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**Multiple scales of biological variability
in New Zealand streams**

A thesis presented in partial fulfilment of the requirements
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General Abstract

Stream fish communities in Taranaki, New Zealand, were studied for the patterns and drivers of their spatial ecology. The study was focused on three main themes: a) complementarity between geography and landuse in driving regional distribution patterns of stream fish, b) the impact of agriculture on community composition, structure and variability of fish and invertebrates, and c) concordance among environmental distance and community dissimilarities of stream fish and invertebrates.

Stream sampling and data collection for fish was conducted at regional scale using 96 sites distributed in the protected forest (44 sites) of Egmont National Park in Taranaki, and in surrounding farmlands (52 sites). Local scale sampling for fish and invertebrates was carried out at 15 stream sites in pasture (8 sites) and in adjacent forest (7 sites). Environmental data of geography, landuse and local habitat description were also gathered concurrently to biological sampling. The regional scale survey reported fifteen fish species, dominated by longfin eels (*Anguilla dieffenbachia*), redfin bullies (*Gobiomorphus huttoni*) and koaro (*Galaxias brevipinnis*), while 12 fish species and 69 different invertebrate taxa were recorded from the 15 sites at local scale.

Regional scale spatial patterns of fish were mainly driven by landuse pattern. Catchment landuse (characterised by percentage cover of farming/native forest) effectively partitioned the stream fish community structure in Taranaki. Within each level of catchment landuse (farming), abundance and richness of fish species were negatively correlated with the altitude. Moreover, the upstream slope in high elevations and intensive farming downstream limited the distribution of stream fish across the region.

Fish community composition differed significantly but weakly between forest and pasture in the immediate proximity. The dissimilarity of fish communities between forest and pasture increased from regional to local scale, and a similar result was found with stream invertebrate dissimilarity at the local scale. Stream communities (fish and invertebrates) were equally variable among streams between the two land use classes both at regional and local scales. Although the land use difference did not affect within-stream variability of fish, invertebrate communities were less variable within a pasture stream. Trends in in-stream variability of invertebrates were influenced mainly by altitude, stream morphology, pH, and riparian native cover.

In concordance analysis, Mantel and Procrustes tests were used to compare community matrices of fish and invertebrates and the environmental distance between stream sites. The spatial patterns of fish and invertebrates were significantly concordant with each other among the 15 streams at the local scale. Nevertheless, community concordance decreased with lower spatial scales, and the two communities were not concordant at local sites within a given stream. Agriculture had a negative impact on the concordance between fish and invertebrates among streams, and none of the communities correlated with the overall environmental distance between agricultural streams. Community concordance between fish and invertebrates was consistently higher than the community-environment links, and lower trophic level (invertebrates) linked to their environment more closely than the upper trophic level (fish). The overall results suggest a bottom-up control of the communities through the stream food web.

Finally, to inform the regional management and conservation decision, stream sites were partitioned according to the most important bioenvironmental constraints. The ecological similarity was measured by geography, land use pattern and the abundances of influential native fish species within the region, and the streams were clustered into seven distinct zones, using the method of affinity propagation. Interestingly, the dichotomy in proximal land use was not generally represented between zones, and the species diversity gradients were not significantly different across the zonal stream clusters. The average elevation of a given zone did not influence the community variability, while upstream pasture significantly homogenised fish communities between streams within a zone. Nonetheless the zones were based on river-system connectivity and geographical proximity.

This study showed separate effects of confounding geography (altitude) and landuse on stream fish community structure, which has not explicitly been explored by previous studies. Studies with a simultaneous focus on multiple biological (e.g. fish and invertebrates) and environmental (e.g. geography, landuse, stream morphology) scales in varying spatial scales are not common in freshwater ecology. Therefore, this study has a great contribution to the understanding of the spatial ecology of stream communities linked with the control of geography, landuse, environment and likely biological interactions between fish and invertebrates.

Preface

This thesis is based on a research designed to investigate the environmental and biological drivers of freshwater community composition, structure and variability, in New Zealand streams. Taranaki streams were selected, because of the rich species diversity of freshwater fish and invertebrates, reported in previous studies. A special attention was paid to separate the effect of geography and land use, which was not explicitly covered by the other studies previously conducted in Taranaki. The first part of the study explores the important environmental drivers of the fish community in Taranaki, surveyed in a wider geographical extent (96 streams), compared to the study area of 15 streams, in the second phase of this research.

Most of the studies on biological variability cover large geographical areas from ecosystems to ecoregions. Particularly in New Zealand, previous studies have not mainly addressed the inter-site variability change across land-uses and the community concordance between fish and invertebrates, within a small geographical extent. Therefore, I attempted to address the knowledge gap in biological variability and community concordance of stream communities at the local scale, with a special concern about the human impacts to stream fish and invertebrates.

This thesis includes three individual research manuscripts, thus some repetition occurs in the introductions, methods and discussions across the chapters.

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Chapter One

The effect of land use on the spatial ecology of New Zealand stream communities

Biological communities and environmental changes

The global environment has been drastically changed over the last three centuries (Goldewijk & Ramankutty, 2004; Ramankutty & Foley, 1999; Turner, 1990). Land use change (e.g. forest clearance), over-exploitation of species (e.g. animal farming, commercial forestry and floriculture), invasive species, climate change (increase in global temperature and precipitation) and high nutrient applications in agriculture intensification are among key direct anthropogenic drivers of the contemporary status of natural ecosystems worldwide (McDowall, 1990; Morris, 2010; Nelson *et al.*, 2006; Turner, 1990). Human impacts have become increasingly critical determinants of biological diversity, within the framework of biogeographical history, spatial heterogeneity (e.g. topography), and temporal changes such as seasonal variations in precipitation and temperature (Chapin III *et al.*, 2000; Chapman & Reiss, 1998; 2010; Olden, 2006). Biotic communities fluctuate in response to their changing environment, and the particular responses may be informative of the level of environmental disturbances (Conrad, 1977).

Biomonitoring has become a popular tool among resource managers for assessing ecological health and sustainability of natural resources in response to anthropogenic activities such as farming, urbanization and introduced exotic species (Allan, 2004; Death & Joy, 2004; Joy & Death, 2002). It may be useful to identify the most sensitive communities to a particular human impact, in order to focus mitigation strategies. For instance, stream fauna such as fish and invertebrates are widely used to monitor the impacts of land

conversions, particularly for agricultural developments. Hence, in countries with economies largely based on agriculture, such as New Zealand, fluvial habitats are extensively studied to compare the stream communities between upstream natural forests and downstream pasture, to find out the effects of farming on the natural environment and essentially the biological diversity (Cowie, 1980; Death & Joy, 2004; McDowall, 2010).

What is β -diversity?

Biological diversity encompasses the diversity of genes, species, and communities, within life-systems, ranging from a single organism to complex ecosystems or ecoregions (Magurran, 2002). Conventional biological diversity measures (e.g. species richness) have a limited capability to capture variability within and between ecosystems (Leprieur *et al.*, 2011; Munoz *et al.*, 2008; Soininen *et al.*, 2007). Community ecologists have therefore focused on diversity measures that cover greater scales to help with this (Magurran, 1988). The concept of β diversity was introduced by Whittaker (Magurran, 2004; Whittaker, 1960), and has developed extensively in community ecology (Anderson *et al.*, 2011; Koleff *et al.*, 2003; Soininen *et al.*, 2007). β diversity measures the change of diversity between sampling units, across time and/or space, and it has a great utility in exploring community patterns, related to the functionality of an ecosystem (Magurran, 2002).

Since the introduction of Whittaker's differentiation index in 1960, around 24 different measures have been described to measure β diversity for presence/absence data, and several quantitative coefficients such as the Bray-Curtis index (Sørensen quantitative) have also been introduced to measure β diversity with density data in biological communities (Koleff *et al.*, 2003; Oksanen, 2012). All of these β diversity measures fall into three basic categories: 1). Measures of differentiation (difference in α diversity (e.g. number of species)

between two plots), 2). Measures of complementarity (similarity / dissimilarity) and 3). Measures of species-area relationship or average species turnover per area (Magurran, 2002).

New Zealand stream communities and their determinants

Fish and benthic macroinvertebrates are the most extensively studied organisms in New Zealand lotic habitats (Collier & Winterbourn, 2000; McDowall, 2010). New Zealand freshwater fish communities comprise a high proportion of migratory (amphidromous and catadromous) species, 21 exotic species and seven marine species (McIntosh & McDowall, 2004). Generally, nocturnal and benthic native fish fauna include representatives in seven families: Geotridae, Anguillidae, Retropinnidae, Galaxiidae, Pinuipedidae, Gobiidae, and Pleuronectidae, with the majority being galaxiids (*Galaxias* spp.) or bullies (*Gobiomorphus* spp.). Almost the entire fish community feeds on freshwater macroinvertebrates, while larger species such as eels and trout prey on other fish and semi-aquatic birds or mammals as well as invertebrates (McDowall, 2000).

Apart from being a major component of the diet of fish, freshwater macroinvertebrates play an important role in many key ecosystem functions (e.g. breaking down allochthonous organic matter and transferring photosynthetic energy to higher trophic levels) of New Zealand running waters (Closs *et al.*, 2009; Collier & Winterbourn, 2000). Freshwater macroinvertebrates are dominated by insects but include other taxonomic groups ranging from Porifera to Mollusca (Collier & Winterbourn, 2000). New Zealand freshwater insects belong to 58 families in nine orders; Odonata, Ephemeroptera, Plecoptera, Megaloptera, Mecoptera, Hemiptera, Trichoptera, Coleoptera and Diptera (Winterbourn *et al.*, 1989). The ecological role of freshwater insects is mainly related to their functional feeding groups: collector-gatherers, browsers, scrapers, shredders, filter feeders, predators and piercer-suckers (Cowie, 1980; Cowley, 1978; Cummins, 1973; Winterbourn, 2000).

Insects disperse between freshwater habitats by flying, drifting, moving between substrates or banks by walking or swimming (Delucchi, 1989).

New Zealand freshwater communities are affected by several environmental factors, including altitude, distance inland, land use, and migratory barriers (Collier & Winterbourn, 2000; Jowett & Richardson, 2003; McDowall, 1990). However, the impact of each factor varies between habitats, regions and at the national scale (McIntosh & McDowall, 2004). For instance, predator-prey interactions are important habitat scale drivers, while geographical factors such as latitude play a major role in regional or national scale community structure and composition of freshwater communities (Geist, 2011; McIntosh & McDowall, 2004). Conversion of forest to pastoral land results in increased deposited sediments, nutrient enrichment, removal of riparian vegetation and declines in water quality (e.g. high primary productivity, deoxygenation, and ammonia toxicity), and may negatively influence the ecological balance of stream communities (Quinn, 2000).

Importance of studying variability in New Zealand stream communities

Multivariate community assessments are commonly used to explore the environmental determinants of New Zealand freshwater community structure and composition (Death & Winterbourn, 1994; Jowett & Richardson, 2003; Leathwick *et al.*, 2005). Although several studies have looked at the β diversity patterns of freshwater fish and invertebrates, particularly along the geographical extent of the country, there has been no investigation of how community variability is partitioned between land uses (e.g. forest vs. pasture) (Astorga *et al.*, 2014; McDowall, 2010). For example, are the fish faunas more or less variable between streams (β diversity) in pasture than in native forest? In addition, landscape ecology of New Zealand stream communities is yet to be explained in terms of links between the physical environment and trophic levels of the stream food web. Some of

the aspects that have not been explicitly addressed by previous exploratory studies include community concordance, factors of spatial stratification, relative importance of geography, and land use for freshwater communities. Further, the conventional studies are heavily weighted towards assessing the land use impacts and/or national scale biogeography of New Zealand freshwater communities (Collier & Winterbourn, 2000; McDowall, 2010; Winterbourn, 1991). In-depth investigations on the spatial ecology of regional stream communities would provide scientific insights for interest groups such as resource managers, conservationists, and local decision makers. Hence, this study would potentially contribute to the future sustainability of freshwater ecosystems.

Study design and the research goals

This research program was designed in three spatial levels within Taranaki: a) regional, b) local and c) in-stream, to explore the relative effects of bioenvironmental factors and cross-community links for fish and invertebrates between specific spatial levels. Stream fish and invertebrates were selected because of their: a) popularity/applicability in ecological health assessments (Joy & Death, 2002; Lewis *et al.*, 2007), b) high contribution to New Zealand stream food webs (Winterbourn, 1991), and c) biological diversity value in conservation of New Zealand freshwater ecosystems (Geist, 2011). Further, the analyses of this study are based on β diversity of the particular communities, to enhance the predictability of community models alongside multiple bioenvironmental scales. Further, the particular β diversity-based statistical analyses (described in the method sections of this thesis) were more effective and informative in achieving the key research goals of this study. For instance, partitioning the community patterns against land use/ geographical gradients, comparing the community ordinations between fish and invertebrates would have not been straightforward with conventional α diversity measures such as species richness (Magurran, 1988).

Agriculture was considered as the predominant human impact indicator of the Taranaki streams, and the study attempted to gauge the relative importance between land use and elevation as portioning factors (Joy & Death, 2001; Townsend, 1996). The key research goals of the research project include:

- Investigating the relative importance of geography and land use control of the stream communities in Taranaki
- Comparison of the effect of farming for community similarity and variability
- Understanding the likelihood of top-down or bottom-up control of the stream communities through trophic levels
- Measuring the differences in community-environment links between stream fish and invertebrates
- Comparing the importance in community concordance for stream community structure between different spatial levels and land use classes
- To suggest a pragmatic conservation/management approach for the fish community in Taranaki.

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Chapter Two

Spatial patterns of stream fish communities in Taranaki, New Zealand

Abstract

The environmental and biological drivers of the similarity structure of fish communities were studied in 96 streams of Taranaki, New Zealand. Eight fish species occurred in > 5% of the sites. Long fin eels (*Anguilla dieffenbachii*) followed by brown trout (*Salmo trutta*) showed the widest distribution, occurring at 75% and 41% of the sites respectively. Fish community similarity differed significantly between forest and pasture within region. Catchment land use and native riparian cover effectively partitioned fish abundances, and fish species consistently correlated with the altitudinal gradient within different land use and riparian classes. Land use vectors were more important than the habitat factors (e.g. habitat type and substrate type) in structuring fish communities. Upstream slope and farming limited species distribution in the extreme ends of upper and lower catchments, respectively.

Introduction

Stream fauna often reflect the quality of their physical and biological environment via community structure, composition, diversity and variability (Closs *et al.*, 2004). During the past three decades, freshwater fish community structure has become increasingly popular as an indicator of the ecological quality of New Zealand lotic habitats (Jowett & Richardson, 2003; Joy & Death, 2002; Leathwick *et al.*, 2005), because of their well-known biology and

life history information (Karr, 1981; 1990). New Zealand native freshwater fish are characteristic for their migratory patterns, nocturnal behaviour and for generally occupying benthic water layers of streams and rivers (McDowall, 1990). Most of the freshwater fish in New Zealand are primarily riverine, and 17 native species migrate between sea and freshwaters to complete their life cycles. More than 80% of New Zealand migratory fish species are either amphidromous or catadromous and spend most of their life in freshwater. In addition to the 38 native species, 21 exotic fish species have been introduced to freshwater habitats in New Zealand since the 19th century (McDowall, 1990; 2000; 2010; McIntosh & McDowall, 2004).

Determinates of freshwater fish community structure and composition vary with the magnitude of spatial units such as region, reach or microhabitat (Closs *et al.*, 2004; McIntosh & McDowall, 2004). In addition to evolutionary and geological history of the country, altitude and/or inland distance have a strong impact on regional scale distribution of freshwater fish in New Zealand (McIntosh & McDowall, 2004). It is not surprising to observe altitude playing an important role in the distribution of a fish community largely consisting of migratory species, because only the good climbers such as eels (*Anguilla* spp.) and koaro (*Galaxias brevipinnis*) are able to penetrate the steep hills to reach the headwaters. Therefore, the occurrence of migratory species generally declines with increasing altitude in inland freshwater habitats (Joy & Death, 2000; McDowall, 1990). Although the latitudinal diversity patterns of freshwater fish in the country have not been completely explained, all diadromous species occur across almost the entire latitudinal range of New Zealand, while the distribution of non-diadromous species is not consistent throughout the country's geographic extent along latitudes (McDowall, 2010).

In addition to dispersal patterns at large spatial scales (e.g. island-wide), geography may influence species distribution also within a small region or sub-region (Heino, 2001).

However particular within region, patterns are often modified by land use constraints (Ricotta *et al.*, 2014; Turner, 1989). It is therefore difficult to distinguish the effects of land use from regional scale fish community patterns often confounded by geographical factors such as altitude, mainly because of the confusion caused by co-linearity between multiple environmental drivers of community structure in relatively limited spatial scales (Graham, 2003; Olden & Jackson, 2002). Hence, it is important to separate the geographical effects from land use impacts on communities, to understand the ecological processes, which underlie community distribution patterns, particularly in ecosystems impacted by agriculture. Nevertheless, in ecological studies of small regions (or limited areas), there has not been an explicit concern about geographical influence for community distribution patterns, compared to the research interest in prominent land use impacts caused by farming in particular (Heino, 2001; Turner, 1989). In this study, I argue that the influence of geography may exist as ‘signatures’ in species’ distribution patterns, even across different land uses, because of the strong connection between altitude and life cycle strategies of migratory fish species in New Zealand streams (McDowall, 2010). The likely fish distribution patterns influenced by geography (across natural and modified landuse classes) are introduced in this study, as “geo-signatures” of the community structure. The term “geo-signature” was used to reflect the persistence of geographical influence on community patterns, at the presence of a given human modification such as conversion of natural forest to pasture.

At relatively smaller spatial scales such as catchment or reach, vegetation, land use and water quality are strong environmental constraints for the composition of riverine fish communities (McIntosh & McDowall, 2004; Winterbourn, 1991). Farming is the predominant land use practice in New Zealand, and makes a major contribution to changes in freshwater habitats, including nutrient enrichment in water, removal of riparian native canopy and sediment deposition on streambeds (Ling, 2010; Quinn & Hickey, 1990; Zimmermann &

Death, 2002). Pasture streams receive less allochthonous organic matter such as leaf litter compared to the forested streams, but show high levels of algal growth with increased nitrogen levels and reduced riparian shade. Therefore, pastoral land use contributes to a dramatic change in freshwater fish habitats from their natural condition, and hence has a strong impact on reach scale structure and composition of freshwater communities in New Zealand (McDowall, 2001; McIntosh & McDowall, 2004; Winterbourn, 1991).

Despite well-known bottom-up effects of agriculture such as increased in-stream primary production, some researchers argue that top-down control by introduced fish has community-wide effects on stream fish in New Zealand (Flecker & Townsend, 1994; Schlosser, 1995; Simon & Townsend, 2003). Exotic species, for instance brown trout, have been studied for their predation, competition and distribution in relation to population dynamics and diversity changes in native fish, invertebrates, and algal growth in streams. For example, invertebrate densities have decreased and the algal standing crop has increased in streams invaded by brown trout compared to the streams occupied by native galaxiids (Flecker & Townsend, 1994). The particular effects of exotic species have, however, generally been assessed at lower spatial levels (e.g. reach), compared to the regional scale analyses of the effect of geography or land use change on stream communities (Heino, 2001; Jowett & Richardson, 2003). Thus, there is limited information on ecosystem-wide effects of introduced species, in comparison to regional scale impacts of geography and land use on freshwater communities.

Studies largely based on inventory measures (e.g. population density, biomass or species richness) have a limited capacity to capture the full range of changes in spatial distribution patterns of natural communities influenced by multiple anthropogenic stressors (Soininen *et al.*, 2007). Contrary to alpha diversity based on the number of species, beta diversity compares communities between given samples, and quantifies the level of

compositional similarity among the sampling sites. Moreover, community ecologists have developed comprehensive spatial analyses (e.g. homogeneity test of beta diversity), to investigate biological variability and its determinants (Anderson & Walsh, 2013; Clarke & Warwick, 2001; Dale & Fortin, 2014). Comparative analyses based on beta diversity are statistically useful to overcome the limited capability of conventional inventory studies for understanding the complexity of ecological patterns influenced by multiple geographical, anthropogenic and biological constraints. For instance, beta diversity is commonly used to analyse the compositional similarities of communities within and/or between different treatment groups (community partitioning) (Anderson *et al.*, 2011; Magurran, 2002). In this study, I used beta diversity to question: a) Does agriculture partition the regional-scale freshwater fish community similarity? b) Are land-use factors more predictive than the habitat (scale) determinants of fish in freshwater ecosystems affected by agriculture? c) Do geo-signatures exist in the spatial structure of fish communities constrained by land use patterns?

Methods

Study sites

The study sites include 96 streams (Appendix 1) at Egmont National Park, on Mount Taranaki and adjacent area, in the west of North Island of New Zealand (Fig. 2.1). Mount Taranaki peaks at 2,518 m above sea level is at the hub of the Egmont National Park. Protected area is predominately surrounded by pastoral land, dominated by dairy and beef farming, while natural forest covers the most of the area in upper catchments (Joy & Death, 2000; Winterbourn, 1991). Pasture covers more than half of the proximal land use along the total length of Taranaki streams (Taranaki Regional Council, 2010).

About 140 streams and rivers drain in a radial pattern through the Taranaki ring plain. Typically, Taranaki running waters are relatively short (compared to major New Zealand river systems: Waikato, Manawatu) first or second order streams (Joy & Death, 2000; Taranaki Regional Council, 2013). Downstream dams are widespread across the Taranaki region, and likely to obstruct the upstream migration of fish, particularly above 100 m of the sea level, but all of the dams/ structures are not obligatory barriers for migration, and fish-passes have been established by some of the downstream dams (Joy, 1999).

Although the specific history of brown trout introduction to Taranaki streams is unclear, this particular species had been introduced to most North Island rivers since 1872 (McDowall, 1990; Townsend, 1996). Further, studies show scientific records of brown trout in Taranaki streams since the late 1940s (Alien & Cunningham, 1957; Jowett, 1990). In Taranaki streams, the native fish community is mainly characterised by diadromous species (except for two species: *Gobiomorphus basalis* and *G. breviceps*) (Joy & Death, 2001). The sites used in this study sampled 96 different reaches of Taranaki streams in both protected forest areas (44 sites) and pasture (52 sites).

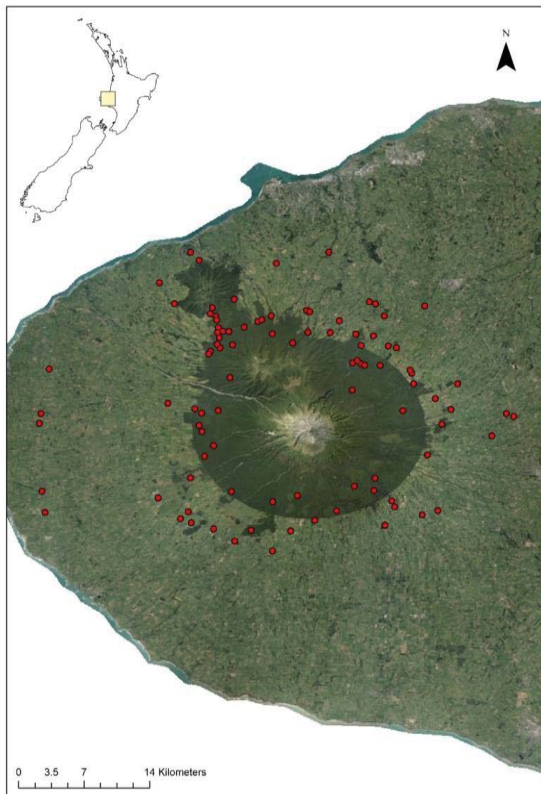


Fig. 2.1 Stream sampling sites in the Taranaki region of New Zealand used to collect fish and habitat data during summer 2012.

Fish sampling and data collection

Night spotlighting for fish species presence and abundance was carried out (once) at 46 sites in Taranaki streams from January to June 2012. These data were supplemented with recent (within 10 years) records from the New Zealand Freshwater Fish dataset (NZFFD). These historical data provided additional species records for 12 of the 46 sampling sites and added another 50 sites; making a total of 96 sites.

A stretch of nearly 150 m was sampled in each stream, using spotlighting and bank side observations, by moving in an upstream direction. Spotlighting was commenced approximately one hour after sunset. Each site was scanned between banks from the downstream end, by using a 30 W spotlight. Smaller fish species (e.g. bullies) were caught

alive using a dip net, and were collected into a container, while large fish were observed closely without catching. Fish species were identified to species level, and the collected fish were released back into their habitats after species identification was completed (McDowall, 2000).

Environmental data were collected in 50 different vectors at habitat, reach and regional scales for each sampling site. Visually observed habitat scale measures of this study include percentage cover of habitat type, substrate type, riparian vegetation type, in-stream vegetation, and leaf litter. Stream size (wetted width and depth) was measured by measuring tapes and rulers. Proximal land use pattern (within 500 m from the stream bank) was recorded by visual observations, and was further confirmed using 1:50,000 maps. Catchment land use data were recorded using 1:50,000 maps and Freshwater Ecosystems in New Zealand (FENZ) geo-based spatial data layers (Leathwick *et al.*, 2010). Water quality parameters including pH, temperature and conductivity were measured by a 'EuTech cyber scan PC-10 pH-conductivity-temperature meter'. Further, I extracted habitat data, including climatic factors (rainfall and air temperature), geological composition (% composition of Ca and P of the surface rocks), proportional upstream land use, total Nitrogen concentration in water, for each sampling site, from the records in geo-based spatial data layers (Leathwick *et al.*, 2010). In addition, NZFFD also provided geomorphological and land use data at habitat, riparian and catchment scales (Appendix II).

Statistical Analysis

Fish and environmental data were compiled into two major categories; a) fish (biological) database of 96 sites and b) environmental data. For fish data set, beta diversity was computed between streams, using Bray-Curtis and Sørensen indices which are popular (dis)similarity measures among ecologists, because they are suitable for communities with

limited numbers of species (Clarke, 1993; Magurran, 1988; 2002). Abundance data were standardised using Wisconsin double standardisation method to increase the gradient detection capability of beta diversity indices (Oksanen, 2008). Bray-Curtis and Sørensen dissimilarities were organised into a triangular matrices (Clarke & Warwick, 2001; Oksanen, 2012).

The non-metric multidimensional scaling (NMDS) method was used to construct a two dimensional ordination between sampling sites, on the biological similarity of fish between streams (Clarke, 1993; Clarke & Warwick, 2001; Ramette, 2007; Wickelmaier, 2003). NMDS models were generated for abundance data matrix. Biological similarity between sites is represented by the distance between points in an NMDS ordination, and the particular distance in a biological ordination is referred to as the biological distance. Euclidean distance between sites was computed, using normalised environmental data, and the environmental distance was compared with the biological distance, by using BIO-ENV/BVSTEP procedures (Clarke & Warwick, 2001). I used the BIO-ENV/ BVSTEP test as an exploratory tool, to find out the most important environmental variables of the fish community structure in Taranaki streams. Because of the large number of environmental variables (46), stepwise matching (BVSTEP) was selected to explore important environmental variables (Appendix II). In addition, I also compared raw density data matrix of fish with the biological similarity matrix, to identify important fish species for the biological distance between streams in Taranaki (BIO-BIO procedure). Significances of the most influential environmental variables and fish taxa of the fish community structure were identified by the Spearman correlation values (Clarke, 1993; Clarke & Warwick, 2001; Zar, 1972).

Fish similarity matrices were used to assess the partitioning dissimilarity of fish between forest and pasture (Oksanen *et al.*, 2013). ANOSIM (Analysis of Similarity) test was

used to find out the effect of factor predictors (forest vs. pasture) on the similarity of fish data between and within groups (Clarke & Warwick, 2001; Oksanen, 2012). ANOSIM detects the importance of factor predictors, in partitioning beta diversity (Anderson & Walsh, 2013). Global R-values measure the degree of separation between selected groups of sites (forest vs. pasture), using average rank dissimilarities and the number of samples in a data matrix (Clarke & Warwick, 2001; Oksanen, 2011). Top contributors for between-group Bray-Curtis dissimilarity were selected by SIMPER (Similarity Percentage) analysis (Clarke & Warwick, 2001; Shepherd *et al.*, 1992).

Further, I compared the average number of species in a stream (α diversity) and total number of species (γ diversity) between the groups of sites significantly different in their group similarities. Within-group variability was compared between impacted and non-impacted sites, using the difference in group homogeneities (Oksanen, 2011). Group homogeneities were computed by partitioning similarities between sites for each factor predictor. In an ordination, distance to the centroid in a partitioned distance matrix was used to quantify the degree of variability within a group of samples. The distance between the group centroid and a sampling site (within a group of sites) was calculated by dividing the sum of squared inter-point (sites are represented as points in an ordination) distances by the number of points (Anderson, 2001). The difference in variability was analysed between groups by using the multivariate analysis of variance. Permutation tests (999) assessed the significance of variation between selected groups of sites.

I used constrained correspondence analysis (CCA) to observe the biological variation, which is explainable by the important community drivers. Compared to previous NMDS models, CCA is rather linear mapping approach that uses Chi-squared distances between the objects (sites) (Ramette, 2007). In the CCA of this study, multiple co-linearity between all the gathered environmental constraints was gauged by variance inflation factor (VIF) of

individual factors among full environmental data set, and factors were considered to be fully independent of other variables, when their VIF is < 10 . To minimise the co-linearity effect among factors, a reduced model was constructed by removing the least important variables found by BIO-ENV analysis (Graham, 2003; Oksanen, 2011).

Important environmental constraints were selected by CCA factor fitting approach, which is similar to BIO-ENV procedure. r^2 value of each variable was used to assess the strength of fitting, and significances were derived by 999 permutation tests (Oksanen, 2008). Important vectors of CCA factor fitting results were selected to develop a reduced model, for the removal of co-linearity effect among multiple vectors. Moreover, individual partial models were developed by constraining the biological ordination with selected most important vectors, and the significance of conditioned partial models was assessed by permutation tests. Each partial model was constrained by only one selected factor, but one to three of other explanatory vectors were fitted into each model, using vector fitting and/or surface fitting approaches (Oksanen, 2011). Further, within-strata variation in community composition was analysed from species fitted into their correlating sites in each partial model. Vegan package in R software (version 3.0.2) and PRIMER (6.0) were used for statistical analysis of this study (Clarke & Warwick, 2001; Oksanen, 2011).

