Invertebrates of the Tasman River Plain:
Characteristics of the invertebrate community and an analysis of sampling methods for biodiversity assessment

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Cover: *Raoulia haastii – R. australis* cushionfield, Tasman River. *Photo: Dave Murray*.

Summary

A total of 152,509 invertebrate specimens of 919 unique RTUs representing 165 arthropod families, 21 orders and 5 classes were identified from 438 samples taken from the *Raoulia haastii – R. australis* cushion-field community using four sampling methods over the period 31 October 2005 - 3 February 2006. Of these, 402 were identified to species, 318 to genus, 174 to family and 25 to order. Diversity was dominated by Diptera, Hymenoptera, Lepidoptera and Coleoptera. Hemiptera were less diverse but extremely abundant. Key detritivores (amphipods, isopods, millipedes) were absent and weevil diversity was conspicuously low. The majority of RTUs were found in small numbers and few samples.

Community composition differed significantly between trap types. The highest number of RTUs (69%) were detected using 25 malaise traps set with trough and jar collection devices. Pitfall, pan and light traps collected 49%, 52% and 10% of RTUs respectively, in 210, 168, and 10 samples. Malaise traps were significantly more efficient than pitfalls, which detected fewer taxa per trap, and had high abundances of juveniles as well as adult specimens. Pitfalls, however, detected large predator beetles and spiders, an important functional group missed by malaise traps. Within trap types, moon phase had no effect on community composition but seasonal and spatial trends were apparent. Small differences between vegetation sub-types and sites were driven by position along the length of the river, with 44% of RTUs found in only one section of the river and 37% found only during one of the sampling periods. Diversity was highest in the upper reaches and both peak abundance and diversity were observed in December and February.

Species diversity was strongly correlated to genus and family diversity. Community composition patterns driven by trap type, season and distribution along the river, were detectable when data was aggregated to genus, and in some cases family. Exclusion of juvenile specimens and very small taxa (Collembola and Acari) reduced specimens requiring processing by 46.5% (70,773 specimens).

Based on the analysis of invertebrates collected in this single study, the following recommendations were made:

Recommendation 1: *Use malaise traps with both jars and troughs for general biodiversity values assessment*

Recommendation 2: *Undertake study to compare malaise trap catch with and without troughs, while incorporating increased replication to determine optimal sampling size*

Recommendation 3: *Supplement malaise trapping with methods targeted to key functional groups (large predators) or other groups of relevance to the research question*

Recommendation 4: *Assess other vegetation types to determine if indicator species/groups can be detected for use in rapid river-wide assessments in the future*

Recommendation 5: *To assess spatial and temporal trends in diversity in future studies, process a subset of insect orders only (e.g. Diptera, Hymenoptera, Lepidoptera, Coleoptera, spiders)*

Recommendation 6: *With the current or future datasets, investigate the predictive power and detectability of a subset of taxa that could be easily extracted from large samples, such as species of larger size classes*

Recommendation 7: *Identify specimens to RTU at least to family level, but avoid spending time on assigning specific species names*

Recommendation 8: *Develop a biodiversity index for terrestrial braided river invertebrates as a function of species richness, taxonomic distinctness and functional diversity*

Recommendation 9: *Sample in three periods across the spring/summer season (e.g. early November, mid-December, late January/early February)*

Recommendation 10: *Exclude immatures and taxa <2mm in length from processing*

Recommendation 11: *Provide data templates if multiple individuals or external experts are processing samples or inputting data*

1.0 Background

Invertebrates make up a significant proportion of biodiversity and are integral in ecosystem function. However, their small size and diversity often preclude their inclusion in biodiversity studies or the assessment of land conservation values. Substantial expertise is required to accurately identify most invertebrates beyond the order level, and in combination with the large numbers of individuals usually collected using traditional sampling methods, this often makes biodiversity monitoring prohibitively expensive and time consuming. More efficient methods of monitoring are being sought. Oliver & Beattie (1996) listed five factors regularly used to increase invertebrate sampling efficiency; 1) use of surrogate indicator species, 2) surrogate or restricted sampling, 3) use of morpho-species rather than expert identification, 4) use of taxonomic ranks other than species, 5) extrapolation from species accumulation curves or other models.

Braided river ecosystems are threatened environments occupying about 250,000 ha in New Zealand (O'Donnell et al., 2016). While data on other flora and fauna are available across some or many braided rivers, because of the issues identified above, the invertebrate biodiversity values of braided rivers have not been comprehensively assessed. To begin addressing this, a pilot survey was designed to determine invertebrate biodiversity values and to compare the suitability of different sampling methods for use in future braided river studies. The primary objectives were to determine the optimal number of samples required to answer research questions while minimising sampling and processing time, and identify whether higher level taxonomic identification can be used as a surrogate for species (reducing the need for expert identification). The Tasman River flood plain was selected for the pilot study due to its accessibility, because it had been the focus of earlier studies on the vegetation community (Woolmore, 2011), it has relative inaccessibility for recreational vehicles and therefore reduced risk of intentional or accidental damage to traps, and because it was within the region boundaries of the funding group, Project River Recovery.

This study was set up to address the following questions:

1) What are the key features of the terrestrial invertebrate biodiversity values observed in the Tasman?
2) Which trapping method or combination of methods would be most suitable for rapid biodiversity assessment of other braided river systems in the future, and what are the minimum and ideal sample sizes required?
3) Are there particular insect species of groups that can be used as identifiers of biodiversity values or presence of other species?
4) What is the minimum level of taxonomic discrimination necessary to define biodiversity values?
5) Can we develop best practice rapid sampling and analysis methods to apply to other braided river systems to assess biodiversity values and ecosystem health?

2.0 Methods

2.1 Site selection

A sampling regime was trialled at six sites on the Tasman floodplain (Map 1). An earlier vegetation study (Woolmore, 2011) identified 11 vegetation communities (derived from cluster analyses of plant species composition and percentage cover at each plot) that occur in braided river systems in the upper Waitaki basin. The invertebrate trial focused on the most commonly found community in the Tasman River; the *Raoulia haastii – R. australis* cushionfield community, described as relatively open, with low-growing vegetation dominated (90% cover) by native species (64%) (Woolmore, 2011). The community comprises 113 species of vascular plants, mosses and lichens, with *Carmichaelia australis*, *Raoulia australis, Poa maniatoto*, *Colobanthus strictus* and *Luzula celata* identified as indicator species (Woolmore, 2011). It represents 8% of the sites sampled across the Waitaki Basin rivers, and 39% of sites sampled in the Tasman River.

As vegetation structure is an important determinant of invertebrate diversity that was not incorporated in Woolmore's analyses, the community was re-analysed with the addition of vegetation height as a surrogate for plant structure. This analysis identified four predominant vegetation plant associations within the *R. haastii – R. australis* community. For the invertebrate study, three sites were randomly selected from the most common association, and one site from each of the other associations, giving a total of six sampling sites. Original site codes are provided in Appendix 1.

2.2 Sampling methods

Five pitfall traps, four pan traps (two yellow and two white) and one malaise trap were set at each site (Table 1). All traps contained a 33% solution of ethylene glycol as a preservative, with several drops of detergent added to reduce surface tension. Traps were checked and emptied at 7-8 day intervals coinciding with the four lunar phases, however only the new and full moon samples are including in this report. Servicing dates and given in Appendix 1. Not all malaise traps were in place in the early stages of the study. One light trap was also set at each of sites 2, 3, 4, and 6 during the new moon phase on 3 occasions, however poor weather prevented light trapping at Time 3 (Table 1).

Table 1: Number of sites where traps of each type were open during each successive new (N) and full (F) moon sample period. Samples collected during the intermediate waxing and waning moon phases are not included in this report. Light traps were only set during the new moon phase. Numbers in parentheses beside total sample counts indicate the number of samples included in MDS analysis (see methods) following exclusion of empty samples. *Site 5 missing, ** 1 jar and 1 trough sample per trap. See Appendix 1 for sampling dates T1-T4.

Sample period	T1		T2		T3		T4		
Moon phase	N	F	N	F	N	F	N	Reps per site	Total
Light	2	-	4	-	0	-	4	1	10
Pitfall	6	6	6	6	6	6	6	5	210
Malaise	0	1	1	5*	6	6	6	2**	50
Pan	6	6	6	6	6	6	6	4	168
						Total samples across all sites and trap types			438 (421)
						Total samples without pseudo-replication‡			186 (180)

‡Pseudo-replication was removed by aggregating the 5 pitfall, 2 yellow pan, and 2 white pan replicates per site.

Map 1: Location of sampling sites on the Tasman River Flood Plain, Mackenzie Basin, South Island, New Zealand.

Pitfall traps were 110 mm deep plastic cups with a 105 mm diameter opening set flush with the ground surface. At each site, five pitfalls were set in a line at 6 m intervals, each inside a galvanised iron cylinder to minimise substrate disturbance when servicing traps. Four galvanised metal strips, 500 mm long and 100 mm high, were positioned in a cross formation extending from the edges of each pitfall as guiding barriers. Each pitfall had a 195 x 195 mm plywood rain cover set at a maximum height of 25 mm above the trap.

Each pan trap consisted of two square white 2 L plastic containers (170 x 170 x 80 mm high) set one inside the other and secured together with duct tape. Half of these were painted with Dulux® Sulphur acrylic paint to make the yellow traps. To hold the pan traps in position, a length of thick wire was threaded through the bottom container and rocks were placed on the ends of each wire.

Malaise traps were omnidirectional with a 1 m high apex and 1 m long side panels tapering to 500 mm high. The traps were made of fine white nylon curtain net ("Finesse") with the side panels dyed black. Each side panel had an open collection trough underneath constructed from PVC spouting (170 mm wide x 100 mm high) and secured by wire loops held in place by rocks. A 200 mL collection jar was attached to the apex of the trap, initially by using an opaque 65 mm diameter PVC downpipe bend. The downpipe bend was later modified by replacing the outer curve with a transparent perspex window. A waratah in the centre of the trap secured the net in position, with the ends of each side panel attached to bamboo stakes held in place by cords attached to rocks.

The pitfall and pan traps were opened on 30 October 2005 giving a total of 42 samples each. One malaise trap was set at site two on 8 November, but the remainder were not set at the other five sites until mid-December. As such only 25 (rather than 42) samples were collected. Once in place, traps were run continuously until 3 February 2006.

Light-trapping was conducted using automated light traps (White, 1996) set for one night during the new moon phases only. Adverse weather precluded light-trapping on 4-5 January 2006 (T3). At sites 2, 3, 4 and 6, a single trap was positioned (in the centre of a white sheet) several metres away from the other trap types to avoid any influence of the light on the catch of those traps. For the first 3 hr after dark, invertebrates that were attracted to the light, but did not enter the trap funnel, were collected by hand. The light trap was subsequently left unattended for the remainder of the night and all invertebrates captured were collected from the trap as early as possible on the following morning. Any invertebrates present on or under the white sheet beneath the trap were also collected.

Some additional hand-collecting was undertaken. Invertebrates observed near traps during servicing were collected if it was thought they have not previously been collected at any of the sites, or notes were made of their presence if they were thought to have been collected before. Similarly, during light-trapping, hand-searching of the riverbed surface, under rocks, on vegetation, and in plant litter was carried out in the vicinity of other traps in the 15 minute light trap dark-phase.

2.3 Sample processing

Samples were sieved in the field through squares of the same fine net used to construct the malaise nets, then rinsed with water in the laboratory and stored in 75% ethanol prior to sorting. Invertebrates collected during the new and full moon phases were sorted initially to recognisable taxonomic units (RTUs) (Oliver & Beattie 1993) then identified to the lowest possible taxonomic level (lowest being species) by specialists. Samples collected during the waxing and waning moon phases have not been processed and remain in ethanol storage at the Department of Conservation's Twizel Te Manahuna

District Office. The count of each RTU present in each sample was recorded along with notes on gender (male/female) and life-stage (adult/immature) where possible. Voucher specimens (and additional specimens available for distribution to other reputable repositories and specialists) of each RTU have been deposited in the Lincoln University Entomology Museum to form the basis of a Mackenzie basin braided river invertebrate reference collection.

2.4 Meteorological data

Onset StowAway® temperature loggers were installed at four of the study sites to record temperature at hourly intervals, but logger failure resulted in only two loggers recording data and then only for a small portion of the sampling period. Alternative meteorological data (hourly temperature, relative humidity, wind direction, wind speed, and rainfall) may be obtained from the nearest weather recording station (in Mount Cook village), however this has not been included in the analysis as it cannot account for site-specific climatic variation.

3.0 Data analysis

Prior to analysis, any data rows (where each row represents an RTU from an individual sample) that were incomplete, erroneous or contained duplicate data, were excluded. This included deleting rows where the level of taxonomic information recorded was not sufficient to determine if the specimens represented unique RTUs or not. For samples where a range of values were given for the abundance of an RTU in a sample, the smallest value was used.

All trap types and individual samples were included in initial exploratory analysis, species accumulation curve analysis, diversity index calculations and some analysis for differences between individual trap types. For statistical comparison of trap, time, site and vegetation effects, hand-collecting was excluded as a sampling method, and within-site replicates of other sampling methods were aggregated to avoid pseudo-replication[1]. Aggregation was performed for; a) the 5 pitfall traps per site, b) the 2 yellow pans per site and c) the 2 white pans per site. For the malaise traps, data from the jar and trough collection devices were also combined for statistical analysis as they cannot be regarded as independent given they used the same interception surface per trap and insects caught in the troughs may have been caught in the jars if the troughs were not present. To compare jars and troughs statistically would require each collection device to have been used in association with separate malaise traps.

Graphical and statistical analysis was conducted using the statistical analysis package PRIMER-E. Non-parametric Multi-Dimensional Scaling (MDS) ordination was used to graphically summarise species-composition relationships between samples. Patterns observed were then tested using analysis of similarity (ANOSIM; a non-parametric permutation test applied to the rank similarities, roughly analogous to ANOVA) to statistically compare species composition between trap types, sampling times, sites, moon phases and vegetation types. The ANOSIM test statistic 'R' indicates the proportion of variability between groups that can be attributed to the variable being tested (e.g. trap type). *R* ranges from 0-1, where 0 indicates no differences between groups and 1 indicates all dissimilarities *between* groups are larger than any dissimilarities among samples *within* groups.

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[1] Note that conducting the analyses on all samples *without* combining to avoid pseudo-replication produced almost identical results.

Sample MDS ordinations were based on the 4th root transformed abundance data for all RTUs (adults and immatures combined) collected in all samples with the 5 pitfalls per site, the 2 yellow and 2 white pans, and the jar + trough samples combined as described above. Samples containing zero specimens were required to be removed prior analysis, therefore n = 180 rather than 186 samples (similarly n = 421 rather than 438 when pseudo-replicates were not combined, see table 1). Analyses are based on rank Bray-Curtis similarities, where similarities/dissimilarities refer to the average combined similarities/dissimilarities in species composition between each possible pair of samples from those variables (sites, trap types etc.) being compared. MDS ordination graphs have no axis, instead, points that are close together on sample ordinations are more similar in their species composition than are points that are further apart. A 'stress value' indicates the degree to which the rank order of the distances between point on the plot match those of the original similarity matrix from which it was created. As the rank orders reach perfect agreement stress tends towards 0. Values below 0.1 indicate an excellent ordination which is unlikely to be misinterpreted. Values up to 0.2 indicate a useful ordination but reliance should not be placed on the finer details. If values are >0.2, patterns should be regarded with caution and cross-checked with other techniques.

Similarity percentage analysis (SIMPER) of 4th root transformed data was used to calculate the average contribution of each invertebrate species to the overall Bray-Curtis *similarity* in sample composition within the *a priori* groups (i.e. trap type, site, vegetation community, sample time, moon phase). Similarity profile permutation tests (SIMPROF) were used to test if clusters detected using MDS ordination represented statistically genuine associations between species or samples. Similarity percentage analysis (SIMPER) was used to calculate the average contribution of each species to the overall Bray-Curtis *dissimilarity* between clusters to determine if any individual species or group of species could be used to discriminate one cluster from another.

Permuted species accumulation curves and non-parametric extrapolator indices that attempt to predict the total species number that would be observed if sample number tended to infinity were calculated based on 999 random permutations. *Taxonomic diversity* and *taxonomic distinctness* indices were calculated using the DIVERSE function in PRIMER-E with branch lengths of 1 for each taxonomic level weighted as species = 25, genus = 50, family = 75, order = 100. ANOVA and Tukey post hoc tests (R, version 3.2.2) were applied to test for differences in mean diversity index values (Margalef's index (d), Simpson index (λ), Taxonomic diversity (Δ) and Taxonomic distinctness (Δ^*)) between trap types and sampling times.

Species biostatus data (endemic, indigenous, exotic) was extracted from the New Zealand Organism Register (http://www.nzor.org.nz/).

4.0 Results

4.1 Overview of trap catch

A total of 438 samples (trap x time x site x moon phase x replicate) and an additional 30 hand collections were fully processed to identify specimens to the lowest possible taxonomic level. From these, 152,509 individual invertebrate specimens were identified representing 919 unique RTUs (Table 2). A total of 25 RTUs were identified only to order, 174 to family, 318 to genus and 402 to species (Appendix 2). Adults accounted for 82% of specimens and immatures the remaining 18%. The majority of specimens (but not RTUs) were collected in pitfall traps (67%; Table 2).

Of the 919 RTUs, 633 (69%) were represented in malaise, 52% in pan traps, and 49% in pitfall traps. A total of 442 (48.1%) of all RTUs were collected using only one method, 22.3% using two, 20.1% three, 7.7% four, and just 1.7% (16 RTUs) were collected using all five methods (Fig. 1). The greatest number of 'unique' RTUs (those only collected in only one trap type) were collected using malaise traps (followed by pitfall and pan traps: Table 2, Fig. 1), although the contributions from jar and trough collections were highly dissimilar. Of the 633 RTUs collected in malaise traps, 90% were represented in trough catches and 147 (23.2%) uniquely so. In contrast, only 35 unique RTUs were caught in the jars. Of the species unique to the pan traps, 34 (7.1% of total pan catches) were collected only from white pans, and 35 (7.2%) only from yellow pans. Just 10% of RTUs were represented in hand collections, with Lepidoptera, Diptera and Coleoptera occurring with similar frequencies (see Table 4). Only 10 unique RTUs were detected using this method. Overall, 53% of all spider RTUs and 34% of beetle RTUs were only collected from pitfall traps, while 38% of Trichoptera and 27% of Hymenoptera were only collected in malaise traps.

Table 2: Total (Σ) number of individual specimens and RTUs, including adults and immatures, collected using each trap type and for which complete data were available. The total proportion of specimens collected by each trap type is indicated in the final column. Unique RTUs (and as a % of total RTUs in parentheses) refer to species only collected using the specified trap type. A total of 442 RTUs were collected from only one of the 5 main trap types (411 if malaise and pan traps retained as sub-types).

| Collecting method	Σ No. RTUs	% Σ RTUs	RTUs Unique To Trap	No. Adults	No. Immatures	Σ No. Specimens	% Σ Catch
Hand	**93**	**10.1%**	**10 (1.1%)**	**344**	**42**	**386**	**0.3%**
Light	**112**	**12.2%**	**23 (2.5%)**	**3,827**	**9**	**3,836**	**2.5%**
Pitfall	**452**	**49.2%**	**127 (13.8%)**	**78,298**	**23,942**	**102,240**	**67.0%**
Malaise	**633**	**68.9%**	**198 (21.5%)**	**26,428**	**1,081**	**27,509**	**18.0%**
Jar	258	28.1%	*35*	8,858	11	8,869	5.8%
Trough	569	61.9%	*147*	17,570	1,070	18,640	12.2%
Pan	**481**	**52.3%**	**84 (9.1%)**	**15,529**	**3,009**	**18,538**	**12.2%**
White	358	38.9%	*34*	8,234	1,327	9,561	6.3%
Yellow	*378*	41.1%	*35*	7,295	1,682	8,977	5.9%
Total	**919**		**442 /411***	**124,426**	**28,083**	**152,509**	**100%**
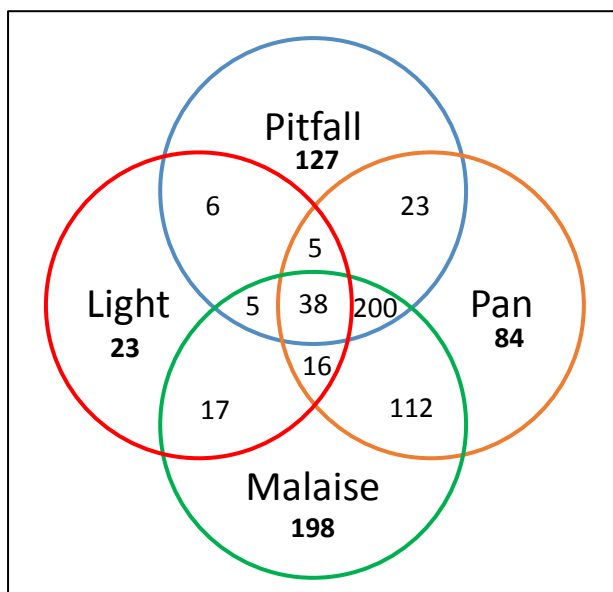
Figure 1: Total number of RTUs common to each combination of the 4 main trap types (yellow + white pans aggregated, malaise trough + Jar aggregated). Combinations not shown are Pan + Light = 2 RTU and Malaise + pitfall = 43 RTUs. The number of RTUs unique to each trap type are in **bold**. Total number of RTUs = 909 excluding the 10 RTUs found only by hand sampling.

4.2 Taxonomic characteristics of the invertebrate community

Specimens collected included representatives of 21 orders from 5 arthropod classes (Table 3). The majority were insects (91.7% RTUs) while arachnids, centipedes, springtails, protura, and crustacea accounted for the remaining 8.3% of RTUs. Spiders (6.0% RTUs) were the most prevalent of the non-insect arthropod groups. No diplopods (millipedes) or amphipods (land hoppers) were detected, both of which are groups that prefer moist habitats such as leaf litter and decaying wood.

Of the 371 insects that could be assigned biostatus with certainty (i.e. those identified to species or classified as endemic or exotic at any taxonomic level), 87% were classified as indigenous, 84% as endemic, and 13% as exotic. True endemism is likely higher, as almost all taxa that were not classified are likely to be indigenous (assuming 13% of the remaining RTUs are exotic, total indigenous = 92%).

The greatest diversity was represented by the Diptera (34.3% of RTUs), Hymenoptera (19.5%) and Lepidoptera (13.2%), followed by Coleoptera, Hemiptera and Araneae (Table 4). Within the flies, the Tachinidae (larvae parasitic on other arthropods, adults visit flowers) and Chironomidae (aquatic midges) were the most speciose (49 and 41 RTUs respectively) with Dolichopodidae ('Long-legged flies', favour moist habitats, adults predatory), Muscidae (house flies etc), Mycetophilidae (fungus gnats) and Ephydridae ('shoreflies' with aquatic larvae) also well represented. Crambidae (32) and Noctuidae (27) were the most common moth families followed by Geometridae and Tortricidae. Of the wasps, bees and ants, Aphelinidae (25), Braconidae (17), Platygastridae (17) and Eulophidae (16), all families of small parasitic wasps, were most speciose. Ten of the 27 species of endemic native bees were collected, predominantly *Lasioglossum sordidum* (Halictidae) followed by *Leioproctus maritimus* and *Leioproctus* sp. (Colletidae). Exotic bees were relatively scarce; *Bombus terrestris*, the most common bumble bee in New Zealand, was the most abundant (98 specimens from 46 samples) while *Bombus hortorum* and *Apis mellifera* (honey bee) were represented by just 2 specimens each. Four ant species were detected, with 99.4% of specimens identified as *Monomorium antarcticum*, a common generalist found in grassland, forest, pasture and gardens throughout New Zealand (Warwick & Harris, 2004). Two unidentified species and *Monomorium smithii*, another generalist endemic that has previously been found in open grassland near Porters Pass and in native forest in both the North and South Islands (Warwick & Harris, 2004), were detected in low numbers.

Table 3: Number of collected RTUs belonging to different arthropod taxa. 'No. Families' refers to the total number of families *definitively* identified within each order. However, as indicated in the final column, additional families may be present as some RTUs were not able to be identified to this level.

Class	Order	No. Families	No. RTUs	RTUs with unident. family
Arachnida	Acari	1	2	1
	Araneae	12	55	1
	Opiliones	1	1	0
	Pseudoscorpionida	3	5	1
Chilopoda	Geophilomorpha*	1	5	2
Crustacea	Copepoda	1	2	1
Ectognatha	Collembola	3	5	1
	Protura	1	1	1
Insecta	Coleoptera	24	91	6
	Diptera	37	315	1
	Ephemeroptera	1	1	0
	Hemiptera	22	74	1
	Hymenoptera	23	179	1
	Lepidoptera	18	121	1
	Neuroptera	1	1	0
	Orthoptera	4	10	1
	Plecoptera	1	4	1
	Psocoptera	3	9	2
	Siphonaptera	1	1	0
	Thysanoptera	3	13	1
	Trichoptera	5	24	1
Total		**165**	**919**	**24**

* 2 RTUs were not identified to order therefore it is unclear if only Geophilomorpha were present in the class Chilopoda.

In the true bugs and beetles, no families were represented by more than 15 RTUs. Aphididae (aphids, 15 RTUs) and Cicadellidae (leafhoppers, 12 RTUs) were most diverse. The diversity of beetles was relatively low (9.9% RTUs) with Staphylinidae (predatory rove beetles) and Scarabidae (herbivores) represented by 15 and 11 species, and herbivorous weevils (Curculionidae) by just 7, despite being the most diverse beetle family in New Zealand. Carabidae (large predatory ground beetles) were also represented by just 7 species, while chrysomelids (leaf beetles), Elateridae (click beetles) and Zopheridae (the fourth most diverse family in New Zealand) had 5 species each. In total, 57 spider RTUs from 13 families were collected. Linyphiidae (12 RTUs, typically minute sheet web spiders showing microhabitat specialisation), Gnaphosidae (11 RTUs, nocturnal ground hunting spiders), Lycosidae (9 RTUs, hunting wolf spiders, primarily associated with open habitats) and Theridiidae (9 RTUs, one of the most species rich spider families in NZ) (Paquin & Vink, 2010) were the most diverse.

Pitfall, malaise and pan traps were all dominated by Diptera followed by Hymenoptera, although the number of RTUs collected in each trap type varied greatly (Table 3). As would be expected, light trap catches were dominated by Lepidoptera (42%), however, only 38.5% of all Lepidoptera detected in the study were represented in light catches. Only 14% of Lepidoptera RTUs were unique to light traps, whereas 24% were only caught in Malaise traps and 8.6% only in pan, pitfall or hand collections combined. Diptera was the next most common order detected by light traps with 31 species (28%), while Hymenoptera were surprisingly scarce (4 RTUs). Spiders and beetles were most commonly detected in pitfalls.

Table 4: Total number of RTUs from each of the main arthropod taxa, and the number represented in samples from each of the 5 collecting methods. Numbers in parentheses indicate the proportion of RTUs in the order that were only collected using that trap type and contributed >20% of order diversity.

Taxa	Total RTUs	% Σ RTUs	Hand	Light	Malaise	Pan	Pitfall
Non-insect arthropods:							
Acari	2	0.2%	0	2	1	2	2
Araneae	55	6.0%	9	3	20	16	50 (53%)
Chilopoda	5	0.5%	2	0	2	0	5
Collembola	5	0.5%	0	0	3	5	4
Copepoda	2	0.2%	0	0	0	0	2
Opiliones	1	0.1%	1	0	1	1	1
Protura	1	0.1%	0	0	0	1	0
Pseudoscorpionida	5	0.5%	3	0	3	3	5
Insects:							
Coleoptera	91	9.9%	15	5	49 (20%)	32	62 (34%)
Diptera	315	34.3%	20	31	235 (23%)	203	122
Ephemeroptera	1	0.1%	0	0	0	0	1
Hemiptera	74	8.1%	7	8	48	41	44
Hymenoptera	179	19.5%	8	4	141 (27%)	104	87
Lepidoptera	121	13.2%	20	47	81 (24%)	47	40
Neuroptera	1	0.1%	0	1	1	1	1
Orthoptera	10	1.1%	4	0	4	3	6
Plecoptera	4	0.4%	0	0	3	1	2
Psocoptera	9	1.0%	1	2	8	3	1
Siphonaptera	1	0.1%	0	0	0	0	1
Thysanoptera	13	1.4%	0	0	10	10	10
Trichoptera	24	2.6%	3	9	23 (38%)	8	6
Total RTUs	**919**	**100%**	**93**	**112**	**633**	**481**	**452**

4.3 Common and rare species

The frequency with which RTUs were detected across all samples (n = 468, including 30 hand collections) ranged from 1 to 247 (Appendix 3). One species (an unidentified mite in the family Prostigmatidae) was found in more than half (52%) of all samples (Table 5) and 28 RTUs (3%) were found in at least 20% of samples. In contrast, 292 RTUs (32%) were collected from just one sample (243 (26% of all RTUs) represented by a single specimen), and 554 RTUs (60%) were each found in 5 or fewer samples (<1%). Overall, 58% of specimens were comprised of just 4 RTUs; Collembola, 3 Hemiptera, and the Prostigmatidae mite noted above (Table 5). Following these, the most abundant insect was New Zealand's second most common and smallest native solitary bee, *Lasioglossum sordidum* (Halictidae), accounting for 2.5% of all specimens and appearing in 36% of samples (Fig. 2a). After mites, the southern ant (*Monomorium antarcticum* (Fr. Smith)), (Fig. 2b) was the most frequently occurring species (47% of samples), followed by *Telenomus* sp. (Platygastridae) a tiny egg parasitoid (45%), and *Balanococcus* sp., a phytophagous sap sucking mealybug (40%) (Table 5).

