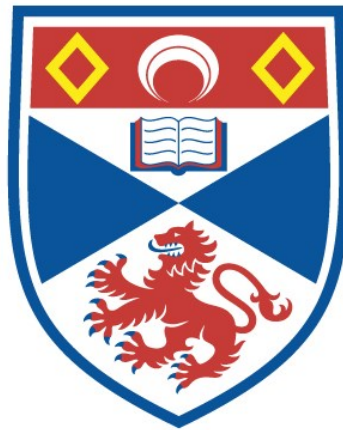


Biological diversity of freshwater fishes in small streams in peninsular Malaysia

Amirrudin Bin Ahmad

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Abstract

Peninsular Malaysia has a diverse flora and fauna, much of which is yet to be documented. The freshwater fishes are one important group that have received little attention. Accordingly, the overarching goal of my study is to investigate the pattern of species richness and analyse the community composition and assemblage structure of fishes in the small streams in Peninsular Malaysia. Small stream habitats appeared to be particularly important repositories of fish biodiversity in this region thus obtaining a reliable census of species occurring in such habitats is critical for conservation and management of biodiversity. Although samplings were far from completed, these habitats support a great variety of species with more than 100 species were recorded from fifty streams sampled in this study. A few are extremely rare with restricted distribution and can thus be considered important in biodiversity conservation of the Peninsular Malaysian ichthyofauna. Human-influenced modification of lowland, headwater stream habitats in Peninsular Malaysia is common and often exemplified by the creation of pools in stretches of rapids and riffles. However, it was not possible to separate pristine and disturbed sites which contained almost identical for species diversity. These findings suggest that local habitat modification does not necessarily cause a decrease in freshwater fish diversity, with only minor negative consequences for other community variables recorded in this study, and therefore raise interesting issues regarding conservation. That said it remains premature to conclude that small stream fishes are insensitive to disturbance and thus their potential utility as bioindicators of disturbance-influenced community changes remain to be confirmed. The maintenance practises being applied to small streams modified for recreational usage were not imposing detectable negative consequences, at least across the sites sampled in this study. The rich diversity of tropical stream environments is the result of both within-habitat (alpha) diversity and between-habitat (beta) diversity. The results showed that there was substantial beta diversity particularly amongst sites that are geographically separated from one another. On the contrary, the lowest beta diversity values were portrayed by contiguous sites. Many fishes exhibited discontinuous patterns of distribution and were considered to be rare while only a handful were widely distributed and abundant. Ordination based on the relative resemblance of fish communities to one another support the existence of two distinct ichthyogeographic divisions in Peninsular Malaysia. It was possible to assign the species recorded to all seven of Rabinowitz's categories of rarity, with at least 10 restricted to a single stream and locally scarce, although not all of these could be described as hyper-endemic. It is recommended that a sizeable augmentation of the existing protected areas is needed to safeguard Malaysia's exceptionally diverse stream-dwelling fauna of which fishes are simply the most well-known inhabitants. Conservation managers should therefore place particular emphasis on small streams since localities in close proximity to one another can exhibit surprisingly high beta diversity, meaning that partial or small-scale habitat protection may prove insufficient.

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Finally, I thank Khamsah – my wife and friend, my sons – Aidil, Fizzy and Bob, my parents and immediate families for their unconditional supports I received during this study.

TERIMA KASIH

In loving memories..

my father,

Ahmad B. Ismail

(1st June 1937 - 19th December 2011)

who taught me how to fish,

and

my brother,

Shaharudin B. Ahmad

(25th February 1980 – 1st January 2008)

who help me fishing..

Rest in peace..

Declarations

I, Amirrudin Bin Ahmad, hereby certify that this thesis, which is approximately 50 000 words in length, has been written by me, that it is the record of work carried out by me and that it has not been submitted in any previous application for a higher degree.

I was admitted as a research student in February, 2008 and as a candidate for the degree of PhD in February, 2008; the higher study for which this is a record was carried out in the University of St Andrews between 2008 and 2011.

I, Amirrudin Bin Ahmad, received assistance in the writing of this thesis in respect of language and grammar, which was provided by Mr. Matthew J. Ford.

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CHAPTER 1

INTRODUCTION

1.1 Freshwater fish diversity in the tropics

Among vertebrates, fishes are the most abundant organisms in terms of number of species (Nelson, 2006; Eschmeyer *et al.*, 2010; Magurran *et al.*, 2011). By late 2006 the total number of fish species worldwide was estimated to be *c.* 28 400 (Nelson, 2006), while Eschmeyer *et al.* (2010) listed 32 042 valid taxa of which 15 170 were obligate freshwater inhabitants. Such a considerable increase in numbers is not necessarily surprising given contemporary advances in systematic techniques which have aided in-depth analysis of both historic and recent field collections. For example, molecular studies incorporating procedures such as DNA barcoding or phylogenetic analyses have proven valuable in demarcating closely related populations occurring within a given species or uncovering new and cryptic taxa (Ardura *et al.*, 2010; Eschmeyer *et al.*, 2010).

Since the last glacial period freshwater fishes have demonstrated a remarkable ability to colonise recently-created inland environments whether fluvial or limnetic (Nelson, 2006). Despite the relatively limited availability of freshwater habitat compared with marine (constituting less than 1% of the world's water) the number of exclusively freshwater fish species comprises *c.* 47% of the global total (see Eschmeyer *et al.*, 2010). The greatest number of species are native to tropical Africa with additional centres of abundance in the Amazon watershed and Southeast Asia. Among these highly biodiverse regions the precise number endemic to the latter is not known, but the estimation of *c.* 1 200 given by Rainboth (1996) should be considered exceptionally conservative. Around 500 species have been reported from Cambodia alone (Rainboth, 1996) but there may in fact be 1 200 or more (Rainboth, 1996). Similarly Dudgeon (2003) hypothesised the presence of 930+ species from 87 families in Indochina and more than 700 species in China. Thailand is thought to contain in excess of 800 species (Magurran *et al.*, 2011), Indonesia more than 1 000 (Kottelat & Whitten, 1996) and Peninsular Malaysia approximately 300 (Magurran *et al.*, 2011). Moreover, existing inventories of Southeast Asian freshwater fishes are far from exhaustive (Dudgeon, 2003) with new records and discoveries reported on a frequent basis.

The precise distribution and occurrence of freshwater fishes is influenced by a complex synergy of environmental and biological factors. For example, tropical monsoons are

thought to play an important role in terms of ecological productivity since they facilitate seasonal fluctuations in planktonic communities which form the basis of food webs within typical aquatic environments (Dudgeon, 2003). In addition, fish species often exhibit a preference for a generalised habitat-type, *e.g.* lakes, swamps, rivers, streams, *etc.* and some may even be adapted and therefore restricted to a specific biotope (Nelson, 2006). In small streams, for example, some fishes are stenotypic inhabitants of riffles and rapids (Kottelat & Whitten, 1996) whereas others are found only in less turbulent stretches. Certain species may have evolved to exploit particular substrate-types (*e.g.*, loaches – families Balitoridae, Cobitidae and Nemacheilidae) or extreme water chemistry such as that encountered in acidic peat swamps (*e.g.*, *Paedocypris* spp.; family Cyprinidae, see Kottelat *et al.* 2006; Britz & Kottelat, 2008).

Nelson (2006) recognised 515 families of living fishes with Cyprinidae, Gobiidae and Cichlidae the most species rich. Among these, members of the former are obligate freshwater dwellers completing their entire lifecycle in the absence of a marine stage and comprising the most speciose family of freshwater fishes known to tropical Asia with *c.* 147 genera recognised to date (Dudgeon, 2003). However, despite this well-recognised taxonomic diversity, there exists little published information regarding the ecology, localised richness and community structure of tropical freshwater fishes in general.

1.2 Freshwater fish diversity in Peninsular Malaysia

Although variation in the nature of flora and fauna inhabiting Peninsular Malaysia has long been recognised, much of the region's biological diversity remains to be documented. Freshwater fish ecology, in particular, has received little attention to date and there is little information pertaining to fish species richness or distribution across the region. There are a wide range of freshwater habitat-types to be found in Peninsular Malaysia, many of which contains heterogeneous fish assemblages, but small streams in the lowlands and foot hills appear to be particularly rich repositories of biodiversity (*e.g.*, Zakaria-Ismail, 1987; 1993; Ahmad & Samat, 2005).

Small lowland and foothill streams are environmentally heterogeneous with many microhabitats. This provides opportunities for ecological specialisation but also means that

dispersal may be limited. Within fluvial ecosystems such ‘habitat specialists’ may be restricted to a single cataract or series of rapids, a handful of headwater streams or a specific tributary drainage within a larger river system, (Kottelat & Whitten, 1996). The variable structure of substrata and riparian zones in small streams also tends to give rise to a large range of shelter, food sources and spawning sites. For these reasons, these stream systems can support a diverse ichthyofauna, with samples collected from stretches of just a few hundred metres in length yielding comparatively high numbers of species relative to other types of freshwater habitat (Kottelat & Whitten, 1996). Peninsular Malaysia has many small streams and a rich freshwater fish fauna, but fish species diversity has never been comprehensively investigated and analyses of community structure are also largely absent.