Results

Fish community composition

Fifteen species of freshwater fish in five families: Anguillidae, Galaxiidae, Gobiidae (Eleotridae), Pinguipedidae and Salmonidae, were observed in the survey. Eight fish species occurred in > 5% of the 96 sites. Long fin eels (*Anguilla dieffenbachii*) occurred at 75% of the sites while koaro (*Galaxias brevipinnis*), shortjaw kokopu (*Galaxias postvectis*) and redfin bullies (*Gobiomorphus huttoni*) were found in more than 27% of the sites. Brown trout (*Salmo trutta*) were found from over 41% of the sites (Table 2.1 and Fig. 2.2).

Fish community structure

Abundance of eight fish species had a significant effect on the community structure. The impact of galaxiids was prominent in their abundance, but their axis correlations varied among species. For example, koaro and banded kokopu showed negative correlations while giant kokopu had positive correlations to both NMDS axes. Additionally, redfin and common bullies had strong positive correlations to NMDS axis 2. Axis correlations of brown trout were positive in both NMDS 1 and 2 (Table 2.2).

Table 2.1: Frequency of occurrence and relative abundances of freshwater fish species reported from the 96 streams and rivers from Taranaki during summer 2012.

Common Name	Scientific Name	% Frequency of occurrence	Relative Abundance (%)
Longfin eel	<i>Anguilla dieffenbachia</i>	75.00	27.58
Brown trout	<i>Salmo trutta</i>	41.67	09.23
Koaro	<i>Galaxias brevipinnis</i>	37.50	17.03
Short jaw kokopu	<i>Galaxias postvectis</i>	31.25	10.44
Red fin bully	<i>Gobiomorphus huttoni</i>	27.08	26.26
Shortfin eel	<i>Anguilla australis</i>	16.67	2.86
Banded kokopu	<i>Galaxias fasciatus</i>	09.38	1.87
Common bully	<i>Gobiomorphus cotidianus</i>	05.21	2.31
Torrentfish	<i>Cheimarrichthys fosteri</i>	04.17	0.55
Giant kokopu	<i>Galaxias argenteus</i>	04.17	0.44
Inanga	<i>Galaxias maculatus</i>	01.04	0.55
Smelt	<i>Retropinna retropinna</i>	01.04	0.22
Cran's bully	<i>Gobiomorphus basalis</i>	01.04	0.22
Upland bully	<i>Gobiomorphus breviceps</i>	01.04	0.22
Bluegill bully	<i>Gobiomorphus hubbsi</i>	01.04	0.22

Table 2.2: Selected fish species important in their abundance to two dimensional NMDS ordination (constructed on Bray-Curtis similarity) of freshwater fish taxa reported from the 96 streams and rivers from Taranaki during summer 2012.

Common Name	Scientific Name	Axis Correlation		r^2	Significance
		NMDS1	NMDS2		
Brown trout	<i>Salmo trutta</i>	0.97	0.26	0.29	0.001 ***
Banded kokopu	<i>Galaxias fasciatus</i>	-0.99	-0.08	0.27	0.001 ***
Koaro	<i>Galaxias brevipinnis</i>	-0.34	-0.94	0.16	0.001 ***
Redfin bully	<i>Gobiomorphus huttoni</i>	-0.03	0.99	0.16	0.001 ***
Shortjaw kokopu	<i>Galaxias postvectis</i>	-0.71	0.71	0.12	0.002 **
Giant kokopu	<i>Galaxias argenteus</i>	0.35	0.94	0.12	0.005 **
Torrentfish	<i>Cheimarrichthys fosteri</i>	0.05	0.99	0.08	0.022 *
Common bully	<i>Gobiomorphus cotidianus</i>	0.21	0.98	0.08	0.027 *

‘*’ $P < 0.05$, ‘**’ $P < 0.01$, ‘***’ $P < 0.001$

Environmental drivers of the fish community structure

Among geographical vectors, a strong negative correlation occurred between NMDS axis 1 and northing ($r_s = -0.97$), and upstream average slope was important for similarity on abundance of fish. Further, the occurrence of fish species was influenced by the gradient of upstream average slope, which is collinear with altitude (Fig. 2.3 and Table 2.7). Strong positive links occurred between NMDS axis 1 and riparian native vegetation in both percentage cover ($r_s = -0.90$) and the proportionate width ($r_s = -0.90$), and in contrast, farming in catchment positively correlated with the same axis of abundance ordination ($r_s = 0.87$). Upstream geology characterised by calcium and phosphorus concentrations in surface rocks had significant but contrasting effects on the fish community ordination. However, in NMDS ordination of fish, the biological variation was poorly explained by environmental factors (very low r^2 values), and multiple co-linearity was common among explanatory variables (Table 2.3).

Table 2.3: Important environmental vectors of NMDS ordination based on fish abundance data and variance inflation factor (VIF) of each vector assessed on constrained community ordination (CCA).

Vector	Axis correlation		r^2	Significance	VIF
	NMDS1	NMDS2			
Northing	-0.97	0.23	0.13	0.003 **	11.70
% Farming©	0.87	-0.49	0.07	0.029 *	1034.07
% Native ®	-0.94	0.34	0.06	0.044 *	793.12
Native riparian cover within 100m	-0.90	-0.43	0.07	0.033 *	10.85
Average slope (US)	-0.93	-0.36	0.07	0.041 *	19.53
Calcium conc. in surface rocks (US)	0.60	0.80	0.07	0.039 *	21.73
Phosphorus conc. in surface rocks (US)	-0.81	-0.59	0.08	0.027 *	9.86

US= upstream, © = catchment, ® = riparian

‘**’ $P < 0.05$, ‘***’ $P < 0.01$, ‘****’ $P < 0.001$

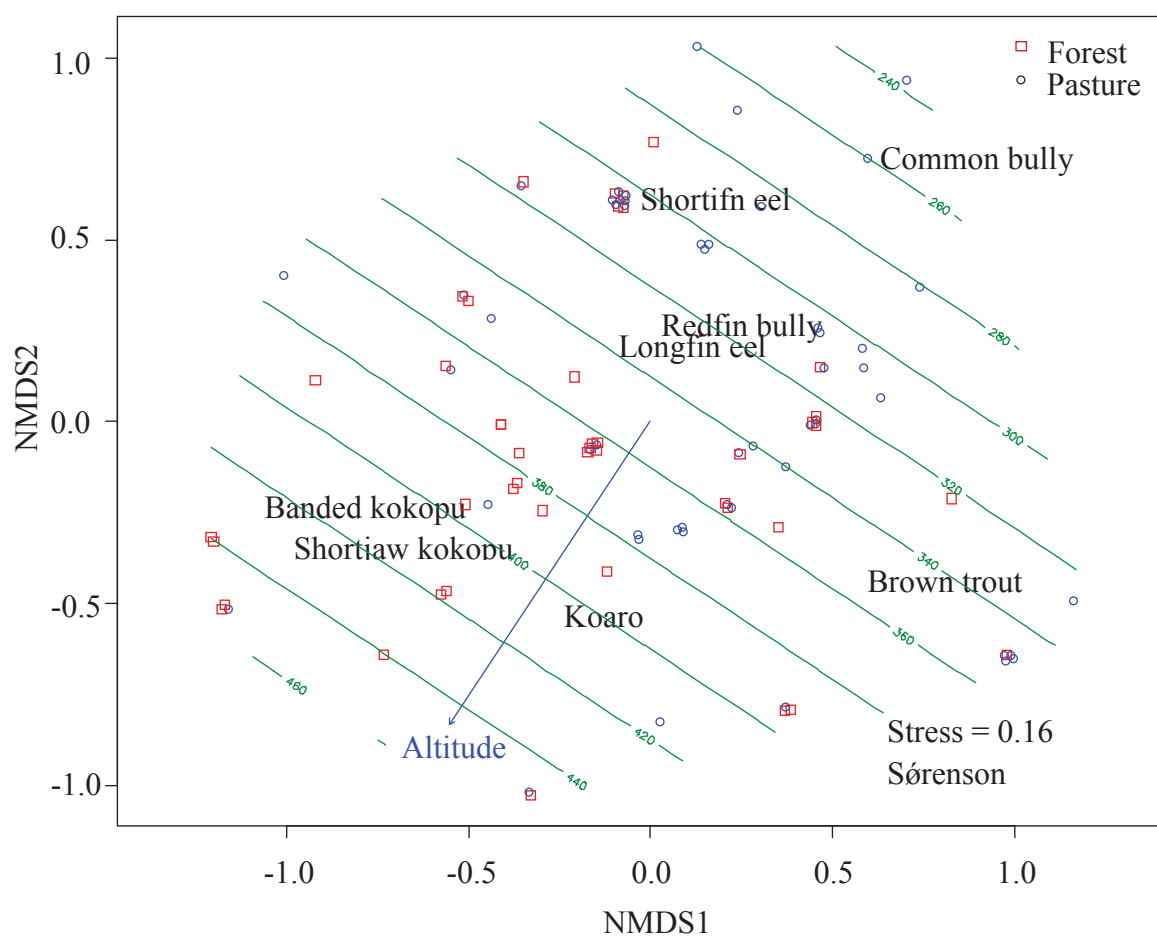


Fig. 2.2 NMDS ordination on fish presence/absence in 96 Taranaki streams fitted with elevation contours (green). Fish species occurring in $> 5\%$ of sites excluded (random noise has been applied to remove the convergence among multiple objects (sites) with identical species composition).

Surface fitting methods revealed that both altitude and northing had a linear relationship. Although the geographic extent of the study area is within a single region, the influence of northing was strong along the NMDS axis 1. Further, the number of forested sites was generally high in higher northings, alternatively to the higher proportion of

agricultural streams clustered on the positive side of NMDS axis 1, showing southern sites of this study (Fig. 2.4).

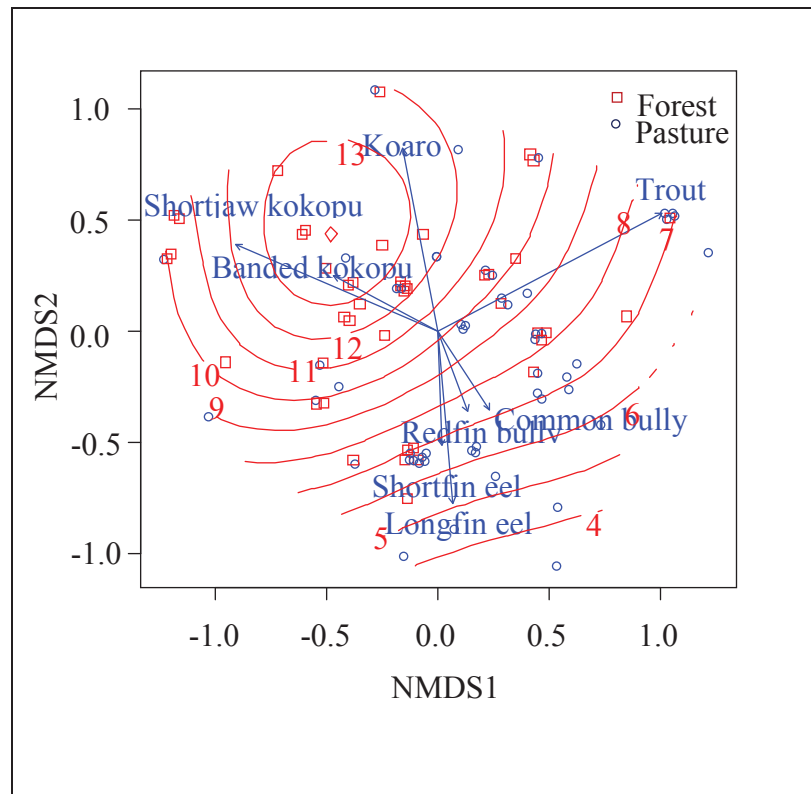


Fig. 2.3 Occurrence of the fish species reported from > 5% of 96 sites, fitted with the gradient in upstream average slope (red contours), on Sørensen similarity ordination between the study sites in Taranaki (random noise has been applied to remove the convergence among multiple objects (sites) with identical species composition).

Co-linearity of fish community drivers

Co-linearity of multiple environmental variables was very prominent among the important drivers (e.g. northing and altitude) of similarity structure considered in this study. However, phosphorus concentrations of the upstream surface rocks remained independent of other environmental vectors ($VIF < 10$) (Table 2.3 and Fig. 2.4).

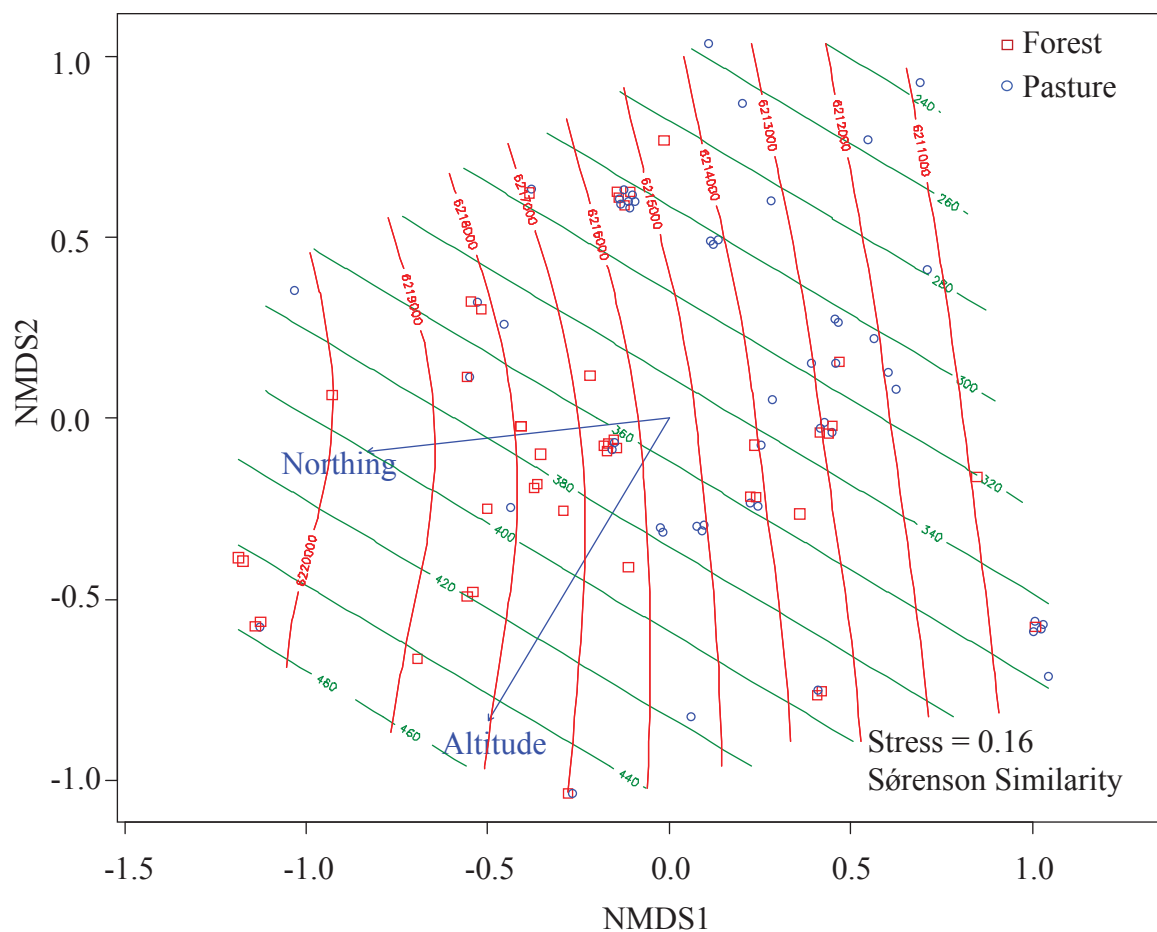


Fig. 2.4 Elevation (red) and northing (green) contours fitted onto the surface of NMDS ordination of Taranaki sites partitioned on proximal land use pattern (random noise has been applied to remove the convergence among multiple objects (sites) with identical species composition).

Partitioning of fish similarity between forest and pasture

Proximal land use had a significant effect on the compositional similarity in fish communities between forested and pasture streams. However, the effect of land use was not very strong on the community similarities among 96 streams in Taranaki (Table 2.4 and Fig. 2.5).

Table 2.4: Results of the Analysis of Similarity (ANOSIM) of Taranaki stream fish data grouped on the change in proximal land use pattern between forest and pasture.

Community Index	Factor	Global R	Significance
Sørensen	Land use	0.059	0.006**
Bray-Curtis	Land use	0.082	0.002**

‘*’ $P < 0.05$, ‘**’ $P < 0.01$, ‘***’ $P < 0.001$

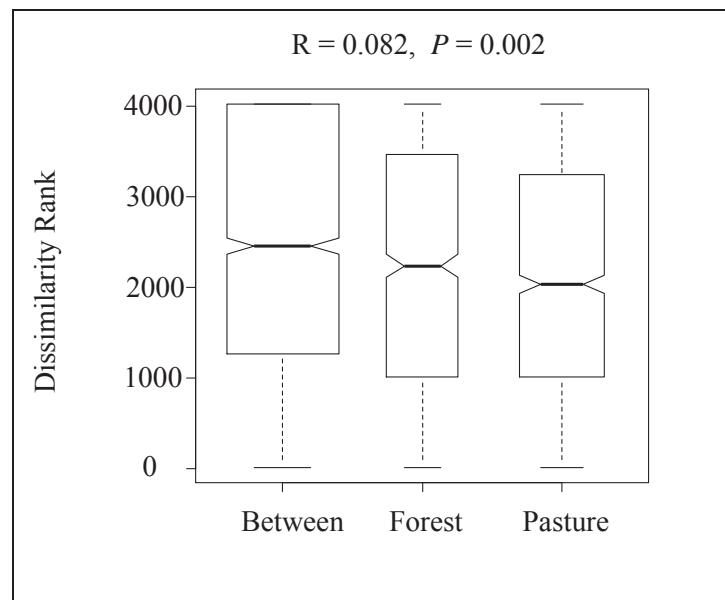


Fig. 2.5 Boxplot diagrams showing the results of Analysis of Similarity (ANOSIM) on fish data collected from Taranaki streams, in 2012. Within and between group differences were compared using average ranked Bray-Curtis similarity, partitioned between forest ($n = 44$) and pasture ($n = 52$).

Table 2.5: Differences in diversity measures of fish between forest (n=44) and pasture (n=52) sites in Taranaki.

Type of Diversity	Measure	Forest	Pasture	F value	P value	Degrees of freedom (d.f.)
α Diversity	Average number of species	2.50	2.63	0.27	0.60	1,94
β Diversity	Group multivariate dispersion	0.46	0.46	0.00	0.99	1,94
γ Diversity	Total number of species	9	15			

Agricultural streams generally had a higher number fish species (15) than the forested sites (9). However, the average species diversity (α) remained similar in streams between two land uses. Moreover, biological variability (within group multivariate dispersion) was not affected by pasture (Table 2.5).

Community changes between forested and agricultural streams

Longfin eels were the most abundant species in both pasture (39.25%) and forest (34.31%), while contributing to 25.86% of the compositional dissimilarity between the two site groups. Koaro, shortjaw kokopu and banded kokopu were clearly more abundant in forest than within the agricultural streams. Brown trout and redfin bullies increased nearly by two fold in their relative abundance within streams from forest to pasture (Table 2.6).

Table 2.6: Ordered contribution by the top six fish species to the Bray-Curtis dissimilarity in species abundances (SIMPER test), between the forest (n=44) and pasture (n=52), in 96 Taranaki streams.

Species	Average abundance (%)		Average dissimilarity	% contribution	Cumulative% contribution
	Pasture	Forest			
Long fin eel	39.25	34.31	18.83	25.86	25.86
Koaro	7.15	23.88	13.00	17.85	43.71
Trout	20.30	8.37	11.63	15.97	59.68
Shortjaw kokopu	6.56	16.88	9.94	13.65	73.33
Redfin bully	15.57	7.22	9.65	13.25	86.58
Banded kokopu	1.49	6.33	3.74	5.14	91.72

Fish community constraints

In the results of constrained correspondence analysis (CCA) of this study, the full range of environmental data explained 70% of the variation in abundance ($P < 0.05$) of the fish community in Taranaki. Amongst the important environmental constraints of fish abundance, land use indicators generally explained a greater biological variation compared to the particular measure explained by geographical vectors. Impact of reach riparian native cover (within 100m), % farming in the catchment, % native cover in the catchment, proximal land use pattern and total nitrogen concentration were significant in the fish CCA model of abundance data. Among the geographical vectors, distance inland and downstream dams remained collinear ($VIF > 10$), even in the reduced model (Table 2.7).

Table 2.7: Axis correlations and variance inflation factor values (VIF) of important environmental vectors in constrained correspondence analysis (CCA model) of overall fish abundance of 96 Taranaki streams.

Category	Factor	CA1	CA2	r ²	Significance	VIF (overall model)	VIF (reduced model)
Geography	Easting	-0.22	-0.98	0.20	0.018 *	22.11	6.57
Geography	Altitude	-1.00	-0.09	0.23	0.008 **	14.68	7.55
Geography	Inland distance (km)	0.03	-1.00	0.35	0.001 ***	47.05	23.95
Habitat	Width (m)	1.00	0.04	0.19	0.029 *	7.84	1.80
Land use	% Native forest©	-0.72	0.70	0.31	0.001 ***	1528.83	5.90
Land use	% Farming©	0.40	-0.92	0.41	0.001 ***	1037.07	4.97
Land use	Native Forest (US)	-0.75	0.66	0.30	0.001 ***	9052.63	Removed
Land use	Pasture (US)	0.75	-0.66	0.29	0.002 **	8883.47	14.41
Land use	Native riparian cover within 100m	-0.78	0.62	0.41	0.001 ***	10.85	4.01
Land use	Total Nitrogen concentration (ppt)	0.74	-0.68	0.23	0.011 *	34.39	9.88
Land use	Proximal Land use [#]	0.82	-0.57	0.35	0.001***	Not included	3.82
Land use	Dams (DS)	0.18	-0.98	0.28	0.006 **	20.79	11.42
Climate	Summer temperature	1.00	0.00	0.29	0.001 ***	37.42	9.52
Geography	Average Slope (US)	-0.81	0.59	0.25	0.007 **	19.53	2.11

US= upstream, DS= Downstream © = catchment ‘*’ P < 0.05, ‘**’ P < 0.01, ‘***’ P < 0.001

[#] = forest or pasture

Partial models

Riparian cover

The proportion of native riparian cover (within 100 m) significantly constrained fish abundance ($P < 0.001$), fish species decomposed mainly into three main strata across the gradient of reach riparian native buffer width ($F = 7.31$, d.f. = 3, 92). In each stratum of the riparian gradient, fish abundances differed in their attachment to the altitudinal range (Fig. 2.6, Table 2.8).

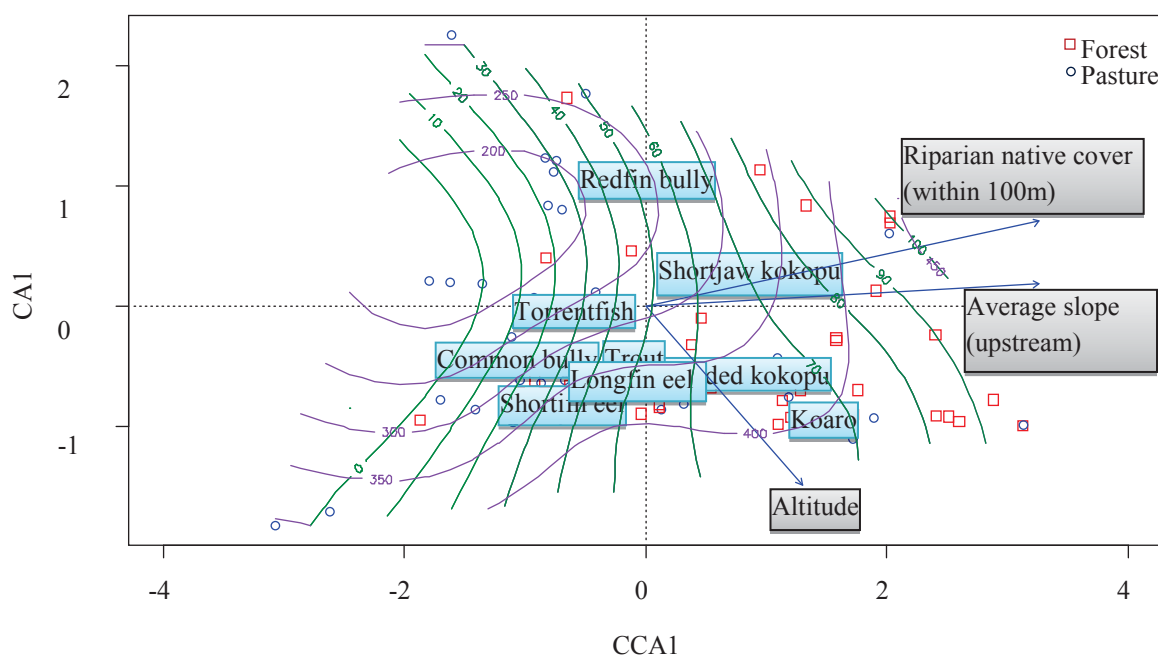


Fig. 2.6 Overall fish abundance of Taranaki streams, constrained by the native riparian cover (green), and fitted with elevation contours (purple) and average upstream slope.

Table 2.8: Selected fish species in Taranaki streams partitioned by the native riparian width and altitude, according to species abundances correlated in the riparian partial model.

Primary constraint	Fitted gradient	Fish species
<i>Reach riparian native cover (%)</i>	<i>Altitude (m)</i>	
20-40	250-300	Torrent fish
	300-350	Common bully, Shortfin eel
40-60	200-250	Redfin bully
	300-350	Longfin eel, Brown trout
	350-400	Banded kokopu
60-70	300-350	Shortjaw kokopu
	400-450	Koaro

Catchment land use

Farming of the catchment partitioned fish community into three main strata ($F = 6.75$, $P < 0.001$, d.f. = 3, 92). Most of the species were abundant when farmlands occurred less than 20% of the catchment. In addition, native forest in the catchment had more or less similar partitioning effect on the overall fish community ($F = 5.32$, $P < 0.01$, d.f. = 3, 92). In the reduced CCA model (Table 2.7), two particular vectors varied independently from each other (VIF= 4.97 and 5.90, respectively), after the removal of other catchment land use vectors such as percentage of exotic forest, scrub, swamp land and alpine (Appendix II and Table 2.7). In both of the partial models constrained by native forest and farming in the catchment, species abundances consistently fitted into altitudinal gradients (Fig.2.7 & Table 2.9).

Table 2.9: Selected fish species in Taranaki streams partitioned by catchment land use and altitude, according to species abundances correlated in the riparian partial model.

Primary Constraint	Fitted gradients	Fish species
<i>Catchment farming (%)</i>	<i>Altitude (m)</i>	
10-20	200-220	Redfin bully
	220-240	Torrent fish
	280-300	Shortjaw kokopu, Brown trout
	320-340	Longfin eel
	380-400	Banded kokopu
	400-420	Koaro
20-30	300-320	Shortfin eel
30-40	280-300	Common bully
<i>Catchment native forest (%)</i>		
80-90	300-350	Shortjaw kokopu
	350-400	Banded kokopu
	400-450	Koaro
70-80	200-250	Redfin bully
	250-300	Torrent fish
	300-350	Longfin eel, Shortfin eel, Brown trout
60-70	250-300	Common bully

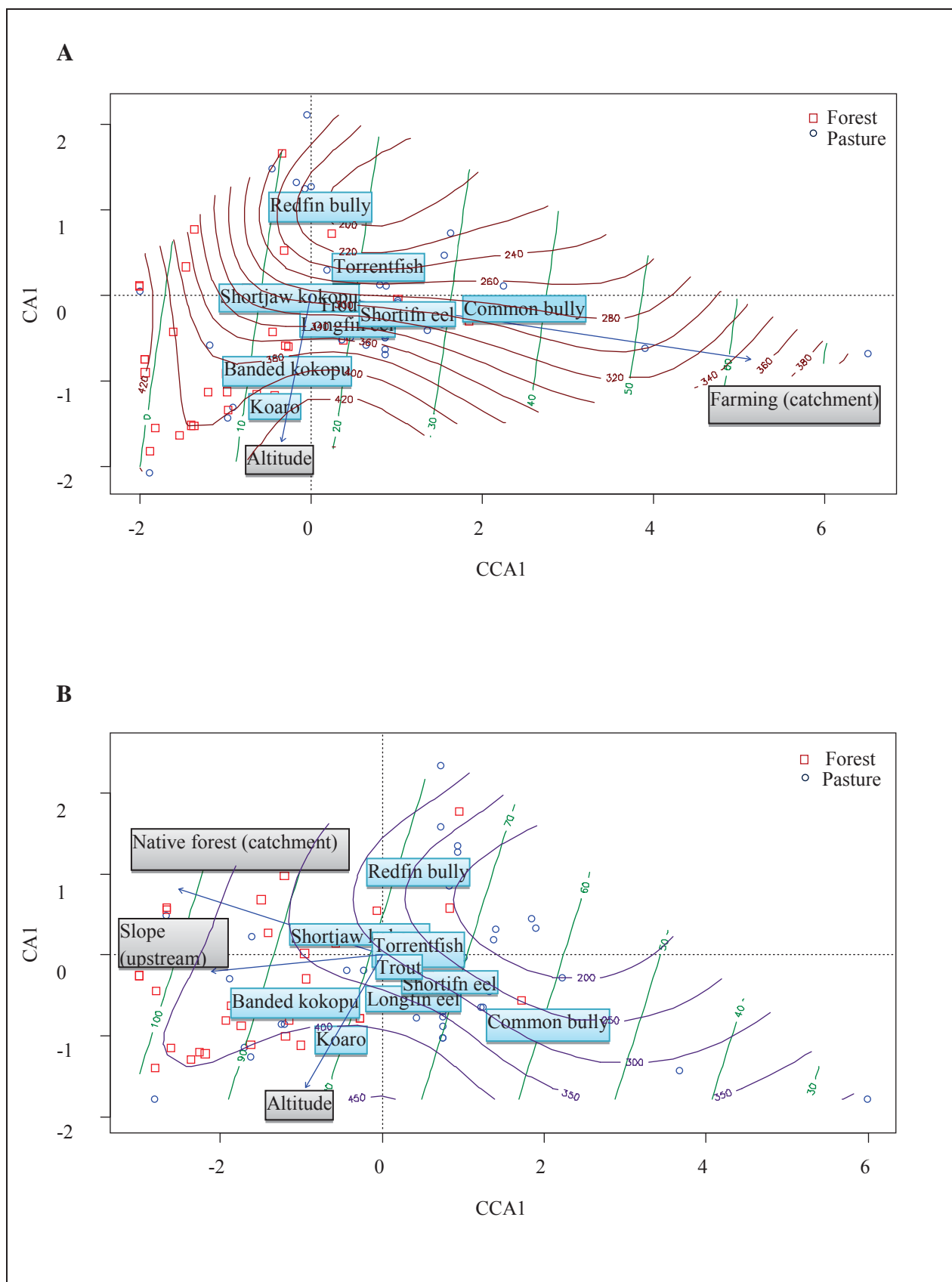


Fig. 2.7 Fish abundances in 96 Taranaki streams constrained by catchment farming (A) and native forest cover (B), fitted into altitude (red (A) & purple (B)) contours and upstream slope.