Table 5: The twenty most frequently occurring RTUs (shaded grey) and an additional 8 RTUs that together make up the 20 most abundant species collected (Ab.Rank = ranked 1-20 from most abundant). Frequency = number of samples in which detected, Abundance = total number of specimens captured.

RTU (Order: Family: species name)	Frequency	Abundance	Ab. Rank
Acari unident unident sp.1	247	7510	5
Hymenoptera: Formicidae: M*onomorium antarcticum*	222	2901	7
Hymenoptera: Platygastridae: *Telenomus* sp.1	210	1495	15
Hemiptera: Pseudococcidae: *Balanococcus* sp.1	187	17036	3
Hemiptera: Pseudococcidae: unident sp.1	179	13268	4
Diptera: Sciaridae: unident sp.1	173	785	
Thysanoptera: Thripidae: *Anaphothrips zelandicus*	172	859	
Hymenoptera: Encyrtidae: *Austrochoreia antipodis*	161	1350	18
Collembola: unident unident sp.1	160	32459	1
Hymenoptera: Halictidae: *Lasioglossum sordidum*	153	3827	6
Hymenoptera: Aphelinidae: unident sp.2	151	1392	17
Araneae: Theridiidae*: Steatoda truncata*	145	335	
Diptera: Tachinidae: *Procissio* sp.1	141	1637	12
Lepidoptera: Gelechiidae: *Kiwaia* sp.1	139	637	
Hemiptera: Lygaeidae: *Nysius huttoni*	124	1828	10
Diptera: Ephydridae: *Nostima duoseta*	122	807	
Hemiptera: Lygaeidae: *Rhypodes chinai*	115	1673	11
Araneae: Lycosidae: *Anoteropsis* sp.1	114	769	
Diptera: Cecidomyiidae: unident sp.1	113	311	
Diptera: Cecidomyiidae: *Dasineura* sp.1	109	343	
Hemiptera: unident unident sp.1	109	18477	2
Diptera: Empididae: *Hilara* sp.1	105	1429	16
Thysanoptera: unident unident sp.1	90	1324	19
Araneae: Lycosidae: *Anoteropsis arenivaga*	84	1314	20
Diptera: Ceratopogonidae: *Dasyhelea* sp.1	81	1503	14
Collembola: Hypogastruridae: unident sp.1	72	1896	9
Diptera: Tipulidae: unident sp.1	65	1557	13
Hemiptera: Lygaeidae: *Rhypodes* sp.1	50	2401	8

Another frequently occurring species was the Thrips *Anaphothrips zelandicus* (37%), thought to be associated with Poaceae (Mound, 1978)). An unidentified Sciaridae (minute flies associated with damp decaying organic matter) was the most frequently occurring fly, however other species were more abundant, E.g. *Dasyhelea* sp. (Ceratopogonidae), *Hilara* sp. (Empididae) and *Scaptomyza fuscitarsis* (native Drosophilidae that feeds on decaying plant matter, widespread (Landcare, 2017), Fig. 2c). The two most frequently occurring (and abundant, barring one unidentified species) beetles were each found in just 84 samples; the ladybird *Diomus* sp.1 (Fig. 2d) and the flightless but widespread Erotylid (pleasing fungus beetle) *Loberus anthracinus* (Fig. 2e). The latter is found throughout New Zealand, most commonly from high altitudes in the South Island, but it has previously been found under rocks in Otago in dry conditions (Leschen, 2003). The most frequently occurring and abundant moth was a *Kiwaia* sp. (Gelechiidae). *Anoteropsis arenivaga*, an endemic wolf spider, was the most abundant Araneae (1,314 specimens from 84 samples), while *Steatoda truncata* (Urquhart) (Theridiidae) (Fig. 2f), *Anoteropsis* sp. (Lycosidae) and *Anzacia gemmea* (Gnaphosidae) were collected

with greater frequency. *Anzacia gemmea* is known to be associated with open country and *S. truncata*, widespread in the South Island but also found in the North Island, is commonly encountered in riverbeds (Hann, 1994).

Of the 402 RTUs fully identified to species only 56 (14%) have been assessed and categorised under the New Zealand Threat Classification System (Appendix 4). One threatened species (Nationally Critical) was detected; *Pimeleocoris roseus* (Hemiptera: Miridae). The bug (Fig. 2g) has previously only been found on a prostrate *Pimelia* on the Waiho River flats, South Westland (Stringer et al., 2012), and given these flats have been severely modified by gravel movement, that population may no longer exist. In the Tasman, a single adult was found in each of the upper river sites in early December; Site 1 in a pitfall, and Site 5 in a pan trap. Four species were classified At Risk Naturally Uncommon; *Anoteropsis arenivaga* (Araneae: Lycosidae), *Eurythecta robusta* (Lepidoptera: Tortricidae), *Neoitamus smithii* (Diptera: Asilidae), *Nysius liliputanus* (Hemiptera: Lygaeidae), and three as Data Deficient; *Anabarhynchus indistinctus* (Diptera: Therevidae), *Matua festiva* (Araneae: Gnaphosidae), *Rhypodes triangulus* (Hemiptera: Lygaeidae). The 41 native species assessed as Not Threatened were all representatives of Araenae, Trichoptera, Plecoptera and Orthoptera, reflecting that only a limited number of arthropod groups have been assessed under the NZTCS to date. Of the 56 RTUs assessed, seven (three bees and four spiders) were listed as Introduced and Naturalised.
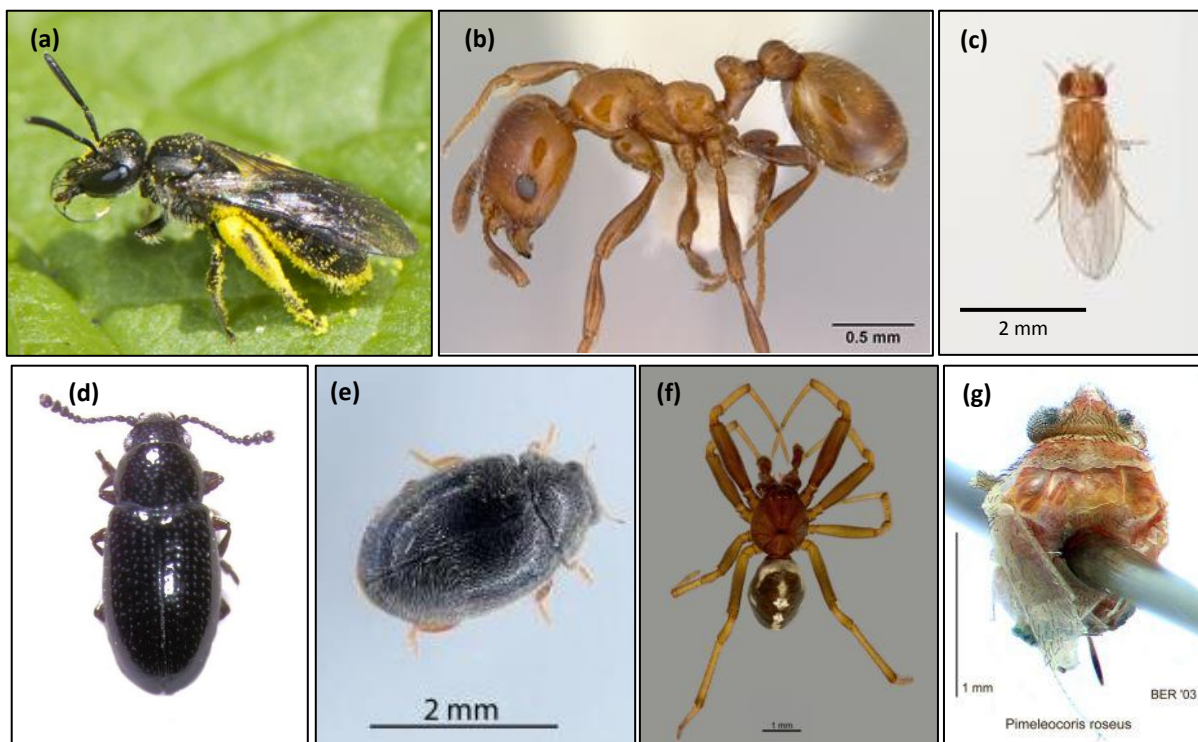

Figure 2: (a) The native Halticid *Lasioglossum sordidum,* one of the most abundant species, collected from 36% of samples including 68% of pan and 66% of malaise samples. **(b)** *Monomorium antarcticum*, the Southern Ant, is New Zealand's most ubiquitous ant, distributed throughout the country. **c-f** examples of abundant or frequently collected species from different orders: **(c)** *Scaptomyza fuscitarsis*, native Drosophilid fly. **(d)** *Loberus anthracinus,* pleasing fungus beetle. **(e)** A *Diomus sp.* Ladybird. **(f)** *Steatoda truncate*, endemic Theridiid spider, **(g)** *Pimeleocoris roseus,* a nationally critical endemic mirid bug. *Photos: a) Landcare Research, b) Plant & Food Research, c) Tim Holmes © Plant & Food Research, d) S. Thorpe, wikimedia commons, e) Nicholas Martin © Plant & Food Research, f) Marinov et al (2014), g) Landcare Research.*

4.4 Juvenile specimens

Of the specimens identified to RTU, 18.4% were recorded as larvae or nymphs. These belonged to 90 RTUs (Appendix 5) in 8 orders (Table 6a), representing just 9.7% of all RTUs identified. Only 2 RTUs (both spiders) were identified solely from juvenile specimens (i.e. no adults of the same RTU were identified); *Diaea* sp.1 (Thomisidae) and an unidentified Salticidae.

Hemiptera accounted for 92% of all juvenile specimens, and these represented > 52% of all the Hemiptera collected. Nymphs were identified for 28% (21/74) of Hemiptera RTUs, primarily in the families Pseudococcidae (mealy bugs) and Lygaeidae (seed bugs). The most commonly sampled were *Balanococcus* sp. 1 (15,847 specimens), another unidentified pseudococcid (6,292 specimens), the endemic Lygaeids *Rhypodes chinai* (1,224), and *Rhypodes* sp. 1 (1,199). *Rhypodes chinai* occurs south of Wellington, has been collected from sea level to 1982 m, and is thought to breed on *Raoulia* and possibly *Celmisia* species. Spiders made up only 6.8% of juvenile specimens, and these included representatives of 70% of all spider RTUs and 49% of the total spider specimens. The Lycosidae, which are commonly associated with open habitats (Vink, 2002), had the highest juvenile abundance, with *Anoteropsis aerescens*, *Anoteropsis* sp. 1 and *A. arenivaga* contributing 346 to 459 specimens each. The most commonly captured Lepidoptera larvae were the Noctuids *Meterana* sp., *Rictonis comma* (Walker) and *Graphania* sp.. All but one of the Orthoptera nymphs were identified as the wētā *Hemideina maori*. Larval Coleoptera and Diptera were generally not identified beyond order, but included one Scarab and one Chironomid RTU respectively.

Juveniles represented almost a quarter (23.5%) of specimens collected in pitfall traps (Table 6b), and only very small proportions of catches from malaise and light traps, both of which favour capture of flying insects.

Table 6: (a) Total number of juvenile specimens collected and number of RTUs to which they were identified. Percent (%) of Juv = proportion of all juvenile specimens contributed by that order. Percent (%) of Total = proportion of all specimens identified for each order that were juveniles. **(b)** Total number of juvenile specimens collected by trap type and proportion of total trap catch (from Table 2) represented by juvenile specimens.

(a) Order	# Juv.	# RTUs	% of Juv	% of Total	(b) Trap Type	# Juv.	% Juv
Araneae	1,911	40	6.8%	48.9%	Pitfall	23,942	23.4%
Coleoptera	123	7	0.4%	7.4%	Pan	3,009	16.2%
Diptera	29	2	0.1%	0.1%	Malaise	1,081	3.9%
Hemiptera	25,867	21	92.1%	52.7%	Hand	42	10.9%
Lepidoptera	99	11	0.4%	2.5%	Light	9	0.2%
Orthoptera	33	2	0.1%	29.7%	**Total**	**28,083**	**18.4%**
Psocoptera	2	2	0.01%	0.9%			
Thysanoptera	19	5	0.1%	0.4%			

4.5 Community composition

Hand collection was excluded from composition analysis as it was not independent of other sampling methods (collections were made when servicing other trap types). MDS ordinations presented below provide a graphical representation of species composition, while ANOSIM and SIMPER tests are used for the statistical comparison of species composition between each pair of trap types, sites, vegetation communities, moon phases and sampling times. Each point on the MDS ordination graphs (e.g. Fig. 3) represents the species composition of a sample, and the relative placement of points indicates how similar the composition of one sample is to all others (close together = similar composition, further apart = more distinct).

Clear distinctions were observed in the community compositions detected using the different trap types (Fig. 3a). There was no effect of moon phase (R=0.005, at 31.6% significance) (Fig. 3b) and a small but significant difference between sample sites (Fig. 3c). Collection date (T1-T4) also had some influence on species collected by all trap types (Fig. 3d). The stress value of 0.22 is high, indicating the coarse patterns (e.g. clustering by trap type) give a good representation of the data but the finer details (e.g. significance of site and time) require further examination. The influence of trap type, time and site/vegetation type are detailed further below.
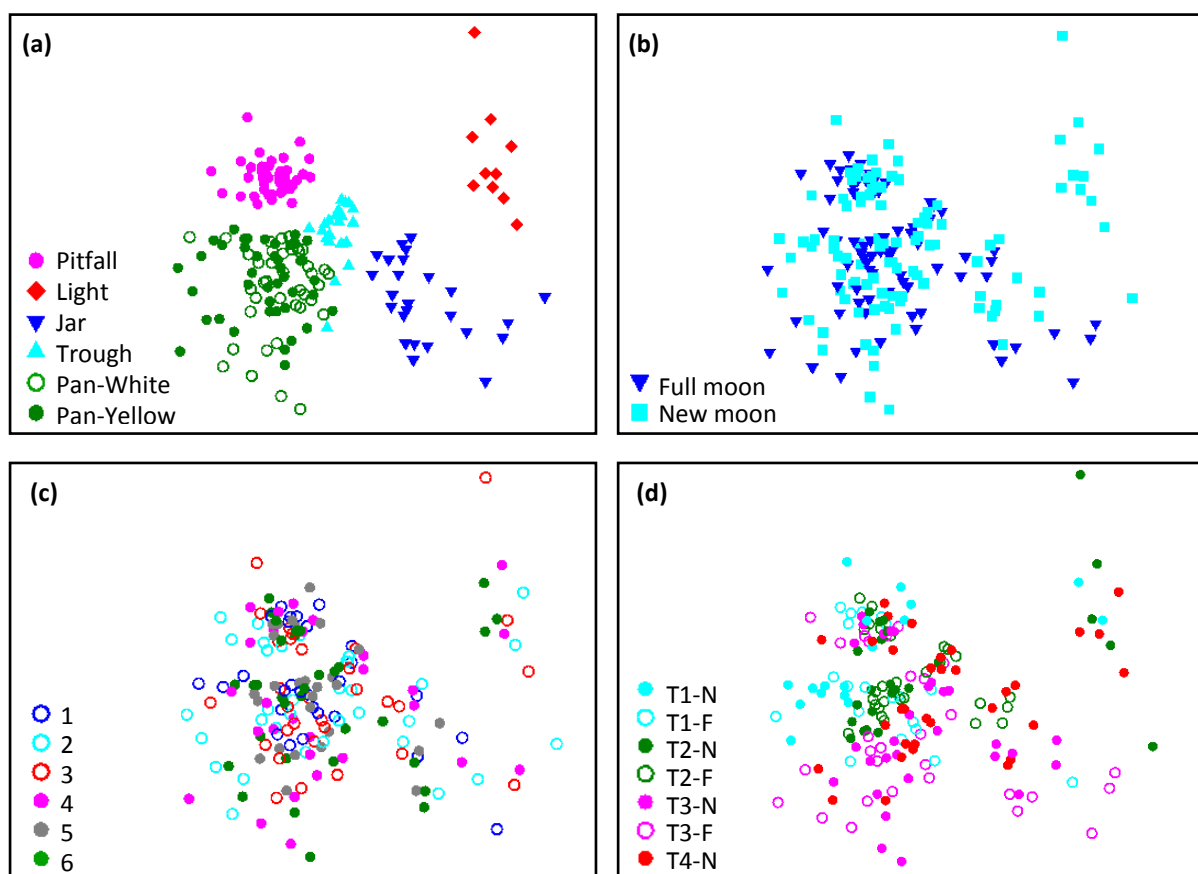

Figure 3: MDS sample ordination showing relative species composition delimited by (**a**) trap type (**b**) moon phase, (**c**) sampling site/vegetation type (sites 1-3 = vegetation type A (open circles), site 4 = C, site 5 = D, site 6 = B), (**d**) sampling time period (T1 – T4, see appendix 1 for exact dates). *n* = 180 samples. *Stress* = 0.22.

4.5.1 Trap type effect – is the community detected dependant on sampling method?

ANOSIM conducted on all trap types (i.e. light, malaise-jar, malaise-trough, pitfall, pan-white, pan-yellow, Fig. 3a) indicated the community composition captured was significantly different for all pairs of trap types (Global R=0.667, p=0.001), and this was supported by cluster analysis (Appendix 6). There was a statistically significant difference between communities detected by the two pan colours (Fig. 4a), however the R coefficient (R=0.139, p=0.001) was extremely low, indicating only a small proportion of the variation was explained by trap colour. As such, pan colours were aggregated for subsequent analysis. For malaise samples, jar and trough composition was significantly different (R=0.659, p=0.001; Fig. 4b), with the trough sample composition sharing only 20.18% similarity with the main cluster of jar samples. However, as noted earlier, the two collection methods were not independent of each other and were therefore also aggregated in subsequent statistical analysis (but see recommendations).
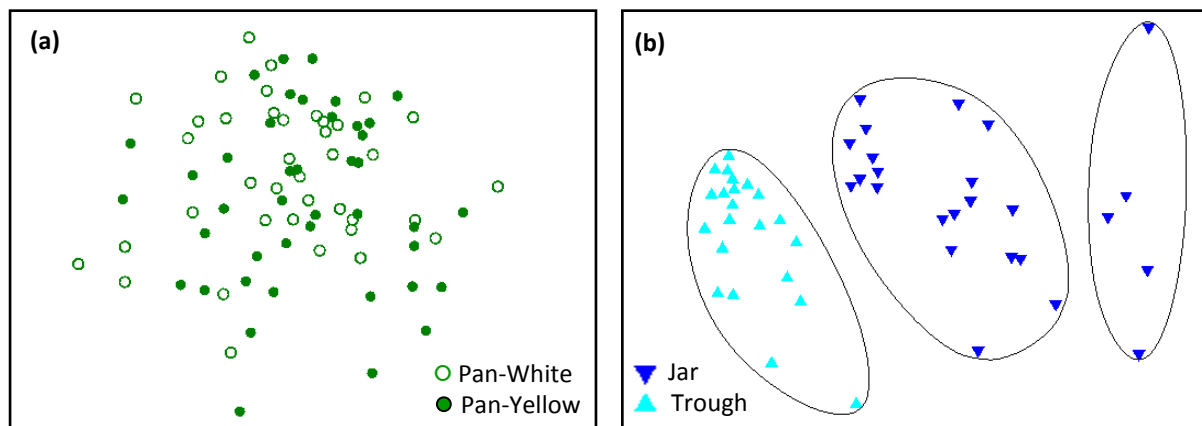
Figure 4: MDS sample ordination showing relative species composition of **(a)** white vs. yellow pan traps (n=42 samples each, *stress* = 0.27) and **(b)** jar vs. trough collection devices on malaise traps (n=25 samples each, stress = 0.14). The low stress value for the malaise ordination indicates a good representation of rank similarities at a fine scale and the ordination is overlaid with a hierarchical cluster analysis showing the species composition of trough samples differs significantly from jar samples at 20.18% similarity (Pi = 4.71, 4.7% sig.).

ANOSIM on a subsequent MDS ordination of all data with yellow and white pan samples aggregated and jar and trough samples aggregated indicated significant differences between all four trap types (Global R=0.591, p=0.001). The greatest compositional differences occurred between light samples and all other trap types (Table 7). Pitfall and malaise catches were more different to each other than either were from pan catches, reiterating the fact that of these three trap types, pans captured fewer unique RTUs (9.1% vs. 13.8% Pitfall and 21.5% Malaise).

Table 7: Average dissimilarity from SIMPER analysis, and R coefficients from ANOSIM comparing the community composition detected for each pair of the four main trap types based on fourth root transformed ranked-abundance sample data. Global R=0.591, p=0.001. Significant differences at the 5% level are indicated by * after Bonferroni corrected p-values for multiple comparisons.

Trap Pair	Ave. Dissimilarity	R value	p value	Significance
Malaise – Light	90.93	0.747	0.001	*
Malaise – Pitfall	84.87	0.646	0.001	*
Malaise – Pan	82.99	0.473	0.001	*
Light – Pitfall	95.25	0.998	0.001	*
Light – Pan	95.54	0.984	0.001	*
Pitfall – Pan	80.54	0.506	0.001	*

Species contributions to trap effect – are particular taxa representative of trap type?

Species that occur consistently within samples of a given group may be useful as indicators of that group. Here, no individual RTU was a strong indicator of trap type. The highest contributing species to within-trap sample similarity contributed just 6.4-15.3% (Table 8). Light traps showed the smallest number of species contributing to sample similarity. Just 7 RTUs accounted for 50% similarity (compared to 14 for malaise and pitfall and 13 for pan) with the greatest contribution (15.3%) from the moth *Physetica caerulea* (Fig. 5a). RTUs from just 3 orders; Lepidoptera, Diptera and Trichoptera (1 RTU), contributed 82.6% to light sample similarity. Of note, only 1 of 23 RTUs unique to light trap samples (*Wiseana copularis* (Lep: Hepialidae, Fig. 5b) was among those RTUs contributing to 90% of average similarity (3.4% contribution). Similarly, species unique to the other three trap types contributed little to within-trap similarity, reflecting that species unique to a single trap type generally also occurred with low abundance.

Jar similarity (27.7%) was driven by a relatively small number of RTUs contributing greater proportions (50% similarity made up of just 6 species contributing 5.5-15.4% each). Trough samples had a greater average similarity (36.5%) but the contribution of each species was lower (25 RTUs contributing to 50% similarity, each contributing <3.8%). The RTUs driving jar composition similarity were the same as those driving overall malaise similarity (Table 8), reiterating the greater distinction between jar catches and other trap types compared to trough catches (Fig. 3a).

The *dissimilarity* between trap types was also driven by very small contributions from many species, rather than one or more strong indicator species. The highest single contribution, just 3.0%, was made by *Collembola* unident. sp.1, which was found with an average abundance of 3.7 per pitfall sample compared to 0.2 per pan sample (Table 9). The same species made the highest contribution to malaise vs. pitfall and also light vs. pitfall dissimilarity. The moth *P. caerulea* was the highest contributing species distinguishing light trap composition from both malaise and pan traps, and the sandfly *Austrosimulium* sp.1 for malaise vs. pan traps (just 1.6%).

Table 8: Average species composition similarity (%) within samples for the four main trap types, and the individual RTUs contributing most to this similarity (showing up to a cumulative total of 20%).

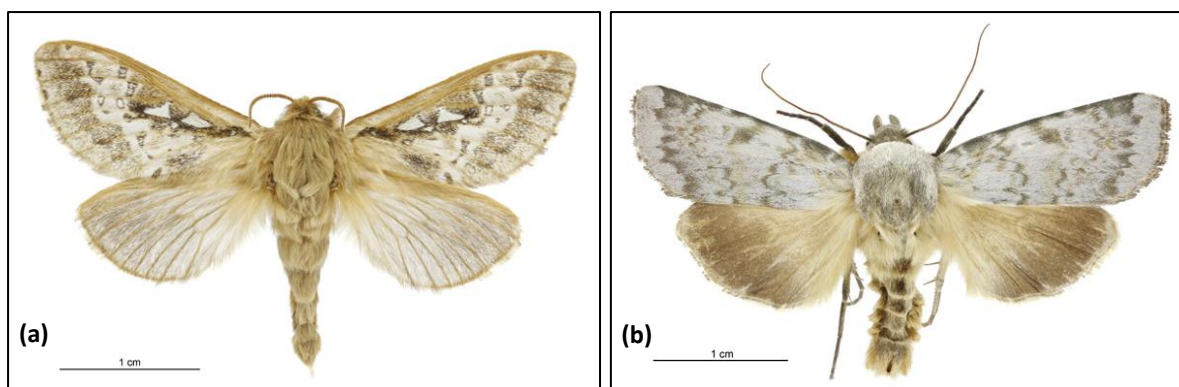| Trap	Ave. Similarity	Contributing Species	% Contribution
Malaise	24.33	*Austrosimulium* sp.1 (Diptera: Simuliidae)	7.34
		Orthocladinae sp.8 (Diptera: Chironomidae)	6.02
		Chironomidae sp.8 (Diptera)	5.76
		Lasioglossum sordidum (Hym: Halictidae)	4.33
Light	37.39	*Physetica caerulea* (Lepidoptera: Noctuidae)	15.28
		Diptera unident sp.1 (Tipulidae)	8.18
Pitfall	36.91	*Monomorium antarcticum* (Hym: Formicidae)	6.37
		Collembola unident. sp. 1	6.28
		Acari unident sp.1	5.44
		Balanococcus sp.1 (Hemiptera: Pseudococcidae)	4.61
Pan	25.97	*Lasioglossum sordidum* (Hym: Halictidae)	7.31
		Pseudococcidae unident sp.1 (Hemiptera)	7.00
		Telenomus sp.1 (Hymenoptera Platygastridae)	4.29
		Leioproctus maritimus (Hymenoptera: Colletidae)	3.94

Figure 5: (a) Male *Physetica caerulea* (Lepidoptera: Noctuidae), the highest contributing species to light trap sample similarity. **(b)** Male *Wiseana copularis* (Lepidoptera: Hepialidae), the only species unique to light trap samples that was included among those RTUs contributing to the top 90% of light sample similarity. Photos: Brigit Rhode (Landcare Research Larger Moths of New Zealand Image Gallery).

Table 9: Highest contributing species to between-trap dissimilarity (Av. trap diss.) determined by SIMPER analysis. The next two data columns show the average abundance of the species per sample for each of the traps compared. Av. species diss = average dissimilarity in the listed species' abundance between trap pairs, Species contrib% = % contribution made by the listed species to the dissimilarity between the trap pair.

Trap pair	Av. trap diss.	Av. species abundance		Av. species diss.	Species diss/SD	Species contrib%
Malaise vs. Light	90.9 %	Malaise	Light			
Physetica caerulea		0.16	2.51	2.44	1.34	2.69
Malaise vs. Pitfall	84.9 %	Malaise	Pitfall			
Collembola unident. sp.1		0.52	3.67	2.09	1.23	2.46
Light vs. Pitfall	95.3 %	Light	Pitfall			
Collembola unident. sp.1		0	3.67	2.67	1.5	2.8
Malaise vs. Pan	83.0 %	Malaise	Pan			
Austrosimulium sp.1		1.46	0.09	1.32	1.2	1.59
Light vs. Pan	95.5 %	Light	Pan			
Physetica caerulea		2.51	0.16	2.71	2.36	2.83
Pitfall vs. Pan	80.5 %	Pitfall	Pan			
Collembola unident. sp.1		3.67	0.22	2.44	1.49	3.03

4.5.2 Time effect – how does sampling time influence the invertebrate community detected?

Total diversity and abundance of invertebrates detected varied over time (Fig. 6). No more than 55% of all 919 RTUs were collected during a single sampling period across all trap types combined, and 25-63% were detected per sampling period for each traping method separately. Low catches were observed in the first session (T1-N) partly because no malaise traps were deployed. Seasonal trends therefore require assessment for each trap type separately. However, it should be noted that peak total abundance was observed in late November despite only one malaise trap having been deployed. This was largely a result of extremely high catches of RTU537 (*Balanococcus* sp. 1) and RTU554 (an

unidentified Hemiptera), particularly in pitfall traps. Full deployment of malaise traps did not result in an increase in either total abundance or diversity from December to January relative to November.