During the first half of the 20th century publications tended to focus on formal descriptions of recently-discovered taxa, new occurrence records for existing species (see de Beaufort, 1933; Herre, 1936; 1940a; 1940b) or general discussion of species distribution, habitats and ecology (Herre & Myers, 1937; Hora, 1941a; 1941b; Hora & Gupta, 1941; Smedley, 1931; Tweedie, 1936; 1940; 1950; 1952). More recently, interest has shifted to aquaculture-based studies (Ismail & Zain, 1978; Khalil, 1982; Aizam *et al.*, 1983; Ali, 1988) of species with high economic values (Aizam *et al.*, 1983; Ali, 1988; 1993; Law, 1986; Saidin *et al.*, 1988), meaning that, to date, the native ichthyofauna has received only modest attention (Ali & Kathergany, 1987; Fernando, 1980; Khoo *et al.*, 1987; Mohsin, 1980; Mohsin & Ambak, 1982).

The last couple of decades have seen renewed interest in the study of taxonomy to the extent that more than 50 additional native freshwater fish species have been recorded, more than half of which are new to science (Lim & Tan, 2002). With the exception of Singapore, the freshwater fishes of Peninsular Malaysia are arguably better known than those of neighbouring countries, and accordingly are the most extensively-studied in the Southeastern Asia subregion. Based on studies published to date the number of freshwater fish species recorded in Peninsular Malaysia is approximately 300 (Figure 1.1).

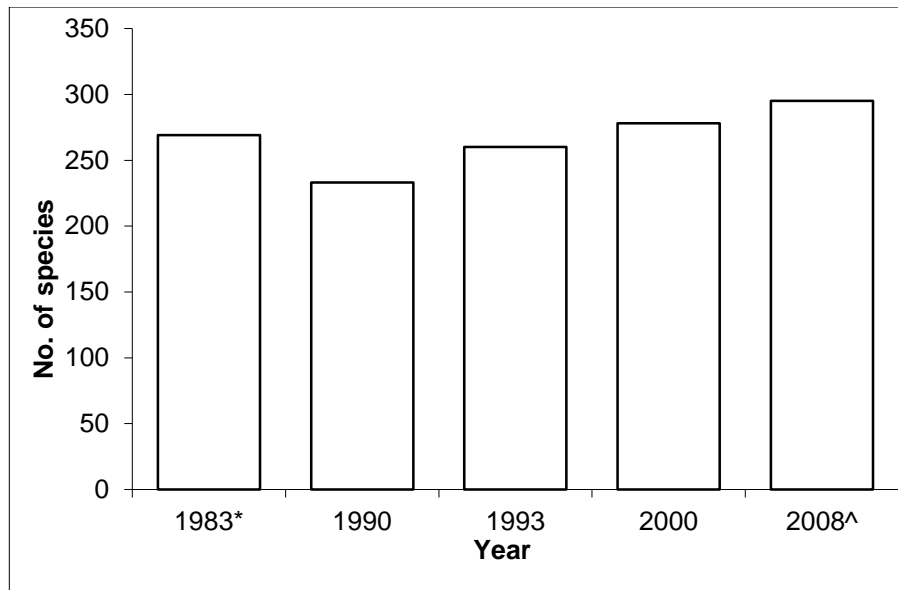


Figure 1.1. Total number of freshwater fish species known to occur in Peninsular Malaysia since 1983. Note:
 * The inflated number of species in 1983 probably included introduced species and synonyms.
 ^The total number of species includes unpublished data collated by the author of this thesis.
 (Source: 1983* – Mohsin & Ambak, 1983; 1990 – cited in Lim *et al.*, 1993; 1993 – Lim *et al.*, 1993; 2000 – Lim & Tan, 2002; 2008 – compilation of A. B. Ahmad; *unpublished*).

1.3 The importance of freshwater fishes

Freshwater fishes are utilised as a source of protein across the globe with the scale of commercial fishing and aquaculture projects expanding tremendously in recent decades. During this period the focus of global fisheries has shifted from large piscivorous to small non-piscivorous species, a change with the potential to cause major disruption to the structure of marine food webs. FAO (2000) estimated that the inland fisheries and aquaculture industry contributes around 15% of total global employment. Unfortunately, bad practice and overexploitation of these resources is well-documented throughout the Asian region in particular (Smith *et al.*, 2005).

Much of this exploitation is simply for subsistence consumption although this is less important in Peninsular Malaysia. However in some South and Southeast Asian countries such as Cambodia, Laos and Bangladesh artisanal fisheries are the dominant model and contribute a significant proportion of the animal protein consumed, particularly in rural communities (Smith *et al.*, 2005). A similar pattern can be observed in certain African countries such as Malawi where inland lake fisheries yield a total annual catch of 35-40

000 t annually (Lowe-McConnell, 2003), that is largely dependent on the number of small zooplanktivorous fishes.

Freshwater fisheries are also exploited beyond the economic context having been utilised as environmental bioindicators, biological control agents, in the ornamental aquarium trade and for recreational sport fishing. Magurran *et al.* (2011) recently highlighted the potential of using 'fish' data to better understand patterns of biological diversity in terms of relative commonness and rarity plus other related attributes. Fishes are particularly appropriate subjects in this respect because they are able to colonise and flourish in an extraordinary range of habitat-types, often occur in great abundance, with correspondent biomass, and exhibit unique growth and behaviour throughout their life histories. Such variable characteristics thus offer myriad possibilities in terms of examining fish community structure.

Although freshwater fishes are diverse (Magurran, 2009) and abundant organisms only a handful of previous studies have concentrated on applying field data to more fully understand the biological diversity concept or increase knowledge of species commonness and rarity. The idea has been explored using other animal groups though while a great deal of biodiversity research has also been focussed on plants (*e.g.*, Colwell & Coddington, 1994; Chazdon *et al.*, 1998; Brose *et al.*, 2003). Among animals, invertebrates are the most commonly-studied group (*e.g.*, Toti *et al.*, 2000; Foggo *et al.*, 2003) whereas among vertebrates mammals (*e.g.*, Vazquez & Gaston, 2004) and birds are far more popular subjects than fishes (*e.g.*, Walther & Martin, 2001; Herzog *et al.*, 2002). Research into commonness and rarity has also tended to involve large mammals (Arita *et al.*, 1990; Dobson & Yu, 1993; Yu & Dobson, 2000; Baquero & Telleria, 2001; Vazquez & Gaston, 2004) and birds (*e.g.*, Goerck 1997; Gaston, 1998; Jankowski & Rabenold, 2007) although Magurran (2009) highlighted that fishes have the potential to be similarly useful. This study therefore attempts to explore and analyse species diversity while examining patterns of commonness and rarity within small stream fish communities in the megadiverse region of tropical Peninsular Malaysia, and to discuss these findings in terms of native species conservation and management.

1.4 Human impact on fish diversity

According to Lévêque (1997) fish community assemblages can be influenced by biotic processes such as predator-prey interactions (Mittlebach *et al.*, 1995; Olsen *et al.*, 1995; Williams *et al.*, 2003), while Grossman *et al.* (1998) reason that abiotic factors, such as artificial disturbance or variation in environmental conditions (Godinho *et al.*, 2000; Ostrand & Wilde, 2002), also play a key role in structuring fish assemblages. Over the past few decades, for example, the increasing spread of invasive, non-native species introduced by humans has resulted in reductions in species richness across the globe (Garcia-Berthou & Moreno-Amich, 2000; Cambray, 2003). Magurran (2009) highlighted one of the threats to freshwater fishes as exotic species besides fragmentation of natural habitat, habitat degradation and over-collecting of native fishes for ornamental fish trade.

The specific impact(s) that biological invasion events exert on native species richness are poorly-understood in the case of Peninsular Malaysia, whereas anthropologically-driven disturbances are known to result in detrimental consequences for both terrestrial and aquatic environments (Zakaria-Ismail, 1994; Kottelat *et al.*, 2006; Magurran, 2009). Excessive conversion of land for intensive cultivation and other agricultural activities has been largely held to blame for the disappearance of ancient peat swamp forest, and thus loss of habitat for many unique and endemic fish species, across much of Southeast Asia (Kottelat *et al.*, 2006). In many areas such macro-scale alteration of land brings about severe adverse repercussions for local stream ecosystems (Matson *et al.*, 1997; Iwata *et al.*, 2003).

Rapid changes in species' ranges and abundance are often driven by environmental degradation (Mace *et al.*, 2010) which is itself commonly induced by human activity (Magurran & Dornelas, 2010). Various studies have shown that such 'impacted' ecosystems are generally less species-rich (*e.g.*, Karr *et al.*, 1985; Townsend *et al.*, 1997; Ganasan & Hughes, 1998; Collares-Pereira & Cowx, 2004). While habitat degradation is typically associated with reduced species richness, this is not invariably the case. Connell (1978) proposed a concept known as the "intermediate disturbance hypothesis" which proposes that species diversity is maximised at an intermediate level of disturbance. A number of later studies have contributed supporting evidence for the theory (Molino &

Sabatier, 2001; Bertrand *et al.*, 2004) although a handful, *e.g.*, McCabe & Gotelli (2000) fail to do so.

Zakaria-Ismail (1994) demonstrated that intensive land development has caused native fish populations of the Gombak River to decline by over 40% in little more than 20 years since the previous official survey (Bishop, 1973). Despite normally functioning as important refugia to many organisms, small streams tend to make only a minor contribution to inland fisheries, and though in many cases they may have been utilised for long-term recreational purposes by local residents, little attention has focussed on better understanding the potential effects these prolonged, small-scale disruptions may exact upon the resident ichthyofauna.