Nitrogen concentration

The total Nitrogen concentration of reaches significantly stratified the fish abundances ($F=4.21$, $P < 0.05$, d.f. = 4, 91). Most of the species were abundant in streams, when the total nitrogen concentration ranged between 0.6 and 1.4 ppb (parts per billion). Shortjaw kokopu, banded kokopu and brown trout abundances correlated with sites having less than 0.8 ppb of total nitrogen in streams. Species abundances further stratified across elevation gradients within each stratum of nitrogen concentration values in streams (Fig.2.8 & Table 2.10).

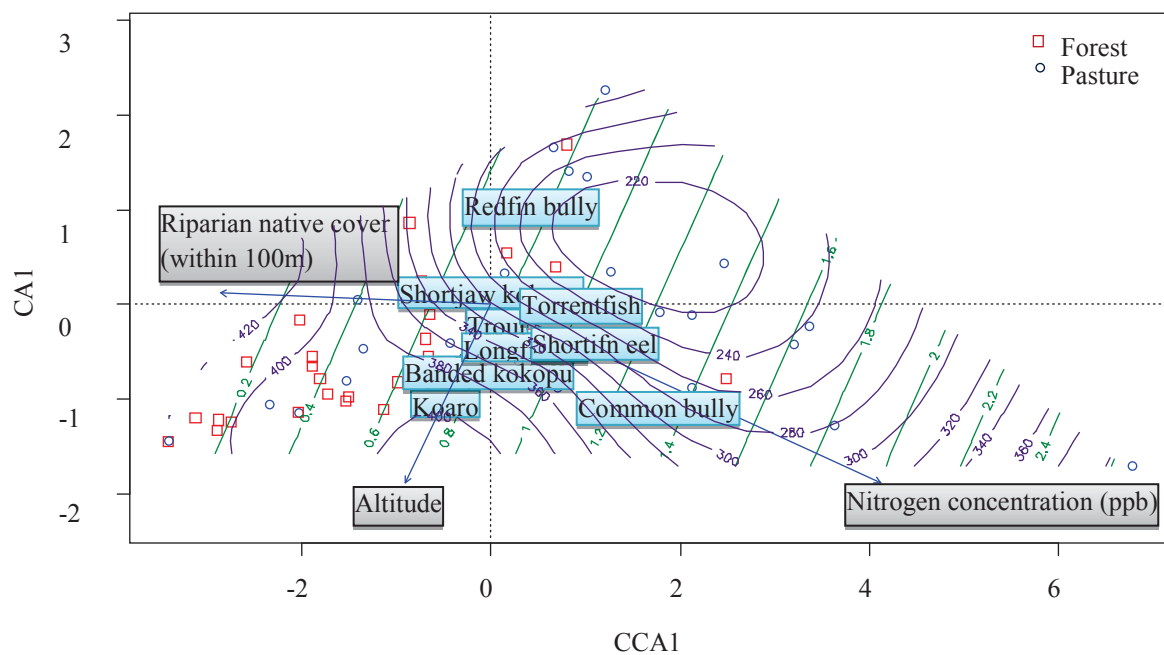


Fig. 2.8 Overall fish abundance of Taranaki streams, constrained by nitrogen concentration (ppb), and fitted with elevation contours (purple) and riparian cover

Table 2.10: Selected fish species in Taranaki streams partitioned by nitrogen concentration and altitude, according to species abundances correlated in the riparian partial model.

Primary constraint <i>Total Nitrogen concentration (ppb)</i>	Fitted gradient <i>Altitude (m)</i>	Fish species
0.6-0.8	280-300	Shortjaw kokopu, Brown trout
	360-380	Banded kokopu
	380-400	Koaro
0.8-1.0	220-240	Torrent fish
	300-320	Shortfin eel
	320-340	Longfin eel
1.2-1.4	260-280	Common bully

Discussion

The magnitude of the spatial scale is one of the most important factors in understanding the structural and functional diversity of a biological community (Ingels & Vanreusel, 2013). In this study, I attempted to investigate the key regional scale drivers of the fish community over Taranaki freshwater ecosystem from geographical, biological and anthropic perspectives. Regional-scale studies contribute to link our informative understanding of communities in their natural habitats, to the state of continental and global ecology (Cheruvilil *et al.*, 2013), and therefore play a vital role in conservation and management measures.

The first hypothesis of this study questions not only the importance of agriculture for the fish community, but also the most effective mechanism of regional scale control of the top consumers of stream community food web. Studies have shown that New Zealand stream fish are feeding generalists, thus differences in fish community composition do not affect the diversity of their prey communities (Flecker & Townsend, 1994; McDowall, 2000). Results of this study show that brown trout is an important component of the fish communities of

Taranaki streams, because of their wide distribution and high relative abundance. However, the presence of brown trout has shown to be less significant in ecosystem scale fish community changes, compared to dairy farming, which shares a similar history with the trout in the Taranaki region (Jowett, 1990; McDowall, 2010; Townsend, 1996). Moreover, from ecosystem ecology point of view, brown trout is unlikely to qualify as a ‘keystone species’ of New Zealand freshwaters, as shown in previous studies (Davic, 2003; Payton *et al.*, 2002). Nonetheless, this study was mainly focused on the effects of land use and geography on fish communities in Taranaki.

In contrast to having lack of evidence for top-down effects from brown trout, land use constraints have led the (regional scale) structural and compositional changes in the fish community considered in this study. Land use change from natural forest to pasture has consistently partitioned both distribution and abundance of fish community. Thus, the fish community considered in this study is clearly predicted by the catchment land use and, in particular, by variables such as percentage forest cover, percentage farming or total nitrogen concentration. However, most of the habitat quality measures and land use vectors showed a high degree of co-linearity, in terms of their variance inflation factor (VIF). Multiple co-linearity among environmental factors can confuse the statistical interpretation of community structure matched with large environmental data matrices (Graham, 2003). Although co-linearity effect reduces the statistical importance of a particular variable in a community model, *priori* assumptions are required to assess the nature of co-linearity between interested environmental vectors, since some vectors are co-linear in nature, for instance temperature and elevation, while regional vectors such as geographical distance may confound with land use practices because of the human interference. Thus, co-linearity requires careful discussion, in both statistical and ecological senses. In this study, three types of co-linearity occurred between the important environmental vectors of fish community: a). Natural co-

linearity (e.g. altitude and slope), b). Impact related co-linearity (e.g. forest cover and pasture) and c). Complex multiple co-linearity associated with habitat scale vectors potentially influenced by several other factors (e.g. % mud and sand).

To resolve the confusion of co-linearity, I reduced the number of variables to constrain biological ordinations considered in this study. Reduced models were advantageous in understanding how geography and land use pattern interactively, but independently, affect the fish community within the ecosystem. Further, the partial models of this study revealed limiting factors of fish dispersal within the ecosystem. For instance, upstream slope and effect of farming have restricted the abundance of fish species at extreme ends of each variable; hence, optimal space for the fish abundance has been reduced by both land use and geography within the ecosystem. Particular independent effects of geo-land use factors for the dispersal of fish are unlikely to be explored in simple bio-environmental data matching methods (Jowett & Richardson, 2003), as well as inventory models, based on alpha diversity (Dudley & Platania, 2007; Joy, 1999; Schlosser, 1995). Therefore, from a meta-community point of reference, the results of this study contribute to explaining the validity of geographical attachment of the species, even in an ecosystem highly affected by agriculture (Leibold *et al.*, 2004; Planque *et al.*, 2011).

Besides having the effect of co-linearity in biological-environmental data matching, the NMDS model explained a very limited variation of the fish community across any given environmental factor (Table 2.3). Even though the NMDS algorithm is popular in exploratory studies (because of its efficiency at identifying the relationships between communities and their environment), linear models such as CCA remain more suitable in explaining the community variations (Ramette, 2007). Therefore, I used both NMDS (non-linear) and CCA (linear) ordination methods to construct the fish community structure. Further, CCA models were very effective in constructing partial models presented in this study.

Although proximal land use effectively partitioned the community composition, most of the important land uses vectors of community structure described catchment or regional scale changes in forest cover and pasture. Therefore, large-scale drivers (e.g. catchment forest cover) are likely to be more effective than medium or small-scale vectors (e.g. bank cover, habitat type), for the inter-site biological distance within the ecosystem. The impact of regional scale vectors consistently occurred from land use, geography, and climate, to the within ecosystem community structure analysed in this study. Hence, it is important considering a zonal clustering approach among particular important drivers, for the regional scale management and conservation plans, to improve the current conservation approach based on the coarse land use dichotomy in Taranaki (Chantepie *et al.*, 2011; Januchowski-Hartley *et al.*, 2011; Roset *et al.*, 2007).

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Chapter Three

Does land use have an effect on the variability of stream communities?

Abstract

Fish and invertebrates were sampled in 15 streams in Taranaki, New Zealand, to investigate the impact of land use on the variability of stream communities. Fish and invertebrate community compositions differed significantly between forested and agricultural streams. Longfin eels (*Anguilla dieffenbanchii*), redfin bullies (*Gobiomorphus huttoni*) and brown trout (*Salmo trutta*) contributed for nearly 78% of the Bray-Curtis dissimilarity of fish, between forest and pasture. *Deleatidium* spp., *Pycnocentroides* spp., Elmidae, Orthocladiinae, *Aoteapsyche* spp. and *Polypedilum* spp. influenced more than 60% of compositional changes of invertebrate communities from forest to pasture. The compositional difference was stronger in invertebrates than in the fish communities between two land use classes.

Despite compositional differences in fish and invertebrate communities between native forest and pasture streams, the stream communities were equally variable between streams, within the two contrasting groups. Fish and invertebrates had similar average in-stream variability across the study sites, regardless of their differences in biology and diversity. While the in-stream variability of invertebrates differed between forest and pasture, stream morphology and habitat quality was among the most important variability-drivers of the particular community within a stream.

Introduction

Since the 19th century, human impact has become a prominent determinate of stream community structure in New Zealand (Alien & Cunningham, 1957; McDowall, 2010). Land use alterations from agricultural intensification have had profound effects on the structure and composition of these communities (McDowall, 1990; Winterbourn, 1991). Most of the lowland rivers have been affected by the removal of native forest cover, in both the upper catchments and adjacent areas (McDowall, 2001). Removal of native buffer strips from rivers may accelerate other agriculture-related impacts, such as nutrient influx, increased runoff of topsoil, sedimentation, bank erosion and loss of habitat stability (Hill, 1996; Newbold *et al.*, 1980). This, in turn, may stimulate changes in the structure and function of streams including increased nitrogen levels, rapid algal growth, loss or reduction of habitat specialists and increases in the abundance of species tolerant to nutrient enrichment (Joy & Death, 2004; Winterbourn, 1991).

In-stream impact assessments, fish and invertebrates are popular bio-indicators of stream ecological health (Adams *et al.*, 1996; Authman *et al.*, 2015; Walsh, 2006). In addition to their diversity and community composition, several secondary inventory measures such as MCI and FBI are available for ecological assessments of fluvial habitats (Hall *et al.*, 2001; Oberdorff *et al.*, 2002). Despite the applicability and popularity of fish and invertebrates as eco-health indicators, researchers have not explicitly focused on the comparative understanding and the relevance of two communities for their predictability for a given environmental factor/s (e.g. water quality and stream morphology) (Paavola *et al.*, 2003).

In addition to differences in community-environment links between different taxa, results of ecological assessment may highly depend on the statistical measures used in a study

(Olden & Jackson, 2002; Soininen *et al.*, 2007). Effect of agriculture has been evaluated on New Zealand stream communities mostly in terms of the changes in their community composition and structure in impacted sites (McIntosh & McDowall, 2004; Quinn, 2000). In most of the impact assessments, community differences are generally expressed in sample-based measures such as population density, relative abundance or alpha diversity rather than the variability, between contrasting site groups (Collier & Winterbourn, 2000). Even if the previous studies have identified agriculture as a strong anthropogenic determinant of New Zealand stream communities, the effect of pasture on the ecological variability of New Zealand stream communities has not been explained yet. For instance, although conventional studies show the compositional difference of stream communities between agricultural and forested streams, particular studies do not necessarily explain how variable the stream communities are across a gradient of a given impact indicator, such as riparian buffer width, the nitrogen concentration in water or stream flow. Moreover, it is difficult to test spatially explicit hypotheses by only depending on mere species diversity.

Biological variability is a useful alternative to species diversity because the variability expresses stress for communities from disturbances, in their habitats (Conrad, 1977). Community variability increases when the natural environment is impacted by anthropogenic factors such as industrial pollutants (Warwick & Clarke, 1993). However, variability changes are not consistent across all spatial, temporal and taxonomic scales (Brown, 2003; 2007; Somerfield *et al.*, 2006). The difference in inter-site variability of marine benthos has been shown to decrease between impacted and non-impacted communities with the physical distance from the source of disturbance, and to increase with the intensity of environmental stressors such as marine oil spills, but comparable studies are rare in freshwater ecology (Warwick & Clarke, 1993).

In contrast to the ‘variability-disturbance’ models suggested by Conrad (1977) and Warwick & Clarke (1993), an alternative theory of ‘community homogenisation’ has been proposed to explain the impact of land use change, particularly from natural forest to agricultural lands (Hendrickx *et al.*, 2007). Homogenisation theory argues that high-intensity agriculture homogenises the vegetation structure over large spaces, thus negatively affects the β diversity, especially with increased patch isolation (Hendrickx *et al.*, 2009; Karp *et al.*, 2012). Further, the particular hypothesis has been tested across a range of different terrestrial communities, including soil microbes, vascular plant, arthropods, carabids and birds, but not explicitly on freshwater communities in agricultural systems (Flohre *et al.*, 2011; Macphail *et al.*, 1990; Vellend *et al.*, 2007).

In studies based on homogenisation theory, results do not always outline a loss of variability from forest to agricultural lands because of the differences in spatial units, communities, and statistical measures of the land use classes between analyses. For instance, Flohre *et al.* (2011) described that agricultural intensification reduces the β diversity of plants across all spatial scales but the change in β diversities of birds and beetles is not consistent through spatial units and is influenced by species richness and the dispersal ability of corresponding communities. Further, most of the studies express variability of communities in terms of their compositional similarity, and is thus less informative about the spatial variability in community structure (Clavero & García-Berthou, 2006; Hendrickx *et al.*, 2007; Marchetti *et al.*, 2006). Therefore, it is important to investigate the relative importance of compositional similarity to community variability across different land use classes and taxonomic groups.

In this study, I investigated whether communities in ‘stressed’ freshwater environments (agricultural streams) differ in community variability from those in contrasting natural habitats. I hypothesised that removal of native vegetation homogenises the

environment and thus the biological communities (Hendrickx *et al.*, 2007). Further, this study discusses differences in composition and variability between fish and invertebrate communities across different spatial scales from reach to local landscapes. Moreover, I asked specifically: 1). Are stream invertebrates more dissimilar than fish communities are between forest and pasture? 2). Do stream fish and invertebrates differ in their community variability across streams? 3). Does agriculture negatively affect the in-stream variability of invertebrates and/or fish?

Methods

Site selection

The Taranaki ring plain consists of more than 140 streams and rivers at a similar range of elevation (Joy & Death, 2000). Nearly 75% of the running waters are first or second order streams, and 58% of the total length of all streams flow through agriculture. In Taranaki, each dairy farm has an average of 6 km of stream, draining through pasture (Taranaki Regional Council, 2010; 2013). Brown trout have become abundant in most of the streams in Taranaki (Joy & Death, 2000; 2001). I selected eight sites in each of pasture (impacted) and forested (non-impacted) areas, in Taranaki, New Zealand. However, only fifteen streams were sampled, because of sampling difficulties related to extremely low flow conditions at one of the forested sites (Fig. 3. 1).

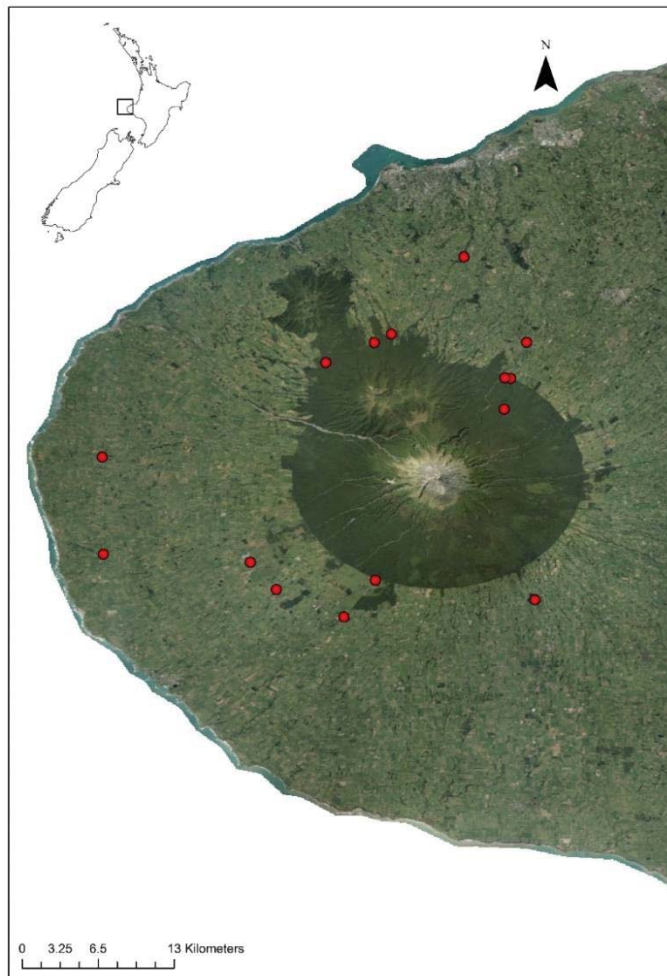


Fig. 3.1 Fifteen streams of Taranaki, New Zealand, selected for sampling fish and invertebrates in the summer of 2013.

Sampling and data collection

Sampling was carried out during the summer in 2012/13 (January/February). A 150m long reach was sampled for fish and invertebrates, at each site. Fish were sampled prior to the invertebrates. Within every 30 m of the 150m long reach, a sample for benthic macroinvertebrates was collected with a Surber sampler (0.1 m^2), by disturbing the stream substrate, using a brush. All invertebrate samples were preserved in 90% ethanol at the

sampling sites, and sieved through a 500 μm mesh in the laboratory. Invertebrates were identified to the lowest possible taxonomic level using Winterbourn *et al.* (1989).

Fish sampling was carried out, using a 'Kainga EFM 300' electrofishing machine with fish collected downstream in a pole-net. The pulses were adjusted to a rate between 60 and 70 Hz, and to a width of 2 ms. Settings were calibrated prior to each application by lowering voltage until less than five lights appear on the electrofishing device, indicating proper setting for each location.

The same stretch sampled for invertebrates was divided into sub-reaches of 15 m, for sampling fish. Electrofishing proceeded on a rectangular area (approximately 3 m long and 2 m wide) in a downstream direction, commencing from one bank at the downstream end. The cathode of the electrofishing machine was always placed between the sampler and the pole netter. When an area was fished, the sampler and the netter progressed one pole width through the waterway and the process repeated until the other side of the sampling area is reached. Then the next equivalent areas were also fished, from downstream to upstream, by the above procedure until the complete area was covered (David *et al.*, 2010). Fish species were identified to the closest confident taxonomic level using keys in McDowall (2000).

Concurrently, environmental data related to stream geomorphology, habitat type, in-stream productivity (periphyton cover, macrophyte, moss and leaf litter), land use and vegetation type in the riparian and proximal land were collected by visual assessments. Stream morphometric data (wetted width, depth and bed exposure) and in-stream water quality (temperature, conductivity and pH) were measured at each site by using measuring tapes/ rulers and a 'EuTech Cyberscan PC-10' meter. Records from FENZ (Freshwater Ecosystems of New Zealand) geo-data base were used to gather data on upstream catchment land use, Nitrogen concentration, geo-climate, geography and geology of the sites, to cover

the full range of environmental information available for the selected sites in this study (Leathwick *et al.*, 2010).

Statistical analysis

The compositional similarity between reaches (sites) was calculated separately for fish and invertebrate communities using the Bray-Curtis index which is one of the most effective dissimilarity measures, popular among community ecologists (Magurran, 1988; Oksanen, 2011). In this analysis, biological variability is expressed as the dissimilarity of each community, among a selected group of sites. Sampling sites were grouped on the land-use pattern. Dissimilarities in each freshwater community between the sites impacted by pasture were compared with the similar measure of a respective non-impacted group of sites in the native forest.

Differences in community composition were evaluated between impacted and non-impacted sites, by using ANOSIM (Analysis of Similarity) test (Oksanen *et al.*, 2013). The mean rank dissimilarities within groups were compared between contrasting groups of streams, related to each freshwater community, separately. The ANOSIM statistic R differentiates two groups of objects (sites), depending on the means of dissimilarity ranks between groups (r_B) and within groups (r_W) as follows,

$$R = (r_B - r_W) / (N(N - 1)/4), \text{ where } N = \text{number of objects.}$$

SIMPER (Similarity Percentage) analysis was used for the comparisons between compositionally different pairs of sampling groups, to explore the species-wise contribution for the overall Bray-Curtis dissimilarity (Clarke, 1993; Oksanen, 2011). Percentage contributions of species for the overall dissimilarity were summarised to the taxonomic groups, such as fish families and insect orders, to observe the community wise differences between contrasting groups of streams. The most influential taxa were selected by the

cumulative percentages of ordered species contributions for the significantly different communities (Oksanen *et al.*, 2013).

Group homogeneities were computed by partitioning similarities between sites for each factor predictor. In an ordination, distance to the centroid in a partitioned distance matrix was used to quantify the degree of variability within a group of samples. The distance between the group centroid and a sampling site (within a group of sites) was calculated by dividing the sum of squared inter-point (sites are represented as points in an ordination) distances by the number of points (Anderson, 2001). The difference in inter-site and in-stream variability between groups was analysed by using the multivariate analysis of variance. Further, linear models were constructed to assess the trends of in-stream variability across each environmental factor considered in this study. Permutation tests concluded the significance of variation between selected groups of sites. I used the R Vegan package functions in R (version 3.0.2) and PERMDISP function in PERMANOVA+ (Clarke & Warwick, 2001; Oksanen, 2011).

Results

Community composition

Twelve fish species and 69 invertebrate taxa were present in the 15 streams surveyed in the study. Fish represented four families, including five species in family Galaxiidae and three species in family Gobiidae. Among six orders of invertebrates reported in the survey, highest diversity occurred in trichopterans (24 taxa), followed by dipterans (16 taxa). In addition, three taxa of gastropods were also reported from the study sites (Table 3.1 and 3.2).

Table 3.1: Relative abundances and frequencies of occurrence of fish species reported from 15 Taranaki streams, in 2013.

Fish species	Scientific Name	Relative abundance (%)	Frequency of occurrence (%)
Longfin eel	<i>Anguilla dieffenbachia</i>	43.86	80.00
Redfin bully	<i>Gobiomorphus huttoni</i>	22.03	26.67
Brown trout	<i>Salmo trutta</i>	18.22	26.67
Koaro	<i>Galaxias brevipinnis</i>	3.60	20.00
Inanga	<i>Galaxias maculatus</i>	3.18	20.00
Banded kokopu	<i>Galaxias fasciatus</i>	2.97	13.33
Shortfin eel	<i>Anguilla australis</i>	2.54	26.67
Torrentfish	<i>Cheimarrichthys fosteri</i>	1.91	6.67
Shortjaw kokopu	<i>Galaxias postvectis</i>	0.64	6.67
Common bully	<i>Gobiomorphus cotidianus</i>	0.42	6.67
Cran's bully	<i>Gobiomorphus basalis</i>	0.42	6.67
Giant kokopu	<i>Galaxias argenteus</i>	0.21	6.67

Table 3.2: Species diversity, relative abundances and frequencies of occurrence of invertebrate taxa reported from 15 Taranaki streams, in 2013.

Invertebrate taxa	Number of species/taxa	Relative abundance (%)	Frequency of occurrence (%)
Order: Ephemeroptera	12	27.28	100.00
Order: Plecoptera	8	3.14	86.67
Order: Trichoptera	24	30.59	100.00
Order: Megaloptera	1	1.04	66.67
Order: Coleoptera	5	14.34	100.00
Order: Diptera (excluding chironomids)	10	3.34	100.00
Order: Diptera, Family: Chironomidae	6	17.45	100.00
Class: Gastropoda	3	2.81	40.00

Table 3.3: Species diversity and in-stream variability (measured in average distance to the group centroid in community ordinations) of fish and invertebrates in 15 Taranaki streams.

Site	Land use	Fish		Invertebrates	
		Number of species	In-stream variability	Number of species	In-stream variability
TK1	Pasture	2	0.08	18	0.35
TK2	Forest	1	0.10	36	0.21
TK3	Pasture	3	0.27	26	0.25
TK4	Forest	4	0.49	29	0.37
TK5	Forest	3	0.24	25	0.30
TK6	Pasture	5	0.40	19	0.21
TK7	Pasture	2	0.04	25	0.17
TK8	Pasture	5	0.40	32	0.27
TK9	Pasture	2	0.32	26	0.25
TK10	Pasture	4	0.45	26	0.19
TK11	Pasture	3	0.24	20	0.14
TK12	Forest	2	0.06	30	0.39
TK13	Forest	1	0.00	19	0.41
TK14	Forest	1	0.00	30	0.40
TK15	Forest	1	0.00	27	0.36

Community dissimilarity between land uses

The composition of both fish and invertebrate communities differed between forested and pasture streams (ANOSIM $R = 0.31$ and 0.50 for fish and invertebrates respectively, $P < 0.005$). Further, the compositional difference was higher in benthic invertebrates than that in fish communities between the two land uses (Fig. 3.2). Longfin eels (*Anguilla dieffenbanchii*), redfin bullies (*Gobiomorphus huttoni*) and brown trout (*Salmo trutta*) contributed for nearly 78% of fish community differences between forest and pasture (Table 3.4). The five invertebrate taxa *Deleatidium* spp., *Pycnocentroides* spp., Elmidae, Orthocladinae, *Aoteapsyche* spp. and *Polypedilum* spp. contributed to more than 61% of the compositional change in invertebrates between the two land uses (Table 3.5).

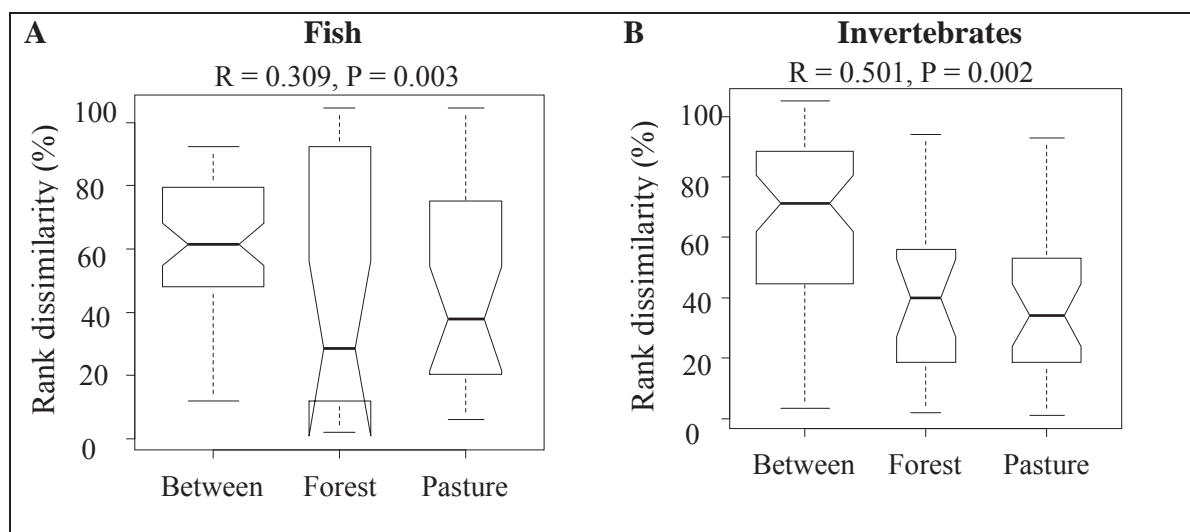


Fig. 3.2 Within and between group rank dissimilarities for fish and invertebrate communities in 15 Taranaki streams, in the forest ($n = 7$) or pasture ($n = 8$) land uses.

Table 3.4: Ordered contribution by the fish species to the Bray-Curtis dissimilarity in species abundances (SIMPER test), between the forest (n=7) and pasture (n=8), in 15 Taranaki streams.

