed substantial overlap in diet community composition between Woolshed Bush and Top Bush (Figure 3.7). PERMANOVA analysis confirmed no significant difference in dietary composition between sites (Table 3.4). The low R^2 value indicates that site location explained only 4.6% of the variation in invertebrate community composition, with the remaining variation related to unmeasured factors.

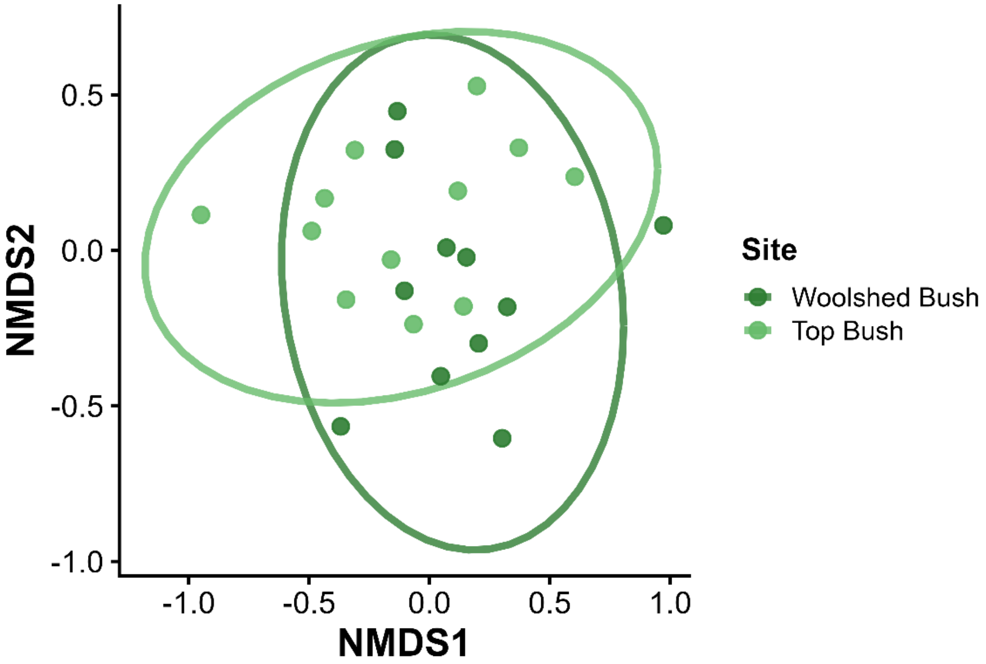

Figure 3.7: Non-metric multidimensional scaling (NMDS) ordination of black robin dietary composition at order level, based on Bray-Curtis dissimilarity of prey taxa detected in faecal samples. Each point represents an individual faecal sample from Woolshed Bush (dark green, n = 11) or Top Bush (light green, n = 12). Ellipses show 95% confidence intervals for each site. Stress = 0.228

Table 3.4: PERMANOVA results testing for differences in black robin dietary composition between Woolshed Bush and Top Bush, based on Bray-Curtis dissimilarity of order-level prey taxa detected in faecal samples. Analysis used 999 permutations.

Term	Df	Sum of Squares	R^2	F-value	p-value

Site	1	0.39	0.05	1.01	0.42
Residual	21	8.04	0.95		
Total	22	8.43	1.00		

3.4.4 Individual Order Comparison

Individual prey orders showed no significant differences in relative abundance between Woolshed Bush and Top Bush sites (Table 3.5). The three most abundant orders (Coleoptera, Diptera, and Orthoptera) which together comprised over 70% of the diet, showed particularly similar abundances between sites. Similarly, less abundant orders showed no significant differences between sites, including Hemiptera, Lepidoptera, and Hymenoptera. The remaining four orders (Scolopendromorpha, Sarcoptiformes, Poduromorpha, and Araneae), which each comprised less than 1% of the diet, also showed no significant site differences. These results are consistent with the overall lack of dietary differentiation detected in the community-level analysis (Section 3.4.3).

Table 3.5: Statistical comparisons of invertebrate order relative abundances between Woolshed Bush (n = 11) and Top Bush (n = 12) sites. Orders are ranked by most to least abundant. Test statistics: W = Wilcoxon rank-sum test statistic; t = t-test statistic (indicates test performed on log-transformed data). P-values were adjusted for multiple comparisons using the Benjamini-Hochberg method.

Order	Test Statistic	p-value	Adjusted p-value
Coleoptera	W = 66.000	1.000	1.000
Diptera	W = 64.000	0.926	1.000
Orthoptera	t = -0.637	0.531	0.979

Lepidoptera	t = -1.148	0.264	0.979
Hymenoptera	W = 79.000	0.396	0.979
Hemiptera	W = 88.000	0.185	0.979
Scolopendromorpha	W = 60.000	0.563	0.979
Sarcoptiformes	W = 66.000	1.000	1.000
Poduromorpha	W = 67.000	0.971	1.000
Araneae	W = 74.000	0.587	0.979

3.4.5 Foraging Analysis

A total of 202 foraging observations were recorded from 106 individually banded and unbanded black robins. The majority of observations were made at Woolshed Bush (n = 168), with fewer Top Bush (n = 34). Of the observed individuals 69 were males, 26 were females, and 103 were of unknown sex. Overall, black robins foraged predominately on the ground (82.2% of observations; Figure 3.8B) and on leaf litter (46.0%) or bare ground (35.6%), with bark gleaning comprising 15.3% of foraging attempts (Figure 3.8A). The most common foraging behaviours were pouncing (43.6% of observations) and gleaning (32.2%), with probing (5.0%), sallying (5.4%), and hover-gleaning (3.0%) occurring less frequently (Figure 3.8C). Prey handling was dominated by immediate consumption, accounting for 94.6% of observations, while prey transport occurred in only 5.4% of observations. Environmental measurements at foraging locations revealed no significant differences between sites in canopy cover (p = 0.966) or litter depth (p = 0.338; Table 3.6). Wind conditions differed slightly between sites (p = 0.039).

Substrate use differed significantly between sites ($\chi^2 = 8.50$, p = 0.037; Figure 3.8 A; Table 3.7). Bark foraging was 2.4 times more common at Top Bush (29.4%) than Woolshed Bush

(12.5%), while leaf gleaning showed the opposite pattern (Top Bush: 32.4%, Woolshed Bush: 48.8%). Foraging height showed a marginal trend toward more above-ground foraging at Top Bush, consistent with increased bark use. Foraging behaviour composition did not differ between sites ($p = 0.190$; Figure 4.4 C), indicating that robins maintained similar prey capture techniques despite using different substrates.

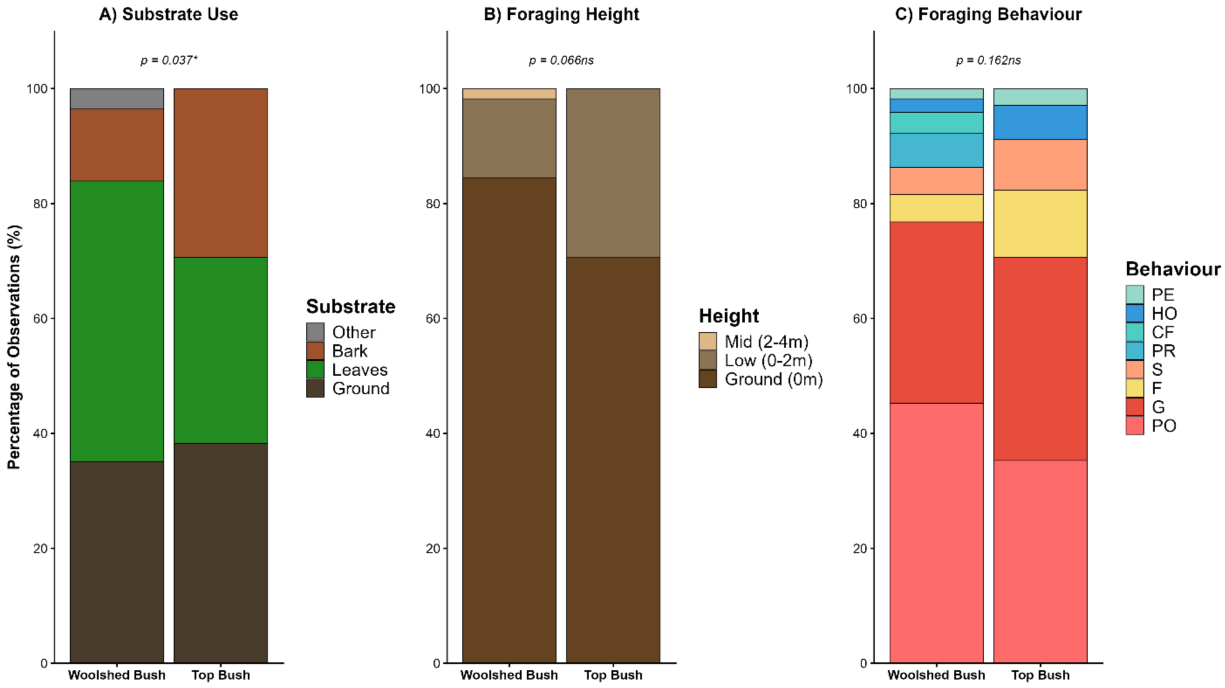

Figure 3.8: Foraging substrate use, height, and behaviour of black robins at Woolshed Bush and Top Bush sites on Rangatira Island, November 2024. Stacked bars show the percentage of foraging observations in each category for (A) substrate type, (B) foraging height, and (C) foraging behaviour type. The asterisk indicates a significant difference between sites from multinomial logistic regression (*$p < 0.05$), while the ns indicates no significance. Sample sizes: Woolshed Bush $n = 168$, Top Bush $n = 34$ observations from 106 individuals. Rare substrate categories (courtship feed and grass, $n = 6$ total) were combined as "Other" for statistical analysis. Foraging behaviours are PE = pecking, HO = hover gleaning, CF = courtship feed, PR = probing, S = sallying, F = flicking, G = gleaning, and PO = pouncing.

Table 3.6: Environmental characteristics at foraging locations for black robins at Woolshed Bush and Top Bush sites.