Commercial logging has been identified as a major driver of anthropogenic environmental change in Peninsular Malaysia, but despite the fact that freshwater environments are known to be impacted the precise effect for fluvial ecosystems and its fauna remain poorly understood (Martin-Smith, 1998a). Evidence collated from streams in Sabah, Borneo suggests that stream fish communities in areas of un-logged forest were slightly dissimilar from those inhabiting recently-logged zones although only a single species was recorded from the pristine river and not the logged area (Martin-Smith, 1998b). No comparable surveys exist for streams of Peninsular Malaysia despite the enduring permanence of small-scale stream habitat modification throughout the region which have traditionally been ignored by park and conservation managers alike.

1.5 Ichthyogeographic division of small stream fishes

The native ichthyofauna of Peninsular Malaysia is broadly similar to that of mainland Asia, possessing a shared Sundaic origin. This close biogeographic relationship has been recognised by numerous previous researchers (*e.g.*, Mohsin & Ambak, 1983; Zakaria-Ismail, 1994; Yap, 2002) and the region can be considered both species rich and highly diverse (Lowe-McConnell, 1987; Kottelat *et al.*, 1993; Martin-Smith, 1998a) in terms of freshwater fishes. Such heterogeneity is typical in the tropics and attributable to a combination of factors including climatic stability, the presence of diverse habitats, high competition and predation plus high primary productivity (Lowe-McConnell, 1987;

Magurran, 2009). Other processes such as colonisation and extinction may also prove important under certain circumstances (Ricklefs, 1987).

Natural geomorphological barriers that prevent cross-colonisation by fish or other organisms are generally thought to be important in defining biogeographical patterns. Peninsular Malaysia has historically been divided into two widely-recognised ichthyogeographic regions, namely the northern and southern ‘crescent’ areas (see Figure 1 in Johnson, 1967: 724), based on freshwater fish distribution. However, Mohsin & Ambak (1983) proposed the existence of three such divisions (Figure 1.2) with the combined north-east and central division representing the most extensive. The diversity and richness of freshwater fish species communities inhabiting these divisions has not previously been examined in detail and one implication raised by ever-deepening knowledge of Peninsular Malaysia’s diverse ichthyofauna is that the current geographic classification may be in need of revision.

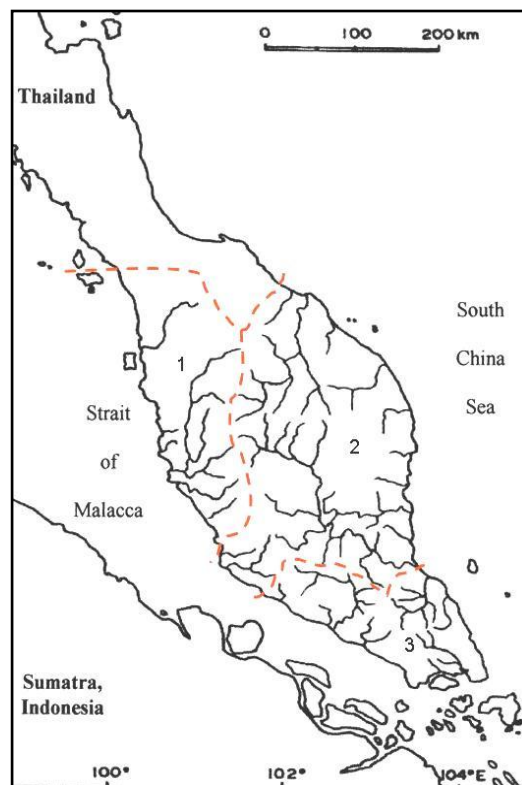


Figure 1.2. Map of Peninsular Malaysia depicting the three ichthyogeographic sub-divisions based on Mohsin & Ambak (1983): (1) north-west division, (2) north-east and central division and (3) southern division.

Various authors have regarded Peninsular Malaysia as a single zoogeographic entity (*e.g.*, Kottelat, 1989; Zakaria-Ismail, 1994; Rainboth, 1996; see also Voris (2000)). Kottelat (1989) recognised a biogeographical zone extending southwards from the north of Peninsular Thailand to the eastern and southern Malay Peninsula (including the Chao Phraya and Meklong drainages of central Thailand), but Rainboth (1996) suggested that the Perak River on the western Malay Peninsula represents a distinct ichthyogeographic region with a native ichthyofauna reminiscent of northern Sumatra. Yap (2002) suggested an alternative zonation encompassing northern Sumatra and Singapore which he termed the “Malay Peninsula biogeographic region”. However, Abell *et al.* (2008) recommended that Peninsular Malaysia be separated into two such regions, *i.e.*, the eastern and western slopes, thus extending further south from the Perak River with the latter including northern Sumatra. In recent years the taxonomy and systematic arrangement of freshwater fishes native to the Malay Peninsula has evolved tremendously with publication of many new species descriptions and systematic revisions. We now have a better understanding of the geographical distribution of species and the extent of their ranges.

1.6 Estimating species richness

Species richness, *i.e.* the number of species present in a particular ecosystem, is one of the most informative ways of characterizing community structure (Gotelli & Colwell, 2001), and is therefore critical to the development and implementation of strategies for conservation and biodiversity management (Pogue, 1999). Informed estimates of species richness can assist in decision-making procedures (Sorensen *et al.*, 2002) and enable conservation managers to prioritise certain objectives. Since it is both costly and time-consuming to physically record every species found in an area (Magurran, 2004), statistical extrapolations based on the results obtained from species richness estimator tools and derived from a subset of data or small indicator groups can be employed to calculate the total number of species in a community (Sorensen *et al.*, 2002).

There are several methods which may be used to calculate or estimate species richness (Colwell & Coddington, 1994). A common procedure is to construct a species accumulation curve using rarefaction, though this relies on availability of a complete species-by-sample matrix of species abundance, or presence and absence data (Colwell &

Coddington, 1994). A second approach involves fitting a parametric model of relative abundance using the number of individuals collected per species. Finally, species richness can also be estimated using non-parametric methods, which give priority to the number of rare species in a sample. There are currently more than 11 estimator tools that have been applied extensively in contemporary investigations of species richness as follows: Chao and Lee 1, Chao and Lee 2, ACE, ICE, Chao 1, Chao 2, first order jackknife, second order jackknife, bootstrap, Michaelis-Menten runs, and Michaelis-Menten means (see Table 1.1). Chao and Lee 1, Chao and Lee 2, ACE and Chao 1 are abundance-based estimators, while the remainder are incidence-based. These nonparametric methods have the greatest potential as estimators of species richness (Colwell & Coddington, 1994) since they make fewer assumptions about the underlying species abundance distribution (Sorensen *et al.*, 2002). The package *EstimateS* (developed by R. K. Colwell – <http://viceroy.eeb.uconn.edu/estimates>) implements these methods of evaluating and predicting species richness.

The performance of these estimators was investigated by Toti *et al.* (2000) in the context of spider community assemblages. Their evaluation demonstrated that different tools generate wildly variable results, a conclusion supported by Sorensen *et al.* (2002) who additionally postulated that their contrasting behaviour is related to disparities in species abundance distribution data between samples. Bossart *et al.* (2006) examined the performance of several estimators and in their appraisal the jackknife2 analysis produced the highest estimate of total richness, although the authors noted that the rank order of all other estimators was inconsistent across sites.

Walther & Morand (1998) assessed the performance of nine estimators and concluded that the most promising results were obtained from the Chao2 and first-order jackknife methods. Lewis & Whitfield (1999) concluded that the bootstrap estimator produces relatively low estimates whereas the incidence-based coverage estimator (ICE) and the Michaelis-Menten means (MM means) give rise to higher totals. Bartels & Nelson (2007) employed seven estimators to predict total species richness in tardigrades (Tardigrada) and ascertained that habitat-type can exert an effect on results in some cases. Hughes *et al.* (2001) evaluated several estimators using data obtained from microbe populations and recommended that large data sets are advantageous to more-accurately gauge bias and precision, at least in the case of incidence-based models.

Table 1.1. Eleven species richness estimators for calculating or estimating the number of the species in an assemblage.

Estimator	Remarks	References
Chao and Lee 1	- abundance-based estimator	
Chao and Lee 2	- abundance-based estimator	
ACE	- modified from the two Chao & Lee (1992) estimators which are known to overestimate richness, especially with small samples -abundance-based estimator	Chao <i>et al.</i> (1993); Colwell & Coddington(1994)
ICE	- modified from the two Chao & Lee (1992) estimators which are known to overestimate richness, especially with small samples - incidence-based estimator relying upon presence/absence data to quantify rarity-based predictions for species found in 10 or fewer sampling units	Lee & Chao (1994); Colwell & Coddington (1994); Lewis & Whitfield (1999)
Chao 1	- abundance-based estimator	Colwell & Coddington (1994)
Chao 2	- incidence-based estimator relying upon presence/absence data to quantify rarity - estimates based on capture-recapture methods or incidence of rare species among samples	Chao (1987); Colwell & Coddington, (1994); Lewis & Whitfield (1999); Pogue (1999)
First order jackknife	- incidence-based estimator relying upon presence/absence data to quantify rarity - estimates based on number of unique and duplicate species plus the number of sites sampled	Colwell & Coddington (1994); Landau <i>et al.</i> (1999); Burnham & Overton (1978); Lewis & Whitfield (1999); Pogue (1999)
Second order jackknife	- incidence-based estimator relying upon presence/absence data to quantify rarity - estimates based on number of unique and duplicate species plus the number of sites sampled	Colwell & Coddington (1994); Landau <i>et al.</i> (1999)
Bootstrap	- incidence-based estimator relying upon presence/absence data to quantify rarity - estimates based upon the proportion of sites containing each species recorded	Colwell & Coddington (1994); Lewis & Whitfield (1999)
Michaelis-Menten runs	- both Michealis-Menten estimators use a similar equation to extrapolate the species accumulation curve but compute it differently	Toti <i>et al.</i> (2000); Colwell & Coddington (1994)
Michaelis-Menten means	- makes use of maximum likelihood to estimate parameters and their variances - makes use of maximum likelihood to estimate parameters and their variances	Toti <i>et al.</i> (2000); Colwell & Coddington (1994); Landau <i>et al.</i> (1999); Lewis & Whitfield (1999); Walther & Morand (1998)

Longino *et al.* (2002) provided a satisfactory estimation of the richness of a tropical rain forest formicid (Family Formicidae) community by utilising three different estimation methods, although observed and estimated richness were generally different, and it was concluded that application of just a single method of species richness estimation would have proved imprecise. The authors added that variation in estimator performance may also be limited by “... *various kinds of edge effect*”, especially in terms of methodology, but suggested that “*combinations of methods and large enough sample sizes may reduce the effects of edge species*”. Evaluation and appraisal of species richness estimators is thus ongoing, and while they typically yield inconsistent results when applied singly, as demonstrated by the above examples, a blended approach should produce more credible results. Taken in combination with species lists generated from biodiversity inventories, accurate species richness totals will undoubtedly assist ecologists and conservation managers in developing best practice in conservation and land use applications.