Species	Abundance/ Stream		Average Dissimilarity	%Contribution for overall dissimilarity	Ordered cumulative % contribution for the dissimilarity
	Forest	Pasture			
Longfin eel	3.43	22.88	26.48	30.03	30.03
Redfin bully	0.00	13.00	24.6	27.89	57.92
Brown trout	4.71	6.63	16.94	19.21	77.12
Koaro	2.43	0.00	4.86	5.51	82.63
Banded kokopu	0.00	1.75	4.41	5.00	87.63
Shortfin eel	0.29	1.25	3.71	4.2	91.84
Inanga	0.00	1.88	2.60	2.95	94.79
Torrentfish	0.00	1.13	2.31	2.62	97.40
Shortjaw kokopu	0.43	0.00	0.88	1.00	98.41
Common bully	0.00	0.25	0.51	0.58	98.99
Cran's bully	0.00	0.25	0.50	0.57	99.56
Giant kokopu	0.00	0.13	0.39	0.44	100.00

Table 3.5: Ordered contribution by the top ten invertebrate taxa to the Bray-Curtis dissimilarity in species abundances (SIMPER test), between the forest (n=7) and pasture (n=8), in 15 Taranaki streams.

Species	Abundance/ Stream		Average Dissimilarity	%Contribution for overall dissimilarity	Ordered cumulative % contribution for the dissimilarity
	Forest	Pasture			
<i>Deleatidium</i> spp.	227.71	439.38	15.58	19.65	19.65
<i>Pycnocentrodes</i> spp.	14.86	400.13	11.16	14.08	33.73
Elmidae	112.14	285.25	9.91	12.50	46.23
Orthcladiinae	77.29	186.00	6.47	8.17	54.40
<i>Aoteapsyche</i> spp.	2.86	175.75	5.65	7.13	61.53
<i>Polypedilum</i> spp.	1.71	94.00	2.91	3.67	65.19
<i>Pycnocentria</i> spp.	4.71	76.38	2.60	3.29	68.48
<i>Aphrophila</i> spp.	38.57	50.00	2.08	2.62	71.10
<i>Potamopyrgus</i> spp.	2.14	75.25	1.95	2.46	73.56
<i>Oxyethira</i> spp.	0.14	33.88	1.53	1.94	75.49
<i>Beraeoptera roria</i>	5.57	36.38	1.53	1.94	77.43

Table 3.6: Percentage contribution by key taxonomic groups of fish and invertebrate to overall the Bray-Curtis dissimilarity in species abundances (SIMPER test), differed between the forest (n=7) and pasture (n=8), in 15 Taranaki streams.

Taxonomic Group	Number of taxa	Percentage contribution to overall dissimilarity	Abundance / stream		Relative abundance within group (%)	
Fish			Forest	Pasture	Forest	Pasture
Family: Anguillidae	2	34.23	3.71	24.13	32.91	49.11
Family: Galaxiidae	5	14.90	2.86	3.75	25.32	7.63
Family: Gobiidae	3	29.04	0.00	13.50	0.00	27.48
Family: Pleuronectidae	1	2.62	0.00	1.13	0.00	2.29
Family: Salmonidae	1	19.21	4.71	6.63	41.77	13.49
Invertebrates			Forest	Pasture	Forest	Pasture
Order: Ephemeroptera	12	26.39	283.86	509.00	39.43	23.72
Order: Plecoptera	8	4.07	70.57	25.38	9.80	1.18
Order: Trichoptera	24	33.72	81.00	778.38	11.25	36.27
Order: Megaloptera	1	1.05	7.43	22.38	1.03	1.04
Order: Coleoptera	5	13.21	125.00	288.75	17.36	13.45
Order: Diptera (excluding chironomids)	10	3.10	41.00	56.88	5.70	2.65
Order: Diptera, Family: Chrionomidae	6	15.98	108.86	389.25	15.12	18.14
Class: Gastropoda	3	2.49	2.14	76.25	0.30	3.55

Biological variability across communities, land uses and spatial units

The inter-site spatial variability of both fish and invertebrates did not differ between the land uses, considered in this study. The multivariate dispersions of group homogeneities did not significantly change from forest to pasture ($F = 0.11, 0.08$, for fish and invertebrates respectively, $P > 0.05$) (Table 3.7). Hence, land use classes or community difference were not influential for biological variability over the 15 sites of this study.

Table 3.7: Within group multivariate dispersion (inter-site variability) of fish and invertebrate communities between Taranaki streams, (grouped as pasture (n=8) vs. forest (n=7)), sampled in January- February 2013, by electrofishing and Surber sampling (0.1 m²)

Community	Treatment	Average distance to the group centroid	F value	P value	Degrees of freedom
Fish	Forest	0.38	0.11	0.75	1, 13
	Pasture	0.42			
Invertebrates	Forest	0.33	0.08	0.78	1, 13
	Pasture	0.35			

Table 3.8: Within stream multivariate dispersion (in-stream variability) of fish and invertebrate communities between Taranaki streams, (grouped as pasture (n=8) vs. forest (n=7)).

Community	Treatment	Average within stream variability	F value	P value	Degrees of freedom
Fish	Forest	0.13	2.98	0.11	1, 13
	Pasture	0.28			
Invertebrates	Forest	0.35	11.64	0.005	1, 13
	Pasture	0.23			

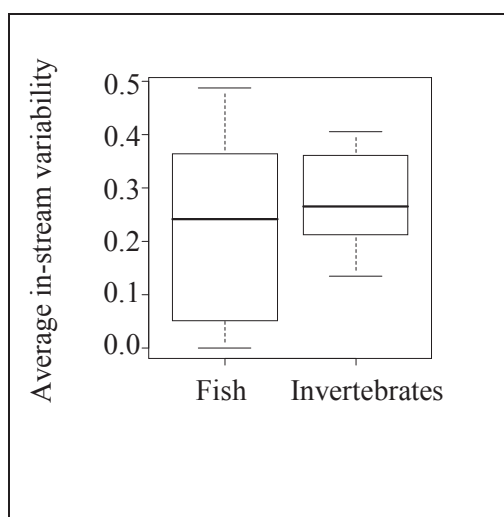


Fig. 3.3 Difference in in-stream variability between fish and invertebrate communities of 15 Taranaki streams, surveyed in 2013.

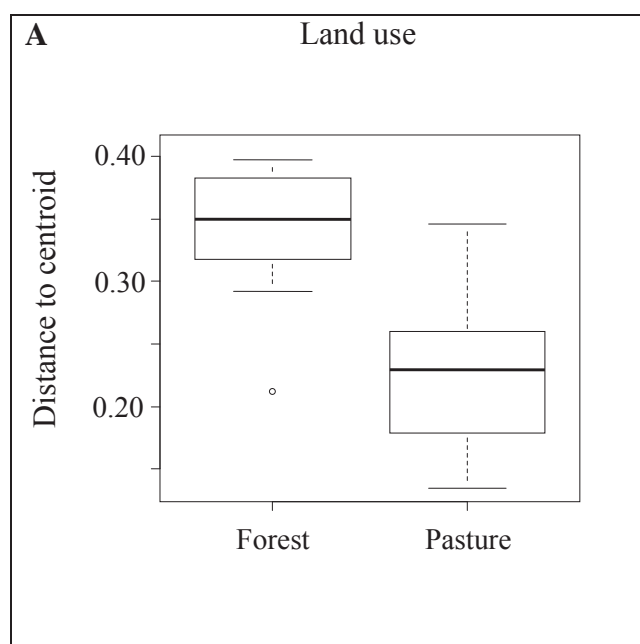


Fig. 3.4 Difference in average multivariate distance to the group centroids (in-stream variability) for invertebrate communities in 15 Taranaki streams, partitioned between contrasting land uses.

At reach scale, average in-stream variability did not significantly differ between the two communities ($F = 2.19$, $P > 0.05$, d.f. = 1, 13), across the 15 streams surveyed in Taranaki (Fig. 3.3), and in-stream variability of fish also remained similar between forest and pasture. However, invertebrates in pastoral streams were less variable than they were within a forested stream ($F = 11.64$, $P < 0.01$, d.f. = 1, 13) (Table 3.3 and 3.6, Fig. 3.4).

Variance in invertebrate habitats between forest and pasture

Stream shape significantly changed from forest to pasture. The increase of wetted width to depth ratio showed a dramatic change in shape of streams ($F = 8.64$, $P > 0.05$, d.f. = 1, 13). Streambank stability decreased by nearly tenfold from agricultural streams to forested habitats ($F = 32.42$, $P > 0.001$, d.f. = 1, 13). However, rather stable stream substrates in forested streams were indicated by higher percentages of bedrocks and bryophytes. Among the water quality measures, relatively high pH (average = 8.32) and temperature (average = 17.65°C) characterised the agricultural streams of this study (Table 3.9 and Fig. 3.5).

Table 3.9: Differences in average values of selected environmental factors between forested (n=7) and pasture (n=8) habitats of Taranaki.

Factor	Group average		F value	Significance	Degrees of freedom
	Forest	Pasture			
Width/Depth ratio	12.66	23.37	8.64	$P < 0.05$	1, 13
% Undercut bank	22.67	2.39	32.42	$P < 0.001$	1, 13
Slope (m/km)	3.76	1.07	32.97	$P < 0.001$	1, 13
% Moss	23.47	2.36	18.52	$P < 0.001$	1, 13
pH	7.59	8.32	7.67	$P < 0.05$	1, 13
Temperature (°C)	13.34	17.65	6.78	$P < 0.05$	1, 13
% Bedrock	10.26	0.06	10.80	$P < 0.01$	1, 13
% Woody debris	28.86	2.20	18.53	$P < 0.001$	1, 13

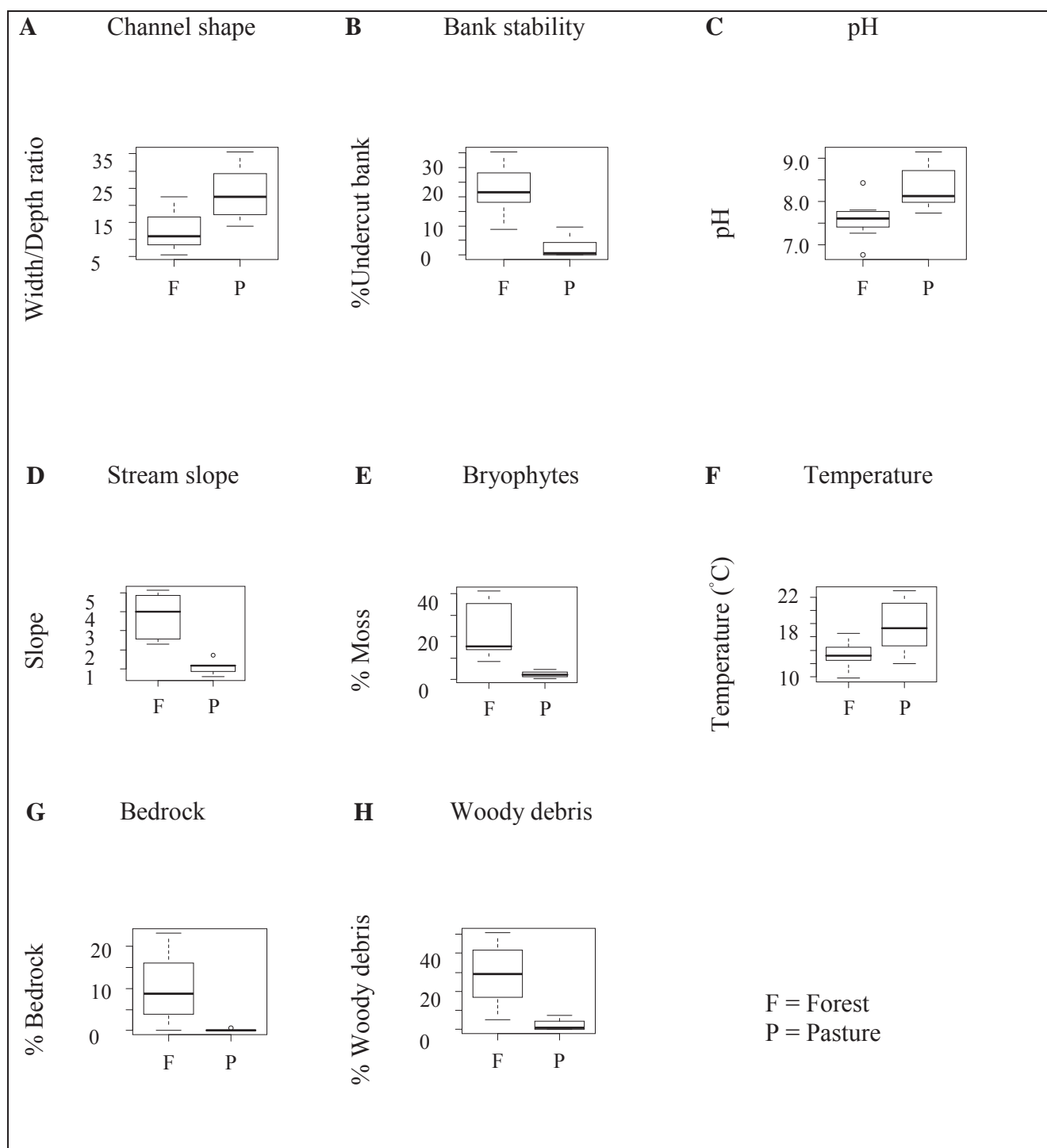


Fig. 3.5 Boxplot diagrams showing the differences of average values in selected environmental factors between forested (n=7) and pasture (n=8) habitats of Taranaki.

Trends in in-stream variability

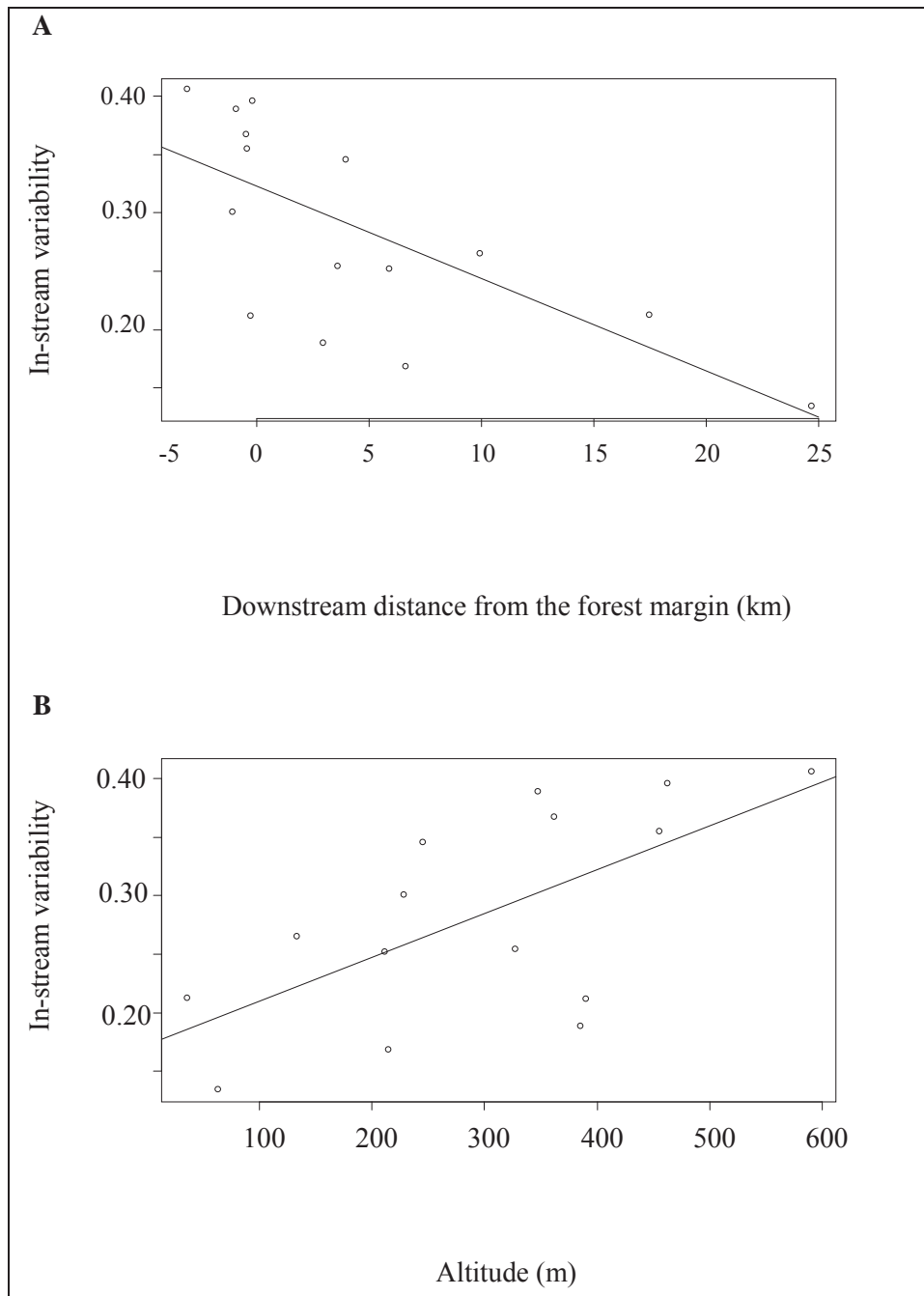


Fig. 3.6 In-stream variability of invertebrates vs. distance from the forest margin (A) and altitude (B), across 15 Taranaki streams, surveyed in 2013.

In-stream variability of invertebrates decreased from forested habitats to pasture streams, along the downstream distance from the forest margin, and a similar trend occurred between within stream variability of invertebrates and altitude. Variability of fish within a

stream did not significantly change across downstream distance or altitude (Fig. 3.6 and Table 3.10).

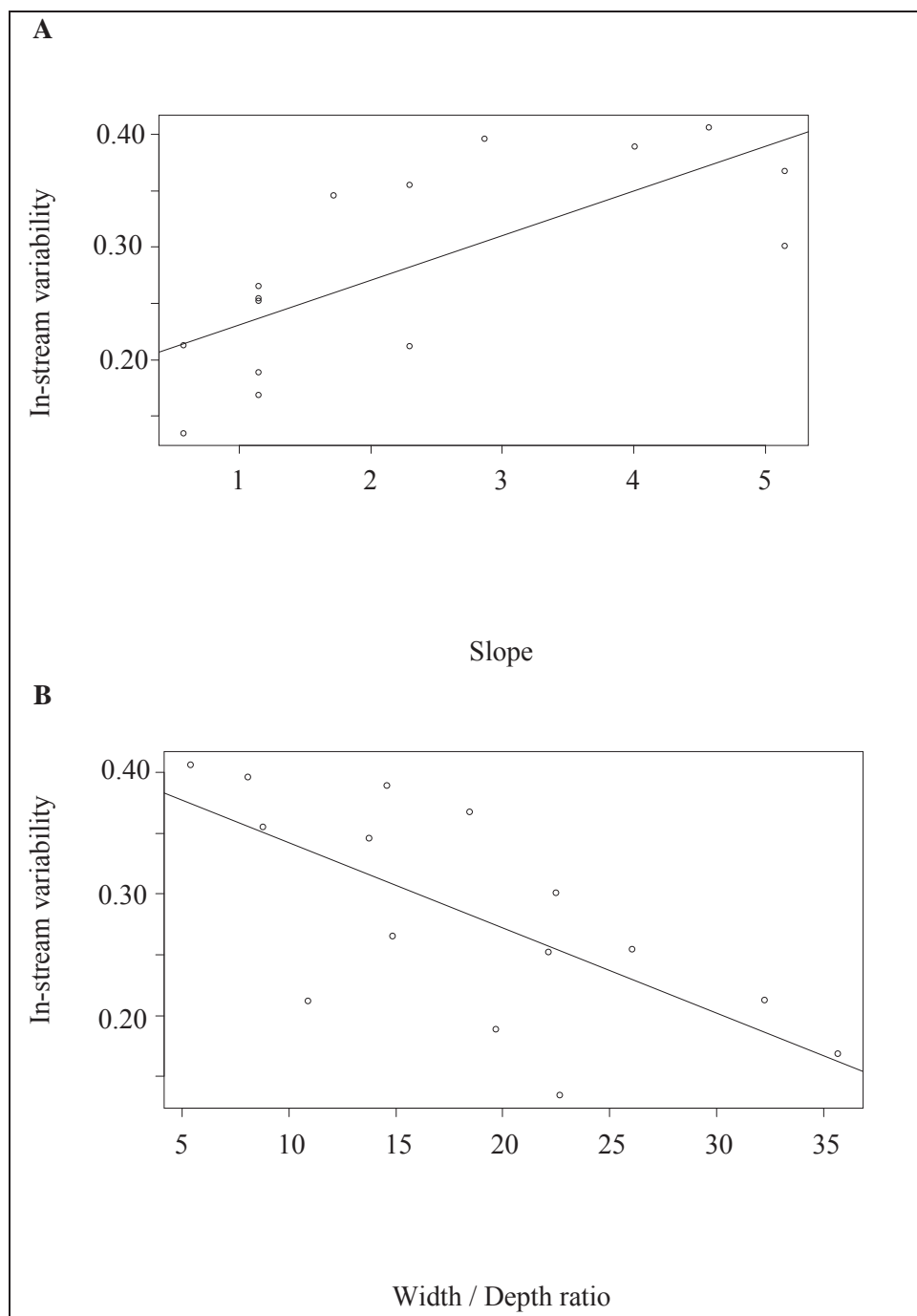


Fig. 3.7 In-stream variability of invertebrates vs. slope (A) and width / depth ratio (B), across 15 Taranaki streams, surveyed in 2013.

Among stream morphological factors, the wetted width of the stream had significant but contrasting effects on in-stream variability of fish and invertebrates. Within stream variability of fish increased with the stream width, while variability of invertebrates decreased with this particular environmental factor. Similarly, fish and invertebrates showed increasing and decreasing trends with stream depth, respectively. Channel shape (width/depth ratio) had a strong negative correlation with invertebrate variability within a stream, while the particular measure of invertebrates increased with the habitat slope (Fig. 3.7 and Table 3.10). Nonetheless, the variability of fish did not change significantly across channel shape or habitat slope, but flow variability showed a negative effect on the variability of fish within a stream (Table 3.10).

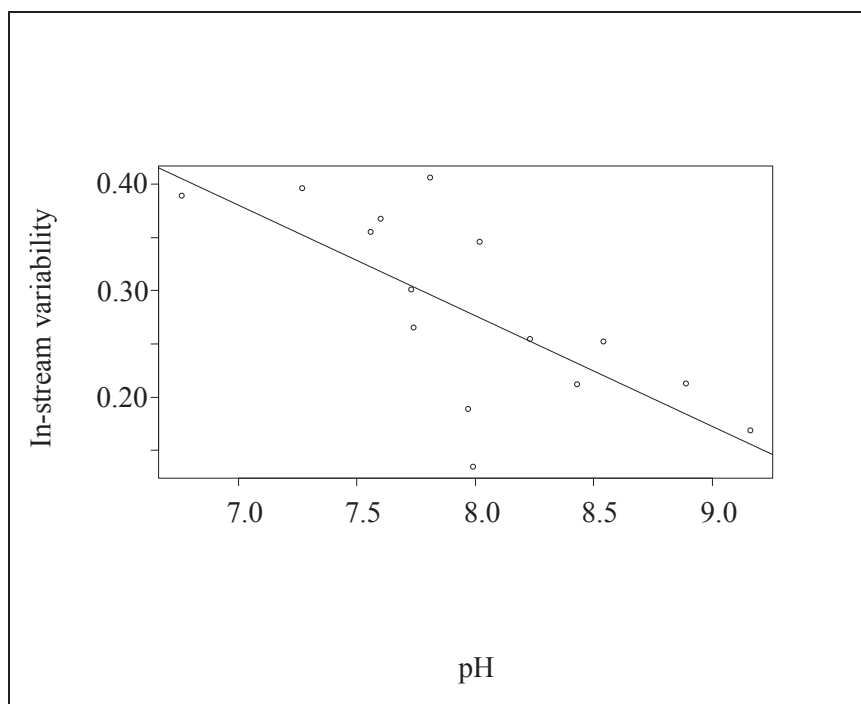


Fig. 3.8 In-stream variability of invertebrates vs. pH value, across 15 Taranaki streams, surveyed in 2013.

Fish variability did not have significant trends across any of the water quality factors, measured in this study. However, invertebrate communities had a strong positive trend

between their in-stream variability and pH, in contrast to their decreasing variability along conductivity (Fig. 3.8 and Table 3.10).

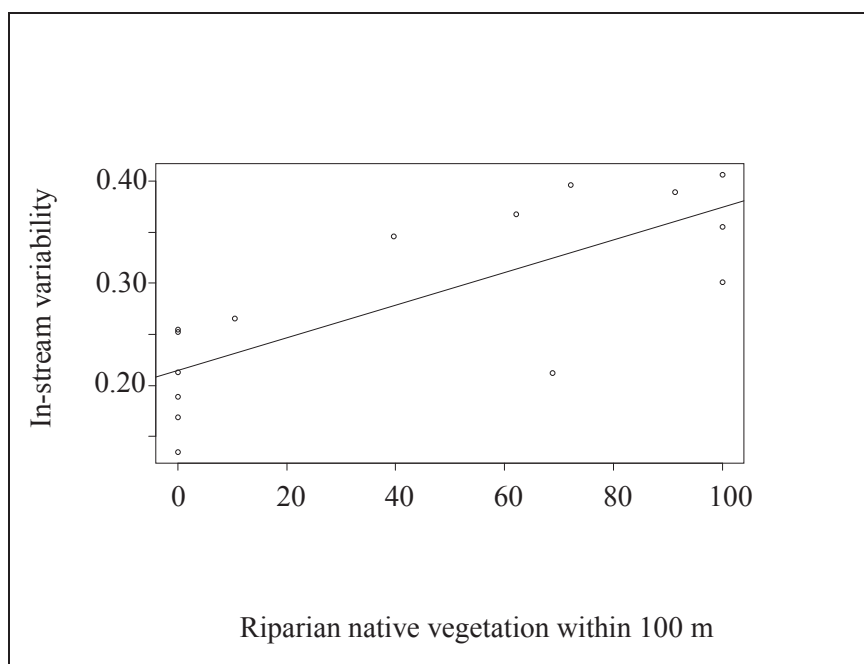


Fig. 3.9 In-stream variability of invertebrates vs. riparian native vegetation within 100 m, across 15 Taranaki streams, surveyed in 2013.

Riparian native vegetation (within 100 m) had contrasting effects on in-stream variability of the two communities. A strong increasing trend occurred between invertebrate variability and native riparian width of stream, while fish community variability reduced with increasing native riparian with (Fig. 3.9 and Table 3.10).

Bryophyte cover (% of moss) positively affected the variability of invertebrates, contrary to the negative trend of fish variability against % moss in streams. Additionally, invertebrate variability reduced with increasing periphyton cover, particularly in downstream habitats. The proportion of undercut banks had a strong positive effect on the in-stream invertebrate variability, while the particular habitat measure did not affect the variability of communities within streams considered in this study (Fig. 3.10 and Table 3.10).

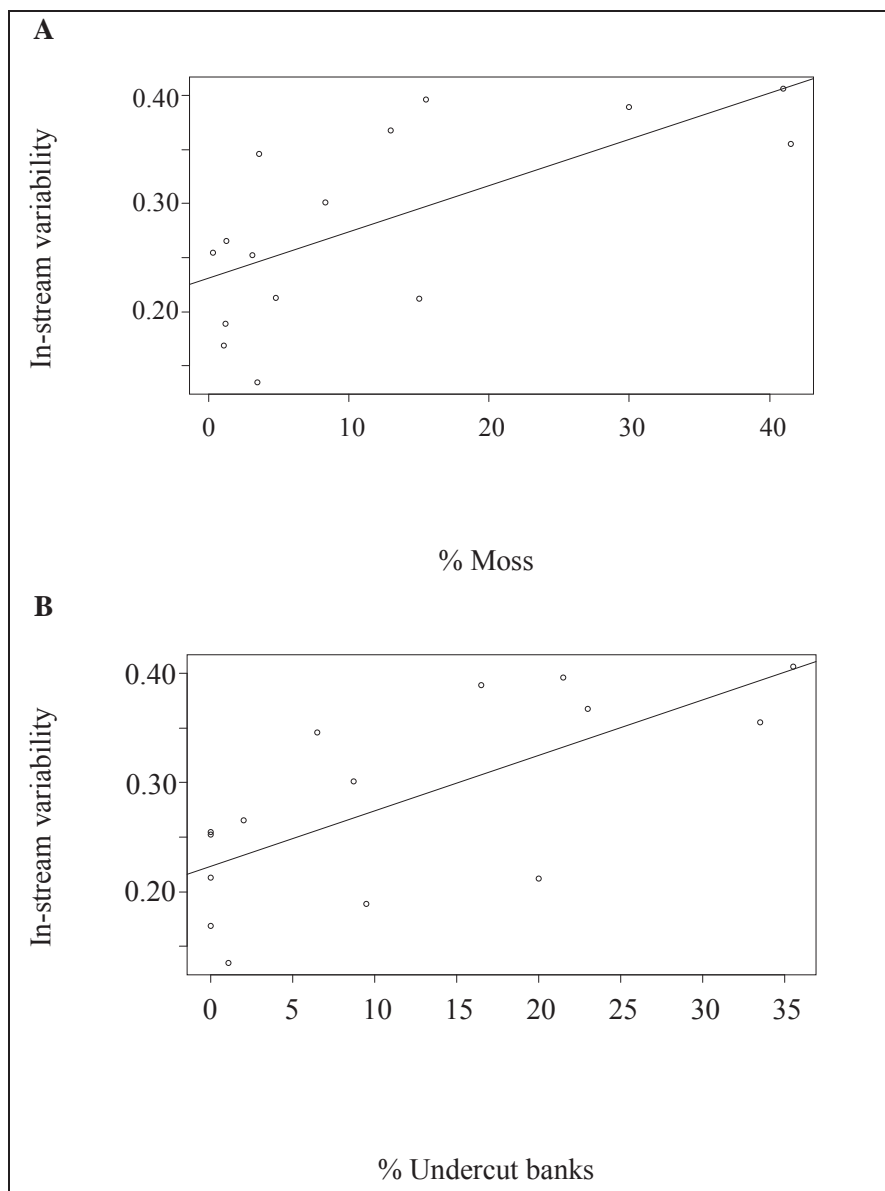


Fig. 3.10 In-stream variability of invertebrates vs. percentage of bryophytes (moss) in streams (A) and % of undercut banks (B), across 15 Taranaki streams, surveyed in 2013.