Variable	Woolshed Bush (mean ± SD)	Top Bush (mean ± SD)	t-statistic	df	p-value
Canopy cover (%)	81.9 ± 15.5	82.0 ± 9.0	-0.04	78.5	0.966
Litter depth (cm)	1.1 ± 1.1	0.9 ± 1.1	0.97	46.6	0.338
Wind (ordinal scale)	1.2 ± 0.9	0.9 ± 1.0	2.12	45.6	**0.039**

Table 3.7: Statistical comparison of foraging substrate, height, and behaviour between Woolshed Bush and Top Bush sites on Rangatira Island, November 2024. Values are count (percentage). Multinomial logistic regression was used to test for site differences in each category. "Other" substrate includes courtship feed and grass. Significant P-values are highlighted in bold.

Foraging Substrate

Category	Woolshed Bush n (%)	Top Bush n (%)	Total n (%)	χ^2	df	p-value
Substrate Type				8.50	3	**0.037**
Leaves	82 (48.8)	11 (32.4)	93 (46.0)			
Ground	59 (35.1)	13 (38.2)	72 (35.6)			
Bark	21 (12.5)	10 (29.4)	31 (15.3)			
Other	6 (3.6)	0 (0.0)	6 (3.0)			
Subtotal	**168 (100)**	**34 (100)**	**202 (100)**			

Foraging Height

Category	Woolshed Bush n (%)	Top Bush n (%)	Total n (%)	χ^2	df	p-value
Foraging Height				5.43	2	0.066

Ground (0 m)	142 (84.5)	24 (70.6)	166 (82.2)			
Low (0-2 m)	23 (13.7)	10 (29.4)	33 (16.3)			
Mid (2-4 m)	3 (1.8)	0 (0.0)	3 (1.5)			
Subtotal	**168 (100)**	**34 (100)**	**202 (100)**			

Foraging Behaviour

Category	**Woolshed Bush n (%)**	**Top Bush n (%)**	**Total n (%)**	**χ²**	**df**	**p-value**
Foraging Behaviour				11.22	8	0.190
Pouncing	76 (45.2)	12 (35.3)	88 (43.6)			
Gleaning	53 (31.5)	12 (35.3)	65 (32.2)			
Probing	10 (6.0)	0 (0.0)	10 (5.0)			
Sally	8 (4.8)	3 (8.8)	11 (5.4)			
Courtship Feed	6 (3.6)	0 (0.0)	6 (3.0)			
Hover	4 (2.4)	2 (5.9)	6 (3.0)			
Peck	3 (1.8)	1 (2.9)	4 (2.0)			
Flick	8 (4.8)	5 (11.7)	12 (6)			
Subtotal	**168 (100)**	**34 (100)**	**202 (100)**			

3.5 Discussion

This study addresses the critical gap in knowledge of the life history of the black robin by combining DNA metabarcoding of faecal samples with dietary behavioural observations to characterise black robin diet and foraging ecology on Rangatira Island. The findings suggest that black robins are generalist insectivores, consuming a diverse range of invertebrate prey dominated by beetles (Coleoptera), flies (Diptera), and wētā (Orthoptera). Black robins demonstrated consistent foraging behaviour across the two habitats, primarily foraging at ground level, with slight differences in some behaviours, such as bark gleaning at Top Bush. While this study focused on the black robin population found on Rangatira Island, it did not include Mangere Island, where a small but crucial population has experienced recent decline and struggles to establish other territories within Mangere Island (Parker, Parlato, et al., 2023). Repeated studies of invertebrate communities and prey availability between these islands would provide valuable insights into factors potentially limiting black robin success at Mangere (discussed further in Chapter 4).

3.5.1 Dietary Composition and Prey Availability

DNA metabarcoding revealed that black robins consume a taxonomically diverse range of invertebrate prey, with three Orders, Coleoptera (beetles), Diptera (flies), and Orthoptera (wētā), comprising over 70% of their diet. This finding aligns with previous observational records from McLean *et al* (1994), Kennedy (2009), and DOC staff, indicating that black robins are wholly insectivorous and consume many invertebrate taxa including beetles, moths, wētā, worms, flies, and caterpillars.

Within these dominant orders, family-level analysis revealed that weevils (Curculionidae) and darkling beetles (Tenebrionidae) were the most abundant Coleopteran families preyed upon, while Diptera were represented by parasitoid flies (Tachinidae), true flies (Heleomyzidae), and grass flies (Chloropidae). Notably, all Orthopteran sequences were assigned to Rhaphidophoridae (cave wētā), with two species *Talitropsis megatibia* and *Novoplectron serratum* detected at high frequency (96% of samples), while no ground wētā (family Anostostomatidae) sequences were detected despite this family potentially occurring on Rangatira Island. This diet composition appears broadly consistent with other New Zealand forest passerines. North and South Island robins (*Petroica australis*) similarly consume predominantly Coleoptera, Diptera, and Lepidoptera larvae, with beetles and wētā forming important dietary components (Steer, 2006).

However, family-level comparisons with invertebrate sampling reveal selective foraging patterns. Ground beetles (Carabidae) were the most abundant Coleopteran family in pitfall traps yet were rarely detected in faecal samples, suggesting active avoidance potentially due to defensive chemical compounds common in this family (Bonacci, 2025). Conversely, weevils and darkling beetles, which lack such defences, were consumed more frequently than their relative abundance in samples would predict.

The prevalence of Coleoptera, Diptera, and Orthoptera in black robin diet broadly matches their relative abundance in invertebrate sampling on Rangatira Island (Chapter 2), suggesting opportunistic foraging at the order level. However, closer examination reveals selectivity within these orders. Cave wētā appear to be consumed disproportionately relative to their abundance in pitfall traps, indicating potential selection of these large-bodied, high-quality prey items. Similarly, Coleoptera are slightly overrepresented in diet compared to invertebrate samples, though this pattern could be driven by consumption of specific families (Curculionidae, Tenebrionidae) rather than beetles as a whole. This suggests black robins employ a mixed foraging strategy: opportunistically consuming abundant prey orders while selectively targeting energetically valuable prey within those orders.

An important limitation of DNA metabarcoding is the inability to determine prey life stage. For example, lepidoptera could represent caterpillars or adult moths, while cave wētā may be consumed across multiple development stages that vary dramatically in body size. Understanding whether robins selectively target large-bodied prey has direct implications for translocation planning, as larger prey provide greater caloric return (Nyffeler et al., 2018). Black robins are highly trainable (Van Horik & Burns, 2007), presenting opportunities for feeding trials to test prey size preferences and complement metabarcoding approaches.

The relatively low success in identifying dietary items below the order level (32.2% to genus) reflects the limited representation of Chatham Island invertebrates in global reference databases, a common challenge in metabarcoding studies of endemic island fauna (Keck et al., 2023; Watts et al., 2019). Despite this limitation, metabarcoding provided substantially more dietary information than traditional observation methods could achieve for a small forest species. Behavioural observations conducted during this study highlighted this challenge. Black robins frequently foraged in dense vegetation where prey were obscured and consumed items too rapidly for identification Similar metabarcoding approaches have successfully characterized diets of other insectivorous birds, revealing dietary diversity and flexibility that would be difficult to detect through visual observation alone (Stenhouse et al., 2023; Villsen et al., 2022). Continued development of Chatham Island-specific reference databases would substantially improve future metabarcoding studies and enable more detailed dietary analyses. Species-level identification would improve translocation planning by identifying specific invertebrate taxa critical for black robin persistence and enable monitoring of dietary responses to environmental change or management interventions.

However, DNA metabarcoding of faecal samples has inherent biases that may influence dietary interpretation. Although all invertebrates have exoskeletons, differential DNA degradation rates can lead to underrepresentation of taxa with softer or thinner exoskeletons (e.g., caterpillars, some spiders) relative to heavily sclerotized prey such as adult beetles or wētā, potentially inflating the apparent importance of Coleoptera and Orthoptera in metabarcoding results (Deagle et al., 2019; Pompanon et al., 2012). Additionally, PCR amplification bias may favour certain taxonomic groups depending on primer specificity (Piñol et al., 2015), and variation in prey biomass versus DNA quantity means that read abundance does not directly translate to dietary proportions by mass (Thomas et al., 2016). These methodological biases should be considered when interpreting the dominance of Coleoptera and Orthoptera in black robin diet, as the technique may underrepresent certain prey types while overrepresenting others. Despite this limitation, metabarcoding remains a powerful tool for characterising the diets of small species and provides insights that would be impossible to obtain through observation alone.

Comparison of dietary composition with invertebrate community sampling (Chapter 2) revealed both similarity and selectivity in prey consumption. At the order level, Coleoptera, Diptera, and Orthoptera were dominant in both diet and invertebrate samples, indicating that black robins largely consume prey in proportion to availability. However, closer examination revealed potential selectivity patterns. Coleoptera appear proportionally more abundant in their diet (28.6%) compared to their representation in invertebrate samples, suggesting possible preference for beetles or their greater detectability during foraging (Razeng & Watson, 2015). Conversely, Diptera were proportionally more abundant in environmental samples than in dietary data (22.9% of diet), potentially indicating avoidance of certain fly taxa or reduced capture success for highly mobile aerial prey. Although these results are insightful, these patterns must be interpreted cautiously, as they are based on order-level data. Higher resolution family and genus level analyses would be needed to definitively showcase prey selectivity.

3.5.2 Dietary Differentiation Between Habitat Types

Black robin diet showed no significant differences between Woolshed Bush and Top Bush at the order level of taxonomic resolution used in this study. Alpha diversity values (observed richness, Chao1 richness estimator, Shannon diversity, and Simpson index) between sites were statistically indistinguishable, and PERMANOVA confirmed no significant differences in overall dietary composition. This finding suggests that both sites may provide similar access to invertebrate prey at the broad taxonomic level examined here. However, these results do not necessarily indicate that both habitats provide adequate prey resources for black robin populations, as we lack a reference baseline for what constitutes sufficient prey availability for black robin. Additionally, similar dietary composition does not account for potential differences in foraging effort—black robins at one site may require substantially more time and energy to capture comparable prey, a fitness cost that would be undetectable through faecal analysis alone.