1.7 Thesis outline

This thesis is divided into three major sections, totalling five chapters. The initial section and first chapter in particular focuses on analysis of ichthyodiversity at a local scale. In Chapter 2 the topic is the estimation of fish species richness based on field data collected from small streams in Peninsular Malaysia, and I ask whether species richness estimator tools can generate reasonable estimations of diversity even when data have been collected using different sampling procedures.

The second section comprises an investigation into the effect of human intervention on local fish species richness. In Chapter 3 the consequence(s) of assorted forms of disturbance for fish species diversity and community structure within specified stretches of small streams is appraised. Data collected during field work from nine stream systems located in the north, south and east of Peninsular Malaysia are used to test the effects of disturbance. Chapter 4 thus examines the impact of minor habitat alteration in terms of fish diversity and community structure in three small stream drainages. Abundance data collected from both ‘natural’ and ‘modified’ pools are analysed and used to test the prediction that artificial habitat modification exacts a detectable, negative impact on species richness. Prior to data analysis it was predicted that disturbed sites would be

relatively less diverse with concurrent reductions in abundance and species richness compared with undisturbed localities.

In the third and final section an assessment of regional biodiversity in Peninsular Malaysia is conducted. Spatial patterns of species richness, employing data collected from various streams of Peninsular Malaysia, are explored in Chapter 5 using a range of methods, and patterns of freshwater fish diversity within-and-between regions, plus throughout Peninsular Malaysia are reviewed. My initial prediction is that the fish community composition will be more similar at the local scale, *i.e.* within the same region, than at the regional scale. Chapter 6 incorporates an investigation of freshwater fish species-range size distribution in Peninsular Malaysia, based around the hypothesis that certain species should be of particular prominence in specific areas with a significantly greater number shared between areas.

The predominant goal of this study is the investigation and resolution of species richness (diversity), plus the analysis of community composition and community assemblage structure among freshwater fishes dwelling in small, lowland and foot hill stream environments of Peninsular Malaysia. I also hope to enhance understanding and knowledge of the diversity and assemblage structure of small stream fishes in Peninsular Malaysia. These data will allow a comparative analysis of assemblage structure of fish in the small streams and enable to test a range of hypotheses proposed to explain the high fish diversity in such systems.

CHAPTER 2

SPECIES RICHNESS AND COMMUNITY STRUCTURE OF SMALL STREAM FISHES IN PENINSULAR MALAYSIA

2.0 Abstract

The fish fauna in small streams in Peninsular Malaysia is diverse but under threat, and obtaining a reliable census of species occurring in such habitats is critical for conservation and management of biodiversity. In this study, I examined the community structure and attempted to estimate fish species diversity of two small lowland stream systems in the eastern region of Peninsular Malaysia. I used species richness estimator tools to measure species richness; these have been applied to fish species communities from both temperate and tropical streams and rivers with varied outcomes, but the non-parametric techniques in particular tend to yield promising results. To compare species diversity between the two stream systems I used rarefaction analysis; this technique allows comparison between unequally sampled streams by standardising samples, therefore measurement can be made by using a subsample (of the smallest abundance) from each data set rather than all samples. Thirty-seven species representing 12 families were identified from 547 individuals collected from 13 plots of a small, 3rd order stream (Sg. Peres) and 42 species representing 14 families of fishes were identified from 740 individuals collected from 12 tributaries of Sg. Dungun, Terengganu. In both streams, the family Cyprinidae dominated the fish species collected, with 13 (> 34%) and 18 species (> 42%) respectively, followed by Balitoridae and other families. In this study, sampling effort was considered adequate for species accumulation and estimates curves to converge. Chao 2 performed adequately for the Sg. Peres data set, where the number of rare species was low, and showed signs of convergence with the species accumulation curve. However, for the Sg. Dungun data set, where there is a predominance of rare species, Chao 1 performed best. In general, sampling effort was insufficient to accurately estimate species richness in either stream system. Observed species richness curves failed to reach asymptote for either stream, indicating that sampling was far from adequate. Rarefaction curves suggested that more species inhabit Sg. Dungun compared with Sg. Peres, but that overall species diversity in the two habitats is not significantly different. The majority of rare species recorded in this study were regarded as an artefact of *edge effects* with potamodromous species comprising a significantly high proportion of this group. Some species were rare because sampling was not extended to include different times of year plus the fact that limited fish capture methods were employed. Only a handful of rare species with known limited distribution in Peninsular Malaysia were captured at the two study sites, and always in low numbers. The estimated species richness results are probably representative of small streams in Peninsular Malaysia. These habitats support a great variety of species, of which a few are extremely rare with restricted distribution and can thus be considered important in biodiversity conservation of the Peninsular Malaysian ichthyofauna.

2.1 Introduction

One of the most frequently asked questions in the field of conservation biology is ‘How many species are there?’ The primary goal in species inventory studies is therefore to assess how many species exist in a particular habitat. Species richness (*i.e.* number of species) is the most commonly used biodiversity indicator, one of the fundamental units of biodiversity, and frequently used as a measure of diversity (DeVries *et al.*, 2009) and ecosystem status (Gonzalez-Oreja *et al.*, 2010). Documentation of species richness is both costly and time consuming (Palmer, 1990) and requires extensive resources in terms of field staff and taxonomic expertise. Further, it is particularly challenging to sample mobile, aquatic organisms, such as fishes (Bayley & Peterson, 2001). Therefore, observed species richness (S_{obs}) is frequently employed and is the most convenient and direct measure of diversity (Gotelli & Colwell, 2001; Beck & Schwanghart, 2010) but it depends largely on sampling effort and will be biased if there is undersampling (Beck & Schwanghart, 2010). Observed species richness increases with sampling effort (Gonzalez-Oreja *et al.*, 2010).

2.1.1 Estimation of species richness

In recent years, a variety of methods have been developed in order to streamline the process, but very few studies have compared or evaluated these techniques when applied to tropical aquatic fauna such as freshwater fishes. In the last few decades, several species richness estimators have been developed, and have become important tools for biodiversity estimations (Colwell & Coddington, 1994; Chazdon *et al.*, 1998). Colwell & Coddington’s (1994) and many subsequent studies show that there are at least four categories of species richness estimation: (1) extrapolations of species-area curves; (2) fitting of species-abundance distributions; (3) modelling of species accumulation curves, and (4) nonparametric techniques (Palmer, 1990; Colwell & Coddington, 1994; Walther & Morand, 1998; Herzog *et al.*, 2002; Foggo *et al.*, 2003). Species richness estimators attempt to predict the asymptote of the species accumulation curve, and consequently correct underestimated biases of observed species richness. Estimated species richness (S_{est}) utilises coverage and abundance as well as frequency of occurrence to estimate the number of species, and usually tends to produce higher estimated values, *i.e.* overestimation of the number of species based on the samples provided. The performance

of these methods has been evaluated by several researchers studying various groups of organisms (see Table 2.1).

Table 2.1. Examples of species richness estimator performance when applied to different groups of organisms as conducted by various researchers over the last two decades.