Table 3.10: Results of regression analyses between community variability (in-stream) and selected environmental factors (significant values ($P < 0.05$) are in bold letters)

Factor	Fish		Invertebrates	
	r	P	r	P
DS distance (km)	0.36	0.19	-0.70	0.004**
Altitude (m)	-0.47	0.08	0.65	0.009**
Width (m)	0.63	0.01*	-0.71	0.003**
Depth (m)	0.60	0.02*	-0.54	0.04*
Width/Depth	0.45	0.10	-0.69	0.005**
Slope	-0.20	0.50	0.73	0.002**
Conductivity (μ S)	0.00	0.90	-0.63	0.01*
pH	0.17	0.52	-0.71	0.003**
% Periphyton	0.00	0.85	-0.58	0.02*
Flow variability	-0.56	0.03*	0.41	0.13
% Shade (riparian)	-0.51	0.05	0.71	0.003**
% Riparian native vegetation	-0.55	0.03*	0.77	0.001***
US rain	-0.35	0.21	0.57	0.03*
US indigenous forest	-0.57	0.03*	0.54	0.04*
US native	-0.41	0.12	0.62	0.01*
US pasture	0.41	0.12	-0.62	0.01*
Average bed sediments	-0.20	0.50	0.35	0.21
% Undercut bank	-0.47	0.08	0.71	0.003**
% Stone bank	0.61	0.02*	-0.10	0.78
% Moss	-0.60	0.02*	0.68	0.005**
% Still	-0.40	0.13	0.57	0.03*
% Riffle	0.17	0.55	-0.56	0.03*
% Rapids	0.26	0.34	-0.53	0.04*
% Fine gravel	-0.61	0.02*	0.57	0.03*
% Cobble	0.56	0.03*	-0.41	0.12
% Bed rock	-0.55	0.03*	0.41	0.13

‘*’ = $P < 0.05$, ‘**’ = $P < 0.01$, ‘***’ = $P < 0.001$ DS = Downstream, US= Upstream

Among other habitat measures, % stones in bank, % fine gravels, % cobbles and % bedrock of stream substrates had significant effects on the variability of fish. Additionally, in-stream invertebrate variability was affected by % fine gravels, % rifles, % rapids and % still habitats. Upstream land use pattern characterised by pasture and native vegetation only

affected invertebrate variability, while upstream indigenous forest cover influenced the in-stream variability of both fish and invertebrates. In addition, number of days raining up stream was important for invertebrate variability (Table 3.10).

Discussion

According to the results of this study, stream invertebrate communities are more indicative of the effects of agriculture than are fish communities. For instance, compositional separation and the difference of in-stream variability of invertebrates was clearer than those of fish between the two land uses, and the variability of invertebrates were more predictive of habitat gradients considered in this study. Clarity in the compositional difference of invertebrates may have occurred because of relatively high species diversity and limited dispersal ability of the particular community. Taranaki streams showed a dramatic difference in invertebrate densities between the two land uses. For instance, the density of EPT (order: Ephemeroptera, Plecoptera and Trichoptera) taxa increased by threefold when streams flow from forest to pasture. The low flow in forested streams may have influenced the reduction of invertebrate densities in forested streams, during the summer. Among EPT taxa, mayflies and stoneflies decreased in relative abundance from forest to pasture, while caddisflies, chironomids and gastropods dominated the streams in Taranaki farmlands. Although agricultural effects on composition can vary between different regions (Quinn, 2000), declining EPT diversity and recolonisation by pollutant tolerant taxa (e.g. chironomids) are commonly observable effects of farming on stream invertebrate communities in New Zealand (Scarsbrook & Halliday, 1999; Storey & Cowley, 1997).

In these Taranaki streams, fish community composition clearly differed between forested and pasture sites. Forested streams had species in family Galaxiidae, Anguillidae and

Salmonidae, while the pasture streams consisted of fish species in five families, including Pinguipedidae and Gobiidae (Eleotridae), in addition to the families found in forested streams. Eels (family; Anguillidae) and bullies (family; Gobiidae) contributed to more than 63% of overall dissimilarity between forest and pasture. The overall contribution of galaxiids was nearly 15% between the two land uses.

In New Zealand, fish communities of small forested streams are generally dominated by native galaxiids, such as banded kokopu, short jaw kokopu, giant kokopu and koaro. Additionally, eels and red fin bullies in low numbers may also occupy. In contrast, pastoral streams are characterised by a different community, consisting of blue-gilled bullies, upland bullies and large numbers of red fin bullies. Eels, particularly the longfin eels, are common, but native galaxiids are rare and may be replaced by brown trout in streams running through pasture (McDowall, 1990). In summary, fish communities of Taranaki show more or less similar compositional changes in streams between the two land use patterns, described by McDowall (1990); 1). Galaxiids are widely distributed and more abundant in forested streams, 2). Bullies are more abundant and frequently occur in pasture sites and 3). Trout are relatively more distributed over the agricultural streams than in the forested habitats.

In addition to McDowall's (1990) observations, Allibone *et al.* (2010) have shown that 13 freshwater fish species are declining in New Zealand streams, because of several factors including agriculture, forestry and water abstraction. Among the fish communities reported in this survey, few fish species including shortjaw kokopu, torrent fish, koaro, inanga and giant kokopu are relatively less abundant and/or distributed (see Table 2.1 and 3.1) over the study sites. The particular limited occurrence/ abundance of fish species in Taranaki streams might have caused by the effect of landuse change, as shown by Allibone *et al.* (2010). Nevertheless, low occurrence or distribution of a particular species has to be carefully discussed along with their natural distribution patterns across the country. For

instance, bluegill bully (reported in Table 2.1 but absent in Table 3.1) is naturally rare in the Taranaki region (McDowall, 1990 and Allibone *et al.*, 2010).

The fish community change is less prominent than that of invertebrates between the two land-use classes of this study. In addition to low species counts and relatively high dispersal ability, limited sensitivity for sampling would also have affected the overall results. However, the applicability of monitoring invertebrates remains high, because of their higher predictability of agricultural effects, compared with the similar likelihood of fish communities in impacted habitats.

Despite the dramatic difference in species counts between fish and invertebrates, their in-stream variability remained similar to each other, across the study sites. Further, the two communities clearly differ in diversity, trophic level, dispersal ability and in most of their community-environment links, but co-exist more or less in the same habitats. Although more insightful studies are required to explore the key variability drivers between terrestrial, marine and freshwater systems, the specific study result indicates that community variability is likely to be unambiguous within limited spatial units (e.g. reach) at least across similar types of habitats (Soininen *et al.*, 2007). Moreover, the variability of a given community likely to be linked with multiple scales including their life cycle strategy, dispersal ability biology, operating spatial scale and responses to changing environment across space (e.g. landuse) or time (e.g. seasons). Nonetheless, it is challenging to draw firm conclusions on how/if different types of ecosystems sustain biological variability across different communities, mainly because of limited literature available in the particular field of study.

Although communities may reflect the environmental stress by changing their biological variability within impacted sites (Conrad, 1977), land use impact considered in this study did not significantly affect the inter-site variability. In the fish community, more

than 70% of community dissimilarity between the impacted and non-impacted sites was caused by three species; brown trout, longfin eel and redfin bully. The variance in relative abundance distributions influences the beta diversity patterns (Erős, 2007). Overall, variability changes are likely to be masked by the limited number of species contributing to most of the community dissimilarity, hence the community changes of galaxiids would poorly be reflected in spatial variability between forested and pastoral streams in this study.

Secondly, the spatial variability changes have been observed over large areas such as river systems longer than 100 km, and the beta diversity is likely to decline within reducing spatial units from landscapes to sampling sites (Erős, 2007). Taranaki streams surveyed in this study are relatively smaller than the major river systems, such as Waikato and Manawatu Rivers in New Zealand (Death & Joy, 2004; Robinson *et al.*, 1995). Therefore, the limited geographical distance between the sites would also have been inadequate to result in a significant difference in inter-site variability of fish communities within the selected groups of streams in this study.

The presence of exotic fish species such as brown trout has reduced the spatial variability between groups of sites in tributaries to the Danube River, Hungary (Erős, 2007). Thus, the homogenising effect of invasive species may lead to equally variable communities between different treatment groups (Clavero & García-Berthou, 2006). In these Taranaki streams, brown trout is generally abundant within most of the selected groups of sites, hence they have the potential to reduce the spatial variability of stream communities between forested and agricultural habitats.

Near the Ekofisk oilfield in the North Sea, biological variability of marine communities has significantly increased, especially within the sites closer to sources of pollution. Variability changes were more apparent between sites when they were

geographically segregated from each other (Warwick & Clarke, 1993). The study sites in Taranaki are not geographically well separated between control and impacted sites. Therefore, the limited geographical distance between the sites would have also resulted in equal inter-site variability between the contrasting communities, in Taranaki. In summary, equal inter-site variability between forest and pasture would have resulted, because of 1. relatively high contribution of limited number of taxa on the overall community composition, 2. the limited geographical extent of the study area, 3. the homogenising effect of invasive species (e.g. *Salmo trutta*) and 4. poor geographical segregation between the contrasting treatment groups.

Even though biological variability did not change across the land use classes and between fish and invertebrate communities of this study, in-stream invertebrate variability decreased from forested streams to pasture. Apparently, land use change has homogenised invertebrate communities within a stream. However, invertebrate variability trends do not directly support that in-stream variability is exclusively driven by agricultural factors such as nutrient effluents, sedimentation and land use pattern. Alternatively, results strongly suggest that habitat quality described by stream morphology, substrate type, bank stability, in-stream vegetation, water quality (pH, temperature) gradients and riparian cover are linked with the in-stream variability gradients of invertebrates. Nonetheless, modifications of natural habitats obviously alter the above mentioned in-stream values, thus the contribution of agriculture to habitat quality should be considered in future research in this field.

Furthermore, two key ecological observations could be discussed with the trends of in-stream variability of fish and invertebrates considered in this study (see Table 3.10). Firstly, in-stream variability of fish is less affected by their environment, in comparison to strong environmental effects on the variability of invertebrates within a stream. Secondly, fish and invertebrates have independently responded to the trends in environmental factors, in

terms of their in-stream variability. For instance, in-stream variability of fish increased with the stream size (width and depth), in contrast to the strong negative correlations between the particular factor of invertebrates and stream size measures. Low in-stream variability of fish in small-shallow streams may potentially be driven by less species counts and abundance. Limited occurrence of fish in small streams is further understandable with their dependency on relatively larger spatial scales, compared to that of invertebrates in particular. Thus, the relevance of fish communities in small-forested streams to local-scale biomonitoring has to be reviewed with their operating spatial scales. It would be insightful, if fish community structure is assessed with their environment and invertebrates simultaneously, to observe cross-community and community-environment links, in varying spatial scales and different land use classes.

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Chapter Four

Community concordance of freshwater fish and invertebrates in Taranaki streams

Abstract

Community concordance was examined between fish and invertebrate communities within 15 streams in Taranaki, New Zealand. Mantel comparison suggested that community patterns of fish and invertebrates are significantly concordant with each other ($r = 0.38$) among the 15 streams sampled in forest and adjacent pastoral lands. Community concordance decreased in lower spatial limits, and the two communities were not concordant within a stream. The cross-community concordance was noticeably high within each land use class. Fish community was best predicted by the invertebrates within the forested sites (Mantel $r = 0.87$). Compared to stream fish and invertebrates in the forest, the two communities were less concordant between agricultural streams ($r = 0.62$), and none of the communities correlated with the overall environmental distance between the sites impacted by pasture. Biological concordance was consistently higher than the community-environment links, while community-environment links were more important in the lower trophic level (invertebrates) than those were in the upper trophic level (fish) considered in this study.

Introduction

Community ecologists often describe environmental quality using biotic communities living in a particular environment (Jackson, 1995; Lenat & Barbour, 1994; Meador &

Goldstein, 2003). Conventional habitat based ecological studies are generally based on a single taxonomic group ranging from a phylum to an order (James & Suren, 2009; Minns *et al.*, 1994; Paavola *et al.*, 2003). For instance in freshwater ecology, either invertebrate or fish communities are largely used to predict the ecological health of their habitats (Humphries *et al.*, 1999; Matthews, 2012; Wren & Stephenson, 1991). Both fish and invertebrate communities may not be similarly affected by their habitat gradients (e.g. water quality and river morphology), hence it is not reliable to extrapolate the spatial relationship between a community and its environment, across all the taxonomic groups within an ecosystem (Paavola *et al.*, 2003).

Concordance studies provide a better alternative to compensate the gaps of knowledge in community-environment links through different taxonomic groups, and has become more commonplace in aquatic ecology (Heino *et al.*, 2003; Paszkowski & Tonn, 2000). Community concordance explains the similarity in community structure between different groups of taxa, living within a given range of habitats (Paszkowski & Tonn, 2000; Peres-Neto & Jackson, 2001). Paavola *et al.* (2003) suggested that both biological and environmental processes might cause similar community patterns across different biotic groups. For example, predation at higher trophic levels in a food web controls the abundance and distribution of their prey species in lower trophic level and hence is likely to influence their overall community pattern (Jackson & Harvey, 1993). Also, different communities may be concordant in spatial patterns because of the common but independent responses to their environment (Paszkowski & Tonn, 2000). Therefore, concordance studies are useful in examining the response of different trophic and taxonomic communities in environmental impact assessment to understand how different communities adhere to each other and to specific environmental gradients such as land use pattern, water quality and habitat morphology (Jackson *et al.*, 2001). Further, the community concordance is a more robust

approach (because of its capacity to capture complex non-linear relationships between data sets) compared to the conventional cross-community investigations based on the changes in population density, relative abundance or biomass of prey species in presence/absence of their predators (Flecker & Townsend, 1994; Stenroth & Nyström, 2003; Townsend & Cowl, 1991).

In stream ecosystems, predation by fish may affect the structure of aquatic communities by reducing the abundance or altering the behaviour of prey species (Closs *et al.*, 2004; Jackson *et al.*, 2001). However, biotic interactions (e.g. predation and competition) are less considered in habitat based ecological studies, which are generally focused on the impact of physical environment on freshwater community structure (Death & Joy, 2004; Karr, 1981). Thus, there is limited knowledge on the relative importance of different trophic levels in structuring stream communities (Closs *et al.*, 2004). Freshwater fish and invertebrate communities are linked by stream food webs and potentially interdependent for their spatial distribution (Backus, 2014; Power, 1990). Further, the degree of community concordance (between stream fish and invertebrates) has been shown in some studies to increase with the spatial extent of their habitats, and is unlikely to be independent from the differences in adherence of particular communities to their environment (Backus-Freer & Pyron; Backus, 2014; Paavola *et al.*, 2003). Nevertheless, the influence of land use change and the spatial limit on cross-community concordance requires further examination, for a comprehensive understating in community ecology.

In this study, I compare the compositional relationship between fish and invertebrate communities in 15 streams in Taranaki, New Zealand. My hypothesis is that stream fish and invertebrates are concordant in their community similarity (Jackson & Harvey, 1993). I predict that both of the communities will follow a similar pattern of spatial distribution, because they are closely linked stream communities through the stream food web (Collier &

Winterbourn, 2000; McDowall, 1990; 2000). This study further questions: 1). Does community concordance increase with the spatial extent? 2). Are stream communities less concordant in the pasture than they are in the forest? 3). Do lower trophic levels (e.g. invertebrates) more closely link with their environment than the high trophic levels (e.g. fish) do? Moreover, I investigated the relevance of environmental distance to the community structure of each of the communities, to compare the important environmental drivers between fish and invertebrate communities (Backus-Freer & Pyron, 2015).

Methods

Study Sites

The Taranaki region is in the west of North Island, New Zealand. More than 140 streams and rivers start from Mount Taranaki, which peaks at 2518m above sea level (Joy & Death, 2000). Most of the fluvial habitats in Taranaki consist of relatively small, first or second order streams. Freshwater macroinvertebrates from more than 110 different taxa and 18 native fish species have been reported from the lotic habitats in Taranaki (Joy & Death, 2000; Taranaki Regional Council, 1997; 2013). A total of 15 sites were selected to collect data for this study in Taranaki (Fig. 4.1).

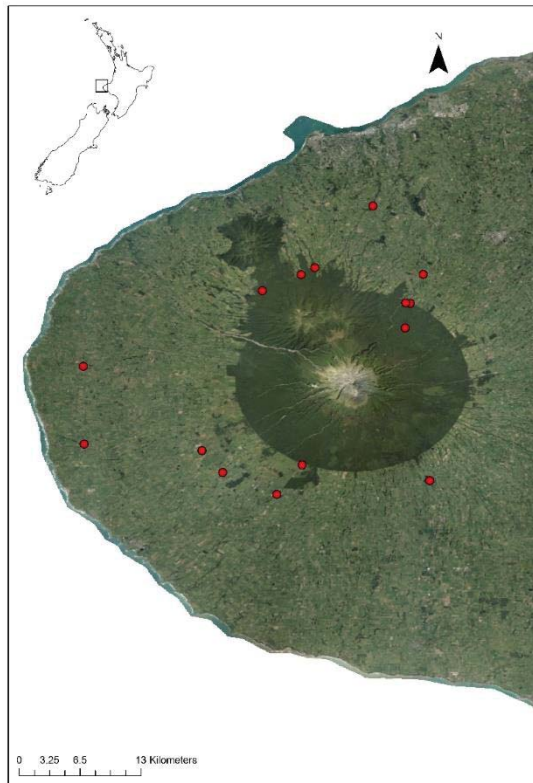


Fig. 4.1 Selected streams in Taranaki, New Zealand, surveyed for fish and invertebrate data, during the summer in 2013.

Sampling and data collection

Field sampling was conducted between January and February, 2013. Fish sampling was carried out by following the protocol proposed by David *et al.* (2010). Invertebrates were collected using the macroinvertebrate sampling protocol of Stark *et al.* (2001). At each of the selected 15 sites, fish data were gathered by moving in an upstream direction along a 150m reach divided into ten equal sub-reaches. A ‘Kainga EFM 300’ electrofishing machine was used with fish collected downstream in a pole-net. The pulses were adjusted to a frequency between 60 and 70 Hz, and to a width of 2 ms. Settings were calibrated prior to each application by lowering voltage until less than five lights appear on the electrofishing machine, showing proper setting for each location.

At each site, five Surber (0.1 m²) samples of benthic macroinvertebrates were collected after fishing, from every second fishing sub-reach. Invertebrate samples were preserved in 90% ethanol at the sites, and sieved by using a 500 µm mesh at the laboratory. Biological samples were identified, to the lowest confident taxonomic level possible (McDowall, 2000; Winterbourn *et al.*, 1989).

Environmental data were collected at each sampling site parallel to the biological survey. Geographical position and elevation were recorded using a ‘GARMIN GPS 72’ personal navigator. Stream geomorphology, habitat type, in-stream productivity (periphyton cover, macrophytes, moss and leaf litter), bank type, substrate type, land use and vegetation cover of riparian and proximal land were assessed visually. Stream morphometric data (wetted-width, depth and bed-exposure) and in-stream water quality (temperature, conductivity and pH) were measured at each site, by using measuring tapes/ rulers and a ‘EuTech Cyberscan PC-10’ meter. FENZ (Freshwater Ecosystems of New Zealand) geo-data base was used to gather data on upstream catchment land use, Nitrogen concentration, climate, geography and geology of the sites, to cover the full range of environmental information available for the selected sites in this study.

Statistical Analysis

The biological similarity between the streams was measured, using the Bray-Curtis (Sørensen quantitative) index, which is one of the most effective ecological similarity measures in observing community patterns (Magurran, 2002; Oksanen, 2011). Two sets of similarities between fish and invertebrates for all sites were constructed into triangular matrices. Non-metric multidimensional scaling (NMDS) in two dimensions was used to plot the similarity of fish and invertebrate communities, between streams. The Mantel test was used to compare fish and invertebrate communities. The significance of the correlation was

assessed between the two communities (fish and invertebrates), using 999 permutation tests (Oksanen, 2011).

NMDS ordinations of fish and invertebrate communities were compared by using the symmetric Procrustes test, to assess any significant correlation between the multivariate structures of the respective communities (Oksanen, 2011). Procrustes analysis computed a symmetric Procrustes residual statistic (m^2) and the Procrustes correlation (r). Procrustes correlation (r) is a derivative of the Procrustes residual statistic ($r = \sqrt{1 - m^2}$). Permutation tests (999) were used to evaluate the significance of the correlation, between two ordinations (Oksanen, 2011). A Procrustes superimposition plot presented the graphical comparison of the fish and invertebrate ordinations.

The Mantel test is popular among community ecologists, because of its straightforwardness and flexibility (Dixon, 2003; Urban, 2006). The key advantage of the Mantel test is its capability of matching both Euclidean (environmental) and non-Euclidean (biological) distances generated by a range of data types such as continuous, binary or ordinal data (Peres-Neto & Jackson, 2001). Jackson (1995) argues that Procrustean superimposition method or PROTEST is a better alternative in cross-community comparisons, due to its usefulness in the visual examination of the association between individual objects (sites) of two different ordinations. Further, the Procrustes test performs more powerfully than the mantel test in non-linear spaces (Peres-Neto & Jackson, 2001). However, each data matching approach remains a choice of testing the community concordance (Oksanen, 2011).

Community comparisons were carried out at three spatial scales; 1). Between streams (aggregated density for each stream was used to construct similarity matrices for fish and invertebrates), 2). Between stream subsets (density data of 75 samples across 15 streams were used for similarity matrices and community ordinations) and 3). Within each stream (In-

stream concordance was tested for each stream, using fish and invertebrate data collected from five subsets within a stream). Land use pattern was the main impact indicator considered for this analysis. Study sites were grouped according to contrasting impacted and non-impacted sites (e.g. forest and pasture). Biological similarities were assessed for fish and invertebrates, and the similarities between two communities were compared within each group of sites, using Mantel test and Procrustes test.

Table 4.1: Environmental factors grouped into relevant categories for measuring the Euclidean distance between 15 streams considered in this study.

Group category	Included environmental vectors
Stream morphology	width, depth and slope*
Habitat type	% cover of still, backwater, pool, run, riffle, rapid and cascade
Substrate type	% cover of mud, sand, fine gravel, coarse gravel, cobble, boulder and bedrock
Water quality	conductivity, pH, temperature and total nitrogen concentration*
Organic carbon input	% cover of periphyton; diatom and algae, moss and leaf litter
Stream bank type	% cover of soil, stones, grass, shrubs, trees, artificial structures and undercut banks
Streamflow	mean annual flow*, mean annual 7-day low flow*, flow variability*
Riparian cover	% cover of native vegetation, exotic , pasture, willow, grass/tussock
Proximal land use	% native, exotic, agriculture, urban and industrial
Upstream land use	upstream indigenous forest*, native forest* and pasture*
Geography	northing, easting and altitude
Climate	upstream average air temperature*, days raining upstream*, summer temperature *
Upstream Geology	hardness, calcium and phosphorus concentration of the surface rocks upstream*

‘*’ = data extracted from FENZ geo-data base

Each of the communities was compared with the Euclidean distances of environmental measures collected in this study. Mantel test was performed to compare community-environment correlation within all 15 sites, in forested and agricultural sites. Further, Euclidean distances were computed for categorised environmental vectors, grouped according to key types of environmental descriptors (Table 4.1). Each set of categorised

environmental factors was compared to fish and invertebrate community matrices (by Mantel test) among all 15 sites, within forested sites and within the pasture (Backus-Freer & Pyron; Backus, 2014; Ramette, 2007). The community comparisons were performed using ‘vegan’ package in R (version 3.0.2) software (Oksanen, 2011; Oksanen *et al.*, 2013).

Results

NMDS ordinations of abundance data among the 15 sites had an excellent goodness of fit, with a stress value of 0.09 for both fish and invertebrate communities. According to the results of Mantel test, fish and invertebrate communities were concordant between streams ($r = 0.38$, $P = 0.001$) (Fig. 4.2). The concordance between two communities decreased with the spatial extent. The Mantel statistic r was 0.21 ($P = 0.001$) for the spatial correlation between habitats (between 75 sub reaches) and average in-stream (between five samples within a stream) concordance was not significant ($r = 0.13$) (Fig. 4.3).

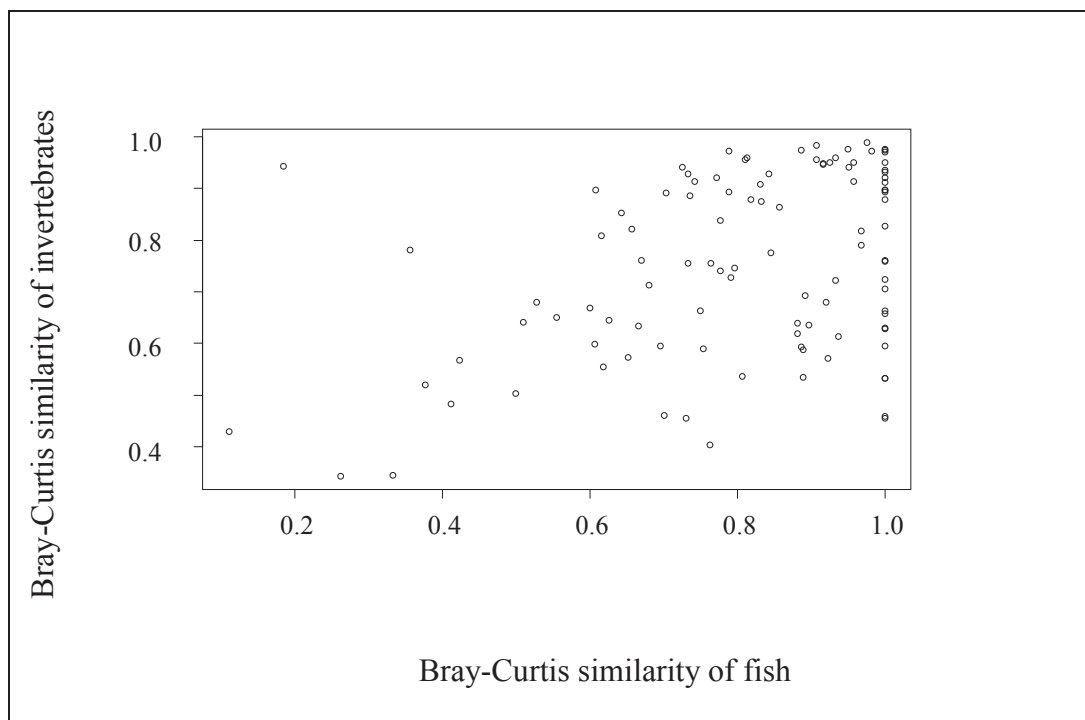


Fig. 4.2 Relationship of biological similarities of fish and invertebrates among 15 streams of Taranaki, surveyed in 2013.

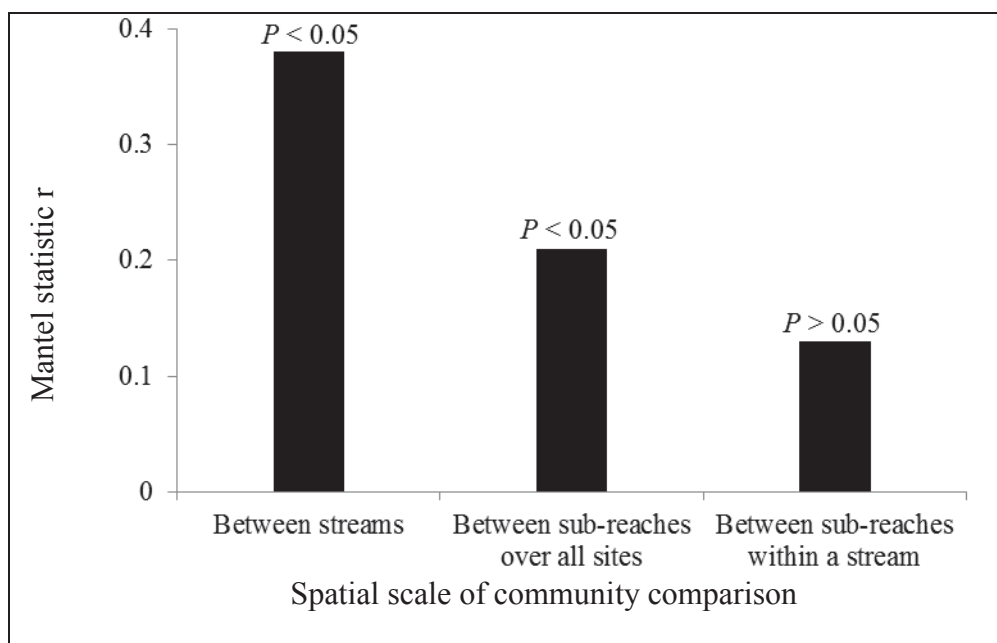


Fig. 4.3 Mantel correlation (r) between fish and invertebrate communities across different spatial units of Taranaki streams, studied in 2013.

In comparison to the spatial correlation of fish and invertebrate communities over the 15 sites, cross-community concordance was noticeably high within each land-use class (forest and pasture). Fish and invertebrate communities in forested streams were more concordant than in agricultural streams ($r = 0.87$ and 0.62 , respectively). Further, in Procrustes test, forest communities showed higher community congruence compared to the stream communities in the pasture (Fig. 4.4, Fig. 4.5 and Table 4.2).

Table 4.2: Results of Mantel and Procrustes tests between fish and invertebrates of Taranaki streams grouped into contrasting land use classes (forest ($n=7$), pasture ($n=8$)).