Interestingly, while mean dietary diversity did not differ significantly between sites, individual variation in diet composition was greater at Woolshed Bush than Top Bush, as shown by the wider spear in Shannon and Simpson diversity indices (Figure 3.6). This suggests that individual black robins at Woolshed Bush exhibited more variation in foraging strategies, with some consuming more diverse prey while others showed more specialised diets. This individual variation could reflect differences in foraging experience, habitat strata use, or individual preference which may influence population resilience to prey community shifts (Mansor & Mohd Sah, 2012).

Three key methodological limitations may explain the lack of dietary differentiation between sites. First, our classification of "habitat quality" was based on black robin abundance patterns reported by DOC management staff rather than measured environmental variables. While field observations during invertebrate sampling noted differences in forest structural characteristics between sites (canopy cover, litter depth, vegetation composition), these were not formally measured or statistically tested. Furthermore, invertebrate community analysis (Chapter 2) found no significant differences in invertebrate abundance or diversity between Woolshed Bush and Top Bush, suggesting that perceived habitat differences may not translate to differences in prey availability. Without systematic habitat assessment incorporating canopy cover measurements, vegetation surveys, and litter depth transects, the assumption that sites differ meaningfully in quality for black robins remains unvalidated, and we cannot definitively conclude that black robins show dietary consistency across a habitat gradient.

Second, the relatively small spatial scale between Woolshed Bush and Top Bush (separated by ~600m of continuous forest) likely allows invertebrate dispersal between sites, reducing prey community differentiation. With no distinct habitat boundaries and similar tree species composition, the sites essentially represent different areas within a contiguous forest rather than discrete habitat types (Auger et al., 2024). Additionally, black robins are territorial but mobile within their territories (Kennedy, 2009; McLean et al., 1994) , and individuals may forage across habitat gradients within their home ranges, further homogenizing site-level differences. Studies of insectivorous birds across larger habitat gradients have revealed dietary shifts associated with environmental differences (Arazmi et al., 2025; Mitchell et al., 2022), but such shifts may not occur over smaller spatial scales or more subtle habitat gradients.

Third, the coarse taxonomic resolution (order-level) used in both dietary and invertebrate community analyses limits our ability to detect finer-scale differences in prey composition or selectivity that could exist at the family or genus level. The lack of differentiation between sites could also reflect the generalist feeding ecology of black robins, which consume a wide range of invertebrate prey. Kennedy (2009) suggested that New Zealand *Petroica* species are relatively generalist insectivores compared to more specialized congeneric species elsewhere, and the taxonomic range observed in this study supports this claim.

Black robins demonstrated strong preferences for specific foraging substrates and heights, with ground-level foraging among leaf litter being their preferred strategy. This behavioural pattern is consistent with the natural history of the *Petroica* species, including the South Island robin (*P. australis*), North Island robin (*P. longipes*), and Chatham Island tomtit (*P. macrocephala chathamensis*), all of which are primarily ground foraging insectivores adapted for searching leaf litter and low vegetation for prey (Boulton, 2006; Kennedy, 2009; McLean et al., 1994). The marginally non-significant trend in substrate use between habitats ($p = 0.054$) warrants careful interpretation. In the low-quality habitat (Top Bush), bark foraging was more common (29.4%) compared to the high-quality habitat (Woolshed Bush) (12.5%), potentially reflecting differences in bark invertebrate communities or vegetation structure between sites. This pattern could reflect subtle behavioural plasticity in response to local prey distributions, with black robins adjusting foraging substrates while maintaining their overall dietary composition. However, the small sample size from low quality habitat ($n = 34$ observations) limits the statistical power to detect differences, and this result should be interpreted cautiously, highlighting the need for replication with larger sample sizes.

These findings have important implications for black robin conservation and future translocation efforts. Black robins demonstrated consistent foraging behaviour across the two study sites, with strong reliance on ground-level leaf litter foraging and limited use of higher vegetation strata. This behavioural consistency, combined with the generalist diet composition (consuming 10+ invertebrate orders), suggests that black robins may be able to establish successfully in a range of forest habitats provided that specific structural requirements are met: intact leaf litter layers, accessible ground-level foraging substrates, and sufficient invertebrate prey availability in lower forest strata (Parker, Patterson, et al., 2023; Stone et al., 2025).

3.5.3 Temporal and Seasonal Considerations

This study's temporal scope limits our understanding of how black robin diet and foraging behaviour may vary throughout the year. Foraging observations were conducted during a single month (November 2023) during the pre-breeding period, while dietary samples spanned September 2023 to March 2024, capturing periods from pre-breeding through chick-rearing and fledging. However, we did not analyse dietary differences across these breeding phases, preventing assessment of how nutritional demands during egg production, incubation, and chick provisioning may influence prey selection. Seasonal variation in invertebrate availability is well documented in temperate ecosystems (Gerlach et al., 2013; Tonkin et al., 2017), and invertebrate sampling on Rangatira Island (Chapter 2) revealed significant differences in prey community composition between November and February, suggesting that black robins likely experience substantial seasonal variation in prey availability. Understanding how black robins respond to these fluctuations, whether through dietary shifts, increased foraging effort, or behavioural plasticity would require sampling across complete annual cycles and multiple breeding phases.

During the pre-breeding period (courtship and nesting), many passerine species increase consumption of calcium rich prey to support egg production, with females showing dietary shifts towards gastropods and other calcium sources (Reynolds & Perrins, 2010). Whether black robins exhibit similar pre-breeding dietary shifts remains unknown, as our dietary samples were collected during chick-rearing and post-fledging periods (December 2023–March 2024) rather than during the pre-breeding phase when such shifts would be most pronounced. Throughout incubation, when adult birds maintain extended periods on the nest, foraging efficiency becomes critical, and prey selection may favour high-energy items that can be captured quickly during brief foraging bouts (Conway & Martin, 2000; Rohwer & Purcell, 2019). Post-breeding, when adults provision nestlings and fledglings, dietary composition often shifts toward larger, more protein-rich prey items, and foraging intensity increases substantially (García-Navas & Sanz, 2011). Samples collected during the chick-rearing and post-fledging periods (December 2023–March 2024) may therefore represent a time of increased foraging activity, potentially masking seasonal constraints that could influence habitat suitability during more demanding phases of the annual cycle.

Additionally, seasonal invertebrate phenology may create temporal bottlenecks in prey availability. Winter, when invertebrate abundance typically reaches its annual minimum in temperate forests, may represent the most critical period for assessing habitat quality and prey sufficiency (Lv et al., 2023; Razeng & Watson, 2015). If black robins can maintain adequate nutrition during winter, when prey is scarce, this would provide strong evidence of habitat suitability year-round. Conversely, habitats that appear adequate during summer may prove insufficient during winter if key prey taxa become unavailable or energetic demands exceed prey supply.

Integrating dietary data with individual reproductive success and survival across seasons would shed light on whether dietary similarity between habitats translates to fitness outcomes. For example, two sites showing similar summer diets might differ substantially in overwinter survival rates, nestling provisioning rates, or fledgling success if seasonal prey availability or quality varies between them. Future research should therefore sample across multiple seasons and breeding stages and ideally link dietary composition to demographic parameters (clutch size, hatching success, fledgling survival) to assess whether diet adequately predicts habitat quality for population persistence.

For translocation planning, these considerations suggest that habitat assessments should extend beyond single-season snapshots. Ideally, potential translocation sites should be evaluated across multiple seasons, with particular attention to winter prey availability and breeding-season provisioning rates. Where year-round assessment is not feasible, winter sampling should be prioritized, as this season likely represents the most demanding test of habitat adequacy for black robin populations.

3.5.4 Conclusion

This study demonstrates that black robins on Rangatira Island are generalist insectivores with diverse diets primarily made up of beetles, flies, and wētā. The lack of dietary and behavioural differentiation between high- and low-quality habitats suggests dietary flexibility in resource use which may have contributed to the species successful population recovery over the past four decades (Butler & Merton, 1992; Parker, Parlato, et al., 2023). Black robins forage predominantly at ground level on leaf litter and ground substrates, emphasizing the importance of intact forest floor environments for this species.

These findings provide crucial baseline data for ongoing conservation efforts and future translocation planning. While black robin showcase tolerance for some habitat variation, successful translocations will require careful attention to prey availability, forest structure, and exclusion of mammalian predators. The methods developed in this study, combining DNA metabarcoding of faecal samples with behavioural observations, provide a repeatable framework for assessing habitat stability at potential translocation sites and monitoring responses in translocated populations.

The black robin's recovery from five individuals in the 1980s to approximately 350 today represents one of New Zealand conservation's greatest success stories, but securing the species' long-term future requires establishing additional populations across suitable habitats (Butler & Merton, 1992; Parlato et al., 2025). By demonstrating that black robins can maintain consistent diets across habitat gradients, this research provides optimism that well-selected translocation sites can support viable populations, bringing this iconic species one step closer to full recovery.

Chapter 4:   General Discussion

4.1 Key Findings

This study provides the first comprehensive quantitative assessment of invertebrate prey communities and black robin foraging ecology across current, previously failed, and potential future translocation sites on the Chatham Islands. In response to a request from the Black Robin Technical Advisory Group, this research addresses critical knowledge gaps by integrating standardised invertebrate sampling (Objective 1), DNA metabarcoding (Objective 2), behavioural observations (Objective 3), and comparative analysis of black robin diet and prey availability (Objective 4) to provide evidence-based information to advise conservation management (Objective 5).

Chapter 2 quantified invertebrate communities across currently inhabited Woolshed Bush and Top Bush (Rangatira | Southeast Island [hereinafter Rangatira island]), previously failed Caravan Bush (Pitt Island), and future potential translocation site Chudleigh Conservation Area (Chatham Island), revealing that predator free sites (Woolshed Bush and Top Bush) supported significantly higher ground-active invertebrate biomass than Caravan Bush and Chudleigh Conservation Area. However, Chudleigh Conservation Area was sampled for five nights compared to six nights at other sites, which limits direct comparison of total abundance. This difference was driven by large-bodied cave wētā (181–205 mg) and ground beetles (112–244 mg), which were abundant at Rangatira but largely absent from Caravan Bush and Chudleigh Conservation area. Body mass distributions extended to 742 mg at predator-free sites (Woolshed Bush and Top Bush) versus predominantly <50 mg at predator-present sites (Caravan Bush and Chudleigh Conservation Area). Critically, Woolshed Bush and Top Bush showed similar invertebrate communities despite differing black robin densities, indicating that prey availability alone does not explain habitat quality.