Author(s)	Organism	Remarks
Palmer (1990)	Trees	Jack1 was the least biased estimator
Baltanas (1992)		Jack1 was the least biased estimator
Colwell & Coddington (1994)	Trees	Favoured Chao2 and jack2
Chazdon <i>et al.</i> (1998)	Trees	Chao2 was less sensitive to aggregate data sets; ACE and ICE performed well with data sets of high species richness with ICE outperforming the others
Walther & Morand (1998)	Parasites of various animals, <i>viz.</i> : woodcreeper, fish, frog, rabbit, owl	Preferred Chao2 and jack1 for real data sets Jack1 performed best at low sampling effort but bootstrap is a better estimator when sampling effort increased
Toti <i>et al.</i> (2000)	Spider	MM performed best as it approached asymptote much quicker than the others
Walther & Martin (2001)	Birds	Chao 2 and Chao 1 were the least biased and most precise estimators
Herzog <i>et al.</i> (2002)	Birds	MMMeans performed best for empirical and most simulated data sets
Brose <i>et al.</i> (2003)	Plants	ICE and Chao2 were less accurate than jackknife estimators Poor accuracy of Chao2 was caused by low precision under low sample coverage and high bias under high sample coverage.
Foggo <i>et al.</i> (2003)	Marine fauna	Chao 1 performed best at intermediate sampling efforts
Foggo <i>et al.</i> (2003)	Pond invertebrates	Chao 2 and ICE we reliable and consistent, Chao 1 performed well for abundance-based estimator
Bartels & Nelson (2006)	Tardigrades	Used seven richness estimators but did not propose performance effectiveness of the estimator
Bartels & Nelson (2007)	Tardigrades	Preferred Chao 1, bootstrap, Chao 2 and Jack 2 respectively to analyse species richness of various samples

Several studies have calculated the species richness of various organisms using *EstimateS* software (developed by R. K. Colwell – see Methodology section) and demonstrated that species richness estimators behave differently in their estimation of true species diversity. Taxa for which the performances of species richness estimators have been compared include seed banks of tropical and temperate forests (Palmer, 1990; Condit *et al.*, 1996; Chazdon *et al.*, 1998), vertebrate parasites (Walther & Morand, 1998), zooplankton (Dumont & Segers, 1996) and marine macrobenthos (Rumohr *et al.*, 2001). In general, some species richness estimators perform better than others (Table 2.1), and nonparametric techniques yield the most promising results. Estimation of species richness based on good datasets has proven fruitful, less time consuming and more viable in an economic sense.

Richness estimators have been successfully applied to estimate fish species richness of both temperate (*e.g.* Lyons, 1992; Angermeier & Smogor, 1995, Hughes *et al.*, 2002) and tropical (*e.g.* Glowacki & Penczak, 2005; dos Anjos & Zuanon, 2007) streams and rivers.

The reliability of diversity measurement techniques depends on adequate sampling. Fish catchability is strongly influenced by habitat type, scale of the sampling area and the range of species presence. Reliable qualitative and quantitative sampling methods plus suitable equipment is needed when species richness and fish assemblage structure are to be determined (Jackson *et al.*, 2001) for conservation and habitat management. In contrast to large rivers, the geomorphological and physical conditions typical of small streams mean it relatively easy to compile species composition and abundance systematically *via* a species inventory, therefore sampling to obtain reliable representation is genuinely viable. To increase species observation records and maximise estimation of richness, data collection at sampling sites should include all stream biotopes, *i.e.* pool, riffle and glide, when possible. With the aid of species richness estimators, it is cheaper and faster to provide a highly dependable method (Coddington *et al.*, 1996) of input useful for decisions relating to biodiversity and conservation management (Coddington *et al.*, 1991).

2.1.2 Fish species richness in the tropics

In the tropics, the fish fauna is diverse and present in a wide range of water bodies. Some species, such as the tinfoil barb (*Barbonymus schwanefeldii*), pangasid catfishes (*Pangasius* spp.) and mahseer (*Tor* spp.) are commercially important and a major source of protein for local communities. Others such as small barbs (*e.g.*, *Puntius hexazona*, *P. dunckeri*), rasboras (*e.g.*, *Rasbora einthovenii*, *Boraras maculata*) and loaches (*e.g.*, *Nemacheilus selangoricus*, *Homaloptera parclitella*) are prized ornamental fishes (Ng & Tan, 1997). The Malay peninsula land mass, extending from the Asiatic continent into the Sunda archipelago is renowned as one of the most diverse regions in the world in terms of freshwater fishes (Abell *et al.*, 2008; Myers *et al.*, 2000). Peninsular Malaysia freshwater fish communities comprise a mixture of Indian, Indochinese and Indo-Borneo (Sundaland) species as well as several endemic to the region (Mohsin & Ambak, 1983; Zakaria-Ismail, 1994; Yap, 2002; Abell *et al.*, 2008). Many species are plentiful throughout the year, have a variety of adaptations, exhibit guild-specific responses to local environmental changes or

occupy specific ecological niches, and showing remarkable within-habitat diversity. Most importantly, they are relatively easy to sample, identify and enumerate.

Many publications on freshwater fishes of Peninsular Malaysia in the first half of the 20th century were either taxonomic descriptions of a new species (see de Beaufort, 1933; Herre, 1936; 1940a; 1940b) or a general discussion on fish occurrences, habitats and ecology (Herre & Myers, 1937; Hora, 1941a; 1941b; Hora & Gupta, 1941; Smedley, 1931; Tweedie, 1936; 1940; 1950; 1952). For many years, studies on fishes focussed chiefly on taxonomy (*e.g.* Kottelat & Lim, 1993; Ng & Ng, 1998; Ng & Kottelat, 2000; Ng, 2002; Kottelat, 2005; Tan & Ng, 2005) with comparatively little attention paid to ecological aspects of fish assemblages and their community structure.

More recently, interest has shifted to aquaculture-based studies (Aizam *et al.*, 1983; Ali 1988; Ismail & Zain, 1978; Khalil, 1982) of species with high economic values (Aizam *et al.*, 1983; Ali, 1988; 1993; Law, 1986; Saidin *et al.*, 1988). To date the native fauna and its diversity have received only modest attention (Ali & Kathergany, 1987; Fernando, 1980; Khoo *et al.*, 1987; Mohsin, 1980; Mohsin & Ambak, 1982). Accurate biodiversity assessment is urgent in diverse but poorly-documented tropical habitats such as small streams. Such streams are common in Peninsular Malaysia and many are under threat due to rapid deterioration *via* land conversion and habitat alteration. Planning and management of tropical forests for recreational used should also take advantage of aquatic diversity, including fishes.

Since 1990, more than 50 native species have been reported and added to the list and more than half of these are new to science (Lim & Tan, 2002). At present, the freshwater fishes of Peninsular Malaysia are probably better known than these in neighbouring countries (except Singapore and Brunei) and this region has probably one of the most extensively studied ichthyofaunas in the Southeastern Asia. Small streams in the lowlands and foothills of Peninsular Malaysia may display differences in species richness and assemblage structure relative to large rivers. Persistent external pressure is prevalent in many forms such as development of new residential districts, increased need for agriculture land, authorised/illegal logging and urbanisation, and these continue to threaten many intact lowland forests (Martin-Smith, 1998c). As a result, the rich aquatic fauna of many small streams is already diminished with the exception of several tolerant species.

Small streams shelter a great variety of fish species despite being less important in commercial fisheries (Lyons, 1996). While some streams may have been utilised for recreational purposes for many decades (see Chapter 4), their biodiversity remains poorly documented. Despite many studies having been conducted on various groups of organisms in order to estimate the diversity of a community and to compare the performance of species richness estimators elsewhere, similar efforts are lacking in tropical countries such as Malaysia and studies involving fishes are correspondingly limited.

In the present study, I assessed local- and landscape-scale fish species richness of small streams in the eastern region of Peninsular Malaysia. I use two data sets and compare usefulness of various statistical approaches in assessing the species richness and diversity of small stream fish communities based on data collated from two stream systems. I also examine the assemblage structure of small stream fishes, characterising differences in species diversity and sampling effort. Finally, since some of these diversity measures are dependent on general abundance, I further examine the ‘natural history’ of rare species to support and increase confidence in recommended diversity measures for small stream fishes in Peninsular Malaysia.

2.2 Methodology

2.2.1 Study areas

Despite their significant conservation value, the biodiversity of Peninsular Malaysia's small streams remain largely undocumented meaning these habitats are consequently underappreciated as reservoirs or refugia for fishes. For this study I sampled two stream systems in the eastern region of Peninsular Malaysia (Figure 2.1); the first was a stream known as Sungai (Malay; Sg. = stream/river) Peres and the second various tributaries of Sg. Dungun in Terengganu. A total of 13 plots, each 25 m in length, were sampled at Sg. Peres, and 12 plots in small tributaries of the upper Sg. Dungun, each approximately 100 to 150 m long (10-20 times mean stream width, MSW) were considered adequate to ensure reliable estimate of species richness and assemblage structure. To maximise data collection, the selected sampling plots encompassed several biotope-types, but not all plots comprised of pool-riffle formations.

Sg. Peres is a small lowland third order stream flowing within the lush lowland forest reserve of Sekayu (Figure 2.2). The stream is a tributary of Sg. Tersat, one of the main tributaries of Sg. Terengganu. The habitat was characterised by relatively steep cascades of short rapids and waterfalls at the upstream limit and low gradients in the mid/downstream sections. In general, these were mostly shallow (water depth less than 1.5 m) with substrates composed predominantly of sand and gravel in the lower reaches or gravel and rocks further upstream. The downstream reaches were often exposed to sunlight with shade usually limited to the stream banks, while the upstream reaches were under vegetative cover extending to almost half of the width of the stream in some cases. Stream width (wet surface) was generally less than 15 m at the downstream reaches and about 5 m at the upstream. The stream margins were typified by riparian tree canopies except the downstream and mid-sections between the two banks of the large section of the stream. Water was usually clear and flowing smoothly, water temperature ranged from 23.3 – 25.6 °C, pH was slightly acidic (6.69) to slightly alkaline (7.25), had relatively low conductivity (28 – 31 $\mu\text{S}/\text{cm}$) and was normally high in dissolved oxygen (7.5 – 8.2 mg/l).