Treatment Group	Mantel test		Procrustes test		
	r	Significance	Correlation	Significance	Protest residual (m^2)
Forest	0.87	0.001	0.72	0.009	0.48
Pasture	0.62	0.013	0.69	0.04	0.52

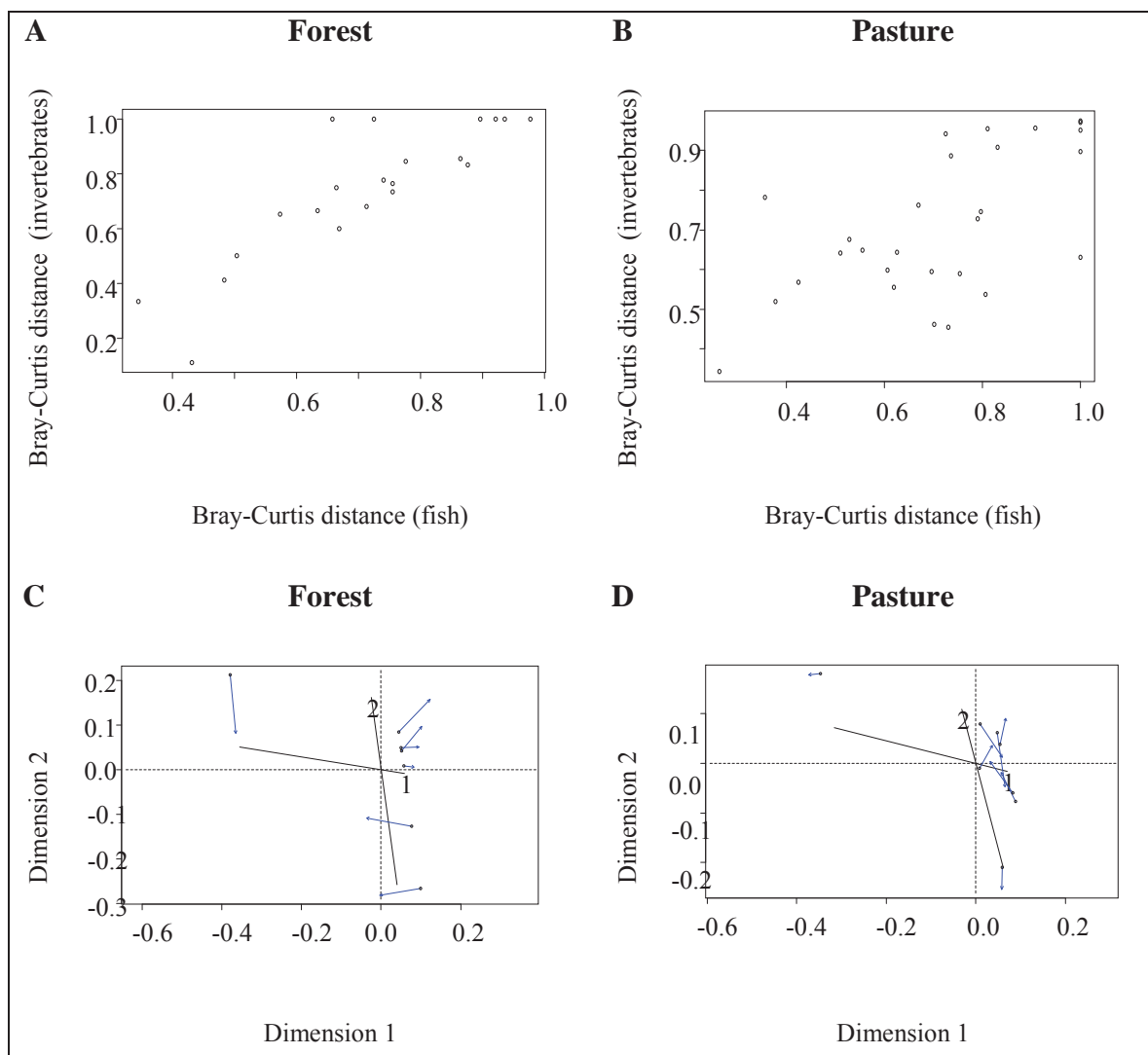


Fig. 4.4 Distance comparisons (A & B) and Procrustes superimposition plots between fish and invertebrates among forested ($n = 7$) and agricultural ($n = 8$) streams in Taranaki.

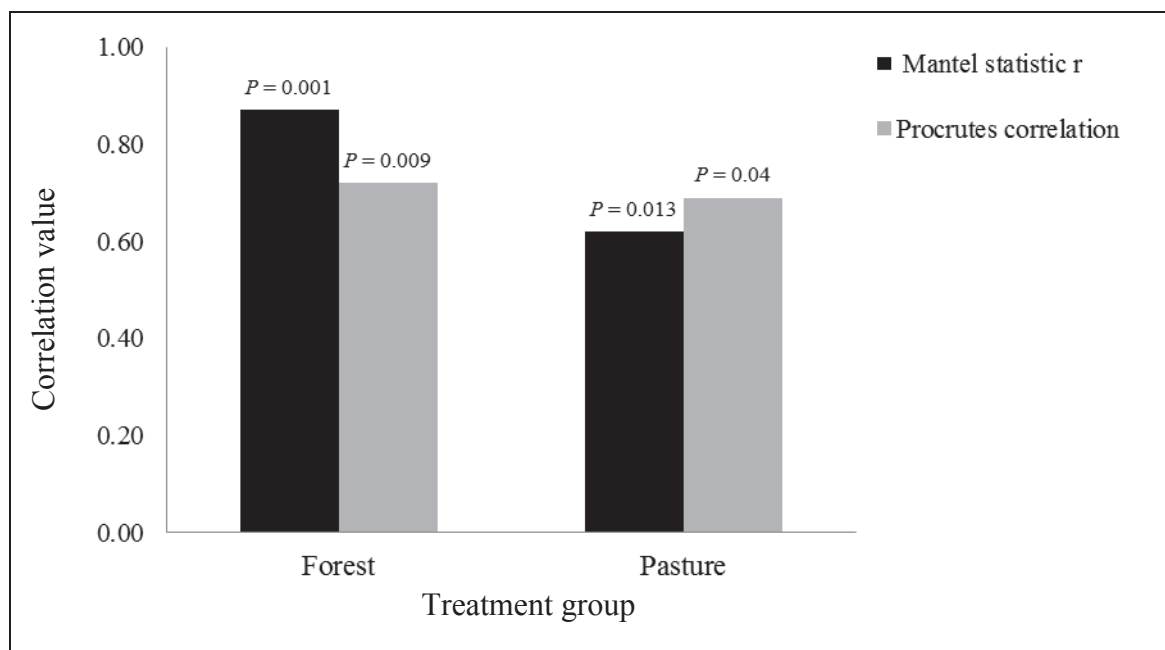


Fig. 4.5 Correlation values of Mantel and Procrustes comparisons between fish and invertebrates among forested ($n = 7$) and agricultural ($n = 8$) streams in Taranaki.

In general, invertebrate communities were more concordant with their environment than fish communities were among the 15 sites (Fig. 4.6). Within the forest, both of the communities significantly correlated with their environment, while community-environment dissimilarities did not link significantly within the pasture sites considered in this study (Table 4.3).

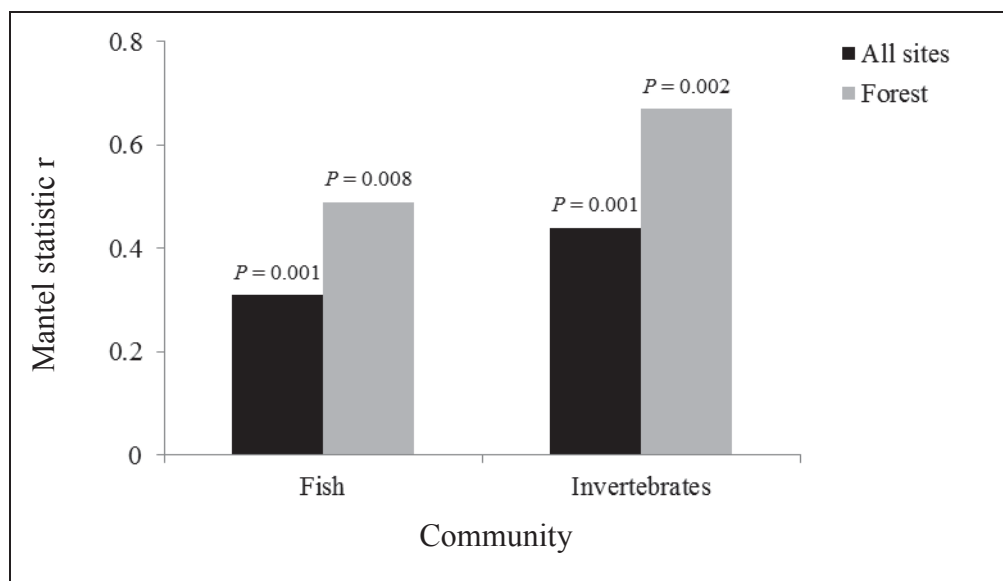


Fig. 4.6 Correlation values of Mantel comparisons between the biological distance (Bray-Curtis) and environmental distance (Euclidean) communities, with respect to fish and invertebrate communities among 15 Taranaki streams and within the subset of forested streams ($n = 7$).

Table 4.3: Mantel Correlations between the biological distance (Bray-Curtis) and environmental distance (Euclidean) of fish and invertebrate communities among 15 Taranaki streams, within the subsets of forested ($n = 7$) and agricultural ($n = 8$) streams.

Group of sites	Fish		Invertebrate	
	r	Significance	r	Significance
All sites	0.31	0.001	0.44	0.001
Forest	0.49	0.008	0.67	0.002
Pasture	0.40	0.09	0.14	0.29

In categorical correlation analyses, community-environment links were more prominent in invertebrates than that in fish communities (Fig. 4.6). Invertebrates correlated with a wider range of environmental distances, compared to the important community-environment links of the fish communities, considered in this study. For instance,

invertebrates correlated with seven categories of environmental matrices, while the fish community adhered only to three different environmental matrices, across the 15 streams of this study (Table 4.4).

Table 4.4: Mantel correlations between the biological distance (Bray-Curtis) and categorical environmental distances (Euclidean) communities relating to fish and invertebrate communities among 15 Taranaki streams and within forested ($n = 7$) streams.

Group of sites	Factor category	Mantel correlation between community and environmental dissimilarities	
		Fish	Invertebrates
All sites	Substrate	0.31*	0.32**
	Organic carbon input	0.11	0.35**
	Stream morphology	0.34**	0.45**
	Stream bank	0.27*	0.25*
	Riparian cover	0.16	0.30*
	Geography	0.17	0.31**
	Climate	-0.01	0.24*
Forest	Habitat type	0.25	0.51*
	Water quality	0.69**	0.45**
	Stream morphology	0.49	0.53*
	Geography	0.85**	0.70**

‘*’ = $P < 0.05$, ‘**’ = $P < 0.01$

Within all the study sites, the most important community-environment links of invertebrates occurred with stream morphology, organic carbon input and substrate type ($r = 0.45$, 0.35 and 0.32 , respectively). In addition, invertebrates correlated with dissimilarities in stream bank type, riparian cover geography, and climate. The fish community linked only with stream morphology, substrate type and stream bank type across the 15 streams in Taranaki.

Among forested sites, geographical distance highly correlated with biological distances of both fish and invertebrates ($r = 0.85$ and 0.70 , respectively, $P < 0.01$).

Additionally, the invertebrates linked with habitat type, water quality and stream morphology, while the fish community interrelated with the water quality distance across the forested streams (Table 4.4).

Discussion

The fish and invertebrate communities considered in this study were predicted to be correlated to each other, mainly because of the trophic relationships between two communities. Almost all the freshwater fish species feed on stream invertebrates in New Zealand (McDowall, 2000) and predation is a key biological driver of the New Zealand stream invertebrates (McIntosh, 2000). The study results support my hypothesis and suggest that the biological environment controls stream communities in addition to the effect of physical constraints, such as geography and land use. However, the relative importance of cross-community links declined from larger to smaller spatial units. For instance, average concordance was low and insignificant between fish and invertebrates within a stream considered in this study. The particular effect may be caused by the difference in mobility between fish and invertebrates within a stream. An individual fish occupies a wider space in a stream than an invertebrate, thus is distributed over several stream subsets, in comparison to the limited distribution of a given invertebrate community. As a result, the particular cross-community link would become less prominent in limited spatial scales of fluvial habitats. Paavola *et al.* (2006) showed that the concordance between fish and macroinvertebrates in Finnish boreal streams are highly dependent on the spatial scale. The particular study further explained that the community concordance significantly declines from large freshwater ecosystems to a single drainage, and concluded that weak concordance in lower spatial scales mainly connected with the dissimilarity in community-environment links between different

communities. However, I argue that community dispersal patterns in a limited space (e.g. single reach) are unlikely to be entirely controlled by the environment, but through a combination of several factors including mobility of individual species, life cycles, feeding behaviour and abundance of predatory species. For instance, Grenouillet *et al.* (2008) showed that the dispersal capacity of organisms is highly influential for the cross-community concordance between stream fish and invertebrate communities of the River Viaur in France.

Consistently, there was a strong connection of invertebrates with environmental factors in a wide range of different categories, compared to the connection between fish communities and their physical environment (Table 4.4). Weakening community-environment links from lower to higher trophic levels possibly shows the bottom-up control of the stream food web. Interestingly, neither of the two communities were concordant with the overall environmental distance between streams in the pasture. Although the insignificance of community-environment concordance does not necessarily suggest the complete absence of environmental control, stream biota in agricultural lands may become less responding to degraded environment, at least because of their high capability to survive in a wide range of environmental conditions, compared to susceptibility of the forest-dwelling species to agricultural impacts. Infante *et al.* (2009) suggested that the scale (intensity?) of land use influences could negatively affect the community responses to their environment, besides differences in susceptibility to agricultural impacts.

When streams run through agricultural lands, inter-community correlation clearly declined but sustained, compared to the dramatic change in community-environment concordance from forest to pasture of this study. However, the negative impact of agriculture was clear on spatial auto-correlation among physical environment, invertebrate and fish communities. This result indicates pastoral stream communities have greatly deviated from the ecological links occur between fish, invertebrates and their environment that occur in

undisturbed habitats. Therefore, I suggest further studies focused on stream food webs, nutrient cycling and energy flow, for a comprehensive understanding of differences in functional ecology between the forested and agricultural streams. Prospective studies may include: a). a complete comparison across all trophic levels in stream food web and, b). comparison of the carbon cycling and transfer of photosynthetic energy via stream food web between the two land use classes. Findings of above mentioned in detail studies would be more insightful than popular bio-environmental data matching method used in conventional impact assessment studies.

The ecological difference in community-environment links was reflected by the high residual value (m^2) generated in Procrustean analysis between fish and invertebrate community ordinations in this study. The residual value of a Procrustean rotation between two community ordinations reflects the ecological and behavioural differences between the communities (Peres-Neto & Jackson, 2001). However, behavioural differences between freshwater fish and invertebrate communities in New Zealand streams have not been studied, compared to their links with the physical environment (Collier & Winterbourn, 2000; McDowall, 2010). Nevertheless, results of this study show that invertebrates are more closely controlled by their environmental heterogeneity than the fish communities are.

Community concordance has been observed more clearly in physically stable freshwater systems, such as boreal lakes in south-central Ontario (Jackson & Harvey, 1993) and deep lakes in north- central Alberta (Paszkowski & Tonn, 2000) than in relatively less stable ecosystems, such as shallow Canadian lakes and Finnish headwaters (Paavola *et al.*, 2003; Paszkowski & Tonn, 2000). Although, relatively large lowland streams are likely to have more physical and hydrological stability than the small shallow forested headwaters, agriculture has a significant negative impact on the ecological and physiochemical stability of streams, mainly because of the high discharges of nutrients, sedimentation and removal of

riparian buffer (Goss *et al.*, 2014). This study showed that there is a higher concordance among the environment and stream communities in the forest than that in the agriculture. Therefore, I suggest that the community concordance is a result of broad ecological stability rather than the physical stability, particularly within a limited spatial extent.

However, previous studies have shown that the impact of physical environment is more important than biological interactions for cross-community spatial auto-correlation, in larger stable systems (Jackson & Harvey, 1993; Jackson *et al.*, 2001). Further, it has been shown that predator-prey interactions affect the communities in larger spatial scales, while the competition (for food and space) is more important in habitats within smaller geographical extents (Jackson *et al.*, 2001). Even though it is evident that fish and invertebrates are more closely linked to each other than they correlate with their environmental distance, stream ecological studies should pay a reasonable attention to discuss further the links between different communities, in addition to the conventional focus on community-environment links of stream communities.

Moreover, it is important to understand the community concordance and its causes, to develop more ecologically meaningful bio-monitoring methods in resource management and conservation practices (Jackson *et al.*, 2001). For instance, the results of this chapter show that fish communities are less dependent on their local environment than invertebrates between streams. This observation has to be reviewed with differences and/or similarities in spatial dependency, life cycles and community-environmental links between the two communities, in order to enhance the utility of bio-monitoring indices based on each community.

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Chapter Five

Is ecological dissimilarity of fish between streams independent from the proximal land use?

Abstract

Fish community data of 96 freshwater habitats in Taranaki was mapped onto a constrained ordination (CCA), and fitted with species abundances and environmental data across the study sites, to identify the most important bioenvironmental factors. Nine environmental factors and four species gradients were chosen to distinguish ecologically dissimilar fish habitat zones within the region. Affinity propagation method suggested seven distinct freshwater habitat clusters, but most of the cluster groups did not specifically discriminate the dichotomy in proximal land use pattern. Fish community gradients were clearly observed in β diversity measures such as similarity and variability, whereas α and γ diversity did not obviously respond to geo-land use factors through the sub-regions. Upstream pasture homogenised the fish communities between streams within a site cluster, while average elevation did not affect the inter-site variability of fish.

Introduction

Ecologists have questioned the validity of conventional biodiversity management plans confined mainly to protected areas, because of the persistence of biotic communities along with human impact (Chester & Robson, 2013). It has therefore been proposed to redesign largely modified natural habitats in conjunction with biodiversity conservation, to preserve communities in impacted habitats (Rosenzweig, 2003). Zonal clustering of habitats has become a robust alternative to conventional conservation measures generally based on

land use dichotomy between protected and impacted sites (Januchowski-Hartley *et al.*, 2011; Kleijn *et al.*, 2001). In zonal clustering of habitats, conservationists use both environmental (e.g. geography and climate) and biological (e.g. species distribution) filters to distinguish different planning/conservation units within an ecosystem (Januchowski-Hartley *et al.*, 2011).

However, integrated planning units such as hierarchical habitat clusters would be less effective in biodiversity conservation if the community gradients between particular units are not been explicitly assessed (Kleijn *et al.*, 2001). For instance, conventional inventory measures such as species richness are less informative than beta diversity in explaining the compositional and structural differences between habitats, thus are incapable of capturing the variability in species composition among non-overlapping spatial units (Soininen *et al.*, 2007). Hence, studies merely based on species numbers would mislead conclusions of community-environment gradient analyses (Magurran, 1988). For example, it is well known that New Zealand lowland rivers consist of a greater number of fish species, and receive the greatest human impact compared to their upstream headwaters, which are generally occupied by fewer fish species. However, limited information is available on trends in the biological variability of streams from headwaters to low elevation rivers (McDowall, 2010; Quinn *et al.*, 1997). In addition, previous studies have not reasonably separated the effects of altitude and land uses have on stream communities in New Zealand, because of the limited focus on beta diversity and confounding gradients between the particular environmental filters (Graham, 2003; Jowett, 1990).

As an alternative to traditional inventory measures, beta diversity has become widely popular among community ecologists, because of its effectiveness and usefulness in testing spatially explicit hypotheses, such as if community variability increases along a given environmental gradient (Legendre *et al.*, 2005; Warwick & Clarke, 1993). Variability studies are important in quantifying the stress of anthropogenic disturbances (e.g. industrial

pollution) and homogenising effect of land use conversions (e.g. from forest to agriculture) (Conrad, 1977; Shepherd *et al.*, 1992; Vellend *et al.*, 2007). Therefore, it is useful to understand variability changes in impacted ecosystems, to precisely conclude the influence of human control on biological diversity (Buckley & Schmidt, 2003; Kleijn *et al.*, 2001).

In this study, I predicted that fish communities are similarity variable between forest and pasture within a given sub-region of Taranaki, because of a). the high proportion of migratory species in the region (Joy & Death, 2000) , b). relatively great dispersal ability (inland penetration) of galaxiids and eels (McDowall, 1990). It was therefore hypothesised that the dichotomy of proximal land use (between forest and pasture) does not clearly distinguish the ecological dissimilarity, while the regional scale ecological dissimilarity is more effectively represented by habitat clusters based on exemplar sites which correspond to the dissimilarity between important bioenvironmental constraints. Further, I asked: 1). Does species diversity represent the ecological difference between landscapes? 2). Is altitude a prominent factor of fish community variability across (sub-regional) habitat groups within Taranaki? and 3). Does upstream pasture homogenise the fish communities between streams? For this analysis, I used the method of hierarchical habitat clustering to partition freshwater habitats in Taranaki, New Zealand, to test the combined partitioning effect of most important bioenvironmental constraints (Januchowski-Hartley *et al.*, 2011). Additionally, the confusion of potential co-linearity between altitude and land use pattern was removed by constraining the biological model by only the land use and geographical filters. Hence, the relative importance of geographical attachment was compared with the influence of agriculture on stream fish communities in Taranaki.

Methods

Study sites

The study area consists of 96 streams (Appendix 1) of the Taranaki region, in the west of North Island of New Zealand (Fig. 5.1). Mount Taranaki of the Egmont National Park is enclosed by agricultural land, controlled by dairy and beef farming, while natural forest covers the most of the area in the upper catchments (Joy & Death, 2000; Winterbourn, 1991). Pasture covers more than half of the proximal land use along the total length of Taranaki streams (Taranaki Regional Council, 2010).

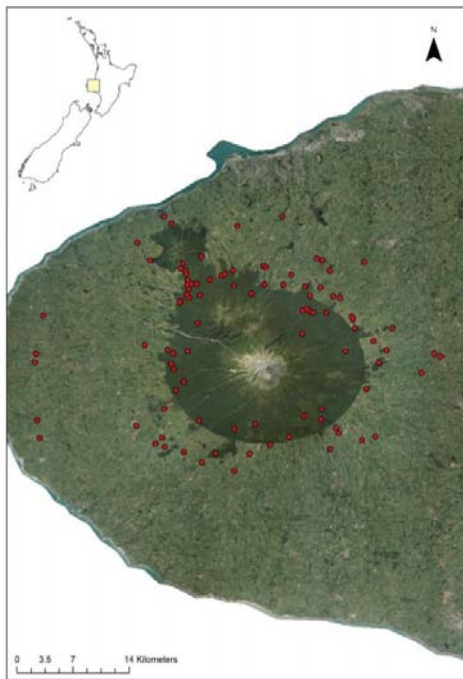


Fig. 5.1 Stream sampling sites of the Taranaki region in New Zealand used to collect fish and habitat data during summer 2012.

About 140 streams and rivers start from the Mount Egmont. Generally, these streams are short first or second order streams (Joy & Death, 2000; Taranaki Regional Council, 2013). The native fish community in the region mainly consists of diadromous species (except for two species: *Gobiomorphus basalis* and *G. breviceps*) (Joy & Death, 2001).

Fish sampling and data collection

Fish were sampled by night spotlighting at 46 sites, between January and June in 2012, and data for 50 other sites were extracted from the New Zealand Freshwater Fish Database (NZFFD). Further, I included historical fish data, from NZFFD, into 12 out of 46 sampling sites, because of inadequate fish records collected from the particular 12 sites.

Approximately 150 m long sections were sampled in each stream, by spotlighting and bank side observations, by heading in an upstream direction. Spotlighting was started approximately one hour after sunset. Each site was observed between banks from the downstream end, using a 30W spotlight. Smaller fish species (e.g. bullies) were captured alive into a dip net, and were transferred into a container, and large fish were examined watchfully. After the species identification was completed, the collected fish were released back to the streams (McDowall, 2000).

I recorded 46 different environmental vectors at habitat, reach and regional scales for each sampling site. The percentage cover of habitat type, substrate type, riparian vegetation type, in-stream vegetation and leaf litter were visually detected, while stream size (wetted width and depth) was measured by measuring tapes and rulers. Proximal land use pattern was visually observed, and further confirmed using 1:50,000 maps. Land use pattern of catchments was verified using 1:50,000 maps and Freshwater Ecosystems in New Zealand (FENZ) geo-based spatial data layers (Leathwick *et al.*, 2010). Water quality parameters measured by a 'EuTech cyber scan PC-10 pH-conductivity-temperature meter', include pH, temperature, and conductivity. Further, FENZ data layers provided habitat details, including climatic factors (rainfall and air temperature), geological composition (% composition of Ca and P of the surface rocks), proportional upstream land use, total Nitrogen concentration in water, for each sampling site (Leathwick *et al.*, 2010). In addition, habitat descriptions of

NZFFD (New Zealand Freshwater Fish Database) records were compared with the collected environmental data corresponding to the study sites (Appendix II).

Statistical Analysis

Fish and environmental data were compiled into two data sets. Constrained correspondence analysis (CCA) was used to select the most important bioenvironmental vectors predicting fish community structure (Ramette, 2007). The important bioenvironmental variables were chosen by factor fitting method for environmental interpretation of biological ordinations, described in the vegan package (Oksanen, 2011). The significance of fitted variables was confirmed with 999 permutation tests. Nine geographical and land use vectors were selected from measured variables (Appendix II) as coarse environmental filters of the fish community structure (Januchowski-Hartley *et al.*, 2011). Fish community structure was also fitted with fish abundance data to select the most important biological constraints. From the important biological constraints, species occurred > 5% of the site were considered as potential biological filters for clustering habitat sites. Selected environmental (geo-land use) and biological (fish species) vectors were compiled into one data set. Fish community ordination was constrained (CCA), using the final bioenvironmental data set, to assess the explainable overall variation of community structure. The variance inflation factor (VIF) was computed for finally selected bioenvironmental filters (of the fish community structure) to assess the co-linearity among the particular vectors and factors were identified as independent vectors if their VIF is < 10 (Graham, 2003; Oksanen, 2011).

To distinguish the habitat clusters that show dissimilarity of the selected bioenvironmental factors, I selected “affinity propagation” method, which uses real value data and clusters data sets on randomly selected representative exemplars by iteratively refining the similarities between objects to form final clusters (Frey & Dueck, 2007). Affinity

propagation approach was used because of its advantages; automatic choice of the number of clusters, suitability for non-metric spaces and efficiency, over alternative k-means clustering approach (Dale & Fortin, 2014; Yu & Dan, 1994).

In affinity propagation, the similarity between pairs of sites is measured using the real value data of selected factors. Pairwise comparisons of the factor variables are performed iteratively to refine the data subsets showing the optimal group dissimilarities. Each subset of objects (e.g. sampling sites) is based on an ‘exemplar’ selected as the centre of the particular subset, through a series of similarity refinements between objects (Frey & Dueck, 2007). Similarities between objects are compared in two-dimensional ordinations based on the Euclidean distances computed on given pairs of factor variables. Each data point in an ordination is matched with initially selected and refined random exemplars and grouped (clustered) with the most corresponding exemplar (Frey & Dueck, 2007; Wang *et al.*, 2007; Yu & Dan, 1994). The structure of hierarchical clusters emerges through affinity propagation can be illustrated in a heat map. A heat map shows the objects of a data matrix in rows and columns of colour coded squares. Each pixel in the heat map is shaded according to the degree of similarity (high similarity is represented by lighter pixels) between row and column numbers corresponding to the original objects (Wilkinson & Friendly, 2009).

Diversity, similarity and variability of affinity clusters was assessed using the community measures used to compare forested and pasture sites in previous chapters, to observe the community differences across the clusters of sites. I computed the average number of species in a stream (α diversity) and the total number of species (γ diversity) of each cluster. The biological and ecological similarity was compared among clusters, through ANOSIM (Analysis of Similarity) test (Clarke & Warwick, 2001; Oksanen, 2012). ANOSIM distinguishes the compositional difference in the fish community among importance of factor predictors in partitioning beta diversity (Anderson & Walsh, 2013). Global R values quantify

the degree of separation between selected groups of sites (e.g. clusters) using average rank dissimilarities and the number of samples in a data matrix (Clarke & Warwick, 2001; Oksanen, 2011).

Within each cluster, variability was assessed in terms of the group homogeneities (Oksanen, 2011). Group homogeneities were computed by partitioning similarities of fish abundances between sites into the clusters. In the NMDS ordination of fish, the distance from sites to the centroid of given a cluster was used to quantify the degree of variability within a group of samples. The average distance between the cluster centroid and a sampling site (within a cluster multivariate dispersion) was calculated by dividing the sum of squared inter-point (sites are represented as points in an ordination) distances, by the number of points (Anderson, 2001). Finally, important descriptors of fish communities across the partitioned clusters of sites were assessed by regression analyses between diversity measures (e.g. variability) and average values of potential environmental drivers within clusters. Statistical software used in this study include PRIMER 6.0, AP Cluster and Vegan packages in R (version 3.0.2) (Clarke & Warwick, 2001; Oksanen, 2011).

Results

Fifteen fish species were reported from the 96 study sites (listed in Table 2.1 of chapter 2). Among them, only five species significantly fitted with the fish ordination (CCA) after 999 permutations, however, two species: Inanga (*Galaxias maculatus*) and Cran's bully (*Gobiomorphus basalis*) occurred in less than 5% of the study sites. Longfin eels (*Anguilla dieffenbachia*), koaro (*Galaxias brevipinnis*), redfin bullies (*Gobiomorphus huttoni*) and common bullies (*Gobiomorphus cotidianus*) were found from more than 5% of the 96 sites and showed a significant correlation to the fish CCA ordination.

Table 5.1: Fitted correlation (CCA) and co-linearity (VIF) values of selected environmental and biological filters of the fish community structure between 96 streams in Taranaki.

Factor	Axis correlations		r ²	Significance	VIF
	CA1	CA2			
Environmental					
Easting	-0.22	-0.98	0.20	0.022 *	3.85
Northing	-0.03	1.00	0.13	0.094	1.73
Altitude	-1.00	-0.09	0.23	0.007 **	5.30
Native forest©	-0.72	0.70	0.31	0.002 **	6.14
Farming©	0.40	-0.92	0.41	0.001 ***	5.75
Native forest (US)	-0.75	0.66	0.30	0.003 **	4065.59
Pasture (US)	0.75	-0.66	0.29	0.003 **	3922.69
Proximal Land use	0.82	-0.57	0.35	0.001 ***	3.93
Biological					
Longfin eel	0.28	-0.96	0.17	0.048 *	1.43
Koaro	-0.92	0.40	0.50	0.001 ***	1.48
Redfin bully	0.78	0.62	0.63	0.001 ***	1.92
Common bully	0.28	-0.96	0.41	0.001 ***	1.94

US= upstream, © = catchment

‘*’ $P < 0.05$, ‘**’ $P < 0.01$, ‘***’ $P < 0.001$

Within the (nine) selected geo-land use vectors, the most influential factor was catchment land use, characterised by farming ($r^2 = 0.41$) and native forest ($r^2 = 0.31$). Dichotomy in proximal land use (forest and pasture) was also significantly important ($r^2 = 0.35$). Additionally, upstream land use, easting and altitude fitted less significantly with the fish ordination (Fig. 5.2, Fig. 5.3 and Table 5.1).