Total diversity detected using pitfall and pan traps, and average diversity detected using malaise traps (to account for differece in the number deployed), showed a common seasonal trend (Fig. 7); increasing from October to late November, declining mid-December to mid-January, then began to increase again in late January. The same trend can not be determined with certainty for light traps because of the absence of samping in mid January.
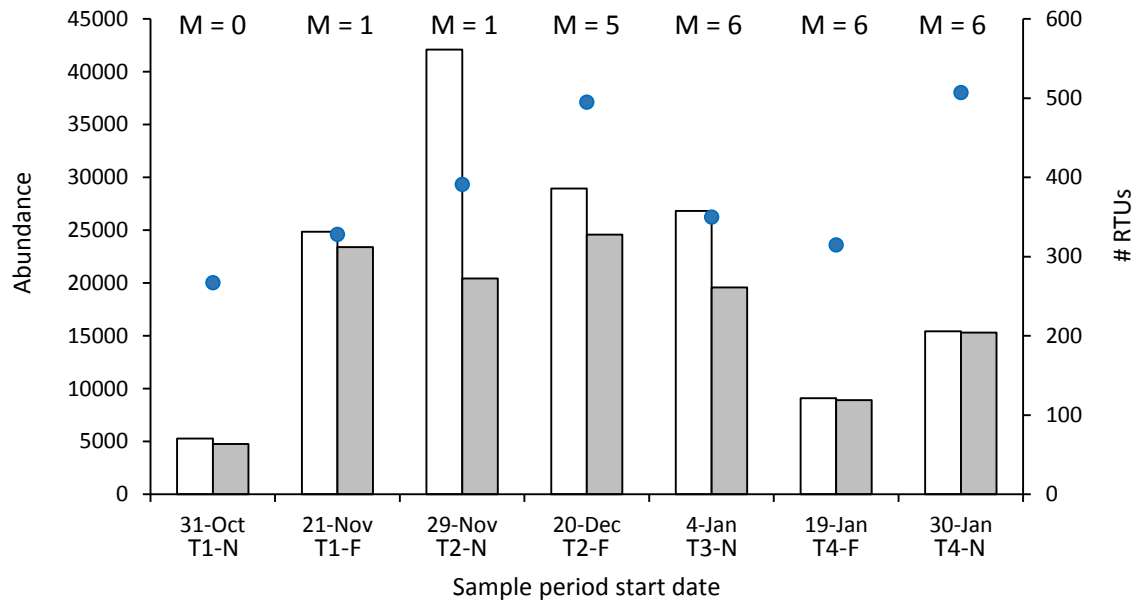
Figure 6: Total abundance (white bars), abundance excluding two dominating Hemiptera (RTU537 & RTU554, grey bars) and total diversity (circles) of invertebrates collected across all 6 sites using all trapping methods at each consecutive sampling period. Light traps were only deployed during the new moon phase (N= new, F = full) and the number of malaise traps (M) deployed ranged from 0 to 6 per session as indicated above each bar.
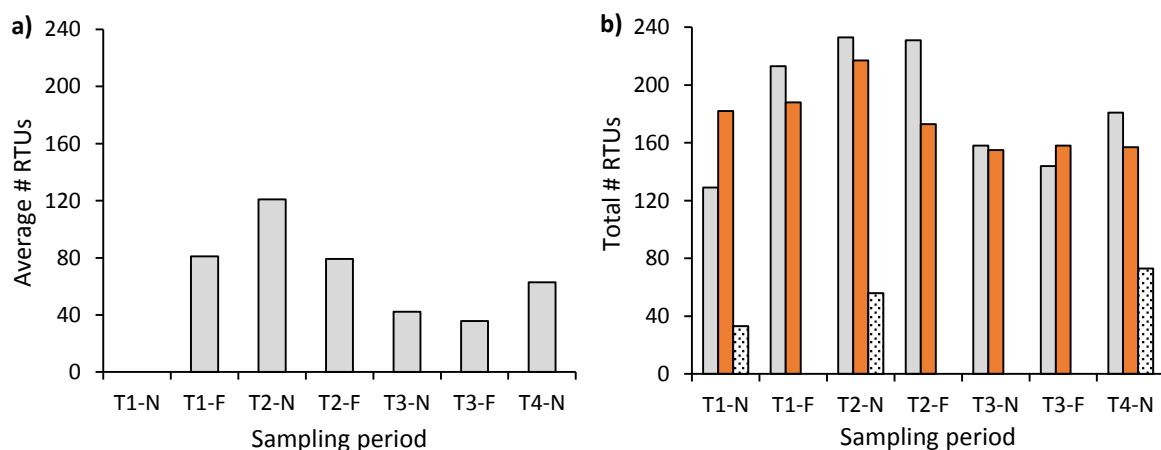
Figure 7: Seasonal trend in species diversity captued across 6 sites using **(a)** malaise and (**b**) pan (grey bars), pifall (orange) and light (stippled) traps. Average RTUs are reported for malaise traps as the numer of traps varied from 1-6 per sampling period. Total RTUs are reported for pan and pitfall (6 traps each) and light traps (1 trap).

To compare abundance data across time, Acari, Collembola and 3 Hemiptera that exhibited extremley high and variable catches, were excluded from analysis. These taxa accounted for 91,471 specimens across all traps, including 83,853 specimens from pitfalls alone. Malaise traps captured relatively few juveniles (Fig. 8b). The peak in adult abundance was driven by high catches of 3 thrips species, 3 Hymenoptera and several Diptera species. The Hymenoptera were the native bee *L. sordidum*, the egg parasitoid *Telenomus* sp. and the scale parasitoid *Austrochoreia antipodis.* The hosts of the latter (Ericoccids) were not detected, possibly because of their sessile habit which would preclude capture in the traps used. At least a dozen Diptera exhibited high catches; the 5 highest contributors were all from different families with catches of 265-855 specimens in a single sampling period. Adults and juveniles caught in pan and pitfall traps (Fig. 8c, d) both peaked early in the season before declining. Although juvenile numbers subsequently remained low, adult catches increased again in January in both malaise and pitfall traps. The three Hemiptera excluded from this analysis showed a similar seasonal trend with a high catch peak in mid or late November followed by a steep decline and a much smaller second peak.
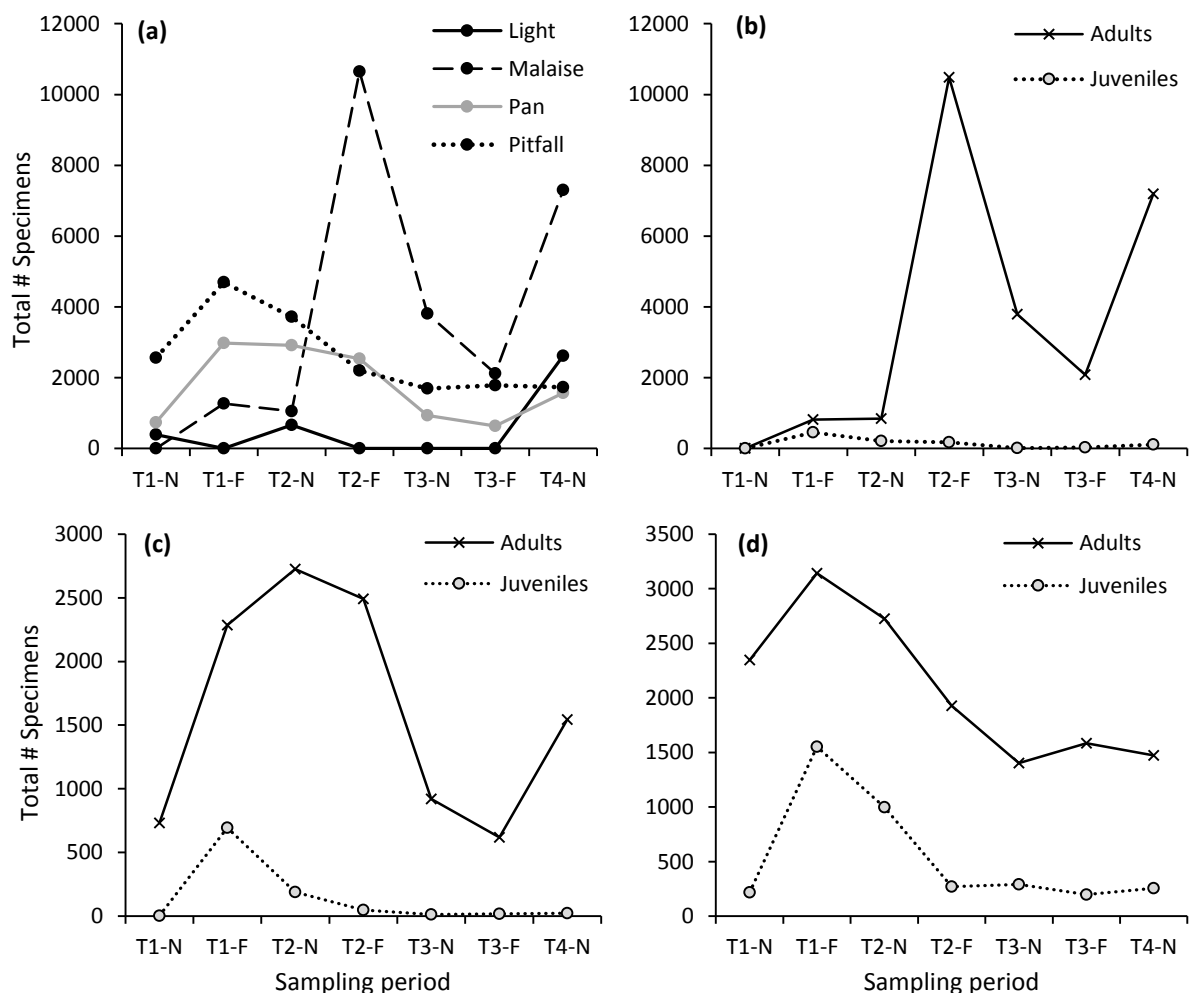

Figure 8: Seasonal trends in total abundance (excluding Acari, Collembola and Hemiptera 537, 541 and 554) for **(a)** adults and juveniles combined, and for **(b-d)** adults and juveniles separately using **(b)** malaise, **(c)** pan and **(d)** pitfall trapping methods.

Seasonal trends in community composition

ANOSIM combining all trap types showed a small but significant overall difference in species composition over time (R=0.194, p=0.001) and between all time-pairs. Dissimilarities ranged from 76.3% (between two consecutive sample periods) to 85.2%, with the three highest dissimilarities occurring between the first sampling period and each of the last 3 periods. Assessment of each trap type separately (Fig. 9) indicated significant differences in sample composition by time for pan (R=0.472, p=0.001), pitfall (R=0.46, p=0.001) and malaise (R=0.271, p=0.001) traps. The strength of the effect on malaise composition was higher when trough and jar samples were analysed separately as is more appropriate (jar R=0.657, p=0.001; trough R=0.442, p=0.001).
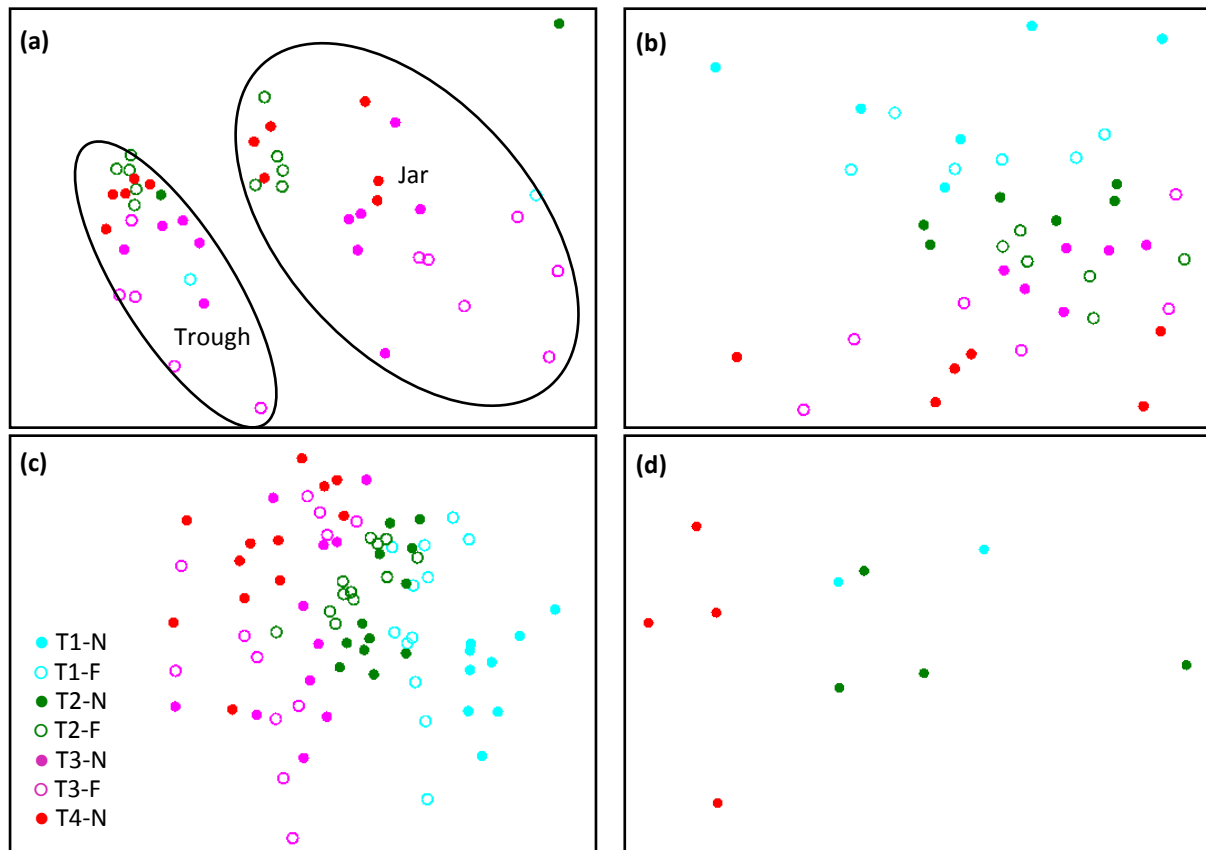
Figure 9: MDS sample ordination showing time effect by trap type **(a)** malaise (n=50, stress = 0.14), **(b)** pitfall (n=42, stress = 0.21), **(c)** pan (n=84, stress = 0.27), **(d)** light (n=10, stress = 0.009). T1-N to T4-N represent sampling periods in chronological order from Oct 2005 to Jan 2006 (see Appendix 1 for dates) during new (N) and full (F) moons. Light sampling was only conducted on new moons. Malaise replication varied across sampling dates.

Cluster analysis (Fig. 10) supported the coarse patterns observed in figure 9, including some statistically significant clusters consisting of a single sampling period or several consecutive periods. Groups incorporating multiple time periods showed an interaction with the distribution of sites across along the riverbed. For example, pan trap (Fig. 10a) samples from the first period formed a distinct cluster (T1-N: 21.5%; Pi = 2.89, p=0.001) while those from the last period formed 3 clusters; one including all samples from sites 2, 3, 4 (T4-N: 25.6%, Pi =2.47, p=0.001), and the other two including samples from T4 and the two earlier January periods from sties 1 and 5 (36.5%; Pi =1.99, p=0.005) and sites 6 (21.5%, Pi =2.96, p=0.024) respectively. Sites 1 and 5 occur in the upper reaches of the river, 2, 3 and 4 in the lower reaches, and 6 in the middle.

Although there are clearly multiple factors influencing species composition on each sampling occasion, and clusters are statistically weak, the temporal changes are likely to be real, reflecting the seasonal emergence of particular species. Although no individual species contributed more than 11.75% to within-time sample composition similarity (Table 10). A total of 344 RTUs were found during only one of the sampling periods; T1-N = 31, T2-F = 36, T2-N = 39, T3-F = 75, T3-N = 25, T4-F = 22, T4-N = 116. Notably, the highest number of 'time-unique' RTUs was observed in the final late January sample, suggesting a late season shift in composition. The low ANOSIM R-values suggest a relative change in abundance and frequency of individual RTUs, rather than a distinct shift in presence/absence. This reflects the fact that although some species were detected during discrete time periods, many other species, or particularly abundant species, were present throughout the study. SIMPER analysis supported this, with several of the highest contributing RTUs appearing across all months and no individual RTUs strongly driving seasonal differences in composition. For example, the highest contribution to sample dissimilarity was just 2.90% between T1-F and T3-N by Pseudococcidae unident sp. 1., an RTU found in 179 samples with an abundance of 13,268.

Table 10: Average composition similarity between samples collected during each sampling period (Time), and the RTUs contributing most to this similarity up to a cumulative total of ~20%.

Time	Ave. Similarity	Species	% Contribution
T1-N	25.12 %	Sciaridae unident sp. 1 (Diptera)	6.71
		Collembola unident sp. 1	5.32
		Rhypodes chinai (Hemiptera: Lygaeidae)	5.13
T1-F	28.37 %	Pseudococcidae unident sp.1 (Hemiptera)	11.75
		Anaphothrips zelandicus (Thysanoptera: Thripidae)	7.70
		Acari unident sp.1	6.10
T2-N	22.38 %	Pseudococcidae unident sp.1 (Hemiptera)	5.91
		Kiwaia sp.1 (Lepidoptera: Gelechiidae)	4.65
		Telenomus sp.1 (Hymenoptera: Platygastridae)	4.36
		Acari unident sp.1	4.24
T2-F	28.37 %	Acari unident sp.1	5.42
		Balanococcus sp.1 (Hemiptera: Pseudococcidae)	4.31
		Telenomus sp.1 (Hymenoptera: Platygastridae)	4.17
		Sciaridae unident sp. 1 (Diptera)	2.73
		Pseudococcidae unident sp.1 (Hemiptera)	2.58
T3-N	21.19 %	*Lasioglossum sordidum* (Hym: Halictidae)	9.13
		Procissio sp.1 (Diptera: Tachinidae)	6.19
		Acari unident sp.1	3.70
T3-F	18.70 %	*Lasioglossum sordidum* (Hymenoptera: Halictidae)	7.26
		Pseudococcidae unident sp.1 (Hemiptera)	6.35
		Orthocladinae sp.8 (Diptera: Chironomidae)	5.16
T4-F	21.51 %	*Nysius huttoni* (Hemiptera: Lygaeidae)	5.14
		Acari unident sp.1	4.01
		Dasyhelea sp.1 (Diptera: Ceratopogonidae)	3.67
		Pseudococcidae unident sp.1 (Hemiptera)	3.19
		Orthocladinae sp.8 (Diptera: Chironomidae)	3.15
		Telenomus sp.1 (Hymenoptera: Platygastridae)	3.13

(a)

T1-N T2-N T3-N T4-N
T1-F T2-F T3-F
(N = new moon, F = full moon)

% Similarity

Site 6   Sites 2, 3, 4   Sites 2, 3, 4, 6   Sites 1, 5   Sites 1, 5
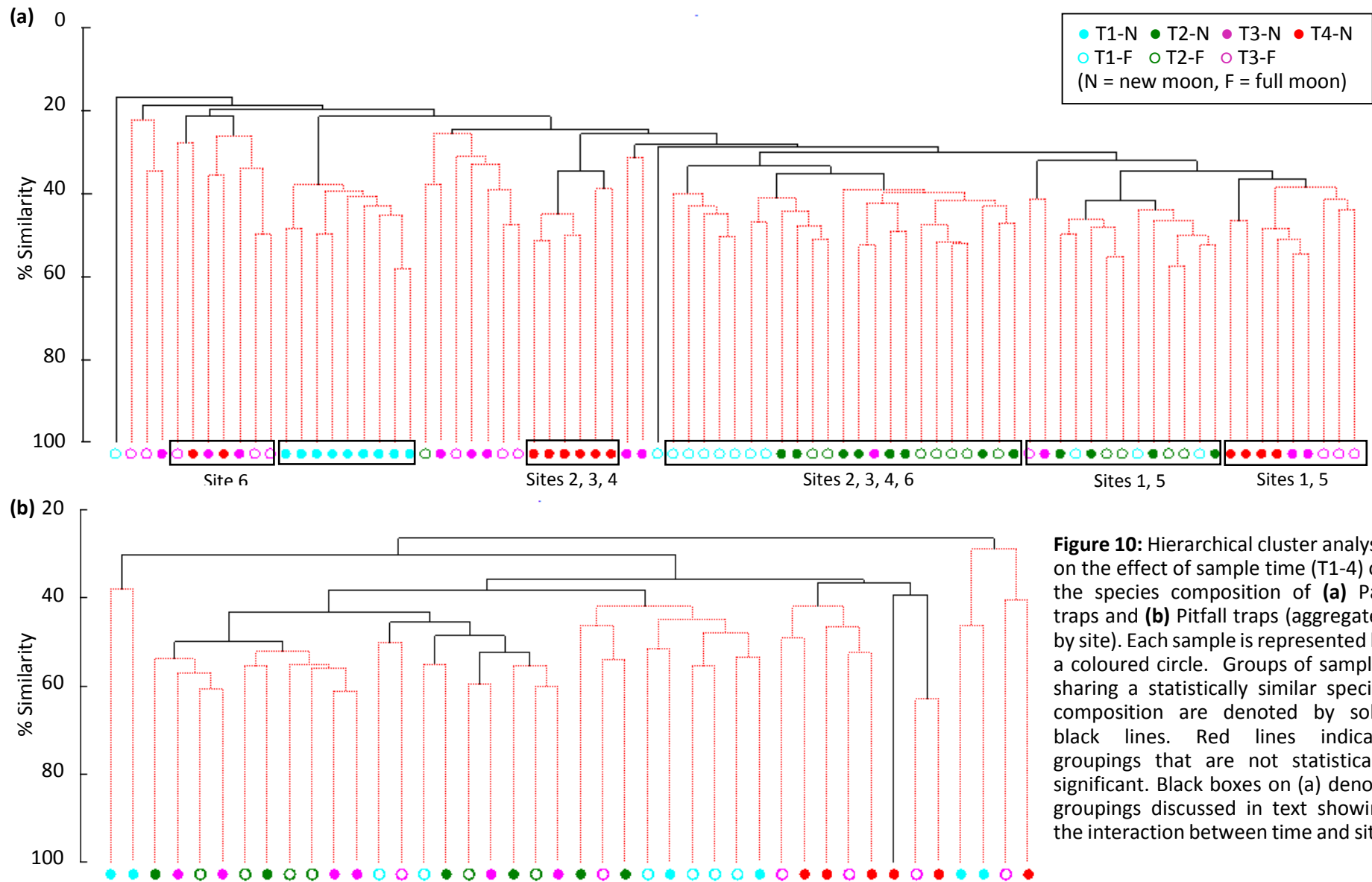
(b)

% Similarity

Figure 10: Hierarchical cluster analysis on the effect of sample time (T1-4) on the species composition of **(a)** Pan traps and **(b)** Pitfall traps (aggregated by site). Each sample is represented by a coloured circle. Groups of samples sharing a statistically similar species composition are denoted by solid black lines. Red lines indicate groupings that are not statistically significant. Black boxes on (a) denote groupings discussed in text showing the interaction between time and site.

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4.5.3 Site and vegetation effects

Statistically significant differences were detected between sites (Global R=0.118, p=0.001%) (Table 11a), however the negligibly small R-values indicate that although not *exactly* the same, site compositions overlapped strongly, and p-values are of limited relevance. The smallest R-values (and therefore compositional differences) were observed for comparisons between the three sites in the lower section of the river (2, 3, 4) and between sites 1 and 5, which were close together in the upper river. Similarly, the largest R-values were between sites 1 or 5 and all other sites. The main exception to this pattern was that site 2 showed minimal difference from any other site, regardless of proximity.

The influence of site distribution along the river can be seen more clearly when sites are grouped for analysis as upper (~680m asl), middle (~600m asl) and lower (~540-550m asl) (Fig. 11). Distribution of samples along the river had a moderate effect on the species composition detected by pitfall (R=0.275, p=0.001) and pan traps (R=0.268, p=0.001), but not malaise (R=0.057, p>1) or light (R=-0.099, p>1), noting the latter only included samples from the middle and lower reaches. For both pitfall and pan, upper site sample composition showed a moderate significant difference from site 6 in the middle, and slightly smaller differences to sites 2, 3, and 4 in the lower reaches (Table 11c). Hierarchical cluster analysis supported the grouping of sites 1 and 5 for both pan (32.2%; Pi=2.56, p=0.001) and pitfall (45.5 % similarity; Pi=1.76, p=0.002) traps. The site 1 + 5 grouping had the highest number of RTUs unique to any single pair of sites (42 RTUs compared to 9-14 RTUs for other pairs) and the lowest average between-site dissimilarity in sample composition (pitfall = 59.9%).

Comparisons of vegetation types also produced very low R-values (Global R=0.058, p=0.058), but indicated species composition of vegetation types B, C, and D showed some small differences while vegetation type A composition overlapped more strongly with all others. Vegetation type A included 3 of the 6 sites dispersed over the full length of the study area, which may account for the relative lack of differentiation.

Table 11: ANOSIM pairwise-comparisons of **(a)** sites, **(b)** vegetation-types, and **(c)** sites grouped by relative location along the river. **(a)** Site-pair differences ranked in order from lowest to highest R value. Sites 1, 2 and 3 all represent vegetation type A, site 4 = C, Site 5 = D, Site 6 = B. Site pairs shaded light blue denote those found relatively close together in the lower (2,3,4) or upper (1,5) river. Site pairs shaded dark grey indicate comparisons between the upper river sites (1, 5) and all others except site 2. **(c)** U = upper stretch of river, M = middle, L = lower. *Note: Bonferroni-type correction for multiple comparisons is not used in PRIMER ANOSIM because p values are strongly affected by sample size therefore adjusting values gives a false indication of certainty.*

| (a)	Site pair	R-value	p		(b)	Veg. pair	R-value	p
	2-3	-0.009	0.258			A-B	0.053	0.144
	2-4	0.016	0.222			A-C	0.095	0.048
	3-4	0.045	0.038			A-D	-0.041	0.735
	2-6	0.067	0.008			B-C	0.133	0.001
	1-5	0.085	0.004			B-D	0.154	0.001
	2-5	0.097	0.004			C-D	0.182	0.001
	3-6	0.112	0.002					
	4-6	0.154	0.001		(c)	Location	R-value	p
	1-2	0.158	0.001		**Pan:**	U-M	0.422	0.001**
	3-5	0.176	0.001			M-L	0.185	0.013**
	5-6	0.179	0.001			U-L	0.268	0.001**
	4-5	0.182	0.001					
	1-6	0.185	0.001		**Pitfall:**	U-M	0.384	0.001**
	1-3	0.199	0.001			M-L	0.042	0.316
	1-4	0.26	0.001			U-L	0.376	0.001**
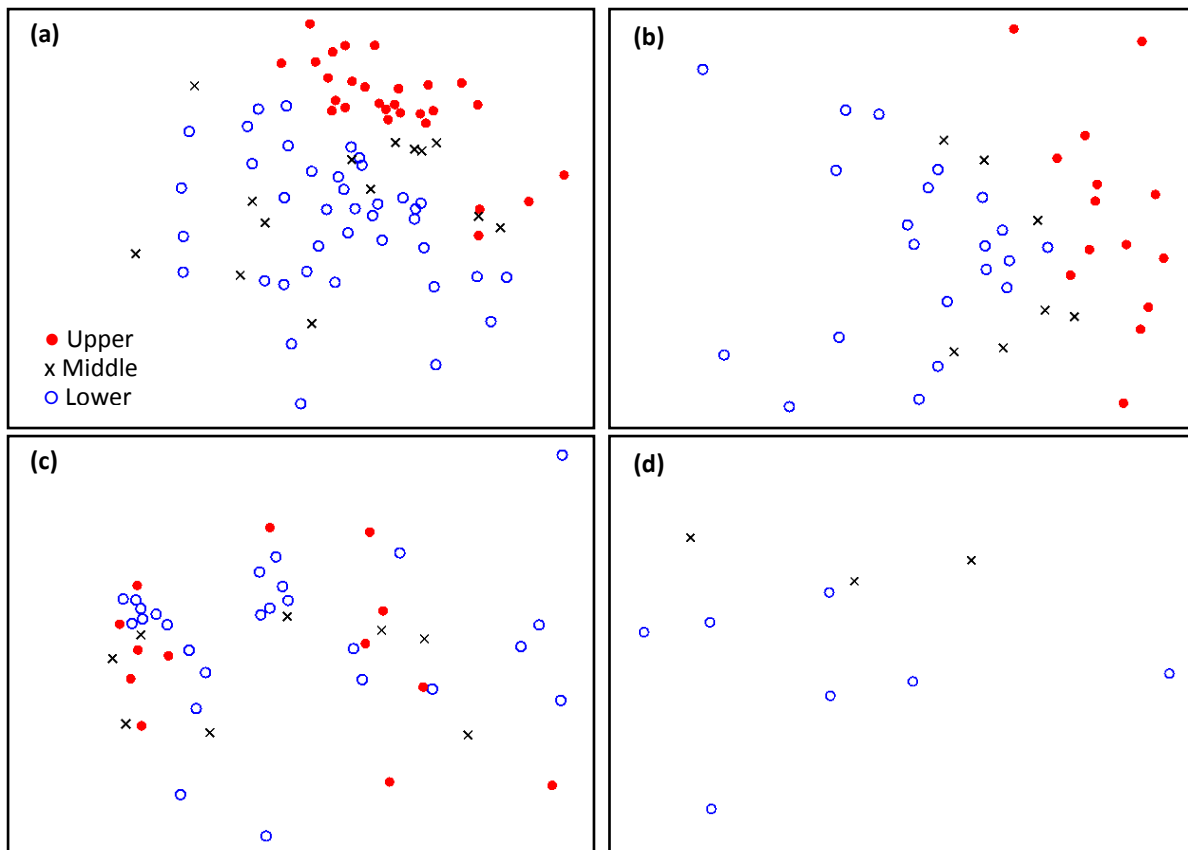
Figure 11: MDS sample ordinations by location along the length of the river for **(a)** pan (*stress* = 0.27), **(b)** pitfall (*stress* = 0.21), **(c)** malaise (*stress* = 0.14 and **(d)** light samples (*stress* = 0.09).

Species contributing to site & vegetation effects

The number of RTUs detected per site ranged from 396-466. No individual RTUs could be identified as strong drivers of sample composition between sites, vegetation types or position along the river. The largest contributions (up to 14.43%) were attributable to large variations in the abundance of very common species including the ant *M. antarcticum*, the native bee *Lasioglossum sordidum*, and unidentified species of Diptera (RTU389), Pseudococcidae (RTU541) and Collembola (RTU161), despite 4th root transformation of data. For example, the abundance of *L. sordidum* ranged from 10-621 across sites, and that of Collembola 161 ranged from 262-11,950.