Chapter 3 characterised black robin diet and foraging ecology, demonstrating that black robins are generalist insectivores with Coleoptera, Diptera, and Orthoptera comprising over 70% of diet. Dietary composition showed no significant differences between Woolshed Bush and Top Bush, indicating consistent resource use across habitat gradients. Foraging observations revealed overwhelming preference for ground-level substrates (82.2% of observations), particularly leaf litter (46.0%) and bare ground (35.6%), with minimal use of higher strata.

4.2 Black Robin Diet and Prey Availability

Black robin diet was dominated by Coleoptera (28.6%), Diptera (22.9%), and Orthoptera (19.9%). These three orders were also the most abundant in invertebrate community samples at Rangatira Island, suggesting that black robins forage primarily on abundant prey taxa. However, the relative proportions differ between diet and environmental availability. Coleoptera appeared proportionally more abundant in diet compared to invertebrate samples, potentially indicating preference for beetles or their greater detectability during foraging. Conversely, Diptera were proportionally more abundant in invertebrate samples than in diet, potentially reflecting avoidance of certain taxa or reduced success of foraging for aerial prey. These patterns must be interpreted cautiously given the coarse taxonomic resolution (order-level), as finer-scale selectivity at family or genus level may exist but cannot be detected with current data.

However, similar invertebrate communities at Woolshed Bush and Top Bush despite different black robin densities indicate that adequate prey is necessary but not sufficient for population establishment. Other factors such as nest cavity availability, vegetation structure, or territory quality likely become limiting once minimum prey thresholds are met (Kennedy, 2009; Lawrence et al., 2017; Massaro et al., 2013). This interpretation should also be viewed cautiously because habitat quality classification relied on field observations and Department of Conservation documents rather than systematic quantitative measurements of forest structure, and because both invertebrate and dietary analyses were conducted at coarse taxonomic resolution (order-level), which may obscure finer-scale habitat-related differences. Despite this limitation, the finding remains critical for translocation planning: sites must meet requirements across multiple ecological dimensions, not just prey abundance alone.

4.3 Habitat Features

Based on comparative analysis across sites, several habitat features and prey community characteristics emerged as associated with black robin foraging and diet. Cave wētā (Rhaphidophoridae) were abundant at current black robin sites (Woolshed Bush: n = 93, mean mass 181 mg; Top Bush: n = 82, mean mass 205 mg) but largely absent from previously failed (Caravan Bush) and potential translocation sites (Chudleigh Conservation Area). While at least one cave wētā species (*Talitropsis megatibia*) is known to occur on Pitt Island and has been recorded at Caravan Bush, it appears to be rare at that site (Trewick, 1999). These large-bodied prey (exceeding 100 mg mean body mass) provide high energetic returns per foraging event, which likely explains their dominance in black robin diet (Nyffeler et al., 2018). The availability and consumption of high-energy prey may be particularly important during energetically demanding periods such as chick provisioning, when adults must increase foraging efficiency to meet nestling nutritional requirements (García-Navas & Sanz, 2011; Razeng & Watson, 2015).

Sites lacking such large-bodied prey may still support black robin persistence if overall invertebrate biomass is sufficient, but reproductive success and population growth rates may be compromised by reduced foraging efficiency (Catry et al., 2013; Kennedy, 2009). Linking dietary composition to individual fitness outcomes, reproductive success, nestling growth rates, fledgling survival, and adult body condition, would better quantify the functional importance of these prey taxa and remains a priority for future research.

Cave wētā populations are likely to respond positively to ongoing habitat restoration efforts at sites such as Caravan Bush, potentially recovering to provide suitable prey for insectivorous birds such as the black robin. Should habitat quality continue to improve sufficiently, such sites may become viable for future black robin translocations. Sites lacking abundant large-bodied prey may still support black robin persistence if overall invertebrate biomass is sufficient, but reproductive success and population growth rates may be compromised by reduced foraging efficiency (Catry et al., 2013; Kennedy, 2009).

Foraging observations revealed that 82.2% of foraging occurred at ground level, with 46.0% specifically targeting leaf litter and 35.6% on bare ground. This strong ground substrate preference emphasises the importance of intact forest floor environments with leaf litter, exposed ground surfaces, and low vegetation structure accessible for pouncing and gleaning behaviours. Sites with degraded forest floors, reduced litter due to browsing or disturbance, or altered ground-layer vegetation may fail to provide ideal foraging conditions even if invertebrate prey are present, as prey accessibility and detection probability influence foraging efficiency regardless of prey abundance (Razeng & Watson, 2015).

The near-complete absence of large-bodied invertebrates at predator-present sites (Caravan Bush and Chudleigh Conservation Area) demonstrates that invasive mammals can exert strong selective pressure on invertebrate communities, eliminating prey taxa that are both vulnerable to predation and nutritionally valuable for black robins (Watts et al., 2022). This pattern aligns with evidence from Aotearoa | New Zealand ecosystems showing that introduced mammals, particularly mice and rats, selectively prey on large-bodied invertebrates (Norbury et al., 2023; Watts et al., 2022). Beyond indirect effects on prey availability, mammalian predators also pose threats to black robins through nest predation and predation on adults, particularly during vulnerable life stages such as incubation when birds are constrained to nest sites (King, 2023; Lawrence et al., 2017).

4.4 Site Assessments

Woolshed Bush and Top Bush on Hokorereoro | Rangatira | Southeast Island represent reference conditions with mature forest, predator-free status, and abundant large-bodied prey (cave wētā) absent from Caravan Bush and Chudleigh Conservation Area (Roberts et al., 2007). The similarity in invertebrate communities between these sites, despite different black robin densities, indicates that once minimum prey thresholds are met, other factors likely affect nest cavity availability, vegetation structure, or territory quality, become limiting. Future translocation sites need not perfectly replicate these communities, provided they meet minimum prey requirements and offer suitable breeding habitat.

Caravan Bush on Rangiauria | Rangiaotea | Pitt Island showed severely lower prey communities: 60% lower ground-active biomass than Rangatira, very low abundance of cave wētā (0 detected vs. 93 at Woolshed Bush), and body masses compressed toward <50 mg. These deficiencies that may be attributable to ongoing mice and cat presence, likely contributed to translocation failure by decreasing foraging efficiency and exposing birds to predation (Parker, Patterson, et al., 2023). Revised efforts to remove or reduce predators from this site will be important for invertebrate recovery, and ongoing monitoring of invertebrate communities following predator management will be critical for evaluating whether prey availability improves sufficiently to support future translocation attempts.

Chudleigh Conservation Area on Rēkohu | Wharekauri | Chatham Island showed lower total biomass (though with one fewer sampling night), absence of cave wētā, and high spatial variability reflecting varying habitat quality. However, ongoing restoration (predator control, native planting) indicates improvement potential (Parker, Patterson, et al., 2023). This site represents a longer-term prospect requiring continued habitat management, sustained predator control, monitoring for large-bodied invertebrate colonisation, and assessment of whether natural recovery is sufficient or if invertebrate translocation may be necessary to establish robust prey populations as well as nest cavity assessment. Ultimately, where assessments reveal suitable habitat structure but potentially inadequate populations of key prey taxa (particularly cave wētā and large-bodied Coleoptera), invertebrate translocations prior to black robin release should be considered to establish self-sustaining prey populations before introducing predators (Holland et al., 2006).

4.5 Future Research Directions

This study revealed several key knowledge gaps that warrant future investigation. Year-round sampling at multiple sites, with particular emphasis on winter when invertebrate abundance is likely most restricted and breeding seasons when chick provisioning demands are highest, would capture seasonal dynamics in prey availability and dietary requirements that may be critical for translocation success but could not be addressed in this study.

A very important limitation of this study is the focus solely on Rangatira Island. While Rangatira Island does support the majority of the black robin population, Maung' Rē | Mangere Island (hereinafter Mangere Island) hosts a small but important population for population recovery (Parker, Parlato, et al., 2023; Parker, Patterson, et al., 2023). The Mangere population has faced issues with black robin remaining in certain areas of the island (K. Parker, personal communication, 2025) and not establishing other apparently more suitable habitats (Parker, Patterson, et al., 2023). Systematic comparison of invertebrate communities, prey availability, and black robin diet between Rangatira Island and Mangere Island could reveal whether invertebrate communities differ between islands and whether prey limitation contributes to the lack of success in populations on Mangere Island.

Enhanced taxonomic resolution through family- or genus-level identification of key prey groups (Coleoptera, Diptera, Orthoptera) would enable detection of finer-scale prey selectivity patterns and community differences. The current study achieved genus-level identification for only 32.2% of metabarcoding sequences, highlighting the need for comprehensive DNA metabarcoding barcode libraries for Chatham Island invertebrate fauna. The invertebrate specimens collected in Chapter 2 provide an ideal foundation for developing such DNA barcode libraries for the Chatham Islands, benefiting not only black robin conservation but broader ecological research and biosecurity efforts across the Chatham Islands.

Linking diet composition to fitness outcomes also represents a critical research gap. Relating individual dietary composition (via faecal metabarcoding) with reproductive success, nestling growth rates, fledgling survival, and adult body condition would contextualise the functional importance of large-bodied prey taxa. This would establish more refined habitat quality thresholds based on demographic outcomes rather than prey availability alone. Additionally, long-term monitoring of sites undergoing predator management would reveal trajectories for invertebrate community recovery, particularly recolonisation of large-bodied taxa, informing realistic expectations for when sites like Caravan Bush might become viable translocation prospects.