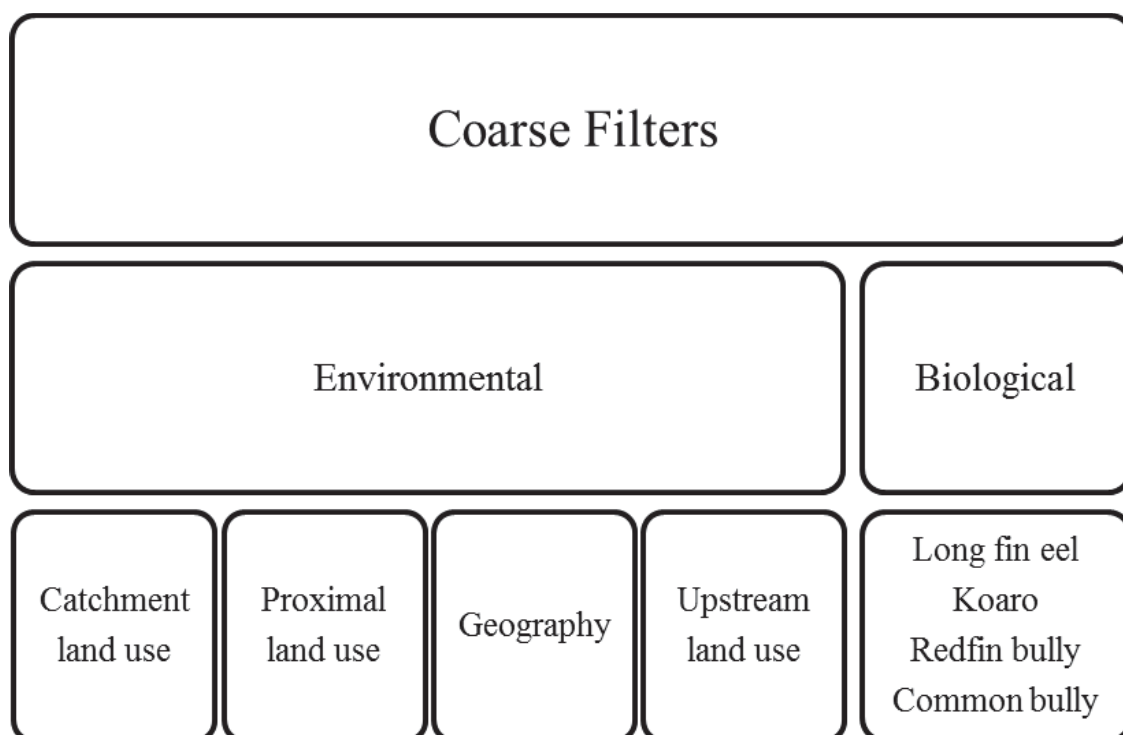


Fig. 5.2 Classification of bioenvironmental filters used for clustering 96 streams considered in this study.

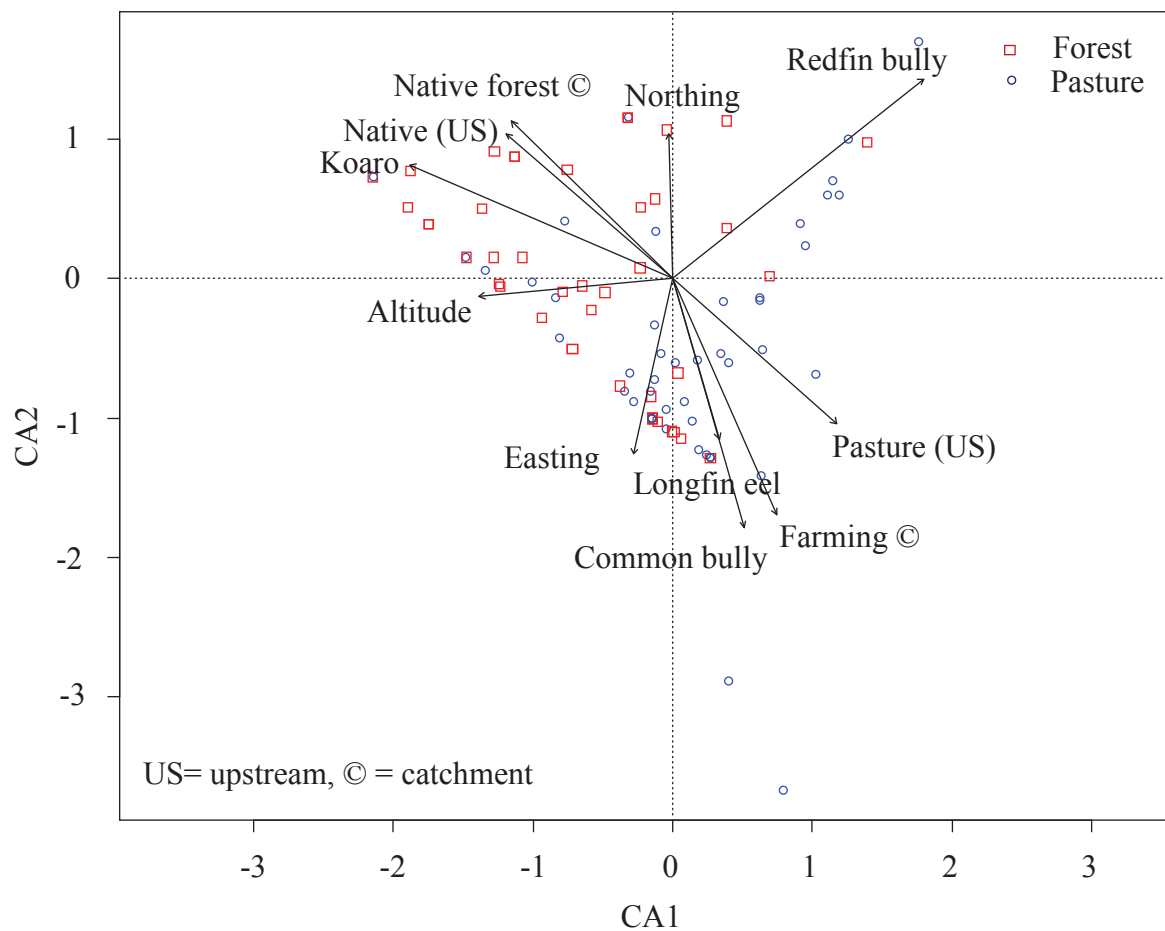


Fig. 5.3 Ordination diagram for the first two axes of Constrained Correspondence Analysis (CCA) of fish abundances in 96 Taranaki streams, fitted with selected bioenvironmental filters.

The affinity propagation procedure suggested an optimal number of seven clusters, after 137 iterations of similarity refinements between 96 sites, based on the selected bioenvironmental factors (Fig. 5.4). However, the number of sites in a cluster varied from 5 to 25, and most of the clusters included both forested and pastoral streams (Fig. 5.5). Further, the site clusters did not geographically overlap with each other.



Fig. 5.4 Two-dimensional similarity ordinations of 96 Taranaki sites (based on Euclidean distances between selected vectors) used in affinity propagation method to distinguish site clusters.

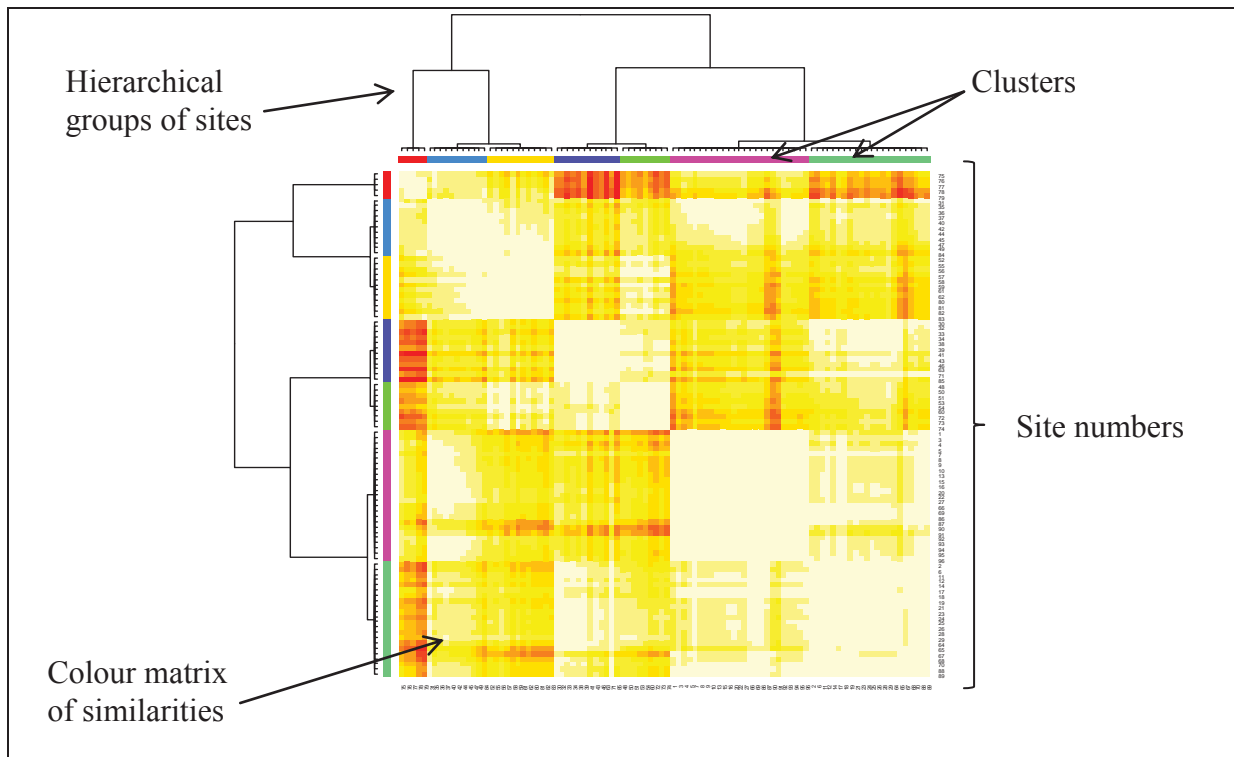


Fig. 5.5 Heatmap of 96 Taranaki sites, represented by colour coded similarities (lighter pixels shows high similarity) in selected bioenvironmental filters.

The sampling sites within each cluster represented several (neighbouring) major catchments of the region. For instance, all the sampling sites of cluster zone 1 were from Oakura River, Timaru Stream or their tributaries, while zone 2 consisted of sites within Waiwhakaiho River and Waiongana River systems. However, streams flowing through intensely farmed areas in the west of the ring plain (zone 7) clustered into a separate zone from their upstream sites in zone 4 (Table 5.2, Fig. 5.6).

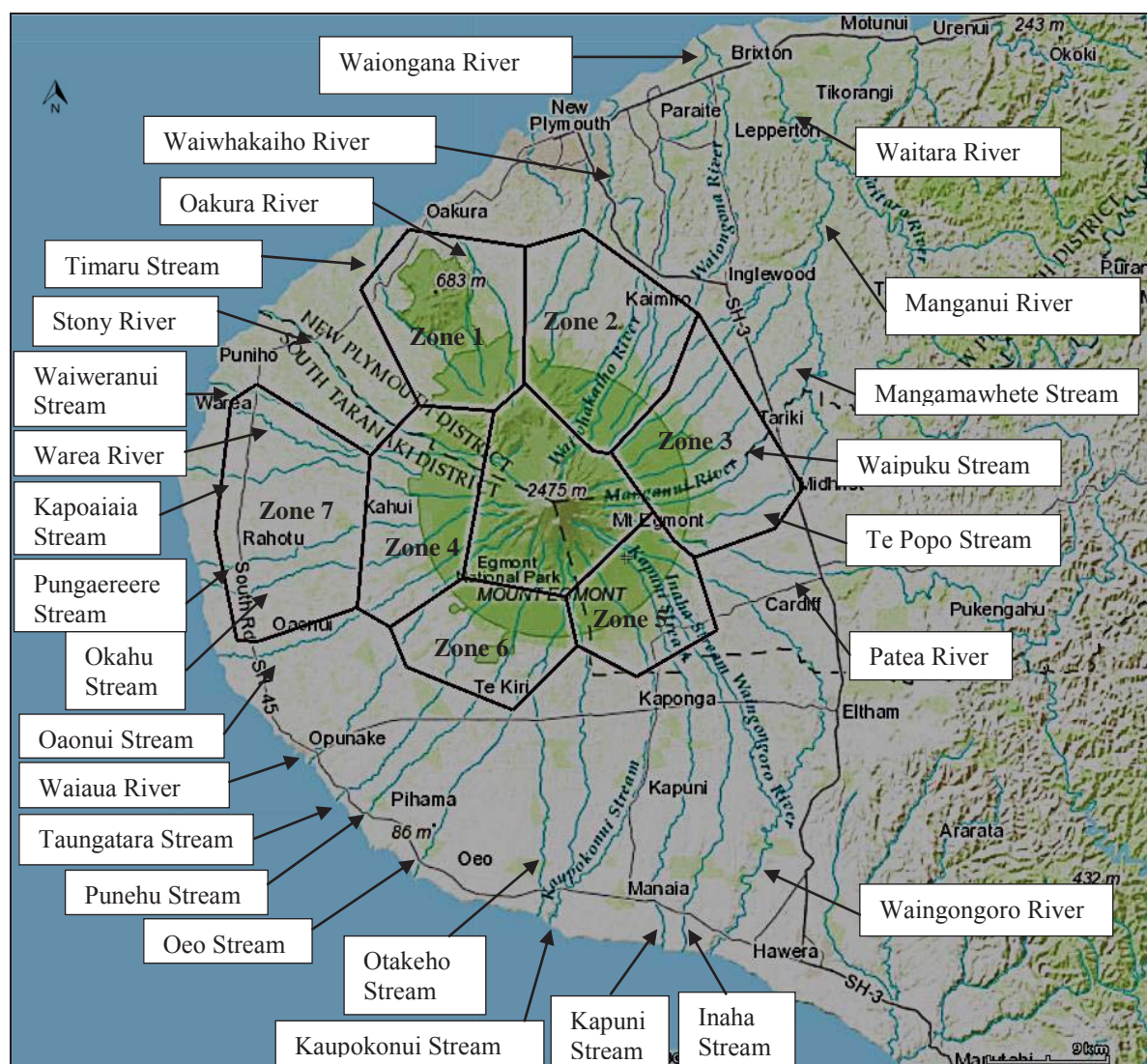


Fig. 5.6 Map of Taranaki streams showing different zones of site clusters referring to neighbouring major catchments.

Table 5.2: Major catchments represented different zones of site clusters in Taranaki.

Zone	Major Catchments
1	Oakura River, Timaru Stream
2	Waiwhakaiho River, Waiongana River
3	Manganui River, Patea River
4	Oaonui Stream, Okahu Stream, Pungaereere Stream, Kapoiaia Stream, Warea River, Waiweranui Stream, Stony River
5	Waingongoro River, Inaha Stream, Kapuni Stream, Kaupokonui Stream
6	Otakeho Stream, Oeo Stream, Punehu Stream, Taungatara Stream, Waiaua River
7	Waiweranui Stream, Warea River, Kapoiaia Stream, Pungaereere Stream, Okahu Stream

Table 5.3: Zonal diversity (γ), local diversity (α), similarity and variability (β) of Taranaki streams partitioned into 7 clusters (zones), using affinity propagation method.

Zone (cluster)	Zonal diversity (total number of species)	Local diversity (number of species/ stream)	Within zone Similarity (Bray-Curtis)	Variability (Average group multivariate dispersion)
1	9	2.92	34.92	0.935
2	12	2.64	31.61	1.033
3	10	2.42	28.40	1.105
4	7	2.00	21.67	1.288
5	7	2.22	37.75	0.885
6	6	2.50	35.01	0.968
7	5	3.00	51.99	0.537

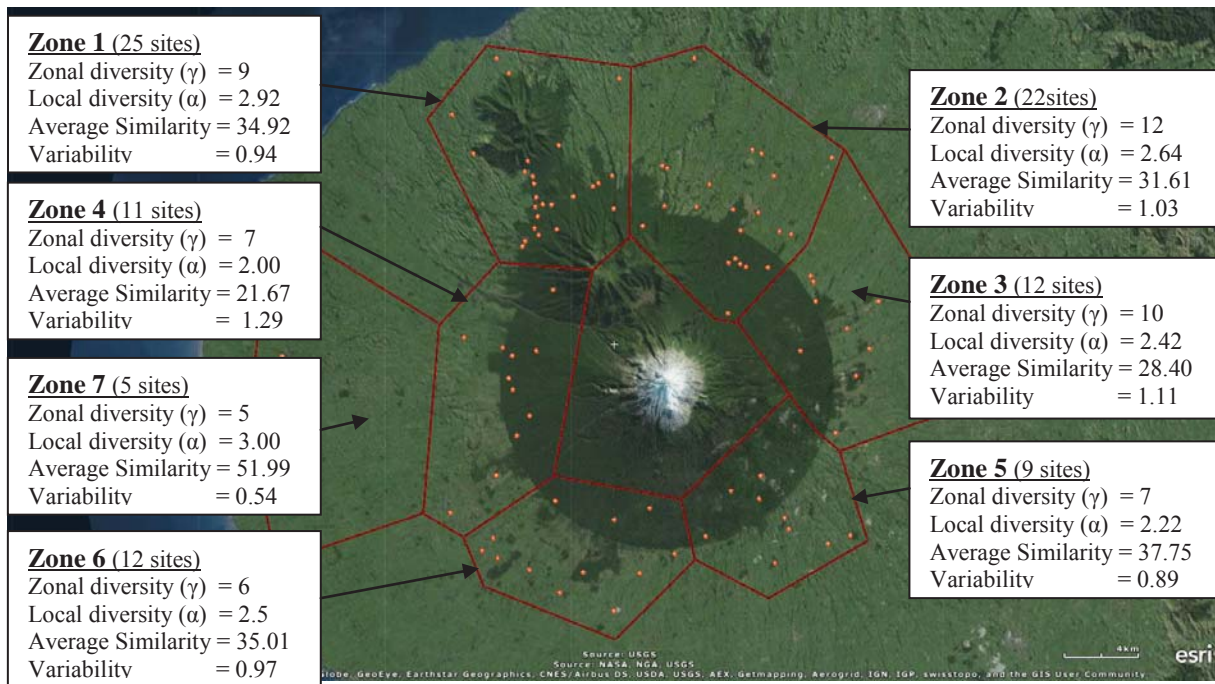


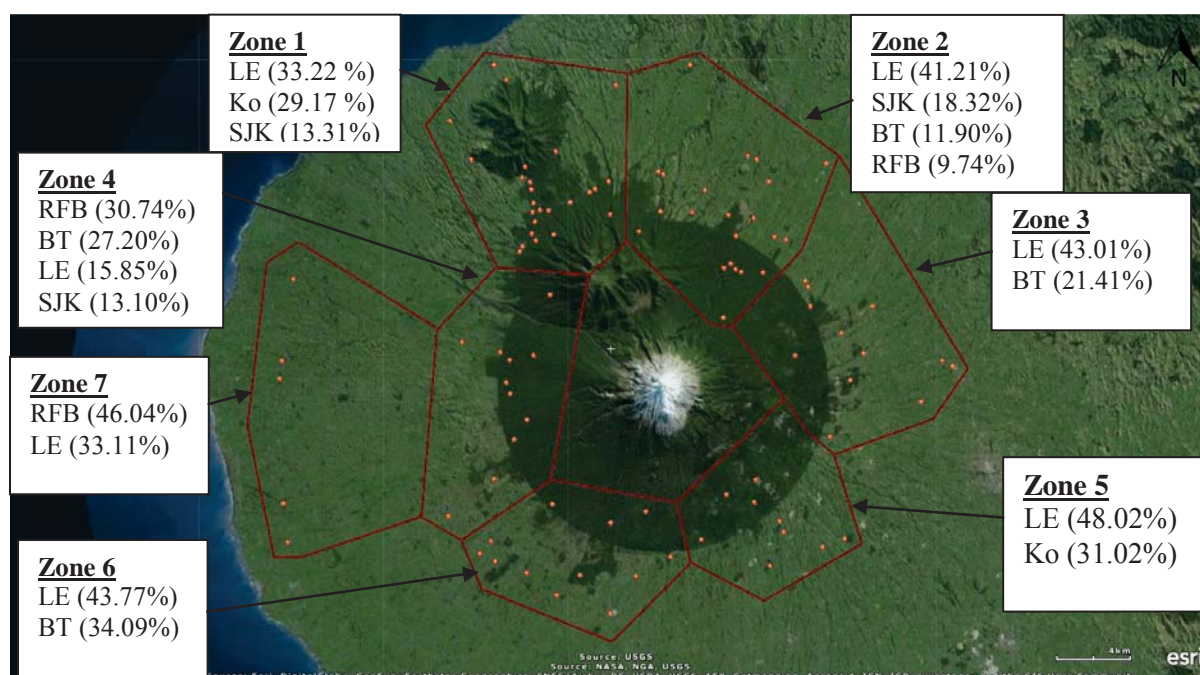
Fig. 5.7 Map of study sites, showing zonal diversity (γ), local diversity (α), similarity and variability (β) of Taranaki streams partitioned into seven clusters (zones), using affinity propagation method.

The number of sites of a zone did not significantly affect the diversity measures; zonal diversity ($r^2 = 0.54$, $P > 0.05$), local diversity ($r^2 = 0.04$, $P > 0.05$), similarity ($r^2 = 0.22$, $P > 0.05$), and variability ($r^2 = 0.01$, $P > 0.05$) considered in this study. The zonal diversity (γ) did not influence local diversity (α) or β diversity (similarity and variability) within a cluster. Although the local diversity (α) explained over 50% of the variations in β diversity measures, the relationships between α and β diversities were not significant. However, similarity and variability had a very strong relationship across the zones (Fig. 5.7, Table 5.3 and Table 5.4).

Table 5.4: Explainable variations of the trends (r^2) between freshwater fish diversity measures across seven clusters of 96 sites in Taranaki.

‘***’ = $P < 0.001$

Local diversity (α)	0.00		
Similarity (β)	0.23	0.52	
Variability (β)	0.21	0.55	0.99***
	Zonal diversity (γ)	Local diversity (α)	Similarity (β)



(LE = Longfin eel, Ko = Koaro, SJK = Shortjaw kokopu, BT = Brown trout and RFB = Redfin bully)

Fig. 5.8 Within zone relative abundances of the most abundant fish species in each cluster zone of 96 Taranaki streams considered in this study.

According to the results of ANOSIM test, the overall biological similarity weakly but significantly differed between the zones (Global $R = 0.12$, $P < 0.05$). Nevertheless, ecological dissimilarities were rather clear between the zones, when geo-land use vectors (Table 5.1) were included in the analysis of similarity (Global $R = 0.33$, $P < 0.01$), and between zone

ecological dissimilarity was significant over 95% of the pairwise comparisons (Table 5.5). Longfin eels dominated the community composition of five zones, while Redfin bullies showed the highest relative abundance in zone 4 and 7 in the west of Mount Taranaki. Shortjaw kokopu were mostly abundant across the northern and western zones (Zone 1, 2 and 4), while koaro was mainly rich in zone 1 and 5. Further, compared to eels and bullies, the galaxiids were very limited in their abundance and occurrence over the seven zones in Taranaki (Fig. 5.8 and 5.10).

Table 5.5: Global R-values of ANOSIM test for the pairwise comparisons of the bioenvironmental similarity, between the seven zones of Taranaki streams.

							‘*’ = $P < 0.05$
							‘***’ = $P < 0.01$
							‘****’ = $P < 0.001$
Zone 2	0.14****						
Zone 3	0.40****	0.14*					
Zone 4	0.20*	0.25**	0.23****				
Zone 5	0.48****	0.36****	0.04	0.22**			
Zone 6	0.37****	0.39****	0.32****	0.1*	0.23**		
Zone 7	0.79****	0.94****	0.67****	0.61**	0.81**	0.89****	
	Zone 1	Zone 2	Zone 3	Zone 4	Zone 5	Zone 6	

Catchment land use or native vegetation of riparian cover was not predictable from the average elevation of a zone considered in this study (Catchment farming; $r^2 = 0.00$, $P = 0.94$, Riparian native cover; $r^2 = 0.30$, $P = 0.12$). Further, the average elevation of a zone did not significantly explain the variation of any of the diversities measured in this analysis.

Upstream pasture did not affect the zonal diversity ($r^2 = 0.15$, $P = 0.39$) or average local diversity ($r^2 = 0.27$, $P = 0.24$). However, both similarity and variability were influenced

by upstream pasture across the zones ($r^2 = 0.62$, $P < 0.05$). Further, increasing upstream pasture negatively affected the inter-site variability of fish in Taranaki (Fig. 5.9).

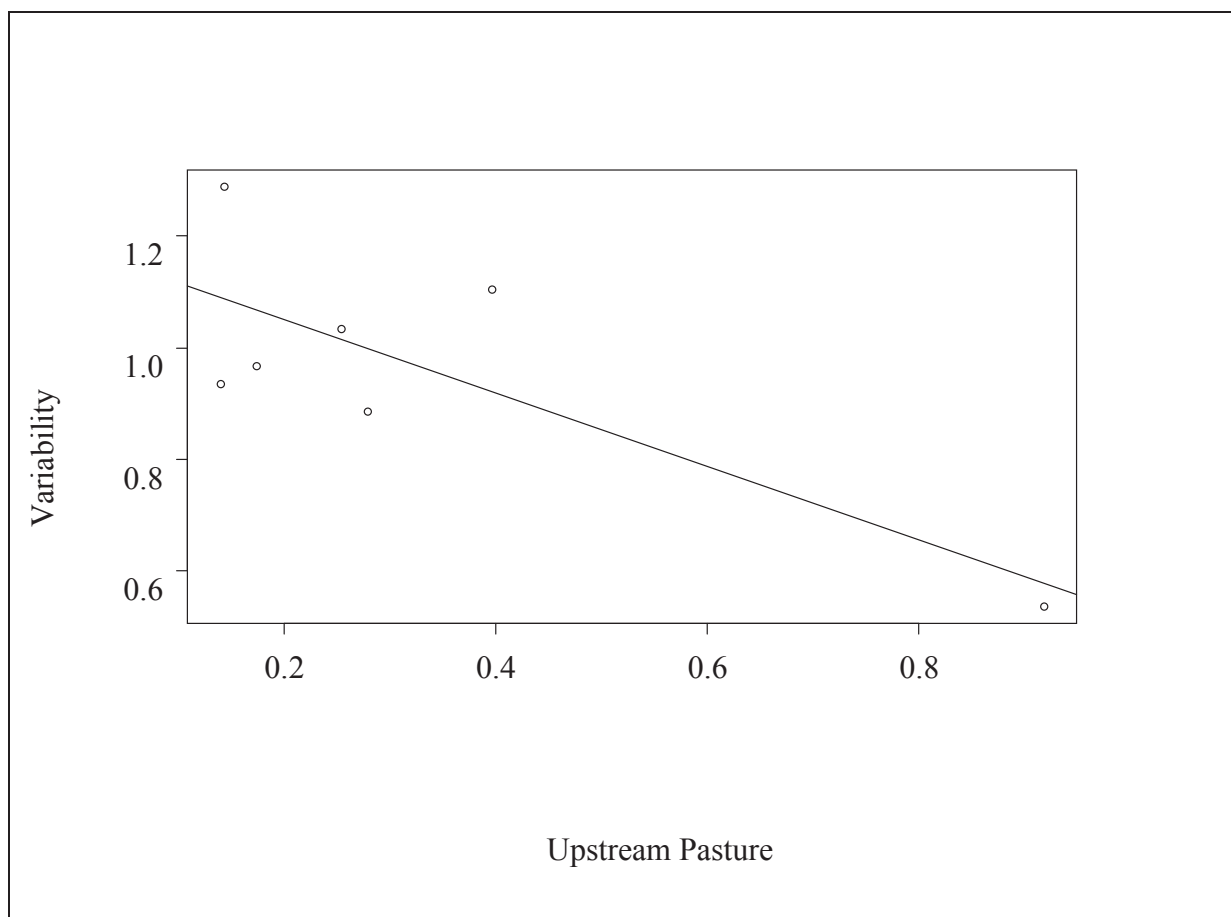


Fig. 5.9 Regression plot between biological variability (mean distance to the group centroid) and upstream pasture across the seven clusters of streams analysed in this study.