No RTUs contributed more than 3.9% of the between-site or between-vegetation type dissimilarity. However, 335 RTUs (just over a third) were found in only one of the six sites, with the number unique to each ranging from 40 to 67. The number unique to vegetation type A was higher than other vegetation types (A = 745, B = 396, C = 410, D = 453), but the mean for the three type-A sites (445) was similar to sites B-D. If sampling was restricted to vegetation type A, which includes sites distributed along the length of the river, only 150 (16.3%) of all RTUs would have been missed, reiterating coverage in space is an important factor. This was supported in that 44% of RTUs were only found in one section of the river (upper = 172, middle = 47, lower = 182). After correcting for differences in sample size, proportionally more site-unique species were detected in the upper (86) vs. middle (47) and lower (66) sites. Species unique to a site tended to be detected at low abundance and as such contributed little to the statistical differences between sites. For example, although sites 1 and 5 formed statistically significant clusters (Fig. 10a, 11a) the 42 unique RTUs they shared contributed only 7.4% and 0.6% to average sample similarity for pitfall and pan traps respectively.

4.6 Taxonomic level of analysis

A strong correlation was observed between total species diversity and genus and family diversity (Appendix 7), suggesting they may be able to be used as surrogates for species level data. MDS sample ordination of community composition compared between datasets including full taxonomic detail (species) vs. aggregation to genus, family and order (Fig. 12) showed the overall patterns observed in trap types communities were retained at all levels, but began to diminish when data were aggregated to the order level (Fig. 12d). Stress values declined as data were aggregated to a higher taxonomic level indicating the patterns observed better represent the ranked similarities between samples and were less likely to be misinterpreted. Similar trends were observed for taxonomic level comparisons of composition between sites, sample times, moon phases and vegetation types, with the patterns generally remaining the same at all levels but beginning to collapse at the order level (Table 12).
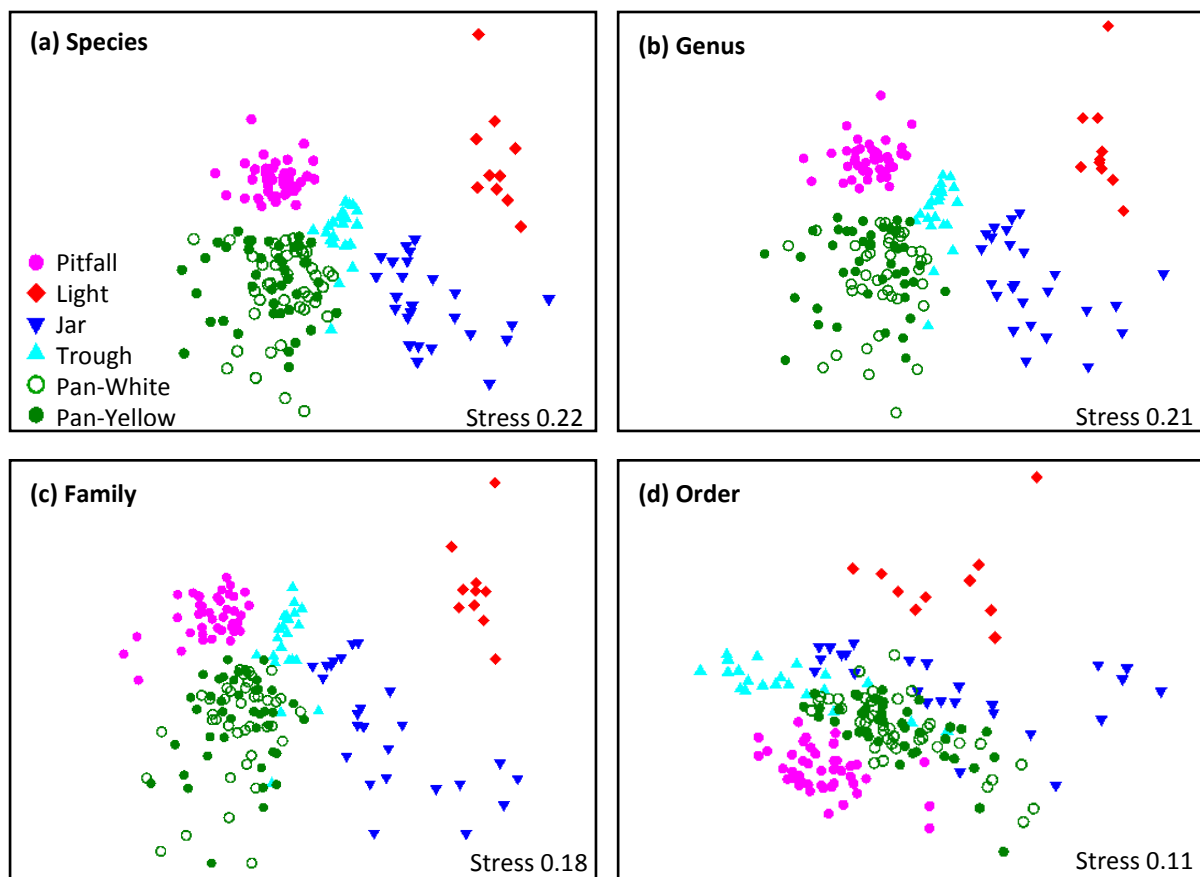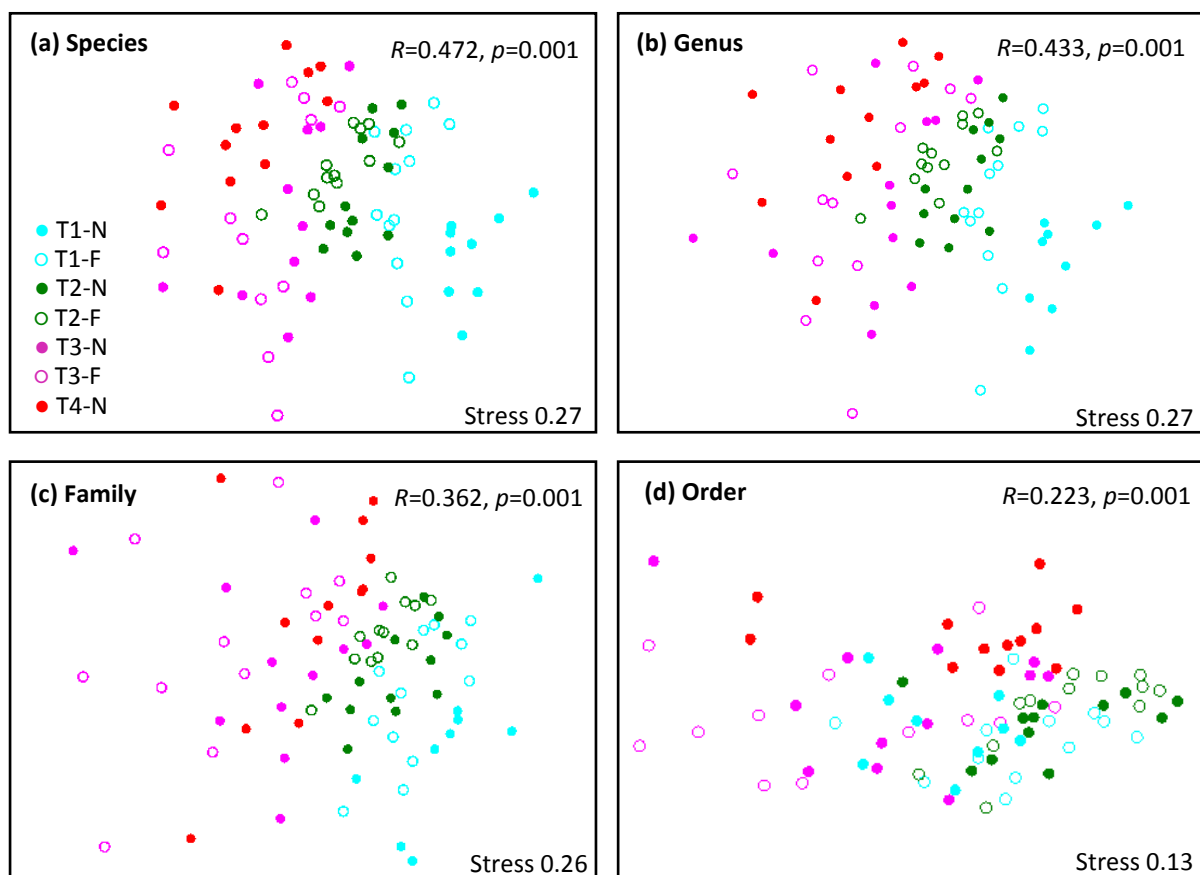

Figure 12: MDS sample ordination showing relative species composition by trap type based on identification of specimens to (**a**) Species (**b**) Genus (**c**) Family or (**d**) Order. *n*=186 samples.

Table 12: Effect of level of taxonomic identification (species, genus, family or order) on differences in community composition (ANOSIM) between trap-types, sampling times, sites, vegetation types and moon phase. Note the diminishing *R* values.

Comparison:	Species		Genus		Family		Order	
	R	*p*	*R*	*p*	*R*	*p*	*R*	*p*
Trap	0.667	0.001	0.598	0.001	0.584	0.001	0.498	0.001
Time	0.161	0.001	0.154	0.001	0.121	0.001	0.096	0.001
Site	0.13	0.001	0.113	0.001	0.076	0.001	0.032	0.004
Vegetation	0.065	0.038	0.061	0.047	0.040	0.150	0.002	0.496
Moon	0.005	0.316	0.004	0.325	0.003	0.390	0.019	0.116

The influence of level of taxonomic identification on the interpretation of data was more clearly seen by examining the details of individual variables within particular trap types. For example, the effect of sampling time on the community composition of pan samples (Fig. 13) can be interpreted with a similar level of certainty when specimens are identified to the genus rather than species level (Fig. 13b), as the variation explained by *time* declines by only 3.5% on average (Table 13). Aggregation to family level would result in less certainty in apparent differences between some sampling periods although a significant effect may still be accepted (e.g. T1-N v T2-N, *R* = 0.731), while differences between other periods may start to be rejected as arbitrary (e.g. T2-N v T4-N, *R* = 0.445). In contrast, identification only to order level (Fig. 13d) would result in a completely different interpretation; with no detectable effect of sampling time on the sample composition. At the order level, variation explained by time declines by 28% on average, and by 71% relative to when insects are identified to the species level.

Figure 13: MDS sample ordination showing relative species composition of Pan trap samples by sampling time based on identification of specimens to (**a**) Species (**b**) Genus (**c**) Family or (**d**) Order level. ●=T1-N, ○=T1F, ●=T2-N, ○= T2-F, ●=T3-N, ○=T3-F, ●=T4-N where N = New moon and F = Full moon.

Table 13: Relative R values (ANOSIM) for differences in the species composition of samples from each pair of time periods (T1N-T4N) sampled when taxonomic identification level is raised to Genus, Family or Order compared to Species level. Change in R indicates the amount by which R declines from Species (S) to each higher level (G = genus, F = family, O = order).

Time Pairs	Level of Identification				Change in R		
	Species	Genus	Family	Order	S-G	S-F	S-O
T1-N, T2-N	0.927	0.907	0.731	0.213	0.020	0.196	0.714
T1-N, T3-N	0.675	0.651	0.500	0.042	0.024	0.175	0.633
T1-N, T4-N	0.887	0.847	0.647	0.293	0.040	0.240	0.594
T1-F, T1-N	0.769	0.742	0.633	0.113	0.027	0.136	0.656
T1-F, T2-N	0.229	0.157	0.147	-0.014	0.072	0.082	0.243
T1-F, T2-F	0.410	0.364	0.324	0.147	0.046	0.086	0.263
T1-F, T3-N	0.492	0.429	0.458	0.288	0.063	0.034	0.204
T1-F, T3-F	0.509	0.461	0.449	0.312	0.048	0.060	0.197
T1-F, T4-N	0.614	0.549	0.505	0.296	0.065	0.109	0.318
T2-N, T3-N	0.315	0.304	0.272	0.317	0.011	0.043	-0.002
T2-N, T4-N	0.621	0.560	0.445	0.297	0.061	0.176	0.324
T2-F, T1-N	0.950	0.947	0.802	0.416	0.003	0.148	0.534
T2-F, T2-N	0.185	0.167	0.109	0.054	0.018	0.076	0.131
T2-F, T3-N	0.313	0.319	0.351	0.455	-0.006	-0.038	-0.142
T2-F, T3-F	0.447	0.416	0.416	0.484	0.031	0.031	-0.037
T2-F, T4-N	0.451	0.405	0.307	0.277	0.046	0.144	0.174
T3-N, T4-N	0.319	0.297	0.229	0.166	0.022	0.090	0.153
T3-F, T1-N	0.729	0.694	0.462	0.100	0.035	0.267	0.629
T3-F, T2-N	0.495	0.476	0.446	0.371	0.019	0.049	0.124
T3-F, T3-N	0.085	0.053	0.037	-0.028	0.032	0.048	0.113
T3-F, T4-N	0.359	0.303	0.199	0.230	0.056	0.160	0.129
				Mean reduction in R :	**0.035**	**0.110**	**0.283**

4.7 Individual orders as indicators

As biodiversity studies are more often restricted to particular insect orders, analysis was undertaken to compare how limiting the focus of the study to key orders could influence the conclusions that may be drawn about optimal sampling approaches and factors influencing the invertebrate community. Unsurprisingly, the diversity of the most species rich orders, Diptera and Hymenoptera, were strongly correlated (R^2=0.78) with total diversity, but Coleoptera (R^2=0.47), Lepidoptera (R^2=0.22) and spiders (R^2=0.24) were only weakly correlated (Appendix 7). The clear separation between the community compositions detected by different trap types was weakened substantially by focusing on only Diptera or Hymenoptera and absent for Lepidoptera and Coleoptera (Appendix 8). The influence of sampling time on species composition was also reduced when focusing on individual orders; for pitfall data there was a weak time effect for Diptera, Hymenoptera and Coleoptera, but not Lepidoptera, and for pan data the effect was absent, except possibly for Diptera (Appendix 9a, b). The effect of sampling location along the length of the river remained apparent in analysis of pan trap data for Diptera, Lepidoptera, and to a lesser extend Hymenoptera, but was absent for Coleoptera (Appendix 8c). In contrast pitfall data indicated a clear but weaker effect for Diptera, Hymenoptera and Coleoptera, but the effect was absent for Lepidoptera data (Appendix 9d).

4.8 Sampling effort

There was a poor correlation (Fig. 14a) between total abundance and total diversity of specimens caught per trap. The correlation was markedly improved by selectively excluding a group of highly abundant taxa (Fig. 14b) that had little impact on diversity. This approach is regularly taken in diversity studies, for example by only sorting specimens > 2mm in length. In this case, excluding the extremely small and ubiquitous Acari (2 RTUs) and Collembola (5 RTUs) could reduce the number of specimens requiring counting and identification by 28%, while also excluding the southern ant and the three highly abundant but tiny Hemiptera, could reduce this by a total of 62%. By contrast, these 11 RTUs accounted for just 1.2% of sample diversity.
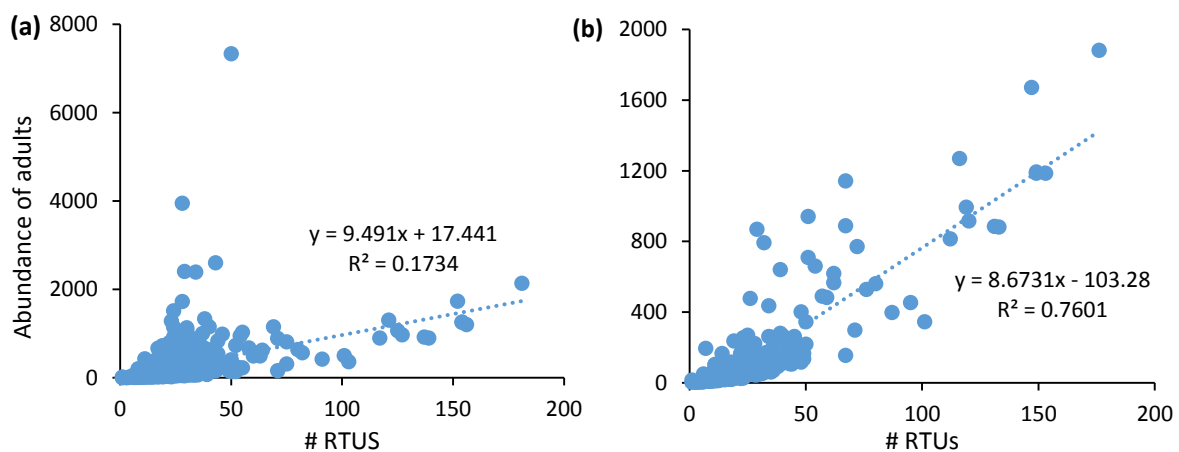
Figure 14: Total abundance vs. diversity of **(a)** all adult specimens sampled across all traps, sites and time periods and **(b)** all adult specimens excluding Collembola (5 RTUs), Acari (2 RTUs) and 3 dominating Hemiptera; Pseudococcidae *Balanococcus* sp.1, Pseudococcidae unident. sp1 and Hemiptera unident sp.

Species accumulation curves for total numbers of RTUs detected (inclusive of all trap types, replicates, sites, and times), indicated species count did not quite reach an asymptote (Fig. 15a), but the rate of accumulation per additional sample was low (<1 RTU per trap) above 300 samples. Extrapolator indices predict the true diversity in the study area to be between 1043 (Bootstrap) and 1206 (Jacknife) RTUs. Malaise trapping, particularly with troughs, proved the most efficient sampling method (Fig 15b, Table 14), with 52.5% of the total predicted diversity captured in just 25 traps, including the highest proportion of RTUs unique to a trap type (21.5%), and highest number of RTUs per samples processed (25.3). Pan and pitfall traps performed similarly with respect to the total proportion of diversity detected and the number of distinct RTUs collected given the number of samples, but the high total number of specimens captured in pitfalls substantially reduced sorting efficiency (0.004 RTUs per specimen, Table 14) relative to all other trap types. Notably, if the dominant Collembola, Acari, and Hemiptera identified above were excluded from processing, RTUs/specimen would increase for pitfall and pan traps to levels as or more efficient (0.029 and 0.039 respectively) than malaise and light traps, which in contrast show no change.

Sequential addition of trapping methods (Fig. 15c) indicates 82% of RTUs detected using all trap methods could be detected using only malaise and pan traps, reducing the number of samples from 442 to 204, and the number of specimens requiring processing from 152,509 to 46,047 (30% of total). The same proportion of RTUs could be detected using malaise and pitfall only with just 138 samples, while the inclusion of pitfall samples increased sample size to 254 and detected 88% of all RTUs.
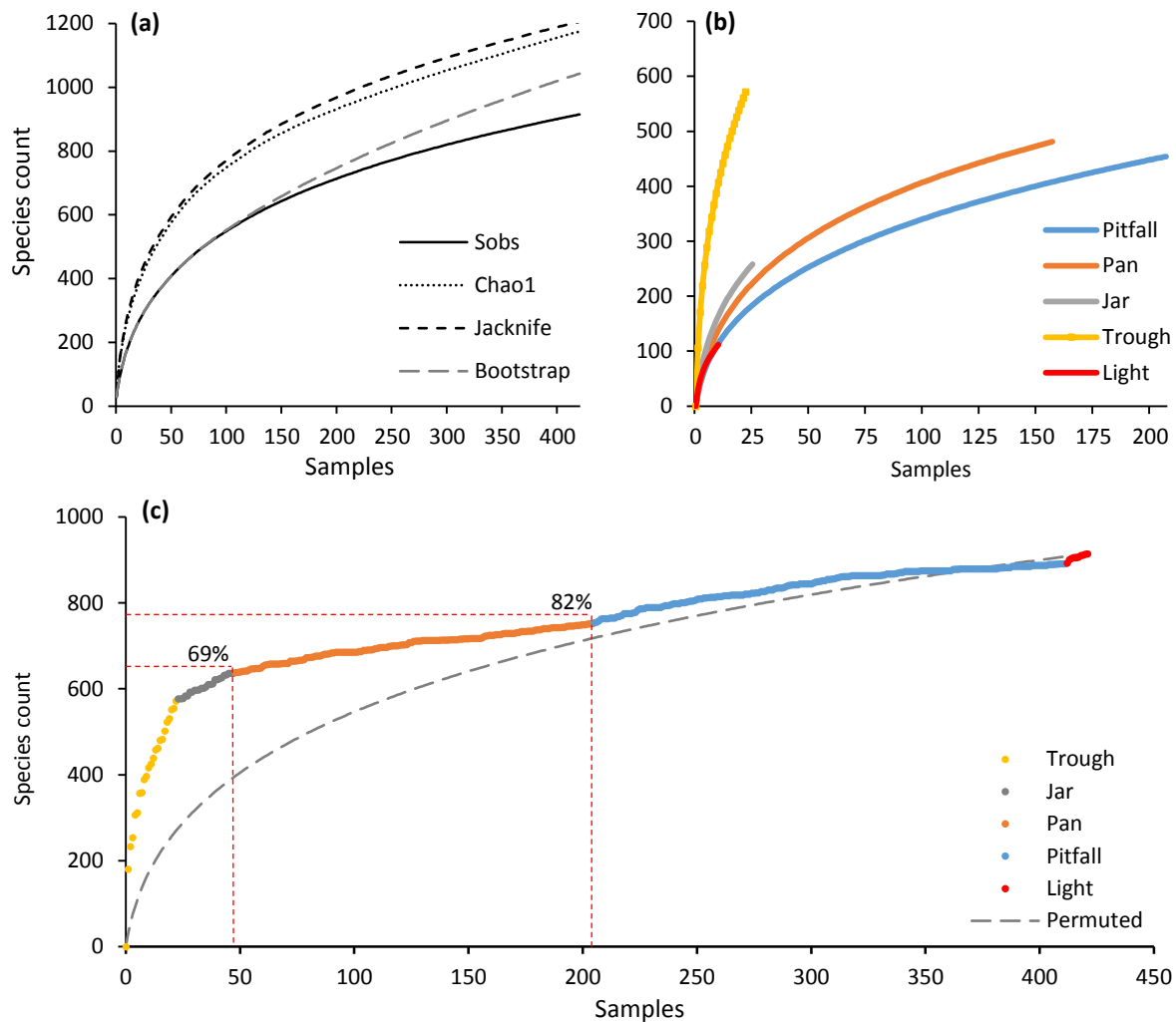
Figure 15: Permuted species accumulation curves for: **(a)** light, pan, pitfall and malaise trap samples combined (*n* = 421, 999 permutations) and **(b)** each trap type separately. Extrapolator indices in (a); Chao1 = a function of the number of species that have only 1 or 2 individuals in the entire pool, Jacknife = a function of the number of species seen in only 1 or 2 samples, bootstrap = a function of the proportion of samples that contain each species. **(c)** Observed vs. permuted accumulation curve for sequential addition of trap types containing the most to least RTUs. Red lines indicate the percentage of total RTUs detected using just malaise or malaise + pan traps.

Table 14: Coarse ranking of sampling efficiency of trap types, and sub-types, to detect invertebrate diversity as a function of the number of RTUs detected per sample and specimen sorted, the percentage of RTUs uniquely detected by each trap type and the percentage of the predicted (jacknife) total species diversity (1206 RTUs) across all trapping methods, sites and sampling times.

Trap	Samples	RTUs	RTU/sample	RTU/specimen	% Unique	% Predicted	Rank
Light	10	112	11.20	0.029	2.5%	9.3%	4
Pitfall	210	452	2.15	0.004	13.8%	37.5%	3
Malaise	25	633	25.32	0.023	21.5%	52.5%	1
Jar	25	258	10.32	0.029	3.8%	21.4%	
Trough	25	569	22.76	0.031	16.0%	47.2%	
Pan	168	481	2.86	0.026	9.1%	39.9%	2
White	84	358	4.26	0.037	3.7%	29.7%	
Yellow	84	378	4.50	0.042	3.8%	31.3%	

Sampling efficiency of trap types was also captured in diversity and equitability indices (Appendix 10). Margalef's *d*, a measure of the number of species present for a given number of individuals (higher score = more efficient detection), was 1.9 to 5 times higher for malaise traps (d=10.53, p<0.001) relative to other sampling methods, and driven by trough diversity (d=15.85). Simpson's index, the probability that any two specimens from a sample will be the same, was significantly higher for hand collection (λ =0.46, p<0.001) relative to all other methods, and for pitfall (λ=0.32) relative to pan (λ=0.16, p<0.001) and malaise traps (λ=0.19, p<0.001) which were both low (p=0.78). Relative to hand and light trap samples, pan, pitfall and malaise trap samples exhibited similarly high (p<0.05) levels of taxonomic distinctness (Δ*), measured as the average taxonomic distance between each pair of specimens in a sample *that are not of the same species* (Appendix 10). However, the average taxonomic *diversity* (Δ), measured as the taxonomic distance between each pair of specimens in a sample *including those of the same species*, was significantly lower for pitfall (Δ=66.5) compared to malaise (Δ=75.3, p=0.014) and pan traps (Δ=80.1, p=<0.001), again reflecting the high abundances of certain RTUs per sample. There was no difference in taxonomic diversity between pitfall, light and hand samples (p>0.05).

A steady accumulation of RTUs was observed over time, reiterating that sampling across the season is required to detect a full complement of species diversity (Fig. 16). However, selectively sampling in only December and February (T2 and T4, 189 samples) would detect 84% of the diversity detected across all sample periods. Restricting sampling to malaise and pan traps within this period detected 70% of total RTUs using only 96 samples (20% of total), while restricting to malaise and pitfall traps detected 73% of total RTUs, using 114 samples.
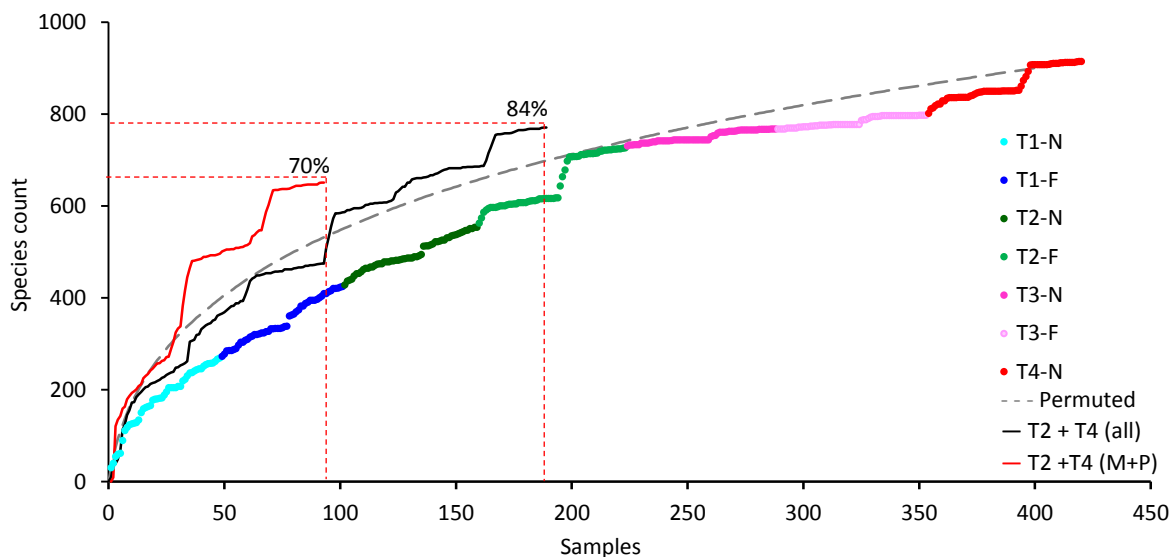

Figure 16: Permuted curve (all samples) vs. observed species accumulation with the sequential addition of all sampling times (multi-coloured line), sampling times T2 and T4 only (Black line), and times T2 and T4 only including only malaise and pan samples (red line). Red dashed lines indicates the percentage of total RTUs detected using reduced selections of samples.

5.0 Discussion and recommendations

The following discussion and recommendations address the 5 key questions identified in the introduction to this report and are based on the analysis of 152,509 specimens collected from 438 trap samples taken across 6 sites over the period 31 October 2005 to 3 February 2006.

1) What are the key features of the terrestrial invertebrate biodiversity values observed in the Tasman River?

A conservative count of 919 unique RTUs were identified from the *Raoulia haastii – R. australis* cushion-field community sampled, representing 165 arthropod families, 21 orders and 5 classes. Of these, 91% were insects, predominantly Diptera, Hymenoptera and Lepidoptera, and, to a lesser extent, Coleoptera. Characteristics of each group are discussed in sections 4.2-4.4. Spiders made up the majority of the 9% of the RTUs that were non-insect arthropods. The most frequently encountered invertebrate species were small bodied mites, Collembola, Hemiptera, flies (parasitic and aquatic) and parasitic wasps, as well as several larger, highly mobile generalists such as the southern ant, spiders and solitary native bees. The moth, *Kiwaia* sp., was also frequently detected. Some groups were notably absent, such as millipedes, amphipods and isopods. This may be an artefact of the collection methods employed but could also be indicative of a reduced detritivore community, possibly limited by the absence of deep, moist, litter layers. Further analyses are required to determine the overall herbivore : predator : detritivore ratio.

Beetle diversity (91 RTUs, 9.9% of total) was relatively low and included only 7 species of weevil, a family of herbivores that is often highly speciose in other environments. Orthoptera were also uncommon. The alpine wētā, *H. maori*, and crickets comprised the majority of specimens, while no cave or ground wētā, and only a few grasshopper specimens (Acrididae) were detected. Although grasshoppers do probably occur with only low abundance in this environment, the low detection rates for wētā may indicate the methods employed are not suitable for obtaining meaningful data on their presence or abundance. The native southern ant and solitary native bee (*L. sordidum*) were extremely common, while exotic honey and bumble bees were scarce. Total endemism could not be determined given many taxa were not identified to species, but for those that were, 13% were classified as exotic, 87% and indigenous and 84% as endemic. Of the 402 RTUs identified to species, only 14% were listed in the NZTCS, including the Nationally Critical mirid bug *Pimeleocoris roseus*.