The black robin's recovery from the brink of extinction represents one of conservation's most remarkable achievements, yet with all individuals confined to two small islands, the species remains critically vulnerable. This thesis builds on the ecological foundation necessary for the next phase of black robin conservation: establishing populations beyond Rangatira and Mangere Islands. By starting to reveal the dietary flexibility, foraging preferences, and prey requirements of black robins, this research demonstrates that successful range expansion is achievable with careful site selection and evidence-based planning. The integrated assessment framework developed here offers conservation managers a practical tool for evaluating translocation sites, bringing the black robin one step closer to long-term security and continuing its extraordinary conservation legacy.

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Appendices

Appendix A: Invertebrate Community Data from 2024 Sampling

Invertebrate samples collected from Woolshed Bush and Top Bush on Rangatira Island in 2024. These data are excluded from cross-site comparisons due to seasonal differences (see Section 2.3.4).

Table A1: Total invertebrate abundance and taxonomic richness across four sites representing different black robin habitats: Woolshed Bush and Top Bush (current habitats).

Site	Total Individuals	Total Orders	Total Families
Woolshed Bush 2024	774	12	17
Top Bush 2024	357	11	18

Table A2: Summary statistics for invertebrate orders captured by suction sampling in 2024, arranged from most to least abundant at each site. Mean body mass (± SD, mg), min (mg), max (mg), and sample size (abundance) are shown for each family at each site (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area).

Woolshed Bush 2024				
Order	**Abundance**	**Mean ± SD**	**Min Mass**	**Max Mass**
Diptera	74	3.14 ± 1.90	0.80	12.48
Hemiptera	25	7.09 ± 3.97	2.50	15.51
Lepidoptera	23	7.18 ± 21.39	0.80	105.11

Coleoptera	2	5.36 ± 0.08	5.30	5.42
Araneae	1	3.61	3.61	3.61

Top Bush 2024

Order	Abundance	Mean ± SD	Min	Max
Diptera	25	3.84 ± 2.27	0.41	11.36
Hemiptera	20	8.98 ± 3.41	4.59	14.04
Lepidoptera	15	4.92 ± 8.65	1.12	35.57
Coleoptera	7	29.77 ± 60.05	2.65	165.24
Araneae	1	1.96	1.96	1.96

Table A3: Summary statistics for invertebrate orders captured by emergence traps in 2024, arranged from most to least abundant at each site. Mean body mass (± SD, mg), min (mg), max (mg), and sample size (abundance) are shown for each family at each site (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area).

Woolshed Bush 2024

Order	Abundance	Mean ± SD	Min	Max
Diptera	224	8.90 ± 13.78	1.18	75.80
Coleoptera	66	19.21 ± 40.53	2.52	230.10

Amphipoda	49	10.81 ± 6.89	2.45	29.17
Isopoda	19	8.08 ± 5.05	2.12	21.27
Lepidoptera	15	13.04 ± 15.87	1.69	51.80
Hemiptera	5	7.00 ± 4.42	3.61	14.48
Orthoptera	3	75.10 ± 39.24	32.65	110.04
Hymenoptera	2	8.74 ± 5.47	4.87	12.60
Araneae	1	20.34	20.34	20.34

Top Bush 2024

Order	Abundance	Mean ± SD	Min	Max
Diptera	119	5.27 ± 10.23	1.09	71.43
Coleoptera	32	29.94 ± 38.67	1.92	141.71
Lepidoptera	5	3.45 ± 2.54	1.09	7.21
Amphipoda	2	9.80 ± 1.02	9.08	10.53
Araneae	2	27.13 ± 31.18	5.09	49.18
Hymenoptera	2	3.18 ± 0.14	3.08	3.28
Isopoda	2	6.75 ± 2.26	5.15	8.35

Orthoptera	1	210.66	210.66	210.66

Table A4: Summary statistics for invertebrate orders captured by pitfall traps in 2024, arranged from most to least abundant at each site. Mean body mass (± SD, mg), min (mg), max (mg), and sample size (abundance) are shown for each family at each site (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area).

Woolshed Bush 2024

Order	**Abundance**	**Mean ± SD**	**Min**	**Max**
Coleoptera	109	49.83 ± 140.76	0.36	1,032.74
Amphipoda	93	9.94 ± 7.47	1.38	46.32
Orthoptera	28	225.75 ± 308.56	4.36	1,220.04
Isopoda	24	14.88 ± 10.78	3.90	44.02
Diptera	3	1.96 ± 0.32	1.65	2.28
Araneae	2	8.24 ± 0.72	7.73	8.75
Haplotaxida	2	51.04 ± 14.34	40.89	61.18
Julida	2	3.55 ± 3.23	1.27	5.83
Collembola	1	0.44	0.44	0.44
Hemiptera	1	5.72	5.72	5.72

Top Bush 2024				
Order	**Abundance**	**Mean ± SD**	**Min**	**Max**
Amphipoda	57	8.47 ± 5.56	1.56	30.41
Coleoptera	44	35.68 ± 71.93	2.36	327.38
Diptera	8	1.72 ± 2.60	0.27	8.01
Isopoda	6	11.28 ± 12.84	4.36	37.27
Orthoptera	5	254.42 ± 275.62	1.03	572.80
Collembola	2	0.80 ± 0.03	0.78	0.82
Araneae	1	49.54	49.54	49.54
Haplotaxida	1	3.55	3.55	3.55

Table A5: Summary statistics for invertebrate families captured by pitfall traps in 2024, arranged from most to least abundant at each site. Mean body mass (± SD, mg), min (mg), max (mg), and sample size (abundance) are shown for each family at each site (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area).

Woolshed Bush 2024				
Family	**Abundance**	**Mean ± SD**	**Min**	**Max**
Talitridae	93	9.94 ± 7.47	1.38	46.32

Zopheridae	78	10.28 ± 8.87	2.21	48.30
Rhaphidophoridae	28	225.75 ± 308.56	4.36	1,220.04
Armadillidae	23	15.16 ± 10.93	3.90	44.02
Carabidae	12	151.56 ± 153.91	2.50	351.09
Curculionidae	9	5.84 ± 2.91	1.88	11.94
Tenebrionidae	5	503.66 ± 378.83	212.87	1,032.74
Staphylinidae	4	55.59 ± 39.33	0.36	92.00
Dolichopodidae	3	1.96 ± 0.32	1.65	2.28
Haplotaxida	2	51.04 ± 14.34	40.89	61.18
Julidae	2	3.55 ± 3.23	1.27	5.83
Linyphiidae	2	8.24 ± 0.72	7.73	8.75
Cerambycidae	1	17.52	17.52	17.52
Entomobryidae	1	0.44	0.44	0.44
Hemiptera	1	5.72	5.72	5.72
Styloniscidae	1	8.35	8.35	8.35
Top Bush 2024				

Family	Abundance	Mean ± SD	Min	Max
Talitridae	57	8.47 ± 5.56	1.56	30.41
Zopheridae	29	4.31 ± 1.33	2.36	7.01
Carabidae	8	68.03 ± 105.22	13.51	327.38
Armadillidae	5	12.66 ± 13.84	4.45	37.27
Rhaphidophoridae	5	254.42 ± 275.62	1.03	572.80
Sciaridae	5	0.58 ± 0.24	0.27	0.94
Curculionidae	3	108.81 ± 90.46	10.75	189.00
Entomobryidae	2	0.80 ± 0.03	0.78	0.82
Tenebrionidae	2	226.55 ± 11.53	218.40	234.70
Dolichopodidae	1	1.97	1.97	1.97
Empipidae	1	0.85	0.85	0.85
Haplotaxida	1	3.55	3.55	3.55
Lycosidae	1	49.54	49.54	49.54
Staphylinidae	1	86.95	86.95	86.95
Styloniscidae	1	4.36	4.36	4.36

Tipulidae	1	8.01	8.01	8.01
Trogossitidae	1	34.12	34.12	34.12

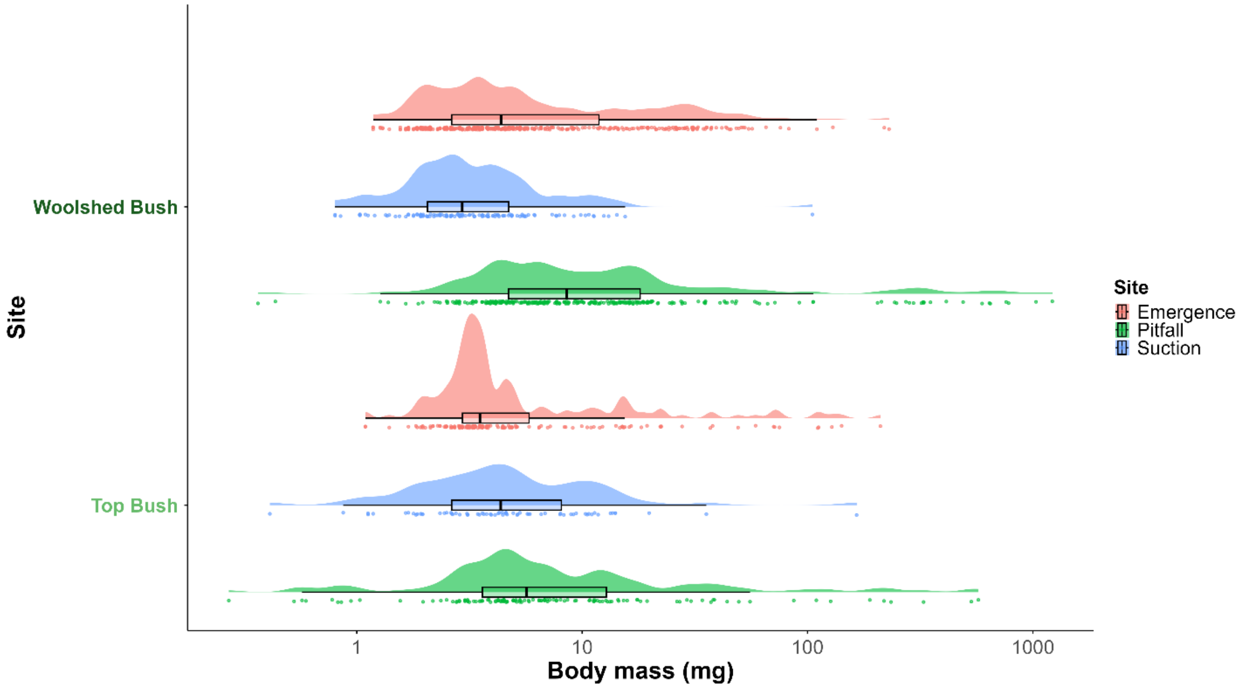

Figure A1: Distribution of individual invertebrate body masses (mg) in 2024 from three habitat strata: understory vegetation (suction), belowground (emergence), and soil surface (pitfall) at four sites. Site names are color-coded to indicate habitat quality for black robin translocation: dark green (current high-quality), light green (current low-quality). Plots combine kernel density distributions (half-violins), boxplots (median, interquartile range, and 1.5× IQR whiskers), and individual data points.