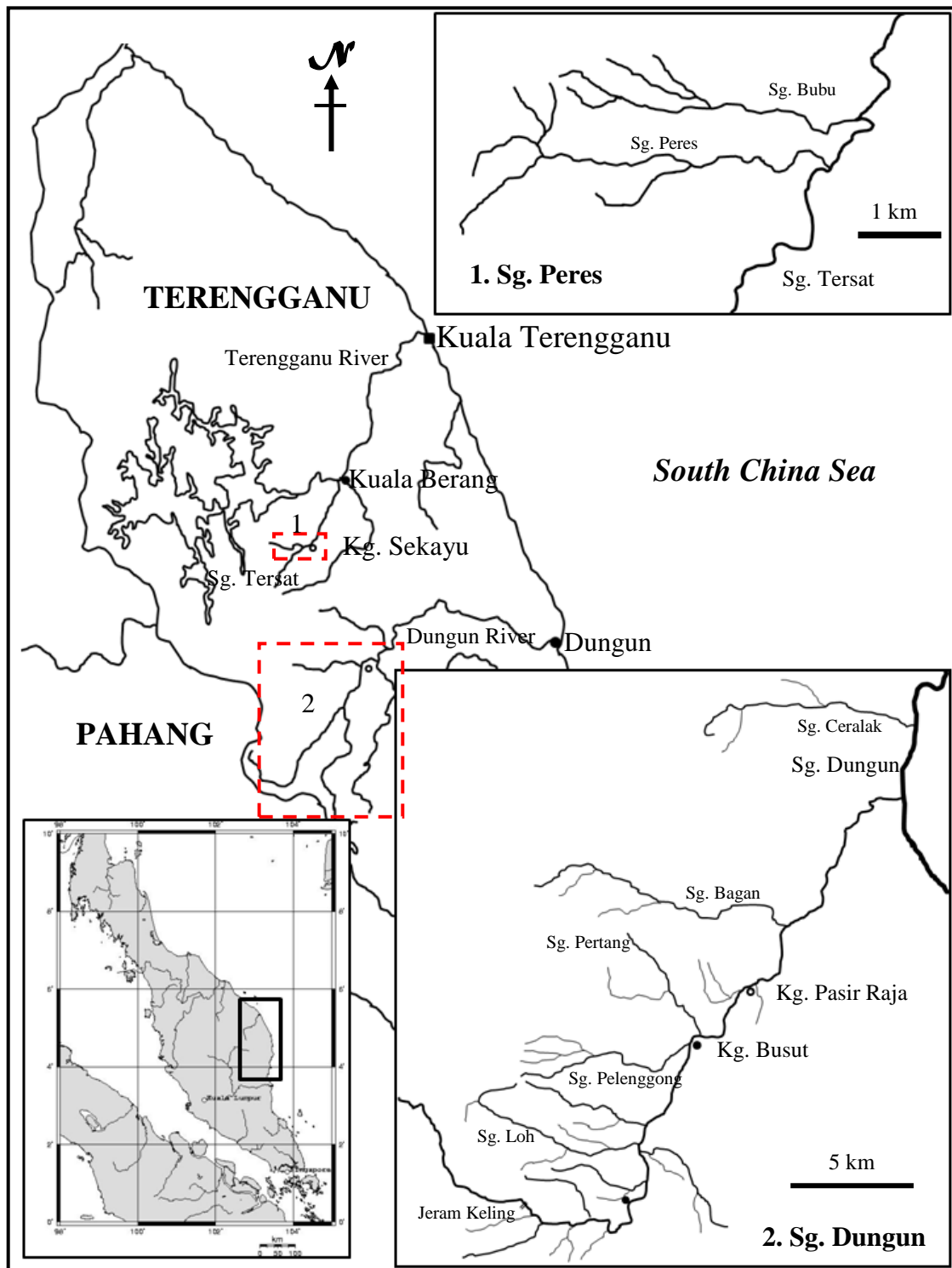


Figure 2.1. Map of Terengganu showing the location of Sg. Peres (1) and Sg. Dungun (2), respectively. The small tributary streams of the Sg. Dungun are not shown in the map. Insert shows a map of Peninsular Malaysia indicating the location of the sampling sites (□).



Figure 2.2. The middle section of Sg. Peres, Terengganu represents a typical small, lowland stream in Peninsular Malaysia, and is frequently used by locals as a picnic spot and for water-related recreational activities.

Prior to that, I sampled 12 small streams at the upper part of Sg. Dungun drainage in June 2004 (Figure 2.3). They were usually shallow with water depth less than 1.5 m, and had predominantly contained sand and gravel bottoms at most sites. Several had a well-developed pool-riffle habitat but the others did not. Within the sampled stream reaches various microhabitats such as small, shallow pools located under banks or brief, and shallow rapids were found. In the latter, the substrate was mostly composed of rock, especially in rapids and riffles, though runs usually featured sandy substrates. Submerged, woody structures such as decomposing leaves, twigs, snags and logs were plentiful. Aquatic plants were absent in many of the streams visited though stream banks were mostly well covered by riparian vegetation consisting mainly of trees and small herbs. Water was usually clear and flowing smoothly, water temperature ranged from 23.3 – 30.4 °C, pH is slightly acidic, had relatively low conductivity (21-98 $\mu\text{S}/\text{cm}$) and was normally high in dissolved oxygen. In general, the two streams displayed similar physiochemical characteristics to other small, lowland streams in Peninsular Malaysia.



Figure 2.3. The lower section of the Sg. Pelenggong, a tributary of the Sg. Dungun, Terengganu represents a typical mid-to-lower section of a small, relatively pristine lowland stream in Peninsular Malaysia which is not being used for human recreational activities.

2.2.2 Sampling techniques

Fishes at all sites were sampled once during a period of base flow (when water levels were lowest) to avoid variability of water flow and volume that could affect catch frequency and fish abundance. In 2006, electrofishing was performed at Sg. Peres using a battery operated electrofisher (model LR 24 Smith-Roots), while in 2004 at the tributaries of Sg. Dungun it was conducted using a generator-powered (model EX350 Honda) backpack electrofisher (model 15- D Smith-Roots). In both sets of sampling, block nets (two seine nets with mesh size of approximately 3 mm) were employed and set at both ends to prevent fishes from either entering or escaping the studied plot. Sampling efforts differed slightly due to varying plot distances. At Sg. Peres, three to five repeated passes were made in an effort to obtain as many fish species and individuals as possible. However, in the Sg. Dungun tributaries, electrofishing was performed with only a single pass in which each microhabitat was carefully sampled by walking upstream in a regular, transverse pattern. Table salt was added upstream to increase electric conductance in order to maximise electrofishing efficiency. At both sampling locations, the same person operated the electrofisher and two people collected the stunned fishes using a long-handled scoop-net. At the fast-flowing stream sections a seine-net was used to block and collect the stunned fishes that drifted downstream. Fishes caught at the downstream block net were also included in the results. Fishes were classified and identified using the taxonomic keys of

Alfred (1969), Roberts (1989), Kottelat *et al.* (1993), Rainboth (1996), Ng & Ng (1998), Ng & Kottelat (2000) and Kottelat (2005) and counted before being released after sampling.

2.2.3 Data analysis

Calculating nonparametric estimators

Estimation of species richness was calculated using the statistical program *EstimateS* 8.2.0 (developed by R. K. Colwell – <http://viceroy.eeb.uconn.edu/estimates>). To estimate total species richness the following non-parametric species richness estimators were selected: coverage-based estimators (ACE and ICE, Lee & Chao, 1994), Chao 1, Chao 2 (Chao, 1987), first-order Jackknife (Burnham & Overton, 1978), second-order jackknife, bootstrap (Smith & van Belle, 1984) and the two Michaelis-Menten estimators (Raaijmakers, 1987). These non-parametric estimators make few assumptions about the underlying species abundance distribution (Sorensen *et al.*, 2002). Two other parameters examined as indicators of inventory completeness (Longino *et al.*, 2002) were the number of “unique” (species that known only from a single collection) and “duplicates” (species known from only two samples).

To determine species richness in each system I used an increasing number of plots for the Sg. Peres data set and the number of plots in individual stream sections for Sg. Dungun. Throughout the calculation, 250 iterations (Longino *et al.*, 2002) were used to randomise the sample in order to produce smooth accumulation curves. Sample patchiness was set at 0.5 (for moderate aggregation of species as perceived from the data sets for both locations) and the coverage-based upper limit of rare species was set at 10 (default value). I follow Walther & Morand (1998) in assuming that the total species richness of the community has been determined if (1) the last 5% of the values of the accumulation curve display equal values (*i.e.* the curve has reached the horizontal asymptote) and (2) the last 50% of the accumulation curve values were within 5% of the final value of the accumulation curve.

Comparison of species assemblages

Despite the differences in data acquisition techniques I made a comparison of species richness between the two stream systems since rarefaction can be used to compare observed species richness between sites or habitats that have been unequally sampled (Hughes *et al.*, 2001). A rarefied curve was generated by averaging randomisations of the observed species accumulation curve (Heck *et al.*, 1975). Rarefaction involved plotting of a smooth species accumulation curve by randomly re-sampling data, then comparing species richness for all sites with the point on the curve corresponding to the number of individuals (or samples) at the site with the lowest sampling effort. The observed richness among samples could then be compared by employing variance from the repeated randomisations (Hughes *et al.*, 2001). Rarefaction analysis was performed using *EcoSims* var. 7.0 with 1000 iterations. Differences in species diversity between each stream were visualised *via* examination of the 95% confidence intervals for individual-based rarefaction curves. In addition, Coleman rarefaction curves (an individual-based rarefaction curve) were generated using *EstimateS* to compare species richness of the two assemblages.