The individual sampling sites and vegetation sub-communities assessed explained little of the variation encountered in the invertebrate community composition. Sampling time through the season had a moderate influence on species detected, and 40% of RTUs were collected during just 1 of the 4 sampling periods. This has implications for sampling design. The distribution of the sampling sites along the river also had a moderate influence on community composition. The greatest diversity and greatest number of RTUs unique to one section of the river was associated with the sites near the head of the river. It is not possible to determine if this reflects a true difference in the invertebrate community relative to further down the river, or whether it is an artefact of topography and habitat patchiness bringing taxa from different communities into closer proximity. To test this, future sampling should incorporate but longitudinal and transverse sampling, and assess species specificity to the 11 major vegetation types identified by Woolmore (2011).

Extrapolating from the available data (only half the samples collected have been sorted to date), true species diversity across the 6 sampling sites is predicted to be between 1043 and 1206 species. Species richness for the entire flood plain is likely to be somewhat higher, particularly for herbivores. This is

because a suite of species with close host-plant associations (e.g. weevils) are likely to have been missed given that 1) sampling methods employed targeted mobile taxa and 2) only 1 of 11 known vegetation communities was assessed limiting the range of plant diversity and structural complexity that was sampled. As the percentage of specialist insects associated with each vegetation community is unknown, it is not possible to extrapolate the current data to obtain true values for invertebrate diversity beyond the minimum numbers given here.

2) Which trapping method or combination of methods would be most suitable for rapid biodiversity assessment of other river systems in the future, and what are the minimum and ideal sample sizes required?

- *Recommendation 1: Use malaise traps with both jars and troughs for general biodiversity assessment*
- *Recommendation 2: Undertake study to compare malaise trap catch with and without troughs, while incorporating increased replication to determine optimal sampling size*
- *Recommendation 3: Supplement malaise trapping with methods targeted to key functional groups (large predators) or other groups of particular relevance to the research question*

A direct comparison of trap suitability and efficiency is difficult given each trap type has different set-up and processing costs (time and money) and targets invertebrates slightly differently (variation in surface areas and numerous other specifications that influence the probability of detecting different taxa). The most appropriate trap type will depend on the specific question being asked of the data. Maximising diversity detected using a single method can be best achieved using malaise traps with troughs (69% of total RTUs and the highest number of RTUs collected in only one trap type), although supplementing this with just one other trap type can increase diversity detected to >80% (see below). Malaise traps detected the highest diversity per sample and for a given abundance of individuals caught (Margalef's index), partly because the relative abundance of a small number of Acari, Collembola and Hemiptera species were substantially lower compared to pan and pitfall traps. This significantly reduces processing time. Equally important is that few immature insects were collected using malaise traps because they target flying and highly mobile insects; juveniles do not fly and, with the exception of predators, are less likely to move between multiple food sources. In comparison, almost a quarter of pitfall specimens were immatures. Unless a study is particularly interested in immature stages, it is beneficial to exclude them to reduce processing time, and increase confidence in correct species identification.

It should be noted the malaise traps used in this study were coupled with collecting troughs at the base of each side panel, rather than relying, as is more common, only on a collecting jar at the highest point of the trap. Although it is not possible to determine if insects caught in the troughs would have eventually been caught in the jars in the absence of troughs, a significantly greater proportion of RTUs were captured in the latter. Therefore, the recommendation to use malaise traps for future biodiversity assessment assumes troughs will be used. As troughs add to the cost and instillation time per trap, a specific study is recommended to compare the performance of traps with only jars versus traps with both jar and trough collection devices, to determine if the troughs are indeed required. Additionally, malaise sampling was not fully replicated in the current study and further investigation is necessary to determine the optimal number of samples, and the spatial and temporal design for this trap type.

Trap choice must also consider the practicalities of the study environment. Although pitfall traps have the benefit of being able to be left in the ground for use in multi-year studies (reducing annual set up

costs) this might not be practical in a riverbed setting where flooding may result in traps being buried or destroyed. Digging pitfalls into such a stony environment is also difficult. Malaise traps may be easier to set up, but are expensive to purchase, highly visible, and cannot be left *in situ* long term. They will be particularly susceptible to damage from strong winds, which are a common in braided rivers, and snow, which may preclude their use in winter.

All trap types added to the diversity detected in this study. A limitation of malaise traps is that they detected fewer large predators. Functional diversity has not been assessed here as this information was not readily available for all 919 RTUs. However, functional diversity is extremely important to ecosystem health and should be assessed for this study at a later date. Large predators, like flightless carabid beetles and spiders, may have keystone roles in the invertebrate community. Greater spider and beetle diversity was detected using pitfalls, and high proportions of these taxa (53% and 34% respectively) were detected only when using pitfalls. To accurately assess the predator guild, or large flightless taxa in general, malaise trapping needs to be replaced by, or supplemented with, pitfall tapping. Pitfalls are cheap, durable and inconspicuous but may be difficult to install in a stony environment. Once in place they can be covered over and reused over multiple years. These factors should be weighed against the possible increase in time required to sort and identify the large numbers of specimens captured.

If tight associations between insects and vegetation communities are of interest other methods should be considered, such as vacuuming, beating or sweep netting, depending on vegetation structure. These methods may detect some of the taxa that were conspicuously uncommon, such as weevils. Rearing hosts of parasitic insects or installing emergence traps over plants to capture the emerging adults of root feeders, or internally-feeding leaf and stem feeders, may also be required. Hand collecting is not recommended for any form of comparative diversity assessment as it is inherently biased towards certain taxa, is not able to be replicated over time or space in a standardised way and is highly dependent on observer skill. In contrast to trapping methods, the capture period for hand collection is limited to the point in time when the observer is present, rather than over a period of many days. Light trapping can be affected by short collection time frames to a lesser degree but has obvious benefit in studies focused on Lepidoptera. Interestingly, the diversity of Hymenoptera collected in light traps here was much lower than expected.

Pan sampling favoured Diptera and Hymenoptera, detecting 62 RTUs from these orders that were not detecting using other methods. Overall, however, less than 10% of RTUs were uniquely detected using pans, and detection rate per pan sample was low, although the initial accumulation rate (e.g. RTUs in the first 25 samples) was higher than for pitfall and light traps. White pan traps caught marginally more specimens than yellow traps, but no greater diversity. Both trap types effectively collected the same number of unique species, however putting out twice as many traps of just one colour could potentially result in the additional species being collected. It is recommended that white traps are used in biodiversity assessments to avoid the complication and reduced replication inherent with using two colours, unless the key question being addressed is targeted towards particular taxa known to respond to different colours.

3) Are there particular insect species of groups that can be used as identifiers of biodiversity values or presence of other species?

- *Recommendation 4: Assess other vegetation types to determine if indicator species/groups can be detected for use in rapid river-wide assessments in the future*

- *Recommendation 5: To assess spatial and temporal trends in diversity in future studies, process a subset of insect orders only (e.g. Diptera, Hymenoptera, Lepidoptera, Coleoptera, spiders)*
- *Recommendation 6: With the current or future datasets, investigate the predictive power and detectability of a subset of taxa that could be easily extracted from large samples, such as species of larger size classes*

A subset of the most diverse orders (Diptera, Hymenoptera, Hemiptera, Lepidoptera, Coleoptera) provided a good representation of the invertebrate community associated with the *Raoulia haasti – R. australis* habitat comparable to that detected using the complete dataset of 21 arthropod orders. No distinct species or small groups were detected that could act as indicators of the community captured by a particular trap type, time or location. This was partly due to the large number of variables being assessed, reducing replication per variable, and the large number of uncommon species. Compositional differences that were observed between trap methods, sampling times and location along the river, were not the result of distinct shifts in species, rather they came from relative differences in the abundances of common species and the presence of many uncommon species in very small numbers; over 92% of RTUs were found in 10% or fewer samples. The lack of useful indicators is not surprising as the study was not designed to answer this question well. An appropriate design would be to compare the species composition of the 11 different vegetation types using a reduced number of sampling methods on 2 or 3 occasions throughout the season (e.g. spring + late summer), controlling for position on the river (e.g. assessing as many vegetation types as possible at the same distance up the river).

Although is common for invertebrate monitoring schemes to focus on a limited taxon set (typically a single order) as a surrogate for total diversity, there is little evidence that this is appropriate. Most studies that do attempt to ground truth against more complete data have been in forest ecosystems (see Barby & Williams 2016). Beetles, ants, and Lepidoptera are regularly selected, due to good taxonomic knowledge. Beetles are commonly targeted as they are considered relatively easy to identify and include representatives of most functional groups. However, in a study of Tasmanian Rain forest beetles, Driscoll (2010) noted the common practice of using 10-20 traps per site is unlikely to detect more than a handful of the most commons species present with 95% confidence. Here, analysis of beetles did not detect the temporal differences in communities observed using all data, or those captured by different trap types, and only the pitfall beetle data reflected the spatial trends seen using the full, multi-taxa, data set. Lepidoptera performed equally poorly, although a spatial trend could be observed in analysis of pan data. Diptera and Hymenoptera were more representative; both pan and pitfall data indicated spatial trends, but temporal trends were coarse or absent. These orders performed better because they dominated the full data set in both species richness and abundance. However, they still failed to strongly reflect the variation in community composition that could be detected by different trap types. Although a full set of comparisons was not conducted here, a better picture of the predictive ability of the above orders may be possible by 'pruning' out some of the more redundant RTUs from analysis (e.g. by including only species contributing more than about 4% of the total abundance in any one sample). To better understand the predictive power of Lepidoptera in particularly, a repeat light trapping study is needed as light trap sample size in this project was extremely low.

Numerous comparisons could be made with the present data to pull out species subsets that provide a good, if not near identical representation of the trends inherent in the full dataset, or individual trap-type datasets. This can be done using the BVSTEP procedure in PRIMER-E by selecting species subsets

(instead of abiotic factors) to link to sample patterns in the full dataset. However, identifying such groups, unless they are whole orders, is unlikely to reduce processing time because the taxa would still need to be identified and sorted out from the large number of specimens in a sample. An alternative not tested here would be assign a size class to each RTU, then compare size class subsets to the full dataset. This approach may be able to inform sampling design to focus on trapping methods that favour target groups or reduce processing by determining whether small specimens can be ignored, and at what size limit. Excluding specimens >2mm or >4mm is commonly used in insect studies allowing samples to by sieved before processing to remove redundant specimens. Identifying a small number of RTUs from the current list that are likely to be consistently distinguishable and could be easily extract from large samples by non-experts, without counting or identifying the majority of other specimens, could also be used as a subset to compare to the full dataset.

To assess broad patterns in diversity, such as in spatial and temporal trends that might reflect ecosystem health, excluding non-insect arthropods (except maybe spiders) and insect orders with relatively low diversity (e.g. Ephemeroptera, Neuroptera, Orthoptera, Plecoptera, Psocoptera, Siphonaptera, Thysanura, Trichoptera) may be an appropriate means to reduce processing time and costs. Some of these orders are good indicators of freshwater health, but this can be more easily assessed using standard water invertebrate sampling methods for juvenile stages. Terrestrial biodiversity assessment most likely needs to include a suite of orders, rather than being restricted to any one order. Carefully excluding abundant ubiquitous taxa, and extremely uncommon taxa may help identify indicator species or groups that were obscured in the current analysis. This might be coupled with some form of biomass analysis on the exclude groups. Noting that these types of analyses are not appropriate to address detailed questions regarding total diversity, or the status of individual species.

4) What is the minimum level of taxonomic discrimination necessary to define biodiversity values?

- *Recommendation 7: Identify specimens to RTU at least to family level*

Species diversity was strongly correlated to genus and family diversity, suggesting identification to these levels may provide a good indication of biodiversity values. The ability to detect overall effects of trap type, sampling time, site etc. on community composition declined as RTU resolution was reduced from species to genus to family to order. Broad patterns and trends in community composition, could be detected with aggregation to genus, and to family in some instances. At the order level details were lost and certainty around trends was low or absent. Although this study has provided an invaluable reference collection, little is likely to be gained from expert identification to species level in future rapid assessment studies. Marine scientists have found identification to family level for macrobenthic fauna, and to genus level for meiobenthic (smaller) fauna, is commonly sufficient to detect temporal trends and responses to environmental perturbations (Clarke & Warwick, 2001). Similarly, non-experts trained to carefully identify terrestrial taxa (ants, beetles, spiders) to morpho-species have been shown to produce results consistent with expert identification to species level (e.g. Oliver & Beattie, 1996, Oliver & Beattie 1993). A conservative morpho-species or RTU approach will miss some diversity, but for large scale investigations into broad patterns, involving the collection of many thousands of specimens, the added cost and time required for expert identification is likely unjustified. This is partly because few taxonomists are available, and they cannot allocate sustained periods of time to processing samples for individual studies. The limited number of experts currently in New Zealand can provide a more valuable service in training and quality control and may need to be consulted if additional information is being sought from the data.

For rapid inventory of braided rivers, an RTU approach is recommended where taxa are identified as far as possible and at least to family, then assigned a morpho-species number if they are clearly distinguishable from other RTUs identified to the same level. This was the approach taken to complete processing in the current study, once it was clear identification to species by experts was not achievable for all groups in the time frame required. This approach is more useful than a complete morph-species approach (assigning all taxa a numerical code with no taxonomic information) as it retains a degree of taxonomic information (which can be achieved with basic training) that will aid in interpretation of data to inform management, and can be built on and explored in future studies. The latter is important given the paucity of braided river invertebrate knowledge. If studies are being conducted by multiple groups or across rivers at different times, it will also assist with sharing reference collections to ensure consistent RTUs are assigned, allowing comparisons between datasets.

5) Can we develop best practice rapid sampling and analysis methods to apply to other braided river systems to assess biodiversity values and ecosystem health?

- *Recommendation 8: Develop biodiversity index for terrestrial braided river invertebrates as a function of species richness, taxonomic distinctness and functional diversity*
- *Recommendation 9: Sample in three months across the season (e.g. early November, mid-December, late January/early February)*
- *Recommendation 10: Exclude immatures and taxa <2mm in length from processing*
- *Recommendation 11: Provide data templates if multiple individuals or external experts are processing samples/inputting data*

Optimal monitoring design depends on how biodiversity values are intended to be used. To rank the relative inherent values of different rivers on a single occasion, it may be sufficient to compare total diversity as some function of species richness, taxonomic distinctness and functional diversity. Further work is required to clarify this. To compare the health of the invertebrate community between multiple rivers, or detect responses to the environmental state (e.g. pollution) or stress (e.g. climate change, fragmentation, response to land management) would require increased focus on the changes in species or functional group composition and abundance over time, potentially based on a subset of species sensitive to the change (See Barby & Williams for review).

Sample collection
Malaise trapping is suggested (*Recommendation 1*) as the most rapid means to estimate diversity, with some supplementation of pitfalls to detect the large predator guild and assess functional diversity (*Recommendation 3*). The appropriate number of pitfalls to detect large carabids could be determined by undertaking a detection probability analysis that calculates the proportion of traps occupied at the sites where the family was found to occur (see Driscoll 2010). This should be assessed for all months versus individual sampling periods to determine the optimal sampling time or frequency. The optimal number of malaise samples required to assess biodiversity values requires further investigation (*Recommendation 2*). One trap per site detected a large number of species, but accumulation per trap was still >5 RTUs after 25 samples. Given a priority to minimise processing time, one trap per site is recommend but the number of sites and seasonal replicates needs to be high enough to counter spatial and temporal variation in diversity and species composition. Malaise traps were less effective at detecting spatial variation; possibly because they target flying taxa (which may travel longer distances), and temporal variation; possibly because early season sampling was not fully replicated. This reiterates the importance of supplementing with pitfall traps. In carrying out recommendation 2,

sample size should be increased by deploying 2 traps (one with jars, one with troughs) at distances of ~2 km (= 10 sites), replicated 3 times during the season (see below). A power analysis on the full dataset versus subsets of the resulting data should be applied to determine if this replication is sufficient to detect changes in diversity given the significant variation that is likely to be detected. Diversity peaked in December and late January. All time periods sampled added new RTUs, with the highest contribution (116) occurring in the late January-early February period. It is like sampling earlier and later in the season would result in even more species being detected. Due to the inherent noise in insect sampling data, and to achieve reasonable coverage of temporal variation, monitoring should be replicated at least three times through spring and summer. Sampling at 6-week intervals in November, December and late January or early February may result in a better estimate of diversity than twice per month over fewer months. Traps should be set for a standard period of time, such as 5 days. As traps measure insect activity, which is strongly influenced by temperature, 'bad weather' days should be excluded i.e. leave traps open for 7 days if two bad weather days occur).

Rapid Processing
In addition to identifying species to RTU at least to family level (*Recommendation 7*), juvenile and very small specimens should be excluded to further expedite processing time. Over 28,000 juveniles were processed in this study, contributing only 2 RTUs that were not also identified from adults. In addition to being difficult to identify, juvenile abundance can be high and patchy. If abundance is of interest (e.g. assessing change in population size over time), it is even more advisable to count only adults, as they provide a biologically meaningful representation of population status. Activity based trapping methods, used here, are also biased towards juveniles of certain taxa, particularly hemimetabolous orders (e.g. Hemiptera), while holometabolous orders (e.g. Coleoptera) are rarely sampled.

Excluding very small specimens from processing, such as those <2mm or <4mm, is a common practice. Excluding mites and Collembola, along with the juvenile specimens noted above, would have reduced the number of specimens processed by 46.5% (70,773 specimens). Although ecologically very important, there is limited information on how to interpret abundances of Acari and Collembola (M. Scott *pers. comm.*) so presence and diversity is sufficient for assessing biodiversity values. Recording presence/absence alone for other highly ubiquitous and abundant taxa could also be considered (e.g. excluding ants and the three Hemiptera noted in Fig. 14 in addition to mites, Collembola and juveniles reduces specimens processed by a total of 68%).

Data management
A key consideration in conducting large scale biodiversity assessments for invertebrates is capturing data in a standardised manner to facilitate rapid processing, ease of analysis and limit errors. The current dataset suffered from having multiple experts providing information in a non-standardised way; for example, some assigned gender to adult specimens only, while others (because of the taxa being dealt with) were able to assign gender to immatures, or did not assign gender at all. Gender information in itself is not required for biodiversity assessment, but its inclusion led to some errors in total counts which had to be fixed manually if and where detected. If multiple individuals are involved in sorting invertebrates and inputting data then identical templates should be used ensure consistency across projects. If samples must be sent to experts they should also be accompanied by a data template and detailed instructions.

6.0 Acknowledgements

7.0 References

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8.0 Appendices

Appendix 1: Original dates (a) and site codes (b) used during sampling and processing and their relation to the TIME and SITE codes used in this report.

(a)	Time code	Moon phase	Sample collection dates
	T1-N	New	31 Oct – 6 Nov 2005
	T1-F	Full	21 – 22 Nov 2005
	T2-N	New	29 Nov – 6 Dec 2005
	T2-F	Full	20 – 21 Dec 2005
	T3-N	New	4 – 5 Jan 2006
	T3-F	Full	19 Jan 2006
	T4-N	New	30 Jan – 3 Feb 2006

(b)	Site code	Original code
	1	TA013
	2	TA021
	3	TA081
	4	TA017SUB
	5	TA133
	6	TA137

Appendix 2: Full list of taxa identified and the trap type(s) by which each was captured. H = Hand collected, L = Light trap, M = Malaise trap, Pn = Pan trap, Pt = Pitfall trap. NB: a small number of duplicate taxa, which were identified subsequent to analysis, are included in the list. These errors resulted primarily from taxonomic synonyms and spelling errors.

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Acari: Prostigmatidae						
Acari RTU1 unident	unident sp.1		*		*	*
Acari RTU2	unident sp.1		*	*	*	*
Araneae: Araneidae						
Araneae RTU3	*Eriophora pustulosa*	*				
Desidae						
Araneae RTU4	*Gasparia rustica*					*
Dictynidae						
Araneae RTU5	*Arangina cornigera*			*	*	*
Araneae RTU6	*Arangina pluva*					*
Gnaphosidae						
Araneae RTU7	*Anzacia gemmea*	*		*	*	*
Araneae RTU8	*Anzacia* sp. 1					*
Araneae RTU9	*Matua festiva*			*	*	*
Araneae RTU10	*Matua* sp. 1				*	
Araneae RTU11	*Matua valida*			*	*	*
Araneae RTU12	*Nauhea tapa*	*		*	*	*
Araneae RTU13	*Zelanda erebus*					*
Araneae RTU14	*Zelanda obtusa*					*
Araneae RTU15	unident sp.1			*	*	*
Araneae RTU16	unident sp.2					*
Hahniidae						
Araneae RTU18	*Alistra* sp. 1				*	
Araneae RTU19	unident sp.1					*
Linyphiidae						
Araneae RTU20	*Diplocephalus cristatus*					*
Araneae RTU21	*Diploplecta* sp.1					*
Araneae RTU22	*Dunedinia pullata*					*
Araneae RTU23	*Erigone prominens*					*
Araneae RTU24	*Erigone* sp. 1					*

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Araneae RTU25	*Erigone wiltoni*					*
Araneae RTU26	*Laetesia* sp. 1					*
Araneae RTU27	*Maorineta* sp. 3					*
Araneae RTU28	*Maorineta* sp. 1				*	*
Araneae RTU29	*Maorineta* sp. 2					*
Araneae RTU30	*Tenuiphantes tenuis*			*		*
Araneae RTU31	unident sp.1			*	*	*
Lycosidae						
Araneae RTU32	*Allotrochosina* sp. 1					*
Araneae RTU33	*Anoteropsis adumbrata*					*
Araneae RTU34	*Anoteropsis aerescens*	*	*		*	*
Araneae RTU35	*Anoteropsis arenivaga*	*		*		*
Araneae RTU36	*Anoteropsis hilaris*			*		*
Araneae RTU37	*Anoteropsis* sp. 1	*		*	*	*
Araneae RTU38	*Anoteropsis* sp. 2					*
Araneae RTU39	*Notocosa bellicosa*					*
Araneae RTU40	unident sp.1			*		*
Pisauridae						
Araneae RTU43	*Dolomedes aquaticus*					*
Araneae RTU44	*Dolomedes minor*					*
Salticidae						
Araneae RTU45	unident sp.1			*		*
Araneae RTU46	unident sp.2	*		*	*	*
Araneae RTU47	unident sp.3			*		
Theridiidae						
Araneae RTU48	*Coleosoma octomaculatum*			*		*
Araneae RTU49	*Coleosoma* sp. 1					*
Araneae RTU50	*Euryopis nana*					*
Araneae RTU51	*Pholcomma* sp. 1					*
Araneae RTU52	*Steatoda lepida*					*
Araneae RTU53	*Steatoda* sp. 1	*		*	*	*
Araneae RTU54	*Steatoda truncata*	*	*		*	*
Araneae RTU55	*Theridion ampliatum*			*		*
Araneae RTU56	unident sp.1					*
Thomisidae						
Araneae RTU57	*Diaea* sp. 1			*		
unident						
Araneae RTU58	unident sp.1		*	*	*	*
Zoropsidae						
Araneae RTU59	*Uliodon* sp. 2					*
Chilopoda: Geophilidae						
Chilopoda RTU60	unident sp.1					*
Chilopoda RTU61	unident sp.2			*		*
Chilopoda RTU62	*Zelanion antipodus*					*
unident						
Chilopoda RTU63	unident sp.1	*		*		*
Chilopoda RTU64	unident sp.2	*				*
Coleoptera: Aleocharinae						
Coleoptera RTU65	unident sp.2			*		
Coleoptera RTU66	unident sp.3			*		
Coleoptera RTU67	unident sp.7			*		
Anobiidae						
Coleoptera RTU68	*Xenocera* sp. 1			*		
Anthicidae						
Coleoptera RTU69	*Anthicus otagoensis*					*
Byrrhidae						
Coleoptera RTU70	*Microchaetes* sp. 1			*	*	*
Carabidae						
Coleoptera RTU71	*Actenonyx bembidioides*	*				*

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Coleoptera RTU72	*Bembidion granuliferum*	*	*			*
Coleoptera RTU73	*Bembidion* sp. 1					*
Coleoptera RTU74	*Bembidion wanakense*	*	*	*		*
Coleoptera RTU75	*Mecodema sculpturatum*					*
Coleoptera RTU76	*Scopodes* sp. 1	*				*
Coleoptera RTU77	unident sp.1					*
Chrysomelidae						
Coleoptera RTU78	*Adoxia* sp. 1			*	*	*
Coleoptera RTU79	*Adoxia* sp. 2			*	*	*
Coleoptera RTU80	*Adoxia* sp. 3			*	*	*
Coleoptera RTU81	*Adoxia* sp. 4			*	*	*
Coleoptera RTU82	*Adoxia* sp. 5				*	
Cleridae						
Coleoptera RTU83	unident sp.1					*
Coccinellidae						
Coleoptera RTU84	*Coccinella leonina*	*		*	*	*
Coleoptera RTU85	*Coccinella* sp. 1	*		*		
Coleoptera RTU86	*Coccinella undecimpunctata*			*		
Coleoptera RTU87	*Diomus* sp. 1			*	*	*
Corticariinae						
Coleoptera RTU88	unident sp.1			*		
Coleoptera RTU89	unident sp.2			*		
Coleoptera RTU90	unident sp.3			*		*
Curculionidae						
Coleoptera RTU91	*Baeosomus iridescens*					*
Coleoptera RTU92	*Goneumus bryobius*					*
Coleoptera RTU93	*Listronotus bonariensis*					*
Coleoptera RTU94	*Peristoreus* sp. 1	*	*	*	*	*
Coleoptera RTU95	*Peristoreus sudus*			*		
Coleoptera RTU96	*Rhopalomerus* sp. 1			*		
Coleoptera RTU97	unident sp.1					*
Elateridae						
Coleoptera RTU98	*Australeeus powelli*					*
Coleoptera RTU99	*Australeeus* sp. 1					*
Coleoptera RTU100	*Australeeus* sp. 2					*
Coleoptera RTU101	*Betarmonides* sp. 1	*		*	*	*
Coleoptera RTU102	unident sp.1					*
Erotylidae						
Coleoptera RTU103	*Loberus anthracinus*	*		*	*	*
Histeridae						
Coleoptera RTU104	*Saprinus detritus*			*		*
Latridiidae						
Coleoptera RTU106	*Melanophthalma* sp. 1			*	*	
Coleoptera RTU107	unident sp.1			*		
Leiodidae						
Coleoptera RTU108	*Paracatops* sp. 1			*		
Melyridae						
Coleoptera RTU109	unident sp.1				*	
Melyrididae						
Coleoptera RTU110	*Dasytes* sp. 1					*
Oedemeridae						
Coleoptera RTU111	*Baculipalpus* sp. 1				*	
Coleoptera RTU112	*Selenopalpus* sp. 1				*	
Paederinae						
Coleoptera RTU113	unident sp.1					*
Ptiliidae						
Coleoptera RTU114	*Ptinella* sp. 1			*	*	*
Coleoptera RTU115	*Ptinella* sp. 2			*		
Scarabaeidae						
Coleoptera RTU116	*Ataenius brouni*				*	*

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Coleoptera RTU117	*Costelytra zealandica*	*	*		*	*
Coleoptera RTU118	*Odontria* sp. 1					*
Coleoptera RTU119	*Odontria* sp. 2					*
Coleoptera RTU120	*Pericoptus punctatus*		*			*
Coleoptera RTU121	*Pyronota otagoensis*					*
Coleoptera RTU122	*Pyronota* sp. 1	*		*	*	*
Coleoptera RTU123	*Pyronota* sp. 2	*		*	*	*
Coleoptera RTU124	*Pyronota* sp. 3	*		*	*	*
Coleoptera RTU125	unident sp.1				*	
Coleoptera RTU126	unident sp.5					*
Scirtidae						
Coleoptera RTU127	unident sp.1			*		*
Coleoptera RTU128	unident sp.2	*		*		
Coleoptera RTU129	unident sp.3					*
Staphylinidae						
Coleoptera RTU130	*Anabaxis* sp. 1			*	*	*
Coleoptera RTU131	*Bledius* sp. 1					*
Coleoptera RTU132	*Carpelimus* sp. 1			*		
Coleoptera RTU133	*Euplectopsis* sp. 1					*
Coleoptera RTU134	*Myllaena* sp. 1			*	*	
Coleoptera RTU135	*Sagola* sp. 1					*
Coleoptera RTU136	*Sagola* sp. 2			*	*	
Coleoptera RTU137	*Stenomalium* sp. 1			*		
Coleoptera RTU138	*Stenomalium* sp. 2			*		
Coleoptera RTU139	unident sp.1			*	*	*
Coleoptera RTU140	unident sp.2			*	*	*
Coleoptera RTU141	unident sp.3			*	*	*
Coleoptera RTU142	unident sp.4			*		
Coleoptera RTU143	unident sp.5			*	*	
Coleoptera RTU144	unident sp.7			*	*	*
unident						
Coleoptera RTU146	unident sp.1			*	*	*
Coleoptera RTU147	unident sp.2					*
Coleoptera RTU148	unident sp.3					*
Coleoptera RTU149	unident sp.4					*
Coleoptera RTU150	unident sp.6					*
Coleoptera RTU151	unident sp.7					*
Coleoptera RTU105	unident sp.8					*
Zopheridae						
Coleoptera RTU152	*Bitoma distans*			*		
Coleoptera RTU153	*Pristoderus otagoensis*					*
Coleoptera RTU154	*Pristoderus* sp. 1					*
Coleoptera RTU155	*Pristoderus undosus*	*		*	*	*
Coleoptera RTU156	*Pycnomerus* sp. 1			*		
Collembola: Entomobryidae						
Collembola RTU157	unident sp.1			*	*	*
Hypogastruridae						
Collembola RTU158	*Hypogastrura* sp. 2				*	
Collembola RTU159	unident sp.1			*	*	*
Sminthuridae						
Collembola RTU160	unident sp.1				*	*
unident						
Collembola RTU161	unident sp.1			*	*	*
Copepoda: Cyclopidae						
Copepoda RTU162	unident sp.1					*
unident						
Copepoda RTU163	unident sp.1					*
Diptera: Agromyzidae						
Diptera RTU164	*Cerodontha australis*			*	*	*
Diptera RTU165	*Cerodontha denticornis*				*	