Appendix B: Statistical Analysis Outputs

Table B1: PERMANOVA results testing for differences in invertebrate community composition among sites (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area) for three sampling methods: suction sampling (understory), emergence, and pitfall (soil surface).

Method	Df	Sum of Squares	R^2	F-value	p-value
Suction	3	1.29	0.29	2.74	**0.007**
Emergence	3	1.10	0.24	2.03	**0.024**
Pitfall	3	2.42	0.40	4.47	**0.001**

Table B2: Homogeneity of multivariate dispersion tests (betadisper) for invertebrate community composition among sites (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area) for three sampling methods: suction sampling (understory), emergence, and pitfall (soil surface).

Method	Df (Groups)	Df (Residuals)	Sum of Squares	Mean Square	F-value	p-value
Suction	3	20	0.17	0.06	2.81	0.057
Emergence	3	19	0.19	0.06	2.64	0.068
Pitfall	3	20	0.09	0.03	1.13	0.347

Table B3: Tukey's HSD post-hoc test results comparing log transformed invertebrate abundance between sites (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area) for each sampling method (Emergence, Pitfall, and Suction). All significant results are highlighted in bold.

Method	Contrast	Estimate	SE	df	t.ratio	p-value
Emergence	Woolshed Bush - Top Bush	0.810	0.41	59	1.975	0.209

	Woolshed Bush - Caravan Bush	0.005	0.41	59	0.013	1.000
	Woolshed Bush - Chudleigh Conservation Area	0.326	0.43	59	0.758	0.873
	Top Bush - Caravan Bush	-0.805	0.41	59	-1.962	0.214
	Top Bush - Chudleigh Conservation Area	-0.484	0.43	59	-1.125	0.675
	Caravan Bush - Chudleigh Conservation Area	0.321	0.43	59	0.745	0.878
Pitfall	Woolshed Bush - Top Bush	-0.095	0.41	59	-0.231	0.996
	Woolshed Bush - Caravan Bush	1.779	0.41	59	4.338	**<0.001**
	Woolshed Bush - Chudleigh Conservation Area	1.600	0.41	59	3.901	**0.001**
	Top Bush - Caravan Bush	1.874	0.41	59	4.569	**<0.001**
	Top Bush - Chudleigh Conservation Area	1.695	0.41	59	4.132	**<0.001**

	Caravan Bush - Chudleigh Conservation Area	-0.179	0.41	59	-0.437	0.972
Suction	Woolshed Bush - Top Bush	0.458	0.41	59	1.116	0.681
	Woolshed Bush - Caravan Bush	-0.370	0.41	59	-0.903	0.803
	Woolshed Bush - Chudleigh Conservation Area	0.564	0.41	59	1.376	0.519
	Top Bush - Caravan Bush	-0.828	0.41	59	-2.019	0.193
	Top Bush - Chudleigh Conservation Area	0.107	0.41	59	0.260	0.994
	Caravan Bush - Chudleigh Conservation Area	0.935	0.41	59	2.279	0.115

Table B4: Tukey's HSD post-hoc test results comparing log-transformed invertebrate abundance between sampling method (Emergence, Pitfall, and Suction) at four sites (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area). All significant results are highlighted in bold.

Site	**Contrast**	**Estimate**	**SE**	**df**	**t.ratio**	**p-value**
	Emergence - Pitfall	0.532	0.41	59	1.297	0.403

Woolshed Bush	Emergence - Suction	2.041	0.41	59	4.978	**<0.001**
	Pitfall - Suction	1.510	0.41	59	3.681	**0.001**
Top Bush	Emergence - Pitfall	-0.373	0.41	59	-0.909	0.637
	Emergence - Suction	1.689	0.41	59	4.118	**<0.001**
	Pitfall - Suction	2.062	0.41	59	5.028	**<0.001**
Caravan Bush	Emergence - Pitfall	2.306	0.41	59	5.622	**<0.001**
	Emergence - Suction	1.666	0.41	59	4.062	**<0.001**
	Pitfall - Suction	-0.640	0.41	59	-1.560	0.271
Chudleigh Conservation Area	Emergence - Pitfall	1.806	0.43	59	4.198	**<0.001**
	Emergence - Suction	2.280	0.43	59	5.300	**<0.001**
	Pitfall - Suction	0.474	0.41	59	1.156	0.484

Table B5: Two-way ANOVA results testing the effects of site, method, and their interaction on log-transformed total invertebrate biomass.

	Df	**Sum of Squares**	**Mean Square**	**F value**	**p-value**
Site	3	6.54	2.18	2.187	0.099
Method	2	94.67	47.34	47.487	**<0.001**
Site:Method	6	52.11	8.68	8.712	**<0.001**
Residuals	59	58.81	1.00		

Table B6: Tukey's HSD post-hoc test results comparing log-transformed total invertebrate biomass between sampling methods (Emergence, Pitfall, and Suction) at four sites (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area). All significant results are highlighted in bold.

Site	**Contrast**	**Estimate**	**SE**	**df**	**t-ratio**	**p-value**
Woolshed Bush	Emergence - Pitfall	0.532	0.41	59	1.297	0.403
	Emergence - Suction	2.041	0.41	59	4.978	**<0.001**
	Pitfall - Suction	1.510	0.41	59	3.681	**0.001**
Top Bush	Emergence - Pitfall	-0.373	0.41	59	-0.909	0.637
	Emergence - Suction	1.689	0.41	59	4.118	**<0.001**
	Pitfall - Suction	2.062	0.41	59	5.028	**<0.001**
Caravan Bush	Emergence - Pitfall	2.306	0.41	59	5.622	**<0.001**
	Emergence - Suction	1.666	0.41	59	4.062	**<0.001**
	Pitfall - Suction	-0.640	0.41	59	-1.560	0.271
Chudleigh Conservation Area	Emergence - Pitfall	1.806	0.43	59	4.198	**<0.001**
	Emergence - Suction	2.280	0.43	59	5.300	**<0.001**
	Pitfall - Suction	0.474	0.41	59	1.156	0.484

Table B7: Tukey's HSD post-hoc test results comparing log-transformed total invertebrate biomass between sites (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area) for each sampling method (Emergence, Pitfall, and Suction). All significant results are highlighted in bold

Method	Contrast	Estimate	SE	df	t-ratio	p-value
Emergence	Woolshed - Top Bush	0.810	0.41	59	1.975	0.209
	Woolshed - Caravan Bush	0.005	0.41	59	0.013	1.000
	Woolshed - Chudleigh Conservation Area	0.326	0.43	59	0.758	0.873
	Top Bush - Caravan Bush	-0.805	0.41	59	-1.962	0.214
	Top Bush - Chudleigh Conservation Area	-0.484	0.43	59	-1.125	0.675
	Caravan Bush - Chudleigh Conservation Area	0.321	0.43	59	0.745	0.878
Pitfall	Woolshed - Top Bush	-0.095	0.41	59	-0.231	0.996
	Woolshed - Caravan Bush	1.779	0.41	59	4.338	**<0.001**
	Woolshed - Chudleigh Conservation Area	1.600	0.41	59	3.901	**0.001**

Method	Contrast	Estimate	SE	df	t-ratio	p-value
	Top Bush - Caravan Bush	1.874	0.41	59	4.569	**<0.001**
	Top Bush - Chudleigh Conservation Area	1.695	0.41	59	4.132	**<0.001**
	Caravan Bush - Chudleigh Conservation Area	-0.179	0.41	59	-0.437	0.972
Suction	Woolshed - Top Bush	0.458	0.41	59	1.116	0.681
	Woolshed - Caravan Bush	-0.370	0.41	59	-0.903	0.803
	Woolshed - Chudleigh Conservation Area	0.564	0.41	59	1.376	0.519
	Top Bush - Caravan Bush	-0.828	0.41	59	-2.019	0.193
	Top Bush - Chudleigh Conservation Area	0.107	0.41	59	0.260	0.994
	Caravan Bush - Chudleigh Conservation Area	0.935	0.41	59	2.279	0.115

Table B8: Maximum likelihood estimates of individual size distribution (ISD) slopes (λ) for invertebrate body mass at four sites (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh

Conservation Area). Values represent slope of the power-law relationship describing the abundance-body mass distribution. More negative values indicate body size distributions with fewer large-bodied individuals. 95% confidence intervals (CI) are provided for each estimate

Location	Abundance	ISD Slope (λ)	Lower 95% CI	Upper 95% CI
Woolshed Bush	783	-1.234	-1.271	-1.198
Top Bush	541	-1.210	-1.256	-1.165
Caravan Bush	623	-1.266	-1.309	-1.223
Chudleigh Conservation Area	508	-1.315	-1.369	-1.262

Table B9: Two-way ANOVA results testing the effects of site, sampling method, and their interaction on log-transformed mean body mass. All significant results are highlighted in bold.

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Site	3	1.02	0.341	0.558	0.645
Method	2	21.64	10.821	17.685	**<0.001**
Site:Method	6	12.49	2.082	3.402	**0.006**
Residuals	59	36.10	0.612		

Table B10: Tukey's HSD post-hoc test results comparing log-transformed mean body mass between sampling methods (Emergence, Pitfall, and Suction) at four sites (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area). All significant results are highlighted in bold.