Species diversity indices including Shannon's index of diversity (H'), evenness (E_H) and Simpson's ($1/D$) were calculated for each plot and stream section using the software Paleontological Statistics (PAST), version 2.01 (Ø. Hammer & D. A. T. Harper, <http://folk.uio.no/hammer/past>). Diversity indices values for both stream systems were plotted against number of individuals and compared. Biological traits were used to characterise the rare species found at the two locations. Principal component analysis (PCA) was performed by PAST software using data compiled from biological traits of all rare species at the localities. Each rare species was assigned and given a score of 1 for presence, 0 for absence of a particular trait. Information regarding biological traits was gathered from various sources especially FishBase (www.fishbase.org) and coded accordingly. Forty traits were selected and each species was assigned a particular trait within three broad biological/ecological bands: 1. Habitat preference (horizontal and vertical feeding position, substrate-type and longitudinal distribution) 2. Trophic level (food preference), and 3. Life history (range of body size, schooling behaviours, swimming speed, migratory patterns, reproductive pattern, seasonality, mating practice and predatory habit. A biplot was generated using the eigenvalue scale of component 1 and component 2.

2.3 Results

2.3.1 Estimation of species richness

Summary and comparison of species richness estimations for the two study sites were given in Table 2.2. Species richness values generated using estimators ranged from 41 (MMMeans) to 55 species (Jack 2), which was between 5 to 18 more than observed at Sg. Peres. In tributaries of Sg. Dungun total species ranged from 46 (Chao 1) to 64 (ICE) compared 42 species recorded during field surveys.

Table 2.2. Summary and comparison of species richness estimations for the two study sites. Randomisation without replacement was done 250 times using *EstimatesS* with classic formulae for Chao 1 and 2, at default (0) value for the coverage-based estimator limit of rare species and patchiness of 0.5 (moderate aggregation).

	Site	Sg. Peres	Sg. Dungun
Observed species (S_{obs})		37	42
No. of samples		13	12
No. of individuals		547	740
Singletons		9 (24.3%)	9 (21.4%)
Doubletons		3 (8.1%)	10 (23.8%)
% Dominance (3 species)			
Shannon's H'		2.75	2.70
Simpson's $1/D$		10.1	9.93
Evenness, $J' = H'/\ln S$		0.762	0.722
Sampling intensity		14.78	17.62
Inventory completeness index		75.68	78.57
% inventory completion		73.27	91.21
Adjusted estimate range		0.37	0.45
Estimators			
ACE		45.44	50.37
ICE		52.60	64.81 [#]
Chao 1		50.50±12.46	46.05*±3.60
Chao 2		51.08±10.40	58.00±10.58
Jack 1		49.00±2.72	56.67±3.67
Jack 2		55.35 [#]	63.94
Bootstraps		42.36	48.65
MMRuns		41.85	51.04
MMMeans		41.60*	49.63
Additional species estimated		4.6-18.35	4.05-22.81

Note. * and [#] denote minimum and maximum value.

For a stream with multiple subplots (Sg. Peres, $n = 13$), neither estimators nor observed species accumulation curves reached the point of asymptote (Figure 2.4) except Chao 2, which appears to converge with the observed species accumulation curve as more individuals were included in the analysis. The latter appeared to stabilise after

approximately 300 individuals were added, but returned relatively higher estimates of species richness (51 species) than the other estimators (see Table 2.2). Conversely, Chao 1 failed to stabilise but estimated a slightly lower total of species. Jack 2 estimated the highest species richness (55.35, see Table 2.2) followed by ICE and Chao 2 with these therefore regarded as ‘higher group’ estimators. The ‘medium group’ comprised Chao 1, Jack 1 and ACE with the two MM estimators and bootstraps forming the ‘lower group’, of which the MMMeans was basal with 41.6 species (Appendix 2.1. Figure A2.1).

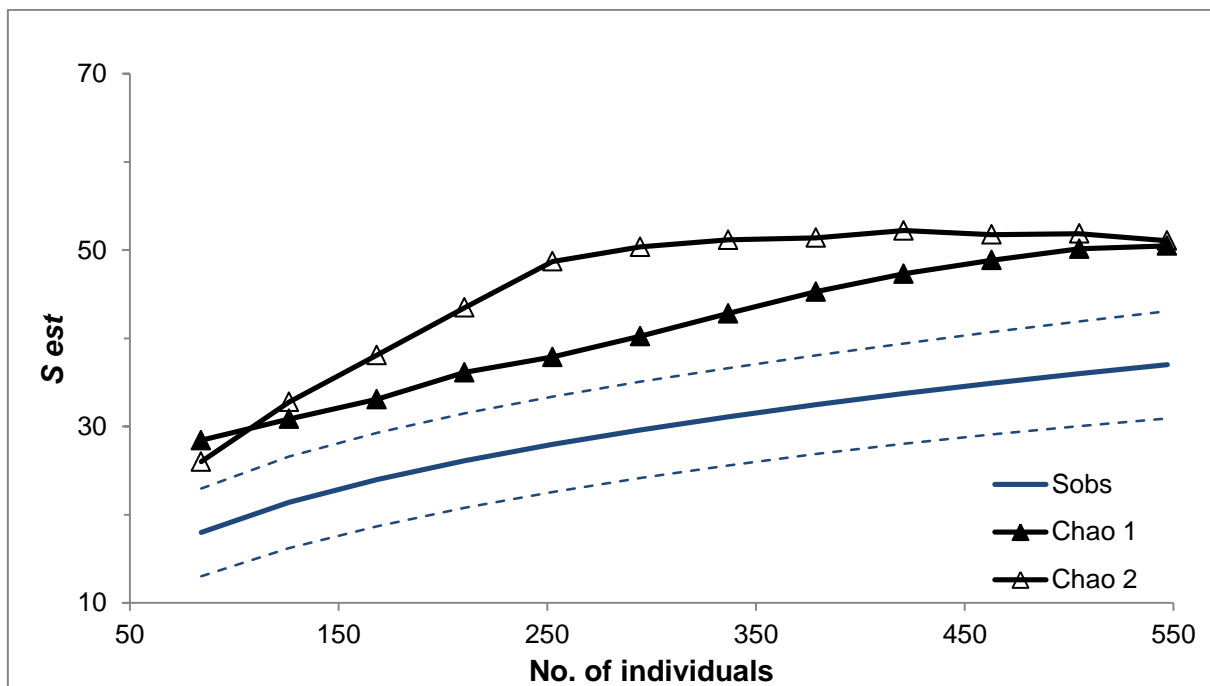


Figure 2.4. Observed and estimated number of fish species in Sg. Peres, Terengganu versus number of individuals collected based on 250 randomised samples and patchiness of 0.5. First value of each curve was removed to improve the clarity of the graph. Thin dashes lines (---) indicate the upper and lower limits of S_{obs} , respectively.

Species richness estimates for the ‘multiple streams’ data set (Sg. Dungun, $n = 12$) varied wildly with none attaining an asymptote (Figure 2.5) except for the two Chao estimators which appear to converge with S_{obs} . Chao 1 ostensibly stabilised more rapidly with Chao 2 somewhat erratic at lower sampling efforts but merging with S_{obs} as sampling effort increased. Chao 1 also returned more favourable estimates (46.2 species) within the limit of S_{obs} . Results for four estimators (ICE, Jack 2, Chao 2 and Jack 1) were closely similar and clustered together towards the upper extreme of species numbers estimated; ICE estimated the highest species richness (64.81 species) followed by Jack 2 (63.94 species). The ‘lower group’ estimators consisted of Chao 1, bootstraps, MMMeans and ACE – Chao 1 predicted the lowest value (46.05) which is nevertheless within the S_{obs} ranges (Appendix

2.1. Figure A2.2). In general, the estimated species richness figures for Sg. Peres exceeded the observed number of species by 12.4 to 49.6% whereas for Sg. Dungun estimated totals ranged between 9.7 to more than 50% beyond those observed (Table 2.2).

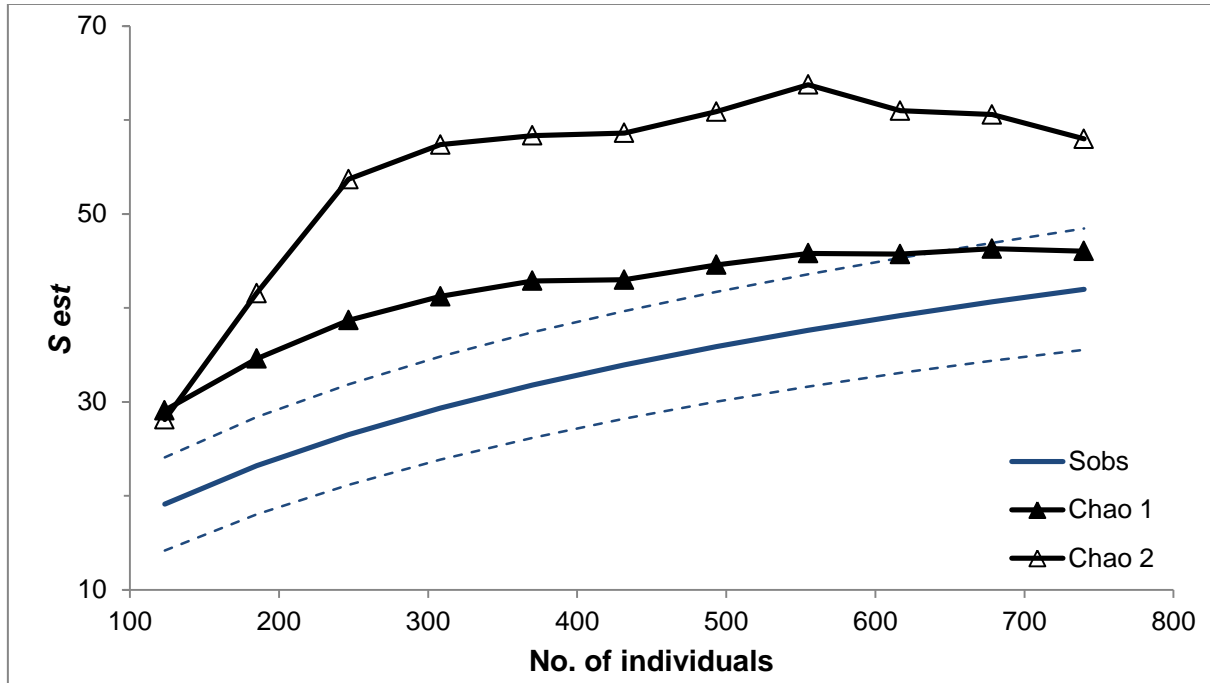


Figure 2.5. Observed and estimated number of fish species in Sg. Dungun, Terengganu versus number of individuals collected based on 250 randomised samples and patchiness of 0.5. First value of each curve was removed to improve the clarity of the graph. Thin dashes lines (---) indicate the upper and lower limits of S_{obs} , respectively.