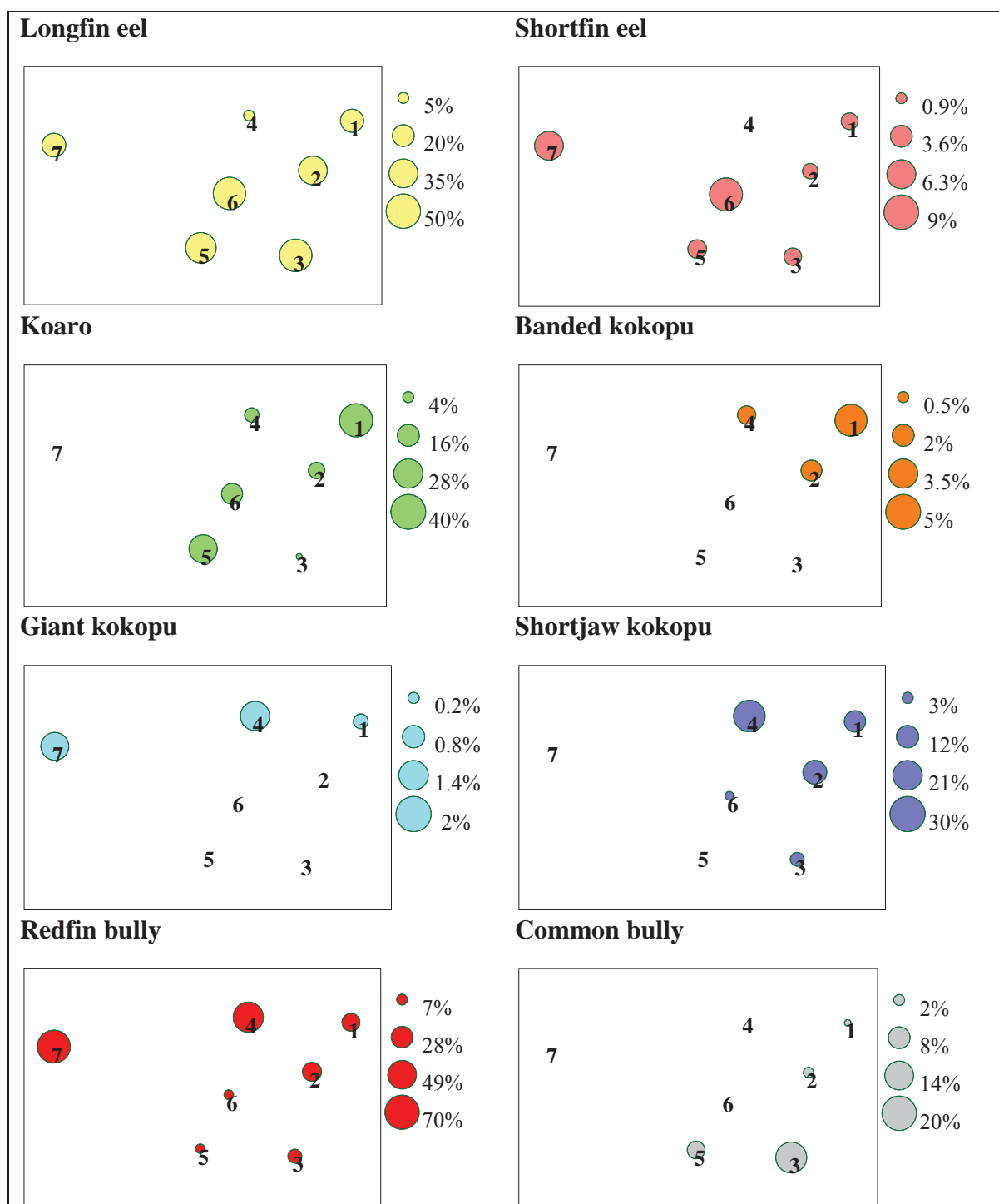


Fig. 5.10 Two-dimensional ordinations (Euclidean distance on selected bioenvironmental filters listed in Table 5.1) between the seven zones (stress = 0.01), superimposed with within group relative abundances of selected fish species in 96 Taranaki streams (sizes of bubbles are proportionate to relative abundances shown in the legends).

Discussion

The outcome of the study challenges traditional conservation measures based on the protected forest at the hub of Taranaki because the most of ecologically dissimilar groups of study sites did not represent the contrast in the proximal land use pattern, most cluster zones included sites from both forest and pasture. In this study, the seven groups of zones, however represented neighbouring catchments rather than the proximal land use pattern. Hence, the study results deeply question the ecological validity of recognising fish communities in terms of proximal land use pattern in general.

As an alternative to traditional conservation designs, ecologists have proposed biodiversity management schemes, based on biology, behaviour, dispersal patterns and the ecology of organisms (Chantepie *et al.*, 2011; Noble *et al.*, 2007). Nevertheless, biodiversity conservation would be rather fruitful, if adjoining human interference is also included in ecological management plans, mainly because it is highly unlikely to resolve the conservation crisis without addressing potential human-environment conflict within a given ecosystem (Grimm *et al.*, 2008). In contemporary biodiversity management, redesigning of nearly a century old conservation areas plays an important role, to implement updated management measures and to enhance the public involvement in conservation. This study suggests one alternative approach: catchment based design for the management of Taranaki freshwater fish community.

Catchment-based management is rather rational to the degree that distribution limitation of fish between different rivers is concerned. Rosenzweig (1995) described that a single river can be considered as district territory of freshwater fish because of the limited lateral movement of fish between different catchments. Although a high proportion of New Zealand riverine fish species have a marine phase in their life cycles, it is more likely for a

given fish population to distribute over adjacent catchments than over different catchments well separated from each other (McDowall, 2010). Even if, the land use pattern is highly influential of freshwater communities in New Zealand (Quinn *et al.*, 1997), the results of this study shows that ecological similarity within a region is not entirely and essentially partitioned by the land use. Nonetheless, it is important to consider the land use pattern as a partitioning factor within an area of similar biogeographic composition.

I further suggest reviewing the popular community assessments based on α diversity indices in conservation, because the study results show that inventory measures such as species diversity are not very explainable of the upstream land use effect among the streams. However, the homogenising effect of upstream pasture was clearly shown by the declining variability across the seven habitat zones of this study. Besides, the particular homogenising effect of land use was independent of the gradients of topography, and species diversity along the groups of sites. Hence, the results of this chapter provide useful insights for understanding the mechanism of community change with the land use impact in Taranaki.

The next best approach would be recognising the most abundant and rare species within sub-regions, in order to restore their habitats, particularly out of the protected areas. Sub-regional habitat restoration will be effective if individual populations of rare species are extensively analysed across time and space. Restoration of natural habitats may be further enhanced by understanding complex cross-community links between different trophic levels and their affinity to the abiotic environment. Nonetheless, it is important to review zonal community patterns within a particular time frame, in order to capture the temporal change in the status of population dynamics of vulnerable species and their local ecology.

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Chapter Six

Concluding Remarks

In this project, I discussed how geo-environmental factors and human impact influence the spatial ecology of stream fish and invertebrates. Beta diversity (Legendre *et al.*, 2005) provided a range of measures reflecting the composition, structure and variability, to analyse stream community patterns against their most important drivers. Although human impact assessments of freshwater communities are common, there has been a limited focus on the relative importance of anthropogenic stressors to natural geo-environmental gradients in control of community patterns (Graham, 2003). For instance, studies often assume the New Zealand running waters partition a general division between upstream-forested habitats and downstream-pasture; hence, the elevation and forest cover shares a great extent of co-linearity (Mosley, 1981; Quinn *et al.*, 1997; Winterbourn, 1991). The results of Chapter 2 showed how altitude and land use interact in driving the regional dispersal pattern of fish in Taranaki streams. Therefore, mere land use change from forest to agriculture is unlikely to explain the entire community structure, unless the interrelationship between geography and land use is carefully analysed, beyond any prior assumption (Erős, 2007).

Confounding multiple effects from the environment and human interference are difficult to resolve, and may counter-drive the spatial patterns of a given community (Smith *et al.*, 2009). In Taranaki streams, the increasing upstream average slope restricted upstream dispersion of fish species (Chapter 2: Fig 2.3 and 2.6), while increased downstream pressure from agriculture homogenised the communities between low elevation rivers (Chapter 5: Fig. 5.9). In addition, previous studies have shown the negative effect of impoundments on the fish distribution in lowland rivers (Joy, 1999; Joy & Death, 2001), and the tendency for the isolation of local communities consist of diadromous species, which may eventually

transform into non-migratory populations (McDowall, 1990). The synergy of all above manmade and natural phenomena is potentially driving the stream fish species from population decline to local extinction of habitat specialist and/or low dispersing taxa, in particular.

According to the results of Chapter 2, Taranaki fish communities are characterised by their biogeographic pattern throughout most of the land-use strata from natural forest to rivers in intensely farmed areas (Fig. 2.7). Therefore, their spatial variability is likely to despite the compositional change of fish communities between the land use classes. In other words, communities are likely to be equally variable between two adjacent land use classes, although there could be the difference in the community composition. However, with accumulating upstream effect from agriculture, species less tolerant to pollution may be absent from the lowland rivers, and communities between particular lowland habitats (heavily impacted by agriculture) would ultimately lose the natural variability as a result.

The possibility of bottom-up control from stream invertebrates was supported by the results of concordance study in this project. The relevance of invertebrates was well observed for fish community pattern between the streams. Stream fish and invertebrate communities within a limited space may have independent spatial patterns (Fig. 4.3) mainly because of the disparity in mobility (between fish and invertebrates) and very low species diversity of fish within a stream. Therefore, the bottom-up effects across environment via trophic levels would not be clearly observable in small-forested streams where the fish communities are less diverse. However, the abundance of fish would negatively affect the population density of invertebrates (via feeding), within a limited space in a stream (Flecker & Townsend, 1994). Further, it was clear that invertebrates show higher affinity to the local environment rather than fish community does between the same habitats (Fig. 4.6). Thus for the spatial patterns, control of the physical environment is very likely to persist through the

food web, unto top consumer communities such as fish in this study. The bottom-up control of spatial patterns might have been more clearly observed through the stream food web, if primary producer communities were also included in the study. However, the project design was rather focused on the diversities of fish and invertebrates, related to their physical environment.

Studies often describe spatial patterns of freshwater communities with respect to the effect of agriculture, but rarely discuss how agricultural impacts would functionally affect the particular communities (Hall *et al.*, 2001; Meador & Goldstein, 2003). Stream ecologists have shown that the control of riverine communities is a complimentary result of several factors, including geographical distance, environmental control, habitat selection, population structure, biological interactions and spatial dependency (Nakagawa, 2014; Planque *et al.*, 2011). Throughout this research, I discussed how geography, environmental control and the trophic relationship of stream communities would interact in different spatial limits ranging from a stream to the wider ecosystem, in Taranaki. The overall results of this study showed that the influence of geography (northing, easting and altitude) is a prominent factor of both fish (Chapter 2 and 5) and invertebrates (Chapter 3: Fig. 3.6 and Chapter 4: Table 4.4) in undisturbed habitats, and likely to persist at least in control of fish even at the presence of agricultural disturbances. However, the control of geography may differ between fish and invertebrates, because the two communities clearly vary in their life cycle strategies and dispersal mechanisms (Cowie, 1980; Delucchi, 1989; McIntosh & McDowall, 2004). For instance, this study shows that fish are attached to elevation classes throughout the region, whereas invertebrate community structure in forested habitats is correlated with the geographical distance between the streams.

The concordance study showed that agriculture weakens the mutual control of the fish and invertebrate community structures between streams. This suggests the likely negative

influence of agriculture on the interaction between trophic levels of stream food web. The particular effect is insightful of understanding the importance of biological interactions that characterise the spatial ecology of stream communities. If agriculture alters the food web of stream communities, traditional bio-environmental data matching approach (generally rely on one taxonomic group) would be less effective in explaining the impact of land use change on the spatial ecology and ecosystem functions in riverine communities. Therefore, it will be more informative if future studies focus on the stream food web structure in order to find helpful answers for restoring ecological health in agricultural streams.

Results of the fourth chapter showed that the environmental distance controls the spatial pattern of stream communities over forested and adjacent pasture sites (Table 4.3). When stream communities are observed among a mixture of forested and pasture sites, invertebrate community structure was driven by several factors, including the differences in stream morphology, organic carbon sources, riparian cover, habitat climate and geographical distance. However, between the streams within the forest, riparian cover, organic input and climatic factors are likely to share a greater within-group similarity, hence varying habitat type, water quality and stream morphology would be more influential for forested stream invertebrate communities characterised by diverse mayfly and stonefly taxa. When streams flow through the pasture, the environmental condition between streams generally become less variable, mainly because of the removal of the natural canopy, high algal growth, the influx of nutrients and sediments. Consequently, the agricultural streams become less suitable for the invertebrates highly dependent on allochthonous organic matter, unpolluted water and riparian cover for their survival and completion of the life cycle; therefore rather generalist and nutrient tolerant caddisflies and chironomids replace taxa such as mayflies and stoneflies (Quinn, 2000). Because of the dominance of habitat and feeding generalist taxa, the link between stream environment and invertebrate communities drops significantly between the

streams within the pasture. Geographical and environmental control of the forested invertebrates (mayflies and stoneflies) is further explainable by moderate or weak flying ability, short adult life span, limited terrestrial dispersal and hemimetabolous development, in contrast to relatively long living (generally several weeks to months), high dispersing, holometabolous trichopterans which dominate agricultural streams (Collier & Winterbourn, 2000; Delucchi, 1989). The limited control of geo-environmental factors may result in a homogenous community structure within a pasture stream. However, relatively high species diversity in trichopterans and dipterans is likely to lead the inter-site variability of agricultural streams to be as high as that of invertebrates among the forested sites.

Spatial patterns and variability of fish within a New Zealand stream is difficult to measure because of low diversity, small fish counts, and limited effectiveness of available sampling methods (Hayes *et al.*, 1989; Minns, 1990). Besides, fish operate in a greater spatial extent (compared to the stream invertebrates). Thus, the difference spatial dependency between fish and invertebrates remains a limitation for community-wide comparisons within small stream sub-sets (Nakagawa, 2014). Between streams within 15 study sites, fish community structure was more concordant with that of invertebrates than the environmental distance (Chapter 4: Table 4.2 and 4.3). The strong spatial link between the two communities explains fish community patterns would be rather reflective of stream food web structure, compared to the direct control of the environment, at least within a given landscape. However, regional level land use and geographical gradients are useful in ecosystem-scale management and conservation of fish, because of their life cycle strategies span over large spatial extents.

In Chapter 5, I questioned the validity of partitioning stream habitats in terms of the proximal land use pattern (based on agriculture in particular), as an approach to the management and conservation of stream fish communities within a region. Despite the

popular conditioning of conservation/management units based on land use practice, organisms persevere beyond so-called biodiversity protection boundaries (Januchowski-Hartley *et al.*, 2011). Lateral and horizontal movements are vital for the continuation of wild communities to maintain their life cycle strategies and to overcome natural disturbances such as droughts (James *et al.*, 2008; McIntosh & McDowall, 2004). Therefore, biodiversity conservation should expand beyond self-imposed demarcations (e.g. boundaries of protected areas) and is to be redesigned according to ensure the sustainability of natural communities (Chantepie *et al.*, 2011; Chester & Robson, 2013). For the conservation of a given wild population, it would be pragmatic to include exploited landscapes alongside the protected areas, to develop robust monitoring plans and implement effective conservation measures. In this study, I attempted to suggest a catchment based management design for Taranaki freshwater fish communities, in light of the overall understanding gathered from the project.

The overall study had several limitations in data collection. Different researchers have collected the historical data (from Freshwater fish database), and different sampling strengths may affect the quality of a data set. However, I used a thorough standardisation method (Wisconsin double standardisation) to enhance the ordination quality (Oksanen, 2008). If the regional scale data were collected by one person/team within the same time, the personal biases and temporal variation of species occurrence would have been minimised (in finer scale studies (Chapter 3 and 4), all data were collected by one person to avoid this bias). In addition, environmental data should have been collected across a much wider range, to improve explanatory analyses. Moreover, with controlled extensive primary data collection the research design would have been tailored to answer more questions in regional scale spatial patterns of fish: for instance, ‘are fish communities more variable between streams in the interface between forest and pasture?’ In contrast, usage of secondary data also has several advantages in quantitative research, including cost-effectiveness, better time

management provided and the ability to gather a large data set for a reasonable exploration (Hox & Boeije, 2005). The low flow effect would also have affected the species counts because the sampling was conducted in summer. In addition, cryptic nature of native fish limits their exposure to samplers, and underestimates of rare species is common in freshwater fish monitoring. I compared species occurrence information from literature (McDowall, 2000) with the data collected for this study, and included historical data where it was practical.

Nevertheless this project has shown that beta diversity greatly improves our understanding of how confounding geo-land use factors interact (complement) in controlling the regional spatial patterns of stream fish and how land use change can potentially affect trophic links in the stream food web. Therefore future management and conservation efforts could be improved with this understanding to sustain not only biological diversity but also the functionality of our stream ecosystems.

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Appendices

Appendix I

Site coordinates, proximal land use, presence/ absence of brown trout, reference object ID and New Zealand reach numbers in FENZ (Freshwater Ecosystems of New Zealand) database, for 96 streams of Taranaki, surveyed in 2012.

Site ID	Easting	Northing	Object ID	NZ Reach	Land use	Presence/absence of trout
TK1	2592928	6229683	94157	6003933	Pasture	Absent
TK2	2607538	6224853	95430	6004587	Pasture	Present
TK3	2595774	6225477	95288	6004681	Pasture	Absent
TK4	2590813	6225063	95381	6004693	Pasture	Absent
TK5	2593963	6224598	95472	6004872	Forest	Absent
TK6	2608243	6223548	95614	6004886	Pasture	Present
TK7	2598913	6221778	96200	6004896	Forest	Absent
TK8	2593783	6223953	95480	6004941	Forest	Absent
TK9	2594248	6223698	95582	6004979	Forest	Present
TK10	2594308	6223278	95582	6004979	Forest	Present
TK11	2605858	6221643	95891	6005065	Forest	Present
TK12	2603728	6221823	95919	6005127	Pasture	Absent
TK13	2594428	6222468	95749	6005133	Forest	Present
TK14	2607313	6221433	95920	6005274	Pasture	Present
TK15	2594368	6221958	95821	6005189	Forest	Absent
TK16	2595313	6222048	95926	6005301	Forest	Absent
TK17	2600593	6220758	96119	6005210	Forest	Absent
TK18	2601868	6221898	95838	6005211	Forest	Absent
TK19	2608528	6220338	96147	6005304	Pasture	Present
TK20	2595598	6220623	96029	6005402	Forest	Absent
TK21	2606278	6220413	96056	6005479	Pasture	Present
TK22	2594548	6220293	95978	6005507	Forest	Absent
TK23	2606218	6218478	96493	6005511	Forest	Absent
TK24	2607823	6218268	96602	6005635	Forest	Absent
TK25	2605543	6218568	96457	6005642	Forest	Present
TK26	2605933	6218808	96270	6005643	Forest	Absent
TK27	2593753	6219963	96264	6005711	Forest	Absent
TK28	2606548	6218313	96493	6005511	Forest	Absent
TK29	2605468	6215658	97140	6005873	Forest	Present
TK30	2610448	6217398	96563	6005952	Pasture	Absent
TK31	2595343	6217128	96676	6006017	Forest	Absent

Cont....

Appendix I cont....

TK32	2610568	6216273	96728	6006122	Pasture	Present
TK33	2614228	6216213	96754	6006172	Pasture	Present
TK34	2612353	6214668	97029	6006506	Forest	Absent
TK35	2590153	6214428	97043	6006687	Pasture	Present
TK36	2592388	6213813	97311	6006781	Pasture	Present
TK37	2594323	6213618	97207	6006725	Forest	Absent
TK38	2613643	6213483	97173	6006726	Pasture	Present
TK39	2609638	6213423	97193	6006747	Forest	Absent
TK40	2592943	6213348	97311	6006781	Forest	Present
TK41	2618233	6212988	97334	6006938	Pasture	Absent
TK42	2592718	6212043	97540	6007108	Forest	Absent
TK43	2612848	6211923	97413	6007066	Pasture	Present
TK44	2592943	6211383	97540	6007108	Forest	Absent
TK45	2593903	6209853	97952	6007361	Pasture	Present
TK46	2611618	6208653	98097	6007743	Forest	Present
TK47	2593138	6208728	94371	6007700	Pasture	Present
TK48	2607238	6206223	94420	6008077	Pasture	Absent
TK49	2591938	6206433	98512	6008122	Pasture	Absent
TK50	2605513	6205383	99075	6008129	Pasture	Absent
TK51	2607133	6204903	99061	6008198	Forest	Absent
TK52	2598733	6203808	99348	6008378	Pasture	Present
TK53	2608603	6203778	99184	6008295	Pasture	Present
TK54	2604013	6202773	99508	6008527	Forest	Present
TK55	2595328	6204933	98850	6008451	Forest	Present
TK56	2600788	6204438	98905	6008444	Forest	Present
TK57	2602198	6201783	99762	6008666	Pasture	Present
TK58	2591713	6202818	99258	6008696	Pasture	Present
TK59	2600173	6200688	99958	6008893	Pasture	Present
TK60	2608003	6201183	99541	6009114	Pasture	Present
TK61	2593798	6200958	99570	6009149	Pasture	Present
TK62	2596888	6200778	99609	6009308	Forest	Present
TK63	2616990	6210614	97696	6007366	Pasture	Present
TK64	2609200	6220158	96216	6005636	Pasture	Present
TK65	2611614	6224564	95455	6004651	Pasture	Absent
TK66	2597727	6223075	96237	6004585	Forest	Absent
TK67	2603712	6230416	94014	6003923	Pasture	Absent
TK68	2607017	6225084	94273	6004577	Pasture	Absent
TK69	2598053	6223256	96237	6004585	Forest	Absent

Cont...

Appendix I cont...

TK70	2604491	6223085	95919	6005127	Pasture	Absent
TK71	2610294	6217736	96478	6006021	Pasture	Absent
TK72	2612392	6202701	99207	6008849	Pasture	Absent
TK73	2608837	6203137	99171	6008475	Pasture	Absent
TK74	2611104	6202246	99436	6008811	Pasture	Absent
TK75	2580330	6218191	96399	6005914	Pasture	Present
TK76	2579477	6212397	97433	6006973	Pasture	Absent
TK77	2579619	6213440	97232	6006803	Forest	Present
TK78	2579625	6205139	98923	6008282	Pasture	Absent
TK79	2579848	6202885	99174	6008835	Pasture	Absent
TK80	2591955	6201642	99448	6009089	Pasture	Absent
TK81	2595532	6199636	99836	6009157	Pasture	Present
TK82	2598647	6198542	99958	6008893	Pasture	Absent
TK83	2591065	6202099	99258	6008696	Pasture	Present
TK84	2589247	6204318	98858	6008450	Pasture	Absent
TK85	2618835	6212665	97358	6007010	Pasture	Absent
TK86	2598849	6223688	96200	6004896	Forest	Absent
TK87	2599343	6229289	94945	6003987	Forest	Absent
TK88	2601781	6224228	95657	6004756	Forest	Absent
TK89	2602057	6224087	95657	6004756	Pasture	Absent
TK90	2592223	6230557	94774	6003820	Pasture	Present
TK91	2589600	6227318	95119	6004609	Pasture	Present
TK92	2593594	6219662	96264	6005711	Forest	Absent
TK93	2594308	6220705	95978	6005507	Forest	Absent
TK94	2594501	6221378	96082	6005408	Forest	Absent
TK95	2594801	6222070	94605	6005300	Forest	Absent
TK96	2596596	6222500	95740	6005239	Forest	Absent

Appendix II

The list of environmental variables considered in the study and the sources of data collection for each variable.

Variable/ Category	Observed/ Measured	Source of Data	
		*FENZ	*NZFFD
Site Variables			
Easting		√	
Northing		√	
Altitude (m)		√	
Inland Distance (km)		√	
Habitat Variables			
Width (m)	√		√
Depth (m)	√		√
Segment slope		√	
% Still	√		√
% Back water	√		√
% Pool	√		√
% Run	√		√
% Riffle	√		√
% Rapid	√		√
% Cascade	√		√
% Mud	√		√
% Sand	√		√
% Fine gravel	√		√
% Coarse gravel	√		√
% Cobble	√		√
% Boulder	√		√
% Bed Rock	√		√
% Over hanging vegetation	√		√
% Debris jam	√		√
% Macrophyte cover	√		√

Cont...

Appendix II cont....

% Moss	√		√
% Shade of the stream before human impact		√	
Nitrogen concentration in water		√	
% Over hanging vegetation	√		√
Catchment Variables			
% Native forest		√	√
% Exotic forest			√
% Farming/ Pasture		√	√
% Scrub			√
% Swamp land			√
% Alpine			√
% Other			√
Upstream Calcium		√	
Upstream Hardness		√	
Upstream Phosphorus		√	
Upstream slope		√	
Riparian Variables			
% Native tree cover	√	√	
% Exotic tress cover	√		
% Pasture	√		
% Grass tussock	√		√
% Scrub willow	√		√
% Raupo or flax	√		√
% Other	√		√

* FENZ = Freshwater Ecosystems of New Zealand, NZFFD= New Zealand Freshwater Fish Database, GIS= Geographic Information System

													Appendix III cont...		
<i>Megaleptoperla</i> spp.	0	96	1	3	0	0	0	0	3	36	0	4	5	1	1
<i>Zelandoperla</i> spp.	4	4	13	33	86	0	2	59	15	18	0	2	0	2	1
<i>Zelandobius</i> spp.	19	0	0	42	78	0	0	4	4	12	0	25	8	28	16
<i>Acroperla</i> spp.	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
<i>Taraperla</i> spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Spaniocerca</i> spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
<i>Archichauliodes</i> spp.	0	35	20	10	7	43	13	41	1	14	47	0	0	0	0
<i>Orthopsyche</i> spp.	19	1	0	3	6	0	0	0	10	0	0	5	0	23	14
<i>Aoteapsyche</i> spp.	0	0	170	0	10	138	303	198	18	65	514	1	1	6	2
<i>Oxyethira</i> spp.	0	1	0	0	0	1	46	191	8	0	25	0	0	0	0
<i>Paroxyethira</i> spp.	0	0	0	0	0	0	0	2	1	1	0	0	0	0	0
<i>Psilochorema</i> spp.	0	0	3	0	0	0	0	6	13	0	0	1	0	0	0
<i>Hydrochorema</i> spp.	0	6	14	0	0	0	0	0	0	0	0	0	0	1	0
<i>Hydrobiosis</i> spp.	0	91	6	8	9	13	27	27	15	0	36	1	0	0	0
<i>Costachorema</i> spp.	0	1	0	0	0	0	0	1	3	0	0	0	0	0	0
<i>Edpercivalia</i> spp.	0	0	7	1	1	0	0	0	13	0	0	2	0	3	0
<i>Neurochorema</i> spp.	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0
<i>Polyplectropus</i> spp.	5	0	0	0	0	0	0	0	0	0	0	3	3	0	0
<i>Plectrocnemia</i> spp.	0	0	0	3	3	5	0	0	27	0	0	1	63	11	25
<i>Hydrobiosella</i> spp.	3	1	0	0	8	0	0	0	13	10	0	9	0	4	5
<i>Cryptobiosella</i> spp.	0	0	0	0	4	0	0	0	0	0	0	0	0	2	2
<i>Helicopsyche</i> spp.	1	8	0	6	0	0	0	0	0	3	0	0	0	0	0
<i>Pycnocentroides</i> spp.	0	29	39	2	73	558	1197	122	3	13	1269	0	0	0	0
<i>Beraeoptera roria</i>	0	28	6	5	4	9	4	23	14	224	11	0	2	0	0
<i>Confluens</i> spp.	0	5	0	1	0	0	0	3	0	0	0	3	0	0	0
<i>Pycnocentria</i> spp.	17	18	4	7	4	250	230	10	2	9	89	0	0	0	4
<i>Olinga</i> spp.	0	7	0	1	2	0	2	0	7	138	0	3	0	1	0
<i>Zelolessica</i> spp.	0	1	0	0	0	0	0	1	0	1	0	0	0	0	1
<i>Triplectides</i> spp.	0	0	0	0	0	0	0	3	0	0	1	0	0	0	0
<i>Pycnocentrella</i> spp.	0	0	0	0	0	0	0	0	0	3	0	2	1	1	1
<i>Triplectidina</i> spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
Staphylinidae	0	2	1	0	0	0	3	1	0	0	2	0	1	0	5
Elmidae	10	689	660	28	31	216	444	78	607	199	68	10	14	1	12
Hydraenidae	2	17	0	7	2	0	0	1	17	0	0	1	0	8	0
Scirtidae	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0
Ptilodactylidae	1	32	0	0	0	0	0	0	0	0	0	0	0	12	1
<i>Northdixa</i> spp.	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Simuliidae	0	0	0	0	0	2	0	10	0	0	9	0	0	0	0
<i>Paraxida</i> spp.	0	0	0	0	0	0	0	3	0	0	0	0	0	1	0
Cont...															

Appendix III cont....														
<i>Mischoderus</i> spp.	0	0	0	0	0	1	0	8	1	0	0	0	0	0
Eriopterini	1	4	11	2	1	0	0	0	3	4	0	0	0	0
<i>Paralimnophila</i> spp.	0	2	0	0	0	0	1	0	0	0	0	0	3	0
Psychodidae	0	1	0	0	0	0	0	0	0	0	0	0	0	0
<i>Aphrophila</i> spp.	2	244	22	1	22	1	133	37	22	89	94	1	0	2
<i>Limonia</i> spp.	0	0	0	0	0	0	0	0	0	0	0	2	0	0
<i>Molophilus</i> spp.	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Tanypodinae	13	0	75	9	67	0	37	13	84	13	0	10	33	16
<i>Maoridiamesa</i> spp.	0	17	34	2	2	5	357	11	0	0	13	0	0	0
Orthcladiinae	3	517	266	10	0	32	294	168	0	0	725	14	0	0
<i>Polypedilum</i> spp.	0	0	434	10	0	7	310	0	0	0	1	2	0	0
<i>Chironomus</i> spp.	0	4	11	0	0	0	21	0	0	0	6	0	0	0
Tanistarsini	0	13	13	0	0	10	28	0	0	0	130	0	0	0
<i>Potamopyrgus</i> spp.	0	14	2	0	0	63	234	6	0	0	297	0	0	1
<i>Physa</i> spp.	0	0	0	0	0	0	1	0	0	0	0	0	0	0
<i>Ferrissia</i> spp.	0	0	0	0	0	0	0	0	0	0	7	0	0	0

Appendix IV

Streams in Taranaki surveyed in 2013.

Site	Stream	Easting	Northing	Altitude (m)	Proximal Land use
T1	Cold creek	2595457	6199592	244.7	Pasture
T2	Clod creek	2597582	6202710	390.0	Forest
T3	Waiaua Stream	2591014	6201982	211.1	Pasture
T4	Momona Stream	2597756	6223041	361.7	Forest
T5	Timaru Stream	2594509	6221370	228.2	Forest
T6	Okahu Stream	2579571	6205137	35.4	Pasture
T7	Oanui Stream	2589322	6204333	214.0	Pasture
T8	Te Henui Stream	2603798	6230307	132.6	Pasture
T9	Waiwhakaiho River	2607875	6222941	326.8	Pasture
T10	Kaupokonui Stream	2608134	6200908	385.0	Pasture
T11	Kapoaiaia Stream	2579580	6213443	62.9	Pasture
T12	Nugtokomi Stream	2598896	6223757	347.5	Forest
T13	Waiongana Stream	2606312	6217237	590.0	Forest
T14	Waiwhakaiho River (tributary 1)	2606780	6219864	462.0	Forest
T12	Waiwhakaiho River (tributary 2)	2606384	6219915	455.0	Forest