Site	Contrast	Estimate	SE	df	t-ratio	p-value
Woolshed Bush	Emergence - Pitfall	-1.11	0.45	59	-2.46	**0.044**

	Emergence - Suction	0.84	0.45	59	1.87	0.156
	Pitfall - Suction	1.96	0.45	59	4.33	**<0.001**
Top Bush	Emergence - Pitfall	-1.55	0.45	59	-3.42	**0.003**
	Emergence - Suction	0.85	0.45	59	1.89	0.151
	Pitfall - Suction	2.40	0.45	59	5.31	**<0.001**
Caravan Bush	Emergence - Pitfall	-0.37	0.45	59	-0.82	0.692
	Emergence - Suction	0.65	0.45	59	1.43	0.330
	Pitfall - Suction	1.02	0.45	59	2.26	0.070
Chudleigh Conservation Area	Emergence - Pitfall	0.69	0.47	59	1.45	0.321
	Emergence - Suction	0.68	0.47	59	1.43	0.333
	Pitfall - Suction	-0.01	0.45	59	-0.02	1.000

Appendix C: Invertebrate Community Data from 2025 Sampling

Table C1: Summary statistics for all invertebrate orders captured by suction sampling in 2025, arranged from most to least abundant at each site. Mean body mass (± SD, mg), min (mg), max (mg), and sample size (abundance) are shown for each order at each location (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area).

Woolshed Bush

Order	Abundance	Mean ± SD	Min	Max
Diptera	25	3.12 ± 4.71	0.78	24.88
Hemiptera	15	13.88 ± 6.21	4.01	23.22
Lepidoptera	14	3.48 ± 2.88	0.70	9.93
Araneae	2	11.00 ± 2.72	9.08	12.93
Isopoda	2	10.34 ± 2.91	8.29	12.40
Hymenoptera	1	1.56	1.56	1.56
Total	**62**			

Top Bush

Order	Abundance	Mean ± SD	Min Mass	Max Mass
Diptera	27	2.49 ± 1.11	0.80	5.10
Hemiptera	6	16.26 ± 3.72	10.95	20.14
Lepidoptera	3	4.34 ± 3.57	0.80	7.94
Araneae	2	6.00 ± 6.08	1.69	10.30
Coleoptera	1	7.73	7.73	7.73
Total	**39**			

Caravan Bush

Order	Abundance	Mean ± SD	Min Mass	Max Mass

Diptera	77	7.46 ± 11.63	0.94	92.85
Lepidoptera	4	12.04 ± 15.79	1.09	35.47
Araneae	2	6.51 ± 5.36	2.72	10.30
Hemiptera	1	17.03	17.03	17.03
Total	**84**			

Chudleigh Conservation Area

Order	**Abundance**	**Mean ± SD**	**Min Mass**	**Max Mass**
Diptera	15	11.84 ± 9.57	2.50	29.52
Araneae	13	5.49 ± 4.79	1.65	19.75
Lepidoptera	6	2.94 ± 1.58	1.48	5.73
Hemiptera	5	123.09 ± 157.14	6.58	325.65
Isopoda	1	7.73	7.73	7.73
Total	**40**			

Table C2: Summary statistics for invertebrate orders captured by emergence traps in 2025, arranged from most to least abundant at each site. Mean body mass (± SD, mg), min (mg), max (mg), and sample size (abundance) are shown for each order at each site (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area).

Woolshed Bush

Order	**Abundance**	**Mean ± SD**	**Min Mass**	**Max Mass**
Diptera	252	8.16 ± 14.58	0.80	70.77
Coleoptera	61	6.61 ± 17.09	1.85	136.46
Amphipoda	40	11.74 ± 6.13	3.60	25.70
Isopoda	28	10.32 ± 5.25	4.45	25.67

Orthoptera	24	163.54 ± 222.97	2.86	750.80
Lepidoptera	11	16.72 ± 16.47	1.03	46.00
Araneae	7	25.29 ± 28.55	6.15	87.98
Hymenoptera	6	3.45 ± 2.44	1.55	8.31
Hemiptera	4	11.07 ± 4.80	5.15	16.88
Total	**433**			

Top Bush

Order	**Abundance**	**Mean ± SD**	**Min Mass**	**Max Mass**
Diptera	146	8.47 ± 10.07	1.21	66.15
Coleoptera	17	8.31 ± 12.85	2.50	57.36
Orthoptera	11	25.96 ± 51.18	3.61	176.61
Araneae	6	15.78 ± 26.29	3.52	69.36
Hymenoptera	4	2.03 ± 0.23	1.79	2.34
Lepidoptera	4	7.23 ± 2.43	4.24	9.88
Amphipoda	3	10.44 ± 4.63	6.01	15.24
Isopoda	3	11.17 ± 2.74	8.55	14.01
Hemiptera	1	11.56	11.56	11.56
Lithobiomorpha	1	9.95	9.95	9.95
Total	**196**			

Caravan Bush

Order	**Abundance**	**Mean ± SD**	**Min Mass**	**Max Mass**
Diptera	445	6.44 ± 7.08	0.45	44.02
Hemiptera	18	186.24 ± 156.43	5.06	434.48

Coleoptera	17	175.52 ± 52.29	2.50	228.38
Amphipoda	5	15.62 ± 2.82	10.85	18.36
Lepidoptera	5	32.86 ± 43.49	1.34	104.10
Araneae	3	4.43 ± 1.17	3.10	5.32
Isopoda	2	13.64 ± 3.72	11.01	16.28
Collembola	1	1.03	1.03	1.03
Hymenoptera	1	1.12	1.12	1.12
Total	**497**			

Chudleigh Conservation Area

Order	**Abundance**	**Mean ± SD**	**Min Mass**	**Max Mass**
Amphipoda	206	3.15 ± 2.16	1.03	22.39
Diptera	158	16.93 ± 26.69	0.80	338.47
Coleoptera	16	213.36 ± 22.81	157.56	254.36
Hymenoptera	9	2.67 ± 2.59	0.80	7.88
Hemiptera	7	282.07 ± 74.77	190.13	389.74
Isopoda	5	12.15 ± 8.63	2.29	26.07
Araneae	3	10.78 ± 5.97	4.24	15.92
Lepidoptera	2	27.13 ± 2.43	25.41	28.84
Collembola	1	7.57	7.57	7.57
Lithobiomorpha	1	12.12	12.12	12.12
Total	**408**			

Table C3: Summary statistics for invertebrate orders captured by pitfall traps in 2025, arranged from most to least abundant at each site. Mean body mass (± SD, mg), min (mg), max (mg), and sample size (abundance) are shown for each order at each site (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area).

Woolshed Bush				
Order	**Abundance**	**Mean ± SD**	**Min**	**Max**
Coleoptera	112	47.64 ± 93.59	0.59	368.76
Orthoptera	93	180.97 ± 209.31	4.27	741.59
Amphipoda	54	10.40 ± 7.23	2.78	31.97
Isopoda	16	12.17 ± 7.02	4.36	27.33
Araneae	4	14.54 ± 13.17	3.10	27.44
Lepidoptera	4	11.10 ± 6.00	3.00	17.40
Diptera	3	37.35 ± 3.99	32.91	40.63
Lithobiomorpha	3	29.06 ± 26.13	1.85	53.96
Dermaptera	1	5.90	5.90	5.90
Julida	1	169.15	169.15	169.15
Total	**291**			

Top Bush				
Order	**Abundance**	**Mean ± SD**	**Min**	**Max**
Amphipoda	136	10.60 ± 6.18	1.65	32.19
Coleoptera	82	66.12 ± 111.42	1.03	444.23
Orthoptera	82	204.60 ± 218.67	3.53	701.10
Isopoda	4	20.02 ± 18.71	4.24	46.80
Araneae	1	35.83	35.83	35.83
Lepidoptera	1	9.93	9.93	9.93

Total	**306**			

Caravan Bush

Order	Abundance	Mean ± SD	Min	Max
Amphipoda	25	15.80 ± 9.48	2.34	42.17
Opiliones	4	23.31 ± 6.68	15.98	31.95
Coleoptera	3	57.06 ± 93.69	2.01	165.24
Diptera	3	16.62 ± 12.33	3.77	28.34
Hemiptera	3	79.24 ± 119.37	7.97	217.05
Julida	3	7.50 ± 6.60	2.80	15.04
Araneae	1	3.82	3.82	3.82
Total	**42**			

Chudleigh Conservation Area

Order	Abundance	Mean ± SD	Min	Max
Amphipoda	35	5.74 ± 4.18	1.69	17.07
Opiliones	12	20.28 ± 4.66	14.66	28.11
Araneae	4	14.77 ± 8.91	5.72	24.34
Coleoptera	4	30.31 ± 7.46	23.53	37.65
Diptera	4	22.77 ± 8.35	12.96	30.46
Isopoda	1	18.99	18.99	18.99
Total	**60**			

Table C4: Summary statistics for invertebrate families captured by pitfall traps in 2025, arranged from most to least abundant at each site. Mean body mass (± SD, mg), min (mg), max (mg), and sample size (abundance) are shown for each family at each site (Woolshed Bush, Top Bush, Caravan Bush, and Chudleigh Conservation Area).