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Diptera RTU166	*Cerodontha* sp. 1				*	
Diptera RTU167	*Liriomyza brassicae*			*	*	*
Diptera RTU168	*Liriomyza chenopodii*			*	*	*
Diptera RTU169	unident sp.1			*		
Asilidae						
Diptera RTU170	*Neoitamus melanopogon*					*
Diptera RTU171	*Neoitamus smithii*				*	*
Diptera RTU172	*Neoitamus* sp. 1				*	
Diptera RTU173	*Neoitamus varius*			*	*	
Diptera RTU174	*Saropogon* sp. 1			*		
Bibionidae						
Diptera RTU175	*Dilophus nigrostigma*			*	*	
Calliphoridae						
Diptera RTU176	*Calliphora quadrimaculata*			*	*	
Diptera RTU177	*Calliphora* sp. 1			*		
Diptera RTU178	*Calliphora stygia*			*		
Diptera RTU179	*Calliphora vicina*			*	*	*
Diptera RTU180	*Lucilia sericata*			*		
Diptera RTU181	*Pollenia* sp. 1			*		
Diptera RTU182	*Xenocalliphora hortona*			*	*	*
Cecidomyiidae						
Diptera RTU183	*Aprionus* sp. 1			*	*	
Diptera RTU184	*Aprionus* sp. 2			*	*	
Diptera RTU185	*Camplomyza* sp. 1			*	*	*
Diptera RTU186	*Dasineura* sp. 1			*	*	*
Diptera RTU187	*Dasineura* sp. 2			*	*	*
Diptera RTU188	*Dasineura* sp. 3			*		
Diptera RTU189	*Mycophila fungicola*					*
Diptera RTU190	*Peromyia* sp. 1			*	*	*
Diptera RTU191	unident sp.1			*	*	*
Diptera RTU192	unident sp.2			*	*	*
Diptera RTU193	unident sp.3			*		
Ceratopoginidae						
Diptera RTU194	unident sp.1				*	
Ceratopogonidae						
Diptera RTU195	*Austrohelea* sp. 1			*		*
Diptera RTU196	*Austrohelea* sp. 2				*	
Diptera RTU197	*Austrohelea tonnoiri*			*	*	*
Diptera RTU198	*Dasyhelea* sp. 1			*	*	*
Diptera RTU199	*Dasyhelea* sp. 2			*	*	*
Diptera RTU200	*Dasyhelea* sp. 3				*	
Diptera RTU201	*Forcipomyia* sp. 1			*	*	
Diptera RTU202	*Palpomyia ementita*			*		
Diptera RTU203	*Palpomyia nelsoni*			*	*	*
Diptera RTU204	*Palpomyia* sp. 1				*	*
Diptera RTU205	*Palpomyia* sp. 2			*	*	
Diptera RTU206	*Paradasyhelea* sp. 1					*
Diptera RTU207	unident sp.1		*	*		*
Diptera RTU208	unident sp.2			*	*	*
Diptera RTU209	unident sp.3					*
Chironomidae						
Diptera RTU210	*Ablabesmyia mala*		*	*		*
Diptera RTU211	*Chironomus* sp. 1	*	*	*	*	
Diptera RTU212	*Chironomus* sp. 2			*		
Diptera RTU213	*Chironomus zelandicus*		*	*		
Diptera RTU214	*Corynocera* sp. 1			*		
Diptera RTU215	*Corynoneura scutellata*			*	*	
Diptera RTU216	*Corynoneura* sp. 1			*		
Diptera RTU217	*Diamesinae* sp. 1			*	*	*
Diptera RTU218	*Eukiefferiella* sp. 1			*		*

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Diptera RTU219	*Macropelopia languidus*		*	*		
Diptera RTU220	*Macropelopia* sp. 1	*	*	*	*	*
Diptera RTU221	*Macropelopia* sp. 2		*			
Diptera RTU222	*Macropelopia* sp. 3					*
Diptera RTU223	*Macropelopia umbrosa*		*			
Diptera RTU224	*Maoridiamessa* sp. 1		*			
Diptera RTU225	*Orthocladinae* sp. 1			*	*	*
Diptera RTU226	*Orthocladinae* sp. 2					*
Diptera RTU227	*Orthocladinae* sp. 3			*	*	*
Diptera RTU228	*Orthocladinae* sp. 4		*	*	*	*
Diptera RTU229	*Orthocladinae* sp. 5			*	*	*
Diptera RTU230	*Orthocladinae* sp. 6			*	*	*
Diptera RTU231	*Orthocladinae* sp. 7			*	*	*
Diptera RTU232	*Orthocladinae* sp. 8		*	*	*	*
Diptera RTU233	*Podonomus* sp. 1					*
Diptera RTU234	*Polypedilum alternans*		*	*		
Diptera RTU235	*Polypedilum canum*			*		
Diptera RTU236	*Polypedilum cumberi*		*	*		
Diptera RTU237	*Polypedilum longicrus*			*	*	*
Diptera RTU238	*Polypedilum luteum*				*	
Diptera RTU239	*Polypedilum* sp. 1		*	*	*	*
Diptera RTU240	*Polypedilum* sp. 3			*		
Diptera RTU241	*Tanytarsus* sp. 1		*	*	*	
Diptera RTU242	unident sp.1	*	*	*	*	*
Diptera RTU243	unident sp.2			*		
Diptera RTU244	unident sp.3			*	*	*
Diptera RTU245	unident sp.4		*	*	*	*
Diptera RTU246	unident sp.5			*	*	*
Diptera RTU247	unident sp.6			*	*	*
Diptera RTU248	unident sp.7				*	*
Diptera RTU249	unident sp.8		*	*	*	*
Diptera RTU250	*Zavrelimyia* sp. 1			*		
Chloropidae						
Diptera RTU251	*Aphanotrigonum huttoni*			*	*	
Diptera RTU252	*Chlorops multisulcatus*			*	*	
Diptera RTU253	*Diplotoxa lineata*			*	*	
Diptera RTU254	*Gaurax duoseta*				*	*
Diptera RTU255	*Gaurax excepta*			*		
Diptera RTU256	*Gaurax flavoapicalis*			*	*	*
Diptera RTU257	*Gaurax mesopleuralis*				*	
Diptera RTU258	*Gaurax neozealandicus*			*	*	
Diptera RTU259	*Tricimba watti*			*	*	*
Diptera RTU260	unident sp.1				*	
Culicidae						
Diptera RTU261	*Culex quinquefasciatus*			*		
Dolichopodidae						
Diptera RTU262	*Chrysotimus nigrichaetus*					*
Diptera RTU263	*Chrysotimus* sp. 1			*	*	
Diptera RTU264	*Chrysotimus* sp. 2			*	*	*
Diptera RTU265	*Chrysotimus* sp. 4			*	*	*
Diptera RTU266	*Chrysotus* sp. 1			*	*	*
Diptera RTU267	*Chrysotus* sp. 2			*		
Diptera RTU268	*Diaphorus parapraestans*			*		
Diptera RTU269	*Diaphorus* sp. 1			*	*	
Diptera RTU270	*Diaphorus* sp. 2				*	
Diptera RTU271	*Micropygus bipunctatus*			*	*	*
Diptera RTU272	*Micropygus pulchellus*			*		
Diptera RTU273	*Micropygus striatus*				*	
Diptera RTU274	*Parentia mobile*			*	*	*
Diptera RTU275	*Parentia modesta*			*	*	

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Diptera RTU276	*Parentia restricta*			*		*
Diptera RTU277	*Scelloides* sp. 1			*	*	*
Diptera RTU278	*Scelloides* sp. 2			*		
Diptera RTU279	*Scelloides* sp. 3			*	*	*
Diptera RTU280	*Scelloides* sp. 4				*	
Diptera RTU281	*Sympycnus* sp. 1					*
Diptera RTU282	unident sp.1			*		
Drosophilidae						
Diptera RTU283	*Drosophila immigrans*			*		
Diptera RTU284	*Drosophila* sp. 1			*	*	
Diptera RTU285	*Scaptomyza elmoi*			*		
Diptera RTU286	*Scaptomyza flava*			*	*	
Diptera RTU287	*Scaptomyza fuscitarsis*			*	*	*
Diptera RTU288	unident sp.1			*		
Empididae						
Diptera RTU289	*Chelifera apicata*			*	*	
Diptera RTU290	*Hilara* sp. 1		*	*	*	*
Diptera RTU291	*Hilarempis* sp. 1			*	*	*
Diptera RTU292	*Isodrapetis* sp. 1			*		
Diptera RTU293	*Platypalpus ementitus*			*	*	
Diptera RTU294	unident sp.1			*	*	
Ephydridae						
Diptera RTU295	*Ditrichophora flavitarsis*			*		
Diptera RTU296	*Ditrichophora* sp. 1			*		
Diptera RTU297	*Hecamedoides affinis*			*	*	
Diptera RTU298	*Hyadina irrorata*			*		
Diptera RTU299	*Hydrellia enderbii*			*		
Diptera RTU300	*Hydrellia novae-zelandiae*			*		
Diptera RTU301	*Hydrellia* sp. 1			*		
Diptera RTU302	*Hydrellia tritici*			*		
Diptera RTU303	*Hydrellia velutinifrons*				*	
Diptera RTU304	*Neoscatella vittithorax*					*
Diptera RTU305	*Nostima duoseta*			*	*	*
Diptera RTU306	*Nostima* sp. 2					*
Diptera RTU307	*Psilopa metallica*			*	*	
Diptera RTU308	*Scatella nitidithorax*			*		
Diptera RTU309	*Scatella nubeculosa*			*		
Diptera RTU310	unident sp.1		*	*	*	
Heleomyzidae						
Diptera RTU311	*Prosopantrum flavifrons*			*	*	*
Diptera RTU312	*Tephrochlamys canescens*				*	
Helosciomyzidae						
Diptera RTU313	*Scordalus femoratus*			*		
Keroplatidae						
Diptera RTU314	*Cerotelion vitripenne*			*	*	*
Diptera RTU315	*Chiasmoneura milligani*					*
Diptera RTU316	*Pyrtaula campbelli*		*	*		
Diptera RTU317	*Pyrtaula* sp. 1			*	*	*
Lauxaniidae						
Diptera RTU318	*Poecilohetaerella bilineata*				*	
Diptera RTU319	*Sapromyza arenaria*			*	*	*
Lonchopteridae						
Diptera RTU320	*Lonchoptera bifurcata*			*	*	*
Muscidae						
Diptera RTU321	*Calliphoroides antennatis*			*		
Diptera RTU322	*Limnohelina bivittata*	*				
Diptera RTU323	*Limnohelina debilis*			*	*	
Diptera RTU324	*Limnohelina smithii*	*		*	*	
Diptera RTU325	*Limnohelina* sp. 1	*	*	*	*	*
Diptera RTU326	*Limnohelina zelandica*		*		*	

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Diptera RTU327	*Millerina* sp. 1	*		*	*	*
Diptera RTU328	*Millerina* sp. 2			*	*	
Diptera RTU329	*Millerina* sp. 3			*	*	
Diptera RTU330	*Millerina* sp. 4			*	*	
Diptera RTU331	*Millerina* sp. 5				*	
Diptera RTU332	*Millerina* sp. 6				*	
Diptera RTU333	*Millerina* sp. 7			*	*	
Diptera RTU334	*Millerina* sp. 8				*	
Diptera RTU335	*Paralimnophora* sp. 1			*		
Diptera RTU336	*Paralimnophora* sp. 2			*		
Diptera RTU337	*Spilogona* sp. 1			*	*	
Diptera RTU338	*Spilogona* sp. 2				*	
Diptera RTU339	*Spilogona* sp. 4				*	
Mycetophilidae						
Diptera RTU340	*Brevicornu maculatum*			*		
Diptera RTU341	*Brevicornu* sp. 1		*	*	*	*
Diptera RTU342	*Exechia* sp. 1			*		
Diptera RTU343	*Mycetophila colorata*					*
Diptera RTU344	*Mycetophila fagi*			*		
Diptera RTU345	*Mycetophila filicornis*				*	
Diptera RTU346	*Mycetophila marginepunctata*					*
Diptera RTU347	*Mycetophila* sp. 1		*	*	*	*
Diptera RTU348	*Mycetophila* sp. 12			*		*
Diptera RTU349	*Mycetophila* sp. 14			*		
Diptera RTU350	*Mycetophila subspinigera*			*		
Diptera RTU351	*Mycomya* sp. 1			*		*
Diptera RTU352	*Parvicellula* sp. 1			*		
Diptera RTU353	*Parvicellula* sp. 2			*		
Diptera RTU354	*Tetragoneura* sp. 1			*		
Diptera RTU355	*Tetragoneura* sp. 2					*
Diptera RTU356	unident sp.12			*		*
Diptera RTU357	unident sp.14			*		
Diptera RTU358	*Zygomyia eluta*			*		
Phoridae						
Diptera RTU359	*Antipodiphora brevicornis*			*	*	
Diptera RTU360	*Antipodiphora nana*			*		
Diptera RTU361	*Antipodiphora* sp. 1			*		*
Diptera RTU362	*Megaselia halterata*			*		
Diptera RTU363	*Megaselia impariseta*			*	*	*
Diptera RTU364	*Megaselia* sp. 1			*		*
Diptera RTU365	*Triphleba* sp. 1			*		
Diptera RTU366	unident sp.1			*	*	*
Diptera RTU367	*Wharia* sp. 1			*	*	
Podonominae						
Diptera RTU368	unident sp.1			*	*	*
Porricondylinae						
Diptera RTU369	unident sp.1			*		*
Psychodidae						
Diptera RTU370	*Psychoda* sp. 1			*		
Diptera RTU371	unident sp.1			*		
Sarcophagidae						
Diptera RTU372	*Hybopygia varia*	*		*	*	
Scatopsidae						
Diptera RTU373	*Coboldia fuscipes*			*	*	
Diptera RTU374	*Coboldia* sp. 1				*	
Diptera RTU375	*Colobostema* sp. 1			*		
Diptera RTU376	*Colobostema* sp. 2			*		
Diptera RTU377	*Colobostemus* sp. 1			*		
Diptera RTU378	*Colobostemus* sp. 2			*		
Diptera RTU379	*Rhegmoclemina* sp. 1			*	*	*

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Diptera RTU380	*Scatopse notata*				*	
Diptera RTU381	*Scatopse vittithorax*					*
Diptera RTU382	unident sp.1			*	*	
Sciaridae						
Diptera RTU383	*Bradysia* sp. 1			*	*	*
Diptera RTU384	*Corynoptera* sp. 1	*		*	*	*
Diptera RTU385	*Corynoptera* sp. 2				*	
Diptera RTU386	*Ctenosciara rufulenta*			*	*	*
Diptera RTU387	*Epidapus ctenosairoides*			*	*	*
Diptera RTU388	*Scythropochroa nitida*			*		*
Diptera RTU389	unident sp.1	*		*	*	*
Diptera RTU390	unident sp.2			*	*	*
Diptera RTU391	unident sp.3				*	
Diptera RTU392	unident sp.4			*	*	
Diptera RTU393	unident sp.5			*	*	*
Diptera RTU394	*Zygonerura* sp. 1				*	
Sciomyzidae						
Diptera RTU395	*Neolimnia* sp. 1			*		
Simuliidae						
Diptera RTU396	*Austrosimulium* sp. 1	*	*	*	*	
Sphaeroceridae						
Diptera RTU397	*Leptocera* sp. 1		*	*	*	*
Diptera RTU398	unident sp.1			*		
Stratiomyidae						
Diptera RTU399	*Odontomyia atrovirens*				*	
Diptera RTU400	*Odontomyia chloris*				*	
Diptera RTU401	*Odontomyia fulviceps*				*	
Diptera RTU402	*Odontomyia* sp. 1			*	*	
Diptera RTU403	*Odontomyia* sp. 2				*	
Diptera RTU404	unident sp.1				*	
Syrphidae						
Diptera RTU405	*Allograpta* sp. 1			*	*	
Diptera RTU406	*Melangyna novaezealandiae*			*	*	
Diptera RTU407	*Melanostoma fasciatum*			*		
Diptera RTU408	unident sp.1				*	
Tachinidae						
Diptera RTU409	*Calcager apertum*			*		
Diptera RTU410	*Calcager* sp. 1				*	*
Diptera RTU411	*Calcageria incidens*			*	*	
Diptera RTU412	*Campylia nudarum*			*	*	*
Diptera RTU413	*Campylia* sp. 1			*		
Diptera RTU414	*Campylia temerarium*			*	*	*
Diptera RTU415	*Erythronychia defecta*			*	*	
Diptera RTU416	*Erythronychia* sp. 1			*	*	
Diptera RTU417	*Gracilicera monticolor*			*	*	
Diptera RTU418	*Gracilicera politiventris*			*	*	
Diptera RTU419	*Heteria appendiculata*	*		*	*	*
Diptera RTU420	*Heteria atripes*			*	*	*
Diptera RTU421	*Heteria extensa*			*		
Diptera RTU422	*Heteria flavibasis*			*		
Diptera RTU423	*Heteria plebeia*			*	*	
Diptera RTU424	*Heteria punctigera*			*	*	
Diptera RTU425	*Heteria* sp. 1			*	*	*
Diptera RTU426	*Medinella flavofemorata*				*	
Diptera RTU427	*Occisor inscitus*			*		
Diptera RTU428	*Occisor versutus*			*		
Diptera RTU429	*Pales* sp. 1			*	*	*
Diptera RTU430	*Pales* sp. 2				*	
Diptera RTU431	*Pales* sp. 3			*	*	*
Diptera RTU432	*Pales* sp. 4			*	*	

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Diptera RTU433	*Pales* sp. 5			*	*	*
Diptera RTU434	*Pales* sp. 6				*	
Diptera RTU436	*Peremptor kumaraensis*			*	*	
Diptera RTU437	*Peremptor* sp. 1			*		
Diptera RTU438	*Plagiomyia smithii*			*		
Diptera RTU439	*Plagiomyia* sp. 1	*		*	*	*
Diptera RTU440	*Plagiomyia turbida*				*	
Diptera RTU441	*Procissio albiceps*			*	*	
Diptera RTU442	*Procissio* sp. 1	*		*	*	*
Diptera RTU443	*Procissio* sp. 2			*		
Diptera RTU444	*Procissio* sp. 5			*		
Diptera RTU445	*Procissio vicina*			*		
Diptera RTU446	*Protohystricia alcis*			*	*	
Diptera RTU447	*Protohystricia huttoni*				*	
Diptera RTU448	*Protohystricia orientalis*			*		
Diptera RTU449	*Protohystricia signata*			*		
Diptera RTU450	*Protohystricia* sp. 1	*				
Diptera RTU451	*Truphia* sp. 1			*	*	
Diptera RTU452	*Uclesiella* sp. 1			*	*	
Diptera RTU453	unident sp.1			*	*	*
Diptera RTU454	unident sp.2				*	
Diptera RTU455	*Zealandotachina nigrifemorata*				*	
Diptera RTU456	*Zealandotachina* sp. 1	*		*	*	*
Diptera RTU457	*Zealandotachina varipes*			*	*	*
Tephritidae						
Diptera RTU458	*Austrotephritis plebeia*			*	*	
Diptera RTU459	*Austrotephritis* sp. 1	*		*	*	*
Diptera RTU460	*Austrotephritis* sp. 5					*
Diptera RTU461	*Tephritis* sp. 1			*	*	
Diptera RTU462	*Tephritis* sp. 2				*	
Diptera RTU463	*Trypanea albopicata*				*	
Diptera RTU464	*Trypanea longipennis*				*	
Diptera RTU465	*Trypanea* sp. 1			*	*	
Diptera RTU466	unident sp.1				*	
Therevidae						
Diptera RTU467	*Anabarhynchus fenwicki*				*	
Diptera RTU468	*Anabarhynchus indistinctus*					*
Diptera RTU469	*Anabarhynchus limbatinervis*				*	
Diptera RTU470	*Anabarhynchus* sp. 1			*	*	*
Diptera RTU471	*Anabarhynchus* sp. 2			*	*	
Diptera RTU472	*Anabarhynchus* sp. 3	*	*	*	*	*
Diptera RTU473	*Anabarhynchus* sp. 4					*
Tipulidae						
Diptera RTU474	*Aphrophila neozelandica*	*	*		*	*
Diptera RTU475	*Molophilus* sp. 1			*	*	
Diptera RTU476	*Molophilus* sp. 2			*	*	
Diptera RTU477	unident sp.1	*	*	*	*	*
Diptera RTU478	unident sp.2			*	*	
unident						
Diptera RTU479	unident sp.1			*	*	*	*
Ephemeroptera: Leptophlebiidae						
Ephemeroptera RTU480	*Deleatidium cornutum*					*
Hemiptera: Acanthostomatidae						
Hemiptera RTU481	unident sp.1					*
Adelgidae						
Hemiptera RTU482	unident sp.1			*	*	*
Aleyrodidae						
Hemiptera RTU483	unident sp.1					*

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Aphididae						
Hemiptera RTU484	*Acrythosiphon kondoi*	*	*	*	*	*
Hemiptera RTU485	*Acrythosiphon pisum*			*		*
Hemiptera RTU486	*Aulacorthum solani*					*
Hemiptera RTU487	*Brachycaudus helichrysi*				*	
Hemiptera RTU488	*Brachycaudus rumexicolens*			*	*	*
Hemiptera RTU489	*Brevicoryne brassicae*			*	*	
Hemiptera RTU490	*Capitophorus eleagni*			*		
Hemiptera RTU491	*Cavariella aegopodii*			*	*	*
Hemiptera RTU492	*Myzus cerasi*			*		
Hemiptera RTU493	*Myzus persicae*			*		*
Hemiptera RTU494	*Nasanovia ribes-nigri*			*	*	
Hemiptera RTU495	*Pemphigus discariae*			*		
Hemiptera RTU496	*Rhopalosiphoninus staphlyeae*			*		
Hemiptera RTU497	*Rhopalosiphum padi*			*	*	
Hemiptera RTU498	unident sp.1			*	*	*
Cantacaderidae						
Hemiptera RTU499	*Cyperobia carectorum*				*	*
Cicadellidae						
Hemiptera RTU500	*Anzygina* sp. 1				*	*
Hemiptera RTU501	*Anzygina zealandica*			*	*	*
Hemiptera RTU502	*Anzygina zelandica*		*			
Hemiptera RTU503	*Arawa novella*			*		*
Hemiptera RTU504	*Arawa* sp. 1		*	*	*	*
Hemiptera RTU505	*Arawa* sp. 2			*		
Hemiptera RTU506	*Batracomorphus adventitiosus*			*	*	
Hemiptera RTU507	*Nesoclutha phryne*			*	*	
Hemiptera RTU508	*Nesoclutha* sp. 1			*		
Hemiptera RTU509	unident sp.1		*	*	*	*
Hemiptera RTU510	unident sp.2			*		
Hemiptera RTU511	*Xestocephalus ovalis*					*
Cicadidae						
Hemiptera RTU512	unident sp.1	*		*	*	*
Coccoidea						
Hemiptera RTU513	unident sp.1				*	
Hemiptera RTU514	unident sp.2				*	
Cryptostigmata						
Hemiptera RTU515	unident sp.1					*
Delphacidae						
Hemiptera RTU516	unident sp.1			*	*	*
Hemiptera RTU517	unident sp.2			*	*	*
Lestremiinae						
Hemiptera RTU518	*Kiwisaldula* sp. 1					*
Lygaeidae						
Hemiptera RTU519	*Nysius huttoni*	*		*	*	*
Hemiptera RTU520	*Nysius liliputanus*			*		*
Hemiptera RTU521	*Nysius* sp. 1			*		*
Hemiptera RTU522	*Rhypodes chinai*	*		*	*	*
Hemiptera RTU523	*Rhypodes myersi*			*		
Hemiptera RTU524	*Rhypodes sericatus*			*	*	
Hemiptera RTU525	*Rhypodes* sp. 1	*		*	*	*
Hemiptera RTU526	*Rhypodes triangulus*				*	
Hemiptera RTU527	unident sp.1	*		*	*	*
Mesoveliidae						
Hemiptera RTU528	*Mniovelia* sp. 1					*
Miridae						
Hemiptera RTU529	*Diomocoris punctatus*	*	*	*		*
Hemiptera RTU530	*Josemiris carvalhoi*			*		
Hemiptera RTU531	*Pimeleocoris luteus*				*	
Hemiptera RTU532	*Pimeleocoris roseus*				*	*

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Hemiptera RTU533	*Tridiplous penmani*			*		
Nabidae						
Hemiptera RTU534	*Nabis maoricus*			*		
Pemphigidae						
Hemiptera RTU535	unident sp.1				*	
Phyloxeridae						
Hemiptera RTU536	unident sp.1					*
Pseudococcidae						
Hemiptera RTU537	*Balanococcus* sp. 1			*	*	*
Hemiptera RTU538	*Balanococcus* sp. 2			*	*	*
Hemiptera RTU539	*Balanococcus* sp. 3				*	*
Hemiptera RTU540	*Balanococcus* sp. 4					*
Hemiptera RTU541	unident sp.1			*	*	*
Hemiptera RTU542	unident sp.2			*	*	*
Hemiptera RTU543	unident sp.3				*	
Hemiptera RTU544	unident sp.4					*
Saldidae						
Hemiptera RTU545	*Saldula* sp. 1					*
Schizopteridae						
Hemiptera RTU546	*Hypselosoma acantheen*			*	*	
Hemiptera RTU547	*Hypselosoma* sp. 1			*		
Tingidae						
Hemiptera RTU548	unident sp.1					*
Triozidae						
Hemiptera RTU549	*Trioza australis*					*
Hemiptera RTU550	*Trioza discariae*		*	*	*	*
Hemiptera RTU551	*Trioza* sp.1			*	*	
Hemiptera RTU552	*Trioza zelandica*		*			
Hemiptera RTU553	unident sp.1			*	*	
unident						
Hemiptera RTU554	unident sp.1	*		*	*	*
Hymenoptera: Aphelinidae						
Hymenoptera RTU555	*Aphelinus* sp. 1			*	*	*
Hymenoptera RTU556	*Aphelinus* sp. 3				*	*
Hymenoptera RTU557	*Aphelinus* sp. 4					*
Hymenoptera RTU558	*Aphelinus* sp. 5			*		*
Hymenoptera RTU561	*Cales* sp. 1					*
Hymenoptera RTU562	*Centrodora* sp. 1			*		
Hymenoptera RTU563	*Coccophagoides* sp. 1			*	*	*
Hymenoptera RTU564	*Coccophagoides* sp. 2			*		*
Hymenoptera RTU565	*Coccophagus* sp. 1			*	*	*
Hymenoptera RTU566	*Coccophagus* sp. 2			*		
Hymenoptera RTU567	*Coccophagus* sp. 3			*		
Hymenoptera RTU568	*Coccophagus* sp. 5			*		
Hymenoptera RTU569	*Encarsia antipodis*			*		
Hymenoptera RTU570	*Encarsia* sp. 1			*	*	*
Hymenoptera RTU571	*Encarsia* sp. 5			*		
Hymenoptera RTU572	*Eupelmus* sp. 3					*
Hymenoptera RTU573	*Eutrichosomella* sp. 1			*		*
Hymenoptera RTU574	*Euxanthellus* sp. 1			*		
Hymenoptera RTU575	*Pteroptrix* sp. 1			*	*	*
Hymenoptera RTU576	*Pteroptrix* sp. 2			*		
Hymenoptera RTU577	unident sp.1			*	*	*
Hymenoptera RTU578	unident sp.2			*	*	*
Hymenoptera RTU579	unident sp.3			*	*	
Hymenoptera RTU580	unident sp.4					*
Hymenoptera RTU581	unident sp.5			*		
Apidae						
Hymenoptera RTU582	*Apis mellifera*			*	*	
Hymenoptera RTU583	*Bombus hortorum*			*		

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Hymenoptera RTU584	*Bombus terrestris*			*	*	
Bethylidae						
Hymenoptera RTU585	*Eupsenella insulana*			*		
Hymenoptera RTU586	*Sierola* sp. 1			*	*	*
Hymenoptera RTU587	unident sp.1			*	*	
Braconidae						
Hymenoptera RTU588	*Aleoides declanae*	*	*	*	*	
Hymenoptera RTU589	*Aleoides* sp. 1		*			
Hymenoptera RTU590	*Apanteles* sp. 1			*	*	
Hymenoptera RTU591	*Apanteles* sp. 5			*		
Hymenoptera RTU592	*Aphidius* sp. 1			*		*
Hymenoptera RTU593	*Aspilota parecur*			*		*
Hymenoptera RTU594	*Cotesia* sp. 1				*	
Hymenoptera RTU596	*Dolichogenidea* sp. 1			*	*	*
Hymenoptera RTU597	*Glyptapanteles demeter*			*	*	
Hymenoptera RTU598	*Glyptapanteles* sp. 1	*		*	*	
Hymenoptera RTU599	*Glyptapanteles* sp. 2			*		
Hymenoptera RTU600	*Macrocentrus* sp. 1			*	*	
Hymenoptera RTU601	*Meteorus pulchricornis*			*		*
Hymenoptera RTU602	*Meteorus* sp. 1			*		*
Hymenoptera RTU603	*Pholetesor* sp. 1				*	*
Hymenoptera RTU604	unident sp.1					*
Hymenoptera RTU605	unident sp.2				*	*
Ceraphronidae						
Hymenoptera RTU606	*Aphanogmus* sp. 1			*	*	*
Hymenoptera RTU607	*Aphanogmus* sp. 2			*		
Hymenoptera RTU608	*Ceraphron* sp. 1			*	*	*
Hymenoptera RTU609	*Ceraphron* sp. 2			*	*	*
Hymenoptera RTU610	*Dendrocerus* sp. 1			*	*	
Hymenoptera RTU611	unident sp.1			*	*	*
Chalchidoidea						
Hymenoptera RTU612	unident sp.2				*	
Hymenoptera RTU613	unident sp.3			*		*
Hymenoptera RTU614	unident sp.4			*		
Colletidae						
Hymenoptera RTU615	*Hylaeus capitosus*			*		
Hymenoptera RTU616	*Leioproctus boltoni*			*	*	
Hymenoptera RTU617	*Leioproctus fulvescens*			*	*	
Hymenoptera RTU618	*Leioproctus huakiwi*			*	*	
Hymenoptera RTU619	*Leioproctus hudsoni*			*	*	
Hymenoptera RTU620	*Leioproctus maritimus*			*	*	*
Hymenoptera RTU621	*Leioproctus* sp. 1			*	*	
Hymenoptera RTU622	*Leioproctus vestitus*				*	*
Diapriidae						
Hymenoptera RTU623	*Belytinae* sp. 1			*	*	*
Hymenoptera RTU624	*Entomacis* sp. 1			*		
Hymenoptera RTU625	*Spilomicrus* sp. 1			*	*	*
Hymenoptera RTU626	*Spilomicrus* sp. 2			*	*	*
Hymenoptera RTU627	*Spilomicrus* sp. 3				*	*
Hymenoptera RTU628	*Spilomicrus vestitus*					*
Hymenoptera RTU629	*Stylaclista* sp. 1			*	*	*
Hymenoptera RTU630	*Stylaclista* sp. 2			*	*	*
Hymenoptera RTU631	*Trichopria* sp. 1			*	*	*
Hymenoptera RTU632	*Trichopria* sp. 2			*	*	
Hymenoptera RTU633	*Trichopria* sp. 5			*		
Hymenoptera RTU634	unident sp.1			*	*	*
Hymenoptera RTU635	unident sp.2				*	
Dryinidae						
Hymenoptera RTU636	*Gonatopus zealandicus*			*	*	
Encyrtidae						

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Hymenoptera RTU637	*Austrochoreia antipodis*			*	*	*
Hymenoptera RTU638	*Austrochoreia* sp. 1			*	*	
Hymenoptera RTU639	*Austrochoreia* sp. 2				*	
Hymenoptera RTU640	*Odiaglyptus biformis*			*	*	*
Hymenoptera RTU641	*Rhopus anceps*			*	*	*
Hymenoptera RTU642	unident sp.1			*	*	*
Hymenoptera RTU643	unident sp.3					*
Hymenoptera RTU644	unident sp.5			*		
Epyrinae						
Hymenoptera RTU645	unident sp.1			*	*	
Eulophidae						
Hymenoptera RTU646	*Aprostocetus* sp. 1			*		
Hymenoptera RTU647	*Aprostocetus* sp. 2			*		
Hymenoptera RTU648	*Elasmus* sp. 1			*		
Hymenoptera RTU649	*Pedobius* sp. 1			*		
Hymenoptera RTU650	*Pedobius* sp. 2			*		
Hymenoptera RTU651	*Pedobius* sp. 3			*		
Hymenoptera RTU652	unident sp.1			*	*	*
Hymenoptera RTU653	unident sp.10					*
Hymenoptera RTU654	unident sp.2			*	*	*
Hymenoptera RTU655	unident sp.3			*	*	
Hymenoptera RTU656	unident sp.4			*	*	
Hymenoptera RTU657	unident sp.5			*		*
Hymenoptera RTU658	unident sp.6			*	*	*
Hymenoptera RTU659	unident sp.7			*		
Hymenoptera RTU660	unident sp.8			*		
Hymenoptera RTU661	unident sp.9			*		
Formicidae						
Hymenoptera RTU662	*Monomorium antarcticum*	*	*	*	*	*
Hymenoptera RTU663	*Monomorium smithii*	*		*	*	*
Hymenoptera RTU664	*Monomorium* sp. 1	*				
Hymenoptera RTU665	unident sp.1			*		
Gasteruptiidae						
Hymenoptera RTU666	*Pseudofoenus* sp. 1				*	
Halictidae						
Hymenoptera RTU667	*Lasioglossum sordidum*	*		*	*	*
Hymenoptera RTU668	*Lasioglossum* sp. 1				*	
Ichneumonidae						
Hymenoptera RTU669	*Aucklandella* sp. 1			*		
Hymenoptera RTU670	*Campoplex* sp. 1	*		*	*	*
Hymenoptera RTU671	*Diadegma* sp. 1	*		*	*	
Hymenoptera RTU672	*Ichneumon* sp. 1			*		
Hymenoptera RTU673	*Lissonota atra*			*	*	
Hymenoptera RTU674	*Lissonota flavopicta*		*	*	*	*
Hymenoptera RTU675	*Mesochorus* sp. 1			*	*	
Hymenoptera RTU676	*Trathala agnina*			*	*	*
Hymenoptera RTU677	unident sp.1			*	*	
Hymenoptera RTU678	unident sp.2			*		
Hymenoptera RTU679	unident sp.3			*		
Hymenoptera RTU680	unident sp.5			*		
Mymaridae						
Hymenoptera RTU681	*Cleruchus* sp. 1			*		*
Hymenoptera RTU682	*Cleruchus* sp. 2					*
Hymenoptera RTU683	*Gonatocerus antipodis*			*		
Hymenoptera RTU684	*Gonatocerus* sp. 1			*	*	*
Hymenoptera RTU685	*Gonatocerus* sp. 2			*	*	*
Hymenoptera RTU686	*Gonatocerus* sp. 3					*
Hymenoptera RTU687	unident sp.1			*	*	*
Hymenoptera RTU688	unident sp.2			*	*	*
Hymenoptera RTU689	unident sp.3				*	*

| RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Hymenoptera RTU690	unident sp.5			*		
Platygastridae						
Hymenoptera RTU691	*Baeus* sp. 1				*	*
Hymenoptera RTU692	*Idris* sp. 1			*	*	*
Hymenoptera RTU693	*Idris* sp. 2			*		
Hymenoptera RTU694	*Idris* sp. 3					*
Hymenoptera RTU695	*Inostemma* sp. 1				*	
Hymenoptera RTU696	*Inostemma* sp. 2			*	*	*
Hymenoptera RTU697	*Inostemma* sp. 4			*	*	*
Hymenoptera RTU698	*Telenomus antipodis*					*
Hymenoptera RTU699	*Telenomus* sp. 1			*	*	*
Hymenoptera RTU700	*Telenomus* sp. 2			*		
Hymenoptera RTU701	*Telenomus* sp. 4			*	*	
Hymenoptera RTU702	*Telenomus* sp. 5			*		
Hymenoptera RTU703	*Trimorus* sp. 1			*	*	*
Hymenoptera RTU704	*Trissolcus* sp. 1			*		
Hymenoptera RTU705	unident sp.1			*	*	*
Hymenoptera RTU706	unident sp.2			*	*	*
Hymenoptera RTU707	unident sp.4			*	*	*
Pompilidae						
Hymenoptera RTU708	*Priocnemis carbonarius*			*	*	
Hymenoptera RTU709	*Priocnemis nitidiventris*			*	*	*
Hymenoptera RTU710	*Priocnemis* sp. 1			*		
Pteromalidae						
Hymenoptera RTU711	unident sp.1			*	*	*
Hymenoptera RTU712	unident sp.10				*	
Hymenoptera RTU713	unident sp.11			*	*	*
Hymenoptera RTU714	unident sp.13					*
Hymenoptera RTU715	unident sp.2			*	*	*
Hymenoptera RTU716	unident sp.3			*	*	
Hymenoptera RTU717	unident sp.4			*	*	
Hymenoptera RTU718	unident sp.5			*	*	*
Hymenoptera RTU719	unident sp.6			*		
Hymenoptera RTU720	unident sp.7				*	
Hymenoptera RTU721	unident sp.8			*		
Hymenoptera RTU722	unident sp.9			*		
Scelionidae						
Hymenoptera RTU723	unident sp.1			*	*	*
Hymenoptera RTU724	unident sp.2			*		
Hymenoptera RTU725	unident sp.3					*
Sphecidae						
Hymenoptera RTU726	*Podagritus albipes*			*	*	*
Hymenoptera RTU727	*Podagritus carbonicolor*				*	
Hymenoptera RTU728	*Podagritus cora*				*	
Hymenoptera RTU729	*Podagritus parrotti*				*	
Hymenoptera RTU730	*Rhopalum zealandum*			*		
Hymenoptera RTU731	*Tachysphex nigerrimus*				*	
Hymenoptera RTU732	unident sp.1			*		
Trichogrammatidae						
Hymenoptera RTU733	*Oligosita* sp. 1				*	*
Hymenoptera RTU734	*Oligosita* sp. 2					*
Hymenoptera RTU735	unident sp.1			*		
unident						
Hymenoptera RTU736	unident sp.1			*	*	*
Lepidoptera: Choreutidae						
Lepidoptera RTU737	*Tebenna micalis*			*		
Coleophoridae						
Lepidoptera RTU738	*Coleophora trifolii*			*		
Crambidae						
Lepidoptera RTU739	*Diasemia grammalis*			*		

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Lepidoptera RTU740	*Diasemia* sp. 1			*		
Lepidoptera RTU741	*Eudonia cataxesta*	*	*	*	*	*
Lepidoptera RTU742	*Eudonia chalara*			*		
Lepidoptera RTU743	*Eudonia diphtheralis*		*			
Lepidoptera RTU744	*Eudonia dochmia*		*			
Lepidoptera RTU745	*Eudonia feredayi*		*			
Lepidoptera RTU746	*Eudonia gyrotoma*			*		
Lepidoptera RTU747	*Eudonia leptalea*		*	*	*	
Lepidoptera RTU748	*Eudonia melanaegis*		*			
Lepidoptera RTU749	*Eudonia oculata*			*		
Lepidoptera RTU750	*Eudonia sabulosella*	*	*	*	*	*
Lepidoptera RTU751	*Eudonia* sp. 1				*	*
Lepidoptera RTU752	*Eudonia submarginalis*		*	*		
Lepidoptera RTU753	*Glaucocharis* sp. 1			*	*	
Lepidoptera RTU754	*Orocrambus aethonellus*				*	
Lepidoptera RTU755	*Orocrambus callirrhous*		*	*		
Lepidoptera RTU756	*Orocrambus corruptus*			*		*
Lepidoptera RTU757	*Orocrambus cyclopicus*		*	*		
Lepidoptera RTU758	*Orocrambus flexuosellus*		*	*	*	*
Lepidoptera RTU759	*Orocrambus lectus*			*		
Lepidoptera RTU760	*Orocrambus lewisi*		*	*		
Lepidoptera RTU761	*Orocrambus ramosellus*		*			*
Lepidoptera RTU762	*Orocrambus* sp. 1	*		*		*
Lepidoptera RTU763	*Orocrambus vittellus*		*	*	*	
Lepidoptera RTU764	*Orocrambus vulgaris*		*	*	*	
Lepidoptera RTU765	*Orocrambus xanthogrammus*	*	*	*	*	*
Lepidoptera RTU766	*Scoparia asaleuta*		*	*	*	
Lepidoptera RTU767	*Scoparia autochroa*			*		
Lepidoptera RTU768	*Scoparia exilis*	*		*		
Lepidoptera RTU769	*Udea flavidalis*			*		
Lepidoptera RTU770	unident sp.1			*		
Elachistidae						
Lepidoptera RTU771	*Cosmiotes ombrodoca*			*	*	
Lepidoptera RTU772	*Cosmiotes* sp. 1			*	*	*
Gelechiidae						
Lepidoptera RTU773	*Athrips zophochalca*			*		*
Lepidoptera RTU774	*Kiwaia cheradias*			*		
Lepidoptera RTU775	*Kiwaia lithodes*			*	*	*
Lepidoptera RTU776	*Kiwaia* sp. 1	*	*	*	*	*
Lepidoptera RTU777	unident sp.1			*		
Gelechoidae						
Lepidoptera RTU778	unident sp.1			*		
Geometridae						
Lepidoptera RTU779	*Arctesthes catapyrrha*	*		*	*	*
Lepidoptera RTU780	*Asaphodes beata*			*		
Lepidoptera RTU781	*Chloroclystis filata*			*		*
Lepidoptera RTU782	*Declana junctilinea*		*			*
Lepidoptera RTU783	*Epicyme rubropunctaria*	*				
Lepidoptera RTU784	*Epyaxa rosearia*		*			
Lepidoptera RTU785	*Gellonia pannularia*		*			
Lepidoptera RTU786	*Helastia corcularia*		*	*		
Lepidoptera RTU787	*Notoreas elegans*			*	*	
Lepidoptera RTU788	*Paranotoreas brephosata*			*	*	
Lepidoptera RTU789	*Pseudocoremia colpogramma*			*		
Lepidoptera RTU790	unident sp.1	*		*	*	*
Lepidoptera RTU791	*Zermizinga indocilisaria*		*	*	*	
Glyphipterigidae						
Lepidoptera RTU792	*Glyphipterix acrothecta*			*		
Lepidoptera RTU793	*Glyphipterix cionophora*			*		
Lepidoptera RTU794	*Glyphipterix* sp. 1			*		

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Gracillariidae						
Lepidoptera RTU795	*Caloptilia elaeas*			*		
Lepidoptera RTU796	*Caloptilia* sp. 1			*		*
Hepialidae						
Lepidoptera RTU797	*Wiseana copularis*		*			
Lepidoptera RTU798	*Wiseana umbraculata*		*			
Lycaenidae						
Lepidoptera RTU799	*Lycaena boldenarum*			*	*	*
Lepidoptera RTU800	*Lycaena* sp. 1	*		*	*	*
Lepidoptera RTU801	*Zizina oxleyi*			*	*	
Noctuidae						
Lepidoptera RTU802	*Aletia cuneata*		*	*		
Lepidoptera RTU803	*Aletia moderata*	*	*	*	*	*
Lepidoptera RTU804	*Aletia obsecrata*		*			
Lepidoptera RTU805	*Aletia* sp. 1					*
Lepidoptera RTU806	*Aletia virescens*		*			
Lepidoptera RTU807	*Bityla defigurata*					*
Lepidoptera RTU808	*Euxoa admirationis*	*	*	*	*	*
Lepidoptera RTU809	*Graphania averiella*			*		
Lepidoptera RTU810	*Graphania disjungens*		*	*		*
Lepidoptera RTU811	*Graphania mutans*		*			*
Lepidoptera RTU812	*Graphania nullifera*	*				
Lepidoptera RTU813	*Graphania paracausta*		*			*
Lepidoptera RTU814	*Graphania phricias*		*	*	*	
Lepidoptera RTU815	*Graphania plena*		*			
Lepidoptera RTU816	*Graphania* sp. 1	*				*
Lepidoptera RTU817	*Graphania ustistriga*		*			
Lepidoptera RTU818	*Ichneutica cana*		*			
Lepidoptera RTU819	*Meterana* sp. 1	*		*	*	*
Lepidoptera RTU820	*Persectania aversa*		*	*		
Lepidoptera RTU821	*Physetica caerulea*	*	*	*	*	*
Lepidoptera RTU822	*Rictonis comma*			*	*	*
Lepidoptera RTU823	*Tmetolophota atristriga*		*			
Lepidoptera RTU824	*Tmetolophota propria*		*			
Lepidoptera RTU825	*Tmetolophota semivittata*		*			
Lepidoptera RTU826	*Tmetolophota toroneura*		*			
Lepidoptera RTU827	*Tmetolophota unica*		*	*	*	
Lepidoptera RTU828	unident sp.1					*
Nymphalidae						
Lepidoptera RTU829	*Argyrophenga antipodum*			*	*	
Oecophoridae						
Lepidoptera RTU830	*Leptocroca* sp. 1					*
Lepidoptera RTU831	*Phaeosaces apocrypta*			*		
Lepidoptera RTU832	*Prepalla austrina*				*	
Lepidoptera RTU833	*Tingena melanamma*			*	*	*
Lepidoptera RTU834	*Tingena* sp. 1				*	*
Lepidoptera RTU835	*Trachypepla* sp. 1				*	
Lepidoptera RTU836	unident sp.1			*	*	
Plutellidae						
Lepidoptera RTU837	*Plutella psammochroa*			*	*	
Lepidoptera RTU838	*Zelleria colpota*			*		
Lepidoptera RTU839	*Zelleria copidota*	*				
Scythrididae						
Lepidoptera RTU840	*Scythris epistrota*	*		*		
Lepidoptera RTU841	*Scythris* sp. 1				*	*
Lepidoptera RTU842	*Scythris triatma*		*	*	*	*
Tineidae						
Lepidoptera RTU843	*Monopis ethelella*			*		
Tortricidae						
Lepidoptera RTU845	unident sp.1			*		

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Lepidoptera RTU846	*Capua semiferana*	*	*	*	*	*
Lepidoptera RTU847	*Ctenopseutis obliquana*			*		
Lepidoptera RTU848	*Epichorista siriana*			*	*	
Lepidoptera RTU849	*Eurythecta robusta*				*	
Lepidoptera RTU850	*Eurythecta* sp. 1			*		
Lepidoptera RTU851	*Eurythecta zelaea*			*		
Lepidoptera RTU852	*Harmologa oblongana*			*	*	*
Lepidoptera RTU853	*Harmologa psammochroa*			*		
Lepidoptera RTU854	*Harmologa* sp. 1		*		*	
Lepidoptera RTU855	*Merophyas leucaniana*					*
Lepidoptera RTU856	*Spherchia intractana*			*		
Lepidoptera RTU857	unident sp.1	*		*		
unident						
Lepidoptera RTU858	unident sp.1			*	*	*
Neuroptera: Hemerobiidae						
Neuroptera RTU859	*Micromus tasmaniae*		*	*	*	*
Opiliones: Phalangiidae						
Opiliones RTU860	*Phalangium opilio*	*		*	*	*
Orthoptera: Acrididae						
Orthoptera RTU861	*Brachaspis nivalis*	*				
Orthoptera RTU862	*Phaulocridium marginale*			*		
Orthoptera RTU863	*Sigaus* sp. 1	*				
Orthoptera RTU864	unident sp.1					*
Anostostomatidae						
Orthoptera RTU865	*Hemideina maori*			*	*	*
Gryllidae						
Orthoptera RTU866	*Bobilla* sp. 1	*				*
Orthoptera RTU867	*Pteronemobius* sp. 1					*
Orthoptera RTU868	unident sp.1					*
Tettigoniidae						
Orthoptera RTU869	*Conocephalus* sp. 1			*	*	
unident						
Orthoptera RTU870	unident sp.1	*		*	*	*
Plecoptera: Gripopterygidae						
Plecoptera RTU871	*Zelandobius furcillatus*			*	*	*
Plecoptera RTU872	*Zelandobius* sp. 1					*
Plecoptera RTU873	*Zelandoperla decorata*			*		
unident						
Plecoptera RTU874	unident sp.1			*		
Protura: unident						
Protura RTU875	unident sp.1				*	
Pseudoscorpionida: Cheliferidae						
Pseudoscorpionida RTU876	*Philomaoria novazealandica*					*
Pseudoscorpionida RTU877	*Philomaoria taierensis*					*
Chernetidae						
Pseudoscorpionida RTU878	*Thalassochernes taierensis*	*		*	*	*
Garypidae						
Pseudoscorpionida RTU879	*Synsphyronus lineatus*	*		*	*	*
unident						
Pseudoscorpionida RTU880	unident sp.1	*		*	*	*
Psocoptera: Caeciliidae						
Psocoptera RTU881	*Caecilius flavistigmata*			*		
Psocoptera RTU882	*Caecilius flavus*			*		
Psocoptera RTU883	*Caecilius semifuscatus*			*		
Psocoptera RTU884	*Valenzuela flavistigmata*		*	*	*	
Psocoptera RTU885	*Valenzuela flavus*			*		
Psilopsocidae						
Psocoptera RTU886	*Psilopsocus stigmaticus*			*		
Psocidae						

RTU identifier	Taxonomic name	H	L	M	Pn	Pt
Psocoptera RTU887 unident	*Ectopsocus briggsi*			*	*	
Psocoptera RTU888	unident sp.1		*	*	*	*
Psocoptera RTU889	unident sp.2	*				
Siphonaptera: Ceratophyllidae						
Siphonaptera RTU890	*Nosopsyllus fasciatus*					*
Thysanoptera: Aeolothripidae						
Thysanoptera RTU891	*Aeolothrips fasciatus*			*	*	*
Phlaeothripidae						
Thysanoptera RTU892	unident sp.1			*	*	
Thripidae						
Thysanoptera RTU893	*Anaphothrips zelandicus*			*	*	*
Thysanoptera RTU894	*Anaphrygmothrips otagoensis*					*
Thysanoptera RTU895	*Aptinothrips rufus*					*
Thysanoptera RTU896	*Chirothrips manicatus*			*	*	*
Thysanoptera RTU897	*Pseudanaphothrips achaetus*			*	*	*
Thysanoptera RTU898	*Thrips obscuratus*			*	*	*
Thysanoptera RTU899	*Thrips* sp. 1			*	*	*
Thysanoptera RTU900	*Thrips tabaci*				*	
Thysanoptera RTU901	unident sp.1			*	*	*
Thysanoptera RTU902	unident sp.2			*		
unident						
Thysanoptera RTU903	unident sp.1			*	*	*
Trichoptera: Conoesucidae						
Trichoptera RTU904	*Beraeoptera roria*			*	*	*
Trichoptera RTU905	*Pycnocentria evecta*		*	*		
Trichoptera RTU906	*Pycnocentrodes aureolus*		*	*	*	
Trichoptera RTU907	*Pycnocentrodes* sp. 1					*
Hydrobiosidae						
Trichoptera RTU908	*Costachorema psaropterum*			*		
Trichoptera RTU909	*Costachorema xanthopterum*			*		
Trichoptera RTU910	*Hydrobiosis clavigera*		*	*		
Trichoptera RTU911	*Hydrobiosis colonica*			*		
Trichoptera RTU912	*Hydrobiosis harpidiosa*		*	*	*	*
Trichoptera RTU913	*Hydrobiosis parumbripennis*		*	*		
Trichoptera RTU914	*Psilochorema bidens*			*		
Trichoptera RTU915	*Psilochorema leptoharpax*			*		
Hydropsychidae						
Trichoptera RTU916	*Aoteapsyche colonica*			*		
Trichoptera RTU917	*Aoteapsyche raruraru*		*	*		
Hydroptilidae						
Trichoptera RTU918	*Oxyethira albiceps*		*	*	*	
Trichoptera RTU919	*Paroxyethira eatoni*	*		*	*	*
Trichoptera RTU920	*Paroxyethira hendersoni*			*		*
Trichoptera RTU921	unident sp.1			*		
Leptoceridae						
Trichoptera RTU922	*Hudsonema alienum*			*		
Trichoptera RTU923	*Hudsonema amabile*	*		*	*	*
Trichoptera RTU924	*Oecetis unicolor*		*	*		
Trichoptera RTU925	*Triplectidina moselyi*			*	*	
Trichoptera RTU926	unident sp.1			*		
unident						
Trichoptera RTU927	unident sp.1	*	*	*	*	

Appendix 3: Frequency with which RTUs were collected from samples across all trap types.
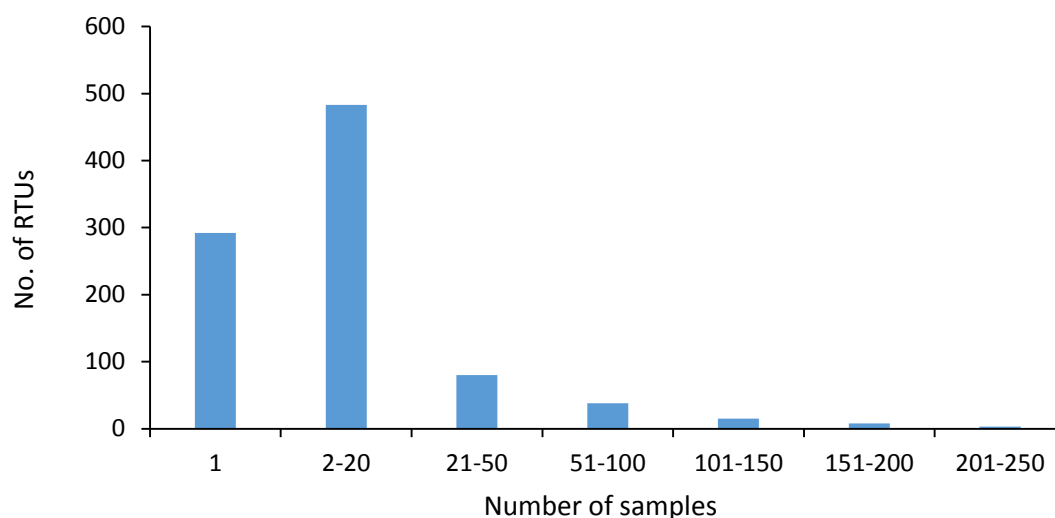
Appendix 4: Threat classifications for the 56 species detected in this study that have been assessed under the New Zealand Threat Classification System (NZTCS). The remaining 346 RTUs that were identified to species, and could therefore be searched for in the NZTCS database, were not found and have either not been assessed or may be listed under a different name.