Woolshed Bush				
Family	**Abundance**	**Mean ± SD**	**Min**	**Max**
Rhaphidophoridae	93	180.97 ± 209.31	4.27	741.59
Zopheridae	63	9.40 ± 15.01	1.85	93.61
Talitridae	54	10.40 ± 7.23	2.78	31.97
Staphylinidae	17	40.01 ± 26.91	0.59	82.84
Armadillidae	15	12.25 ± 7.26	4.36	27.33
Carabidae	13	244.09 ± 131.14	5.29	368.76
Leiodidae	8	8.62 ± 7.79	3.61	24.88
Curculionidae	4	11.21 ± 5.60	4.71	18.08
Lepidoptera	4	11.10 ± 6.00	3.00	17.40
Calliphoridae	3	37.35 ± 3.99	32.91	40.63
Henicopidae	3	29.06 ± 26.13	1.85	53.96
Linyphiidae	3	10.24 ± 12.22	3.10	24.34
Tenebrionidae	3	177.87 ± 151.95	5.30	291.64
Cerambycidae	2	2.86 ± 1.04	2.12	3.60
Scarabaeidae	2	118.20 ± 128.84	27.09	209.30
Forficulidae	1	5.90	5.90	5.90
Julidae	1	169.15	169.15	169.15
Lycosidae	1	27.44	27.44	27.44
Styloniscidae	1	10.95	10.95	10.95
Total	**291**			
Top Bush				

Family	Abundance	Mean ± SD	Min	Max
Talitridae	136	10.60 ± 6.18	1.65	32.19
Rhaphidophoridae	82	204.60 ± 218.67	3.53	701.10
Carabidae	45	112.03 ± 133.81	9.57	444.23
Zopheridae	18	4.21 ± 1.15	2.01	6.58
Leiodidae	12	4.84 ± 0.70	3.90	5.72
Staphylinidae	6	38.05 ± 18.67	1.03	50.98
Armadillidae	2	14.51 ± 4.78	11.13	17.89
Histeridae	1	17.78	17.78	17.78
Lepidoptera	1	9.93	9.93	9.93
Lycosidae	1	35.83	35.83	35.83
Porcellionidae	1	46.80	46.80	46.80
Styloniscidae	1	4.24	4.24	4.24
Total	**306**			

Caravan Bush

Family	Abundance	Mean ± SD	Min	Max
Talitridae	25	15.80 ± 9.48	2.34	42.17
Triaenonychidae	4	23.31 ± 6.68	15.98	31.95
Julidae	3	7.50 ± 6.60	2.80	15.04
Rhyparochromidae	2	10.34 ± 3.34	7.97	12.70
Tipulidae	2	23.04 ± 7.50	17.73	28.34
Carabidae	1	165.24	165.24	165.24
Cicadidae	1	217.05	217.05	217.05

Curculionidae	1	2.01	2.01	2.01
Linyphiidae	1	3.82	3.82	3.82
Stratiomyidae	1	3.77	3.77	3.77
Zopheridae	1	3.92	3.92	3.92
Total	**42**			

Chudleigh Conservation Area

Family	Abundance	Mean ± SD	Min	Max
Talitridae	35	5.74 ± 4.18	1.69	17.07
Triaenonychidae	12	20.28 ± 4.66	14.66	28.11
Linyphiidae	4	14.77 ± 8.91	5.72	24.34
Tipulidae	4	22.77 ± 8.35	12.96	30.46
Nitidulidae	2	23.89 ± 0.51	23.53	24.25
Armadillidae	1	18.99	18.99	18.99
Tenebrionidae	1	35.83	35.83	35.83
Zopheridae	1	37.65	37.65	37.65
Total	60			

Appendix D: Metabarcoding Supplementary Tables

Table D1: Complete list of all families detected in black robin faecal samples through metabarcoding (n = 23 samples). ASVs = number of amplicon sequence variants; Total Reads = total number of sequences; Relative Abundance = percentage of total sequences across all samples.

Order	Family	ASVs	Total Reads	Relative Abundance
Araneae	Linyphiidae	1	279	0.021404

Araneae	Clubionidae	2	273	0.020944
Araneae	Salticidae	1	60	0.004603
Coleoptera	Tenebrionidae	2	110306	8.462476
Coleoptera	Staphylinidae	4	30742	2.35847
Coleoptera	Curculionidae	2	24670	1.892638
Coleoptera	Chrysomelidae	1	3621	0.277797
Coleoptera	Cerambycidae	1	372	0.028539
Coleoptera	Carabidae	1	87	0.006674
Coleoptera	Erirhinidae	1	78	0.005984
Coleoptera	Latridiidae	1	59	0.004526
Coleoptera	Melyridae	1	37	0.002839
Coleoptera	Cleridae	1	30	0.002302
Coleoptera	Buprestidae	1	12	0.000921
Coleoptera	Chaetosomatidae	1	12	0.000921
Coleoptera	Elateridae	1	11	0.000844
Coleoptera	Hydraenidae	1	7	0.000537
Coleoptera	Oedemeridae	1	0	0
Diptera	Agromyzidae	1	144451	11.08202
Diptera	Heleomyzidae	1	14959	1.147627
Diptera	Tachinidae	1	8088	0.620497
Diptera	Chloropidae	1	6445	0.494449
Diptera	Calliphoridae	2	5132	0.393718
Diptera	Stratiomyidae	1	4047	0.310478

Diptera	Anthomyiidae	1	4012	0.307793
Diptera	Limoniidae	1	1207	0.092599
Diptera	Culicidae	1	1092	0.083776
Diptera	Muscidae	1	1021	0.078329
Diptera	Sciaridae	1	748	0.057385
Diptera	Dolichopodidae	2	443	0.033986
Diptera	Phoridae	3	421	0.032298
Diptera	Psychodidae	1	400	0.030687
Diptera	Mycetophilidae	2	276	0.021174
Diptera	Sphaeroceridae	1	161	0.012352
Diptera	Hybotidae	1	101	0.007749
Diptera	Empididae	1	100	0.007672
Diptera	Chironomidae	1	56	0.004296
Diptera	Keroplatidae	1	54	0.004143
Diptera	Drosophilidae	1	47	0.003606
Diptera	Tipulidae	1	42	0.003222
Diptera	Tabanidae	1	41	0.003145
Diptera	Lonchaeidae	1	4	0.000307
Diptera	Ptychopteridae	1	3	0.00023
Diptera	Sarcophagidae	1	3	0.00023
Diptera	Ceratopogonidae	1	0	0
Hemiptera	Cicadidae	5	123518	9.476076
Hemiptera	panagrolaimidae	1	16342	1.253729

Hemiptera	Flatidae	1	2204	0.169087
Hemiptera	Meenoplidae	1	244	0.018719
Hemiptera	Pseudococcidae	1	43	0.003299
Hemiptera	Triozidae	1	18	0.001381
Hymenoptera	Formicidae	3	91868	7.047946
Hymenoptera	Ichneumonidae	2	4996	0.383284
Hymenoptera	Figitidae	1	322	0.024703
Hymenoptera	Braconidae	3	30	0.002302
Hymenoptera	Mymaridae	1	5	0.000384
Lepidoptera	Geometridae	1	33050	2.535536
Lepidoptera	Oecophoridae	1	9180	0.704273
Lepidoptera	Noctuidae	2	6481	0.497211
Lepidoptera	Nepticulidae	1	6263	0.480486
Lepidoptera	Tortricidae	3	2131	0.163486
Lepidoptera	Crambidae	1	406	0.031148
Lepidoptera	Gelechiidae	2	265	0.02033
Lepidoptera	Nymphalidae	1	211	0.016188
Lepidoptera	Cosmopterigidae	1	17	0.001304
Lepidoptera	Tineidae	1	16	0.001227
Lithobiomorpha	Henicopidae	1	334	0.025624
Opiliones	Neopilionidae	1	592	0.045417
Orthoptera	Rhaphidophoridae	6	180958	13.88277
Poduromorpha	Hypogastruridae	3	1258	0.096511

Poduromorpha	Brachystomellidae	1	4	0.000307
Pseudoscorpiones	Cheliferidae	1	10	0.000767
Sarcoptiformes	Proctophyllodidae	1	146	0.011201
Sarcoptiformes	Acaridae	1	29	0.002225
Sarcoptiformes	Suidasiidae	1	7	0.000537
Thysanoptera	Phlaeothripidae	1	54	0.004143

Table D2: Complete list of all genera detected in black robin faecal samples through metabarcoding (n = 23 samples). ASVs = number of amplicon sequence variants; Total Reads = total number of sequences; Relative Abundance = percentage of total sequences across all samples.

Order	Family	Genus	ASVs	Total Reads	Relative Abundance
Araneae	Clubionidae	Clubiona	2	273	0.02094
Coleoptera	Curculionidae	Curculio	1	18	0.00138
Coleoptera	Erirhinidae	Praolepra	1	78	0.00598
Coleoptera	Staphylinidae	Acrotona	1	0	0
Coleoptera	Tenebrionidae	Tenebrio	1	12954	0.99381
Diptera	Calliphoridae	Calliphora	1	5125	0.39318
Diptera	Hybotidae	Oropezella	1	101	0.00775
Diptera	Phoridae	Megaselia	1	4	0.00031
Hemiptera	Cicadidae	Kikihia	4	123154	9.44815
Hymenoptera	Braconidae	Doryctomorpha	1	4	0.00031
Hymenoptera	Formicidae	Chelaner	1	91662	7.03214
Hymenoptera	Formicidae	Technomyrmex	1	26	0.00199

Hymenoptera	Ichneumonidae	Campoletis	1	163	0.01250
Lepidoptera	Gelechiidae	Anisoplaca	2	265	0.02033
Lepidoptera	Noctuidae	Apamea	1	4477	0.34347
Lepidoptera	Tortricidae	Planotortrix	1	68	0.00522
Lepidoptera	Tortricidae	Merophyas	1	20	0.00153
Orthoptera	Rhaphidophoridae	Talitropsis	4	140095	10.7478
Orthoptera	Rhaphidophoridae	Novoplectron	1	40457	3.10379
Poduromorpha	Brachystomellidae	Brachystomella	1	4	0.00031
Poduromorpha	Hypogastruridae	Ceratophysella	3	1258	0.09651
Pseudoscorpiones	Cheliferidae	Philomaoria	1	10	0.00077

Table D3: Statistical comparisons of order-level prey abundance between Woolshed Bush and Top Bush. Test = statistical test used (t-test or Wilcoxon rank-sum test); Statistic = test statistic value; P value = unadjusted p-value; P adjusted = p-value adjusted for multiple comparisons using Benjamini-Hochberg method.

Order	Test	Statistic	P value	P adjusted
Hemiptera	Wilcoxon	88	0.1847	0.9788
Lepidoptera	t-test (log-transformed)	-1.148	0.2639	0.9788
Hymenoptera	Wilcoxon	79	0.3956	0.9788
Orthoptera	t-test (log-transformed)	-0.637	0.5307	0.9788
Scolopendromorpha	Wilcoxon	60	0.5632	0.9788
Araneae	Wilcoxon	74	0.5873	0.9788
Diptera	Wilcoxon	64	0.9264	1
Poduromorpha	Wilcoxon	67	0.9711	1
Coleoptera	Wilcoxon	66	1	1

Sarcoptiformes	Wilcoxon	66	1	1