Name & Authority	Taxonomic classification
Threatened-Nationally Critical (1)	
Pimeleocoris roseus Eyles & Schuh	Hemiptera: Miridae
At Risk-Naturally Uncommon (4)	
Anoteropsis arenivaga (Dalmas)	Araneae: Lycosidae
Eurythecta robusta Butler	Lepidoptera: Tortricidae
Neoitamus smithii Hutton	Diptera: Asilidae
Nysius liliputanus Eyles & Ashlock	Hemiptera: Lygaeidae
Data Deficient (3)	
Anabarhynchus indistinctus Lyneborg	Diptera: Therevidae
Matua festiva Forster	Araneae: Gnaphosidae
Rhypodes triangulus Eyles	Hemiptera: Lygaeidae
Not Threatened (41)	
Anoteropsis adumbrata (Urquhart)	Araneae: Lycosidae
Anoteropsis aerescens (Goyen)	Araneae: Lycosidae
Anoteropsis hilaris (L.Koch)	Araneae: Lycosidae
Anzacia gemmea (Dalmas)	Araneae: Gnaphosidae
Arangina cornigera (Dalmas)	Araneae: Dictynidae
Arangina pluva Forster	Araneae: Dictynidae
Beraeoptera roria Mosely	Trichoptera: Conoesucida
Brachaspis nivalis Hutton	Orthoptera: Acrididae
Costachorema psaropterum McFarlane	Trichoptera: Hydrobiosidae
Costachorema xanthopterum McFarlane	Trichoptera: Hydrobiosidae
Dolomedes aquaticus Goyen	Araneae: Pisauridae

| Name & Authority	Taxonomic classification
Dolomedes minor L. Koch	Araneae: Pisauridae
Dunedinia pullata Millidge	Araneae: Linyphiidae
Eriophora pustulosa (Walckenaer)	Araneae: Araneidae
Euryopis nana (O P.-Cambridge)	Araneae: Theridiidae
Gasparia rustica Forster	Araneae: Desidae
Hemideina maori Pictet & Saussure	Orthoptera: Anostostomatidae
Hudsonema alienum (McLachlan)	Trichoptera: Leptoceridae
Hudsonema amabile (McLachlan)	Trichoptera: Leptoceridae
Hydrobiosis clavigera McFarlane	Trichoptera: Hydrobiosidae
Hydrobiosis harpidiosa McFarlane	Trichoptera: Hydrobiosidae
Hydrobiosis parumbripennis McFarlane	Trichoptera: Hydrobiosidae
Matua valida Forster	Araneae: Gnaphosidae
Nauhea tapa Forster	Araneae: Gnaphosidae
Notocosa bellicosa Goyen	Araneae: Lycosidae
Oecetis unicolor (McLachlan)	Trichoptera: Leptoceridae
Paroxyethira eatoni Mosely	Trichoptera: Hydroptilidae
Paroxyethira hendersoni Mosely	Trichoptera: Hydroptilidae
Psilochorema bidens McFarlane	Trichoptera: Hydrobiosidae
Psilochorema leptoharpax McFarlane	Trichoptera: Hydrobiosidae
Pycnocentria evecta McLachlan	Trichoptera: Conoesucidae
Pycnocentrodes aureolus (McLachlan)	Trichoptera: Conoesucidae
Phaulacridium marginale Walker	Orthoptera: Acrididae
Steatoda lepida (O P.-Cambridge)	Araneae: Theridiidae
Steatoda truncata (Urquhart)	Araneae: Theridiidae
Theridion ampliatum Urquhart	Araneae: Theridiidae
Triplectidina moselyi McFarlane & Ward	Trichoptera: Leptoceridae
Zelanda erebus (L. Koch)	Araneae: Gnaphosidae
Zelandobius furcillatus Tillyard	Plecoptera: Gripopterygidae
Zelandoperla decorata Tillyard	Plecoptera: Gripopterygidae
Zizina oxleyi Felder & Felder	Lepidoptera: Lycaenidae
Introduced and Naturalised (7)	
Apis mellifera Linnaeus	Hymenoptera: Apidae
Bombus hortorum (Linnaeus)	Hymenoptera: Apidae
Bombus terrestris (Linnaeus)	Hymenoptera: Apidae
Diplocephalus cristatus (Blackwall)	Araneae: Linyphiidae
Erigone prominens Bösenberg & Strand	Araneae: Linyphiidae
Erigone wiltoni Locket	Araneae: Linyphiidae
Tenuiphantes tenuis (Blackwall)	Araneae: Linyphiidae

Appendix 5: RTUs that included immature specimens & proportion of specimens the immatures represented. * Denotes RTUs which were *only* represented by immatures.

| RTU	Family	Genus	Species	%	*
Araneae RTU10	Gnaphosidae	*Matua*	sp.1	50.0	
Araneae RTU11	Gnaphosidae	*Matua*	*valida*	27.5	
Araneae RTU12	Gnaphosidae	*Nauhea*	tapa	11.8	
Araneae RTU15	Gnaphosidae	unident	sp.1	49.3	
Araneae RTU16	Gnaphosidae	unident	sp.2	50.0	
Araneae RTU17	Gnaphosidae	*Zelanda*	*erebus*	25.0	
Araneae RTU19	Hahniidae	unident	sp.1	50.0	
Araneae RTU24	Linyphiidae	*Erigone*	sp.1	50.0	
Araneae RTU25	Linyphiidae	*Erigone*	*wiltoni*	29.4	
Araneae RTU26	Linyphiidae	*Laetesia*	sp.1	41.7	
Araneae RTU28	Linyphiidae	*Maorineta*	sp.1	22.2	
Araneae RTU3	Araneidae	*Eriophora*	*pustulosa*	33.3	
Araneae RTU31	Linyphiidae	unident	sp.1	43.6	
Araneae RTU33	Lycosidae	*Anoteropsis*	*adumbrata*	50.0	
Araneae RTU34	Lycosidae	*Anoteropsis*	*aerescens*	73.9	
Araneae RTU35	Lycosidae	*Anoteropsis*	*arenivaga*	26.3	
Araneae RTU36	Lycosidae	*Anoteropsis*	*hilaris*	27.1	
Araneae RTU37	Lycosidae	*Anoteropsis*	sp.1	48.6	
Araneae RTU38	Lycosidae	*Anoteropsis*	sp.2	50.0	
Araneae RTU39	Lycosidae	*Notocosa*	*bellicosa*	83.1	
Araneae RTU4	Desidae	*Gasparia*	*rustica*	37.5	
Araneae RTU40	Lycosidae	unident	sp.1	49.5	
Araneae RTU42	Pisauridae	*Dolomedes*	*minor*	50.0	
Araneae RTU43	Pisauridae	*Dolomedes*	*aquaticus*	25.0	
Araneae RTU45	Salticidae	unident	sp.1	69.2	
Araneae RTU46	Salticidae	unident	sp.2	78.6	
Araneae RTU47	Salticidae	unident	sp.3	100.0	*
Araneae RTU48	Theridiidae	*Coleosoma*	*octomaculatum*	54.5	
Araneae RTU49	Theridiidae	*Coleosoma*	sp.1	16.7	
Araneae RTU5	Dictynidae	*Arangina*	*cornigera*	16.7	
Araneae RTU53	Theridiidae	*Steatoda*	sp.1	47.6	
Araneae RTU54	Theridiidae	*Steatoda*	*truncata*	9.0	
Araneae RTU55	Theridiidae	*Theridion*	*ampliatum*	10.0	
Araneae RTU57	Thomisidae	*Diaea*	sp.1	100.0	*
Araneae RTU58	unident	unident	sp.1	45.7	
Araneae RTU59	Zoropsidae	*Uliodon*	sp.2	50.0	
Araneae RTU7	Gnaphosidae	*Anzacia*	*gemmea*	35.7	
Araneae RTU8	Gnaphosidae	*Anzacia*	sp.1	50.0	
Araneae RTU9	Gnaphosidae	*Matua*	*festiva*	36.8	
Coleoptera RTU126	Scarabaeidae	unident	sp.5	50.0	
Coleoptera RTU146	unident	unident	sp.1	44.3	
Coleoptera RTU147	unident	unident	sp.2	50.0	
Coleoptera RTU148	unident	unident	sp.3	50.0	
Coleoptera RTU149	unident	unident	sp.4	60.0	
Coleoptera RTU150	unident	unident	sp.6	50.0	

| RTU	Family	*Genus*	Species	%	*
Coleoptera RTU151	unident	unident	sp.7	50.0	
Diptera RTU242	Chironomidae	unident	sp.1	1.0	
Diptera RTU479	unident	unident	sp.1	17.5	
Hemiptera RTU481	Acanthostomatidae	unident	sp.1	80.0	
Hemiptera RTU484	Aphididae	*Acrythosiphon*	*kondoi*	4.6	
Hemiptera RTU488	Aphididae	*Brachycaudus*	*rumexicolens*	5.6	
Hemiptera RTU498	Aphididae	unident	sp.1	45.2	
Hemiptera RTU509	Cicadellidae	unident	sp.1	25.3	
Hemiptera RTU511	Cicadellidae	*Xestocephalus*	*ovalis*	50.0	
Hemiptera RTU516	Delphacidae	unident	sp.1	13.3	
Hemiptera RTU519	Lygaeidae	*Nysius*	*huttoni*	5.9	
Hemiptera RTU521	Lygaeidae	*Nysius*	sp.1	25.0	
Hemiptera RTU522	Lygaeidae	*Rhypodes*	*chinai*	73.2	
Hemiptera RTU525	Lygaeidae	*Rhypodes*	sp.1	49.9	
Hemiptera RTU527	Lygaeidae	unident	sp.1	49.2	
Hemiptera RTU528	Mesoveliidae	*Mniovelia*	sp.1	50.0	
Hemiptera RTU535	Pemphigidae	unident	sp.1	50.0	
Hemiptera RTU537	Pseudococcidae	*Balanococcus*	sp.1	93.0	
Hemiptera RTU538	Pseudococcidae	*Balanococcus*	sp.2	68.1	
Hemiptera RTU539	Pseudococcidae	*Balanococcus*	sp.3	50.0	
Hemiptera RTU540	Pseudococcidae	*Balanococcus*	sp.4	96.8	
Hemiptera RTU541	Pseudococcidae	unident	sp.1	47.4	
Hemiptera RTU542	Pseudococcidae	unident	sp.2	42.9	
Hemiptera RTU554	unident	unident	sp.1	0.7	
Lepidoptera RTU762	Crambidae	*Orocrambus*	sp.1	41.2	
Lepidoptera RTU790	Geometridae	unident	sp.1	50.0	
Lepidoptera RTU803	Noctuidae	*Aletia*	*moderata*	8.9	
Lepidoptera RTU816	Noctuidae	*Graphania*	sp.1	50.0	
Lepidoptera RTU819	Noctuidae	*Meterana*	sp.1	50.0	
Lepidoptera RTU822	Noctuidae	*Rictonis*	*comma*	41.4	
Lepidoptera RTU828	Noctuidae	unident	sp.1	50.0	
Lepidoptera RTU834	Oecophoridae	*Tingena*	sp.1	16.7	
Lepidoptera RTU841	Scythrididae	*Scythris*	sp.1	27.8	
Lepidoptera RTU846	Tortricidae	*Capua*	*semiferana*	3.4	
Lepidoptera RTU858	unident	unident	sp.1	29.4	
Orthoptera RTU865	Anostostomatidae	*Hemideina*	*maori*	35.2	
Orthoptera RTU869	Tettigoniidae	*Conocephalus*	sp.1	11.1	
Psocoptera RTU884	Caeciliidae	*Valenzuela*	*flavistigmata*	1.0	
Psocoptera RTU888	unident	unident	sp.1	9.1	
Thysanoptera RTU893	Thripidae	*Anaphothrips*	*zelandicus*	0.6	
Thysanoptera RTU897	Thripidae	*Pseudanaphothrips*	*achaetus*	0.9	
Thysanoptera RTU899	Thripidae	*Thrips*	sp.1	0.6	
Thysanoptera RTU901	Thripidae	unident	sp.1	0.2	
Thysanoptera RTU903	unident	unident	sp.1	0.2	

Appendix 6: Overlay of cluster analysis on MDS sample ordination by trap type. SIMPROF analysis indicates trap type clusters represent statistically genuine groups at 0.1% significance with similarities of (a) Light = 5.8%, Pi = 5.1; (b) Jar = 12.1%, Pi = 4.51; (c) Pitfall = 22.3%, Pi = 1.5; (d) Trough = 24.33%, Pi = 3.19, excluding 2 samples; (e) Pan = 24.33%, Pi = 3.1, excluding 13 samples. Similarity refers to species composition relative other defined groups.
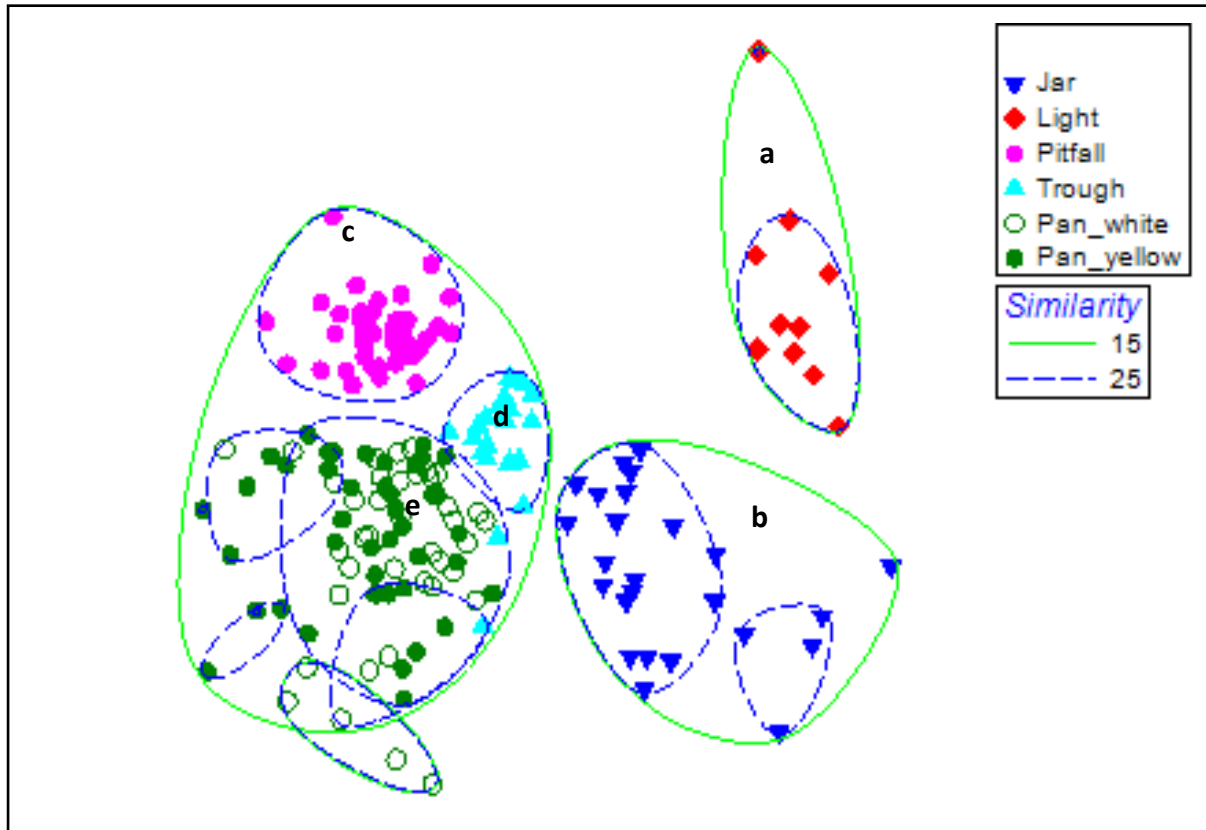
Appendix 7: Correlations between total species diversity and vs. (a) genus, (b) family, (c) order, (d) Diptera, (e) Hymenoptera, (f) Lepidoptera, (g) Coleoptera and (h) spider species.
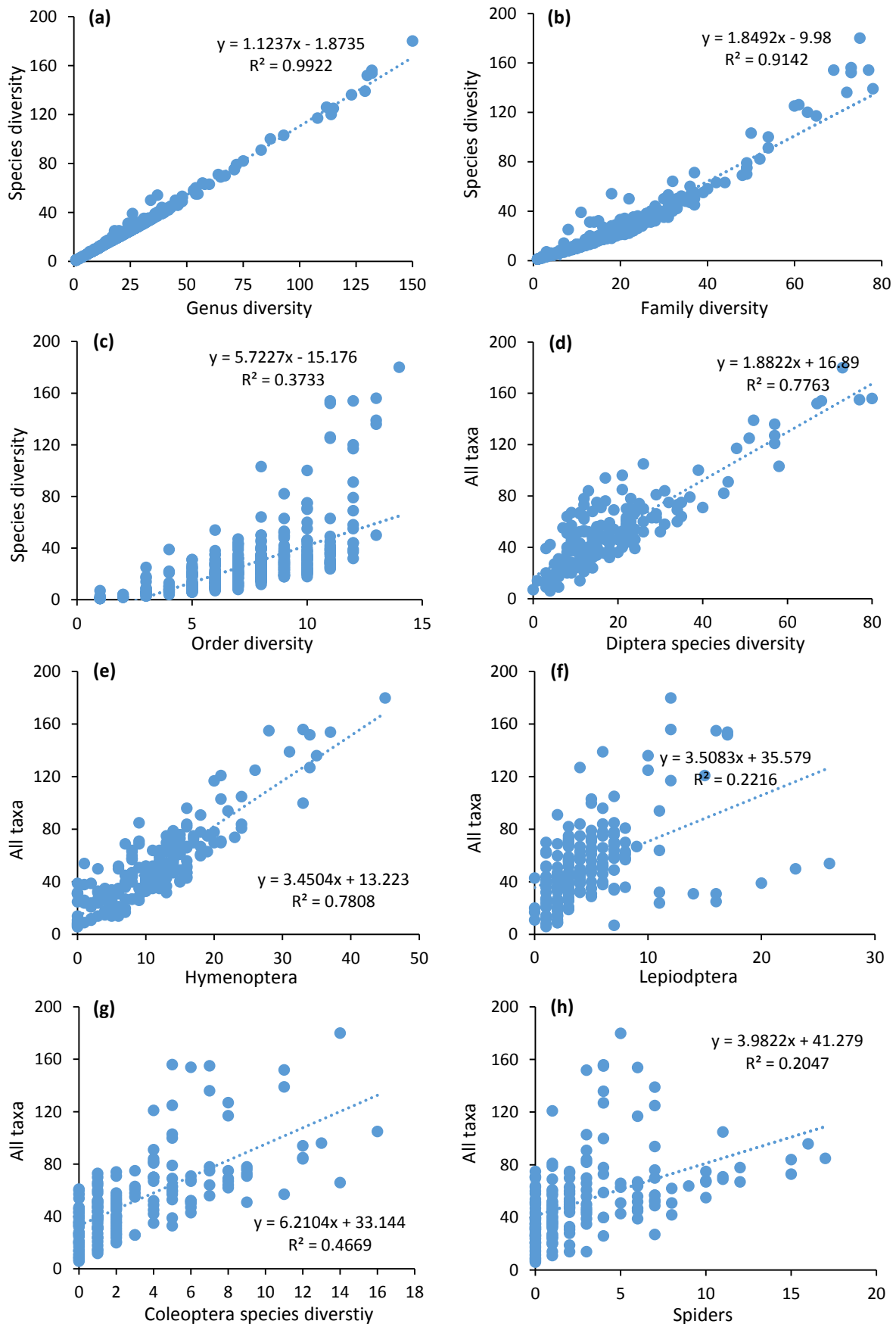
Appendix 8: Patterns of community compositions by trap type able to be detected by **(a)** the full data set of 919 RTUs from 21 arthropod orders (*stress = 0.22*) compared to subsets of particular orders; **(b)** orders with > 20 RTUs (Aranae, Coleoptera, Diptera, Hemiptera, Hymenoptrea, Lepidoptera, Trichoptera), 865 RTUs, *stress = 0.23*; **(c)** Diptera, 315 RTUs, *stress = 0.26*, **(d)** Hymenoptera, 179 RTUs, *stress = 0.24*, **(e)** Lepidoptera, 121 RTUs. *stress = 0.19*, **(f)** Coleoptera, 91 RTUs, *stress = 0.01*. Samples containing no specimens of the order being assessed were excluded in order to plot MDS ordinations (e.g. most light samples (red diamonds) for Hymenoptera). Pitfall samples (pink circles) for Coleoptera are obscured in the centre of graph indicating high compositional similarity.
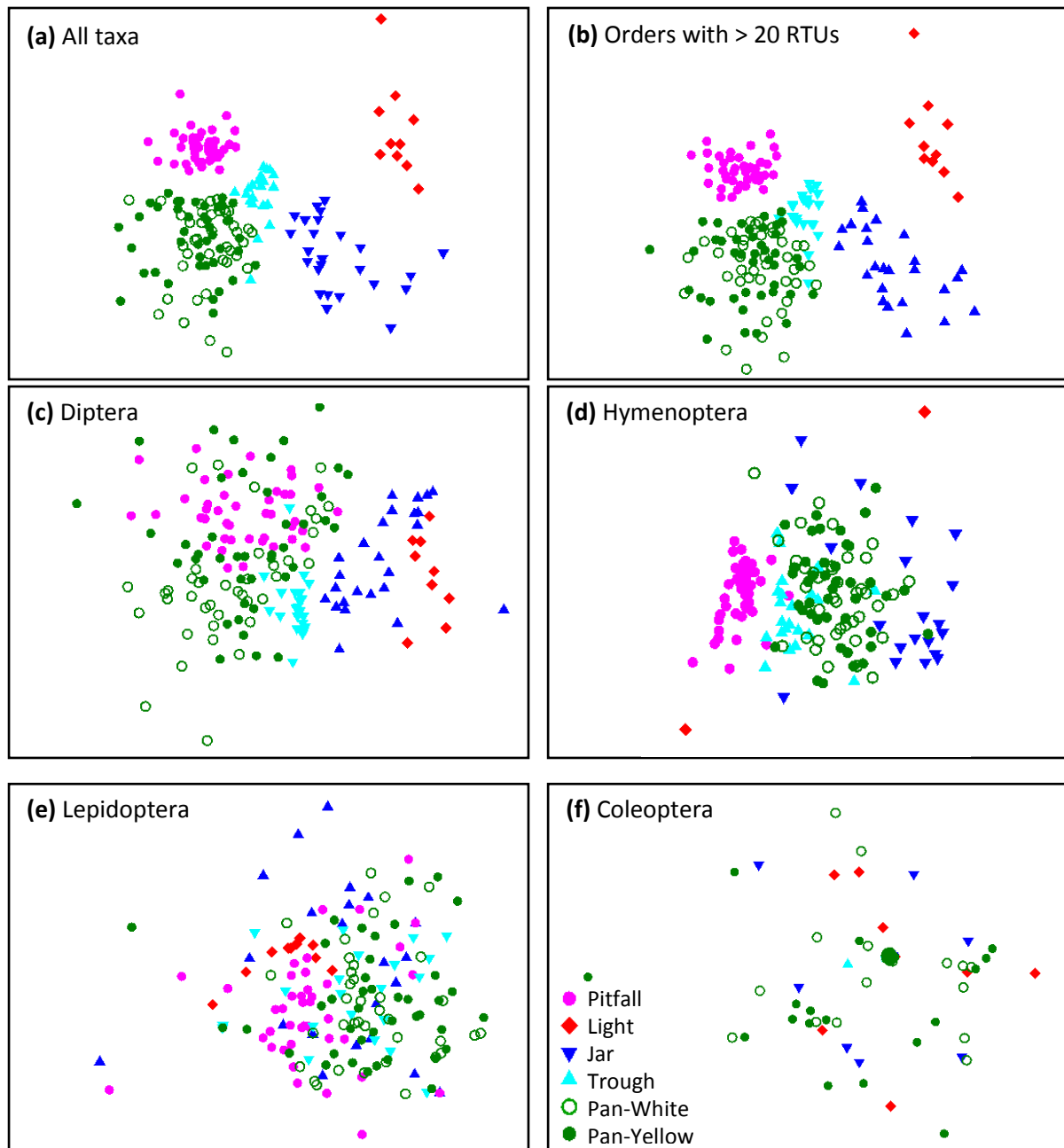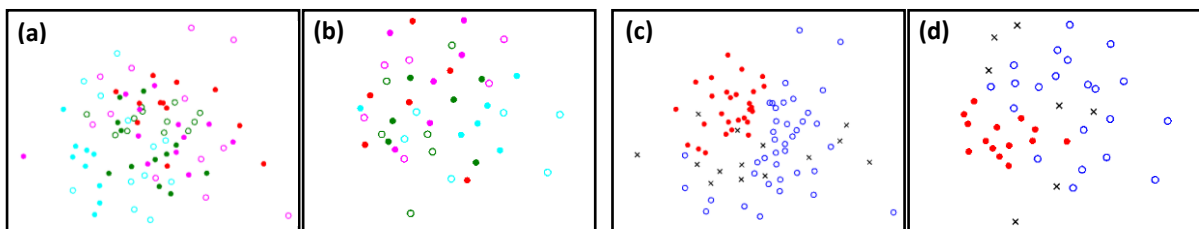
Appendix 9: Comparison of the effects of sampling time **(a, b)** and site position along the Tasman River **(c, d)** on the community compositions that were able to be detected using the full dataset of 919 RTUs vs. subsets of individual orders using pan (left of each pair) and pitfall (right of each pair) data.
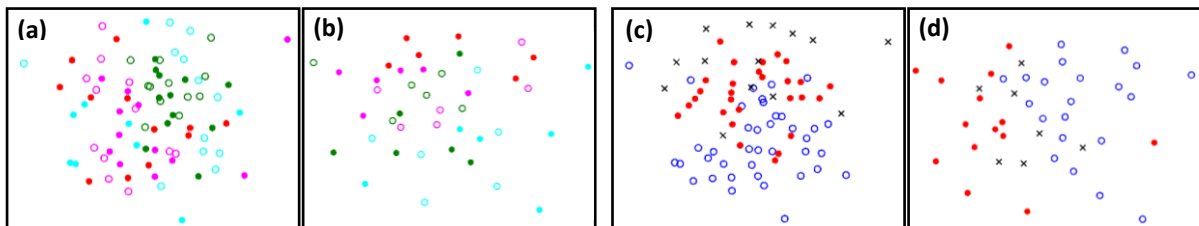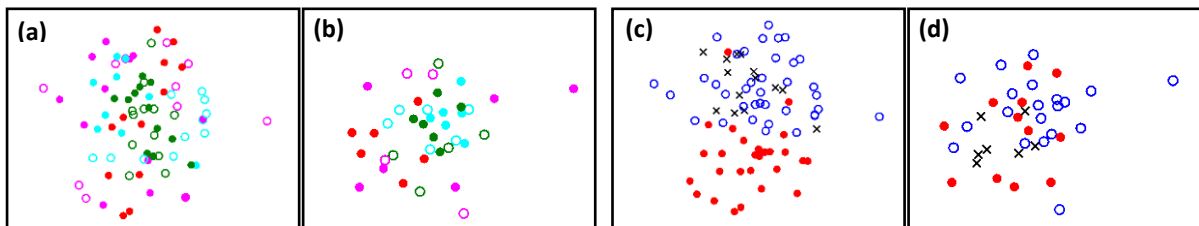
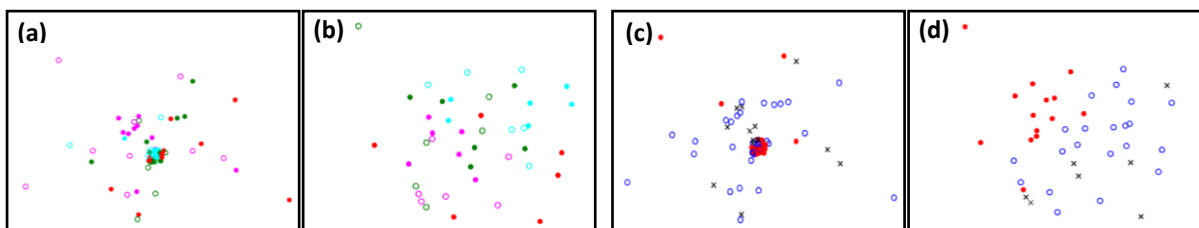**All taxa (919 RTUs)**:
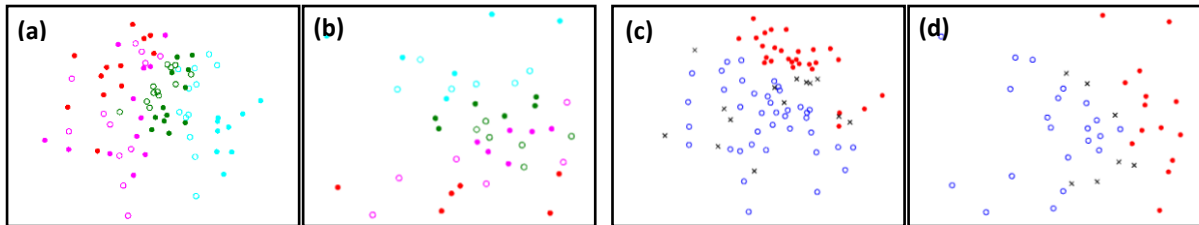
Diptera (315 RTUs):

Hymenoptera (179 RTUs):

Lepidoptera (121 RTUs):

Coleoptera (91 RTUs):

Appendix 10: Mean values for **N** (total abundance) and 9 diversity indices. Shaded columns are measures of dominance/evenness, unshaded columns are measures of species richness: **S** = total species, **d** = Margalef's index (*d* = (S-1)/log(N)), diversity for a given abundance, **Δ** = taxonomic *diversity* (average taxonomic distance apart of every pair of individuals in a sample), **Δ***= taxonomic *distinctness* (average taxonomic distance apart of every pair of individuals in a sample that are not of the same species). **J'** = Pielou's evenness index (H'/log(S)), **H'** = Shannon index (log e), **λ =** Simpson index: **λ** = (SUM(Pi^2)) probability that any two specimens will be the same, values close to 1 indicate assemblage abundance is dominated by one or a few species, **1-λ =** (1-SUM(Pi^2)), evenness index, **1-λ'** = (1-SUM(Ni*(Ni-1)/(N*(N-1)))), evenness index for small sample sizes.

Trap type	N	S	d	Δ	Δ*	J'	H'	λ	1-λ	1-λ'
Hand	12.87	5.83	2.07	60.56	76.83	0.87	1.20	0.46	0.54	0.73
Light	383.60	30.70	5.14	64.49	82.19	0.69	2.25	0.22	0.78	0.79
Pan	118.08	25.85	5.59	80.05	92.63	0.80	2.48	0.16	0.84	0.86
Pan-white	127.48	25.64	5.50	79.69	92.03	0.80	2.45	0.17	0.83	0.86
Pan-yellow	109.48	26.04	5.68	80.39	93.18	0.80	2.51	0.16	0.84	0.86
Pitfall	493.89	22.76	3.92	66.52	95.32	0.59	1.74	0.32	0.68	0.69
Malaise	585.21	68.00	10.53	75.32	92.81	0.69	2.70	0.19	0.81	0.82
Jar	354.72	34.40	5.84	68.94	94.02	0.65	2.08	0.28	0.72	0.74
Trough	847.14	106.18	15.85	82.57	91.44	0.75	3.41	0.10	0.90	0.90

Site/Veg type	N	S	d	Δ	Δ*	J'	H'	λ	1-λ	1-λ'
1	438.85	33.68	5.94	74.31	94.20	0.68	2.25	0.23	0.77	0.78
2	215.19	25.69	5.02	75.88	93.27	0.75	2.17	0.22	0.78	0.81
3	281.99	27.45	5.09	69.31	89.66	0.68	2.00	0.27	0.73	0.76
4 (Veg type C)	218.33	23.44	4.38	70.75	91.82	0.71	1.97	0.26	0.74	0.76
5 (Veg type D)	533.00	30.96	5.76	69.76	92.61	0.66	2.09	0.28	0.72	0.76
6 (Veg type B)	344.84	24.52	4.58	70.16	94.05	0.66	1.97	0.28	0.72	0.74
Veg type A	309.48	28.85	5.34	73.18	92.36	0.71	2.14	0.24	0.76	0.79

Moon	N	S	d	Δ	Δ*	J'	H'	λ	1-λ	1-λ'
Full	327.47	28.44	5.15	69.70	92.56	0.68	2.00	0.28	0.72	0.74
New	346.05	26.97	5.10	73.19	92.63	0.71	2.12	0.24	0.76	0.79

Time sampled	N	S	d	Δ	Δ*	J'	H'	λ	1-λ	1-λ'
T1	268.99	21.93	4.28	68.35	91.42	0.68	1.89	0.30	0.70	0.74
T2	546.44	35.93	6.06	74.87	94.00	0.67	2.24	0.21	0.79	0.80
T3	263.93	22.44	4.51	69.88	91.84	0.71	1.95	0.28	0.72	0.75
T4	211.53	31.07	5.87	74.62	93.34	0.73	2.28	0.22	0.78	0.80

Appendix 10 cont.

Time sampled	N	S	d	Δ	Δ*	J'	H'	λ	1- λ	1- λ '
T1-N	97.83	19.65	4.38	76.66	92.98	0.78	2.18	0.21	0.79	0.83
T1-F	428.34	24.05	4.19	60.61	89.96	0.59	1.62	0.38	0.62	0.65
T2-N	668.13	31.62	5.40	71.35	92.38	0.64	2.08	0.24	0.76	0.77
T2-F	432.01	39.99	6.67	78.18	95.52	0.70	2.38	0.19	0.81	0.82
T3-N	388.54	24.13	4.57	70.65	91.83	0.69	1.95	0.27	0.73	0.76
T3-F	135.60	20.70	4.44	69.08	91.86	0.72	1.95	0.29	0.71	0.75
T4-N	211.53	31.07	5.87	74.62	93.34	0.73	2.28	0.22	0.78	0.80