2.3.2 Species assemblages

A total of 17 families and 52 species of fishes were recorded from the two stream systems (Table 2.2). At Sg. Peres, 37 species from 13 families were recorded from 547 individuals collected. At 12 small streams of Sg. Dungun, 42 species representing 15 families of fishes were identified from 740 individuals collected (see Appendix 2.2 for details). Observed fish species diversity in Sg. Dungun therefore surpassed that in Sg. Peres by a total of five. In both streams, fish assemblages were dominated by family Cyprinidae (36.5%, 19 species) followed by Bagridae and other families. There were more cyprinid fishes recorded at the tributaries of Sg. Dungun (18 species, 42.8% of total) than in Sg. Peres (13 species, 35%).

The number species collected from 13 plots at Sg. Peres and 12 stream reaches at Sg. Dungun was between five to 19 and six to 18 species, respectively. The fish community at

Sg. Peres was dominated by *Glyptothorax major* (family Sisoridae, 130 individuals), followed by *Garra cambodgiensis* (Family Cyprinidae) and *Homaloptera zollingeri* (family Balitoridae). The most frequently encountered were *Homaloptera zollingeri* (present in nine plots), followed by *H. tweediei* (eight plots) plus *Rasbora notura* (Cyprinidae) and *Glyptothorax major* (both seven plots). In the Sg. Dungun tributaries the most abundant species was *Rasbora notura* (140 individuals), followed by *Poropuntius smedleyi* (Cyprinidae) and *Mystacoleucus marginatus* (Cyprinidae) with 110 and 106 individuals, respectively. *Rasbora notura* was collected from 11 stream reaches and by far the commonest fish species in the upper Sg. Dungun drainage. Other common species recorded were *Poropuntius smedleyi* (recorded nine times) followed by four species: *Hemibagrus nemurus*, *Mystacoleucus marginatus*, *Puntius banksi* and *Garra cambodgiensis*.

Shannon's H' diversity measure per plot of Sg. Peres ranged between 0.98 and 2.44, with an overall value of 2.76 for all sampled plots when considered together (Table 2.2). For the Sg. Dungun localities the H' value varied from 1.53 to 2.65, with an inclusive figure of 2.70 (Table 2.2). Therefore when total catch for each stream system was pooled H' was slightly higher for Sg. Peres (2.76) than Sg. Dungun (2.70) although the mean values of H' were not significantly different ($p > 0.05$) (Figure 2.6. See also Appendix 2.3. Figure A2.3a).

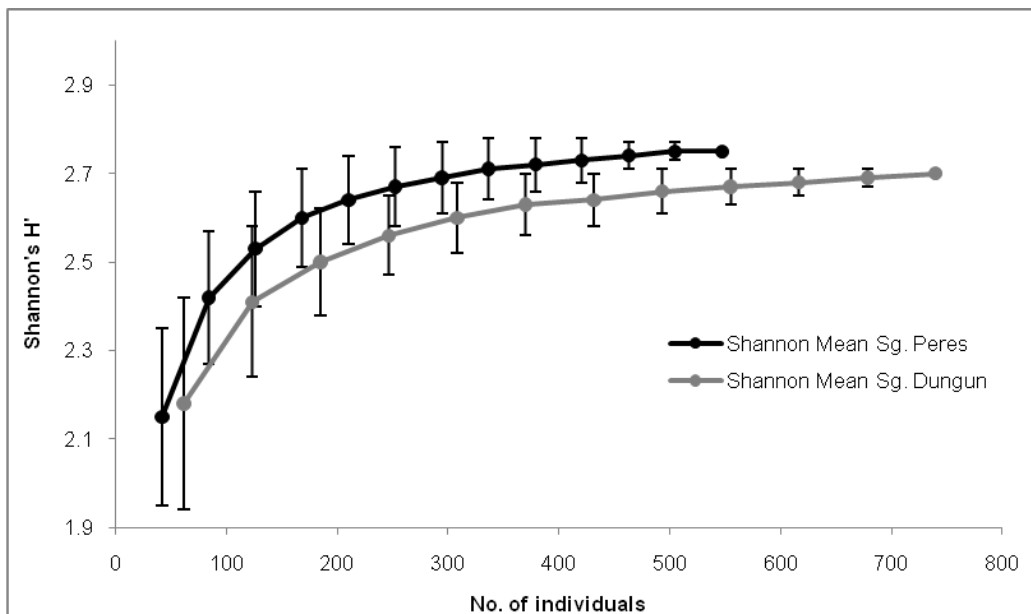


Figure 2.6. Mean of Shannon's (H') for Sg. Peres and Sg. Dungun. The variance decreasing as sample size increases.

Overall, Simpson's reciprocal diversity index also indicated that Sg. Peres was marginally more diverse than Sg. Dungun although as for Shannon's H' , Simpson's $1/D$ values for both streams were not significantly divergent from one another (Figure 2.7. See also Appendix 2.3. Figure A2.3b). The evenness value at Sg. Peres (0.76) slightly exceeded that for tributaries of Sg. Dungun (0.72).

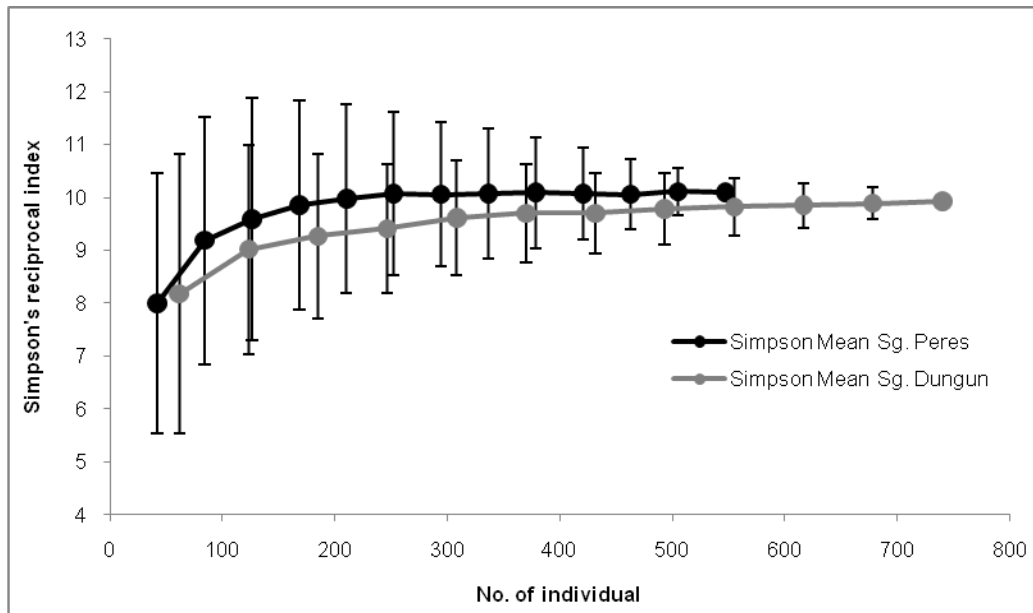


Figure 2.7. Mean of Simpson's reciprocal diversity index ($1/D$) for Sg. Peres and Sg. Dungun.

Sampling intensity (individual : species) for Sg. Dungun (17.6) was notably less-intensive than that for tributaries of Sg. Peres (14.8). However, despite relatively low sampling intensity, the Sg. Dungun tributaries returned more positive results for both the inventory completeness index and percentage of inventory completion than that Sg. Peres (Table 2.2). On the other hand, a smaller adjusted estimate range was recorded at Sg. Peres compared with Sg. Dungun, indicating that sampling at Sg. Peres was close to completion.

In addition, rarefaction analyses showed that at a standardised figure of 547 individuals collected, more species would be recorded from Sg. Dungun (38.9 ± 2.4 species, lower limit = 36 species and upper limit = 42 species) than Sg. Peres (37 species). However, since the variance of diversity curves for the two streams, overlapped one another species richness can be said not to differ significantly between them (Figure 2.8). When sampling effort was calculated and plotted versus observed species richness, no curves for either stream displayed any sign of stabilisation (Appendix 2.4. Figure A2.4), indicating that sampling

was far from sufficient. Coleman rarefaction curves suggest that a considerably greater number of species should be expected from tributaries of Sg. Dungun as opposed to Sg. Peres based on the assembled data (Appendix 2.4. Figure A2.5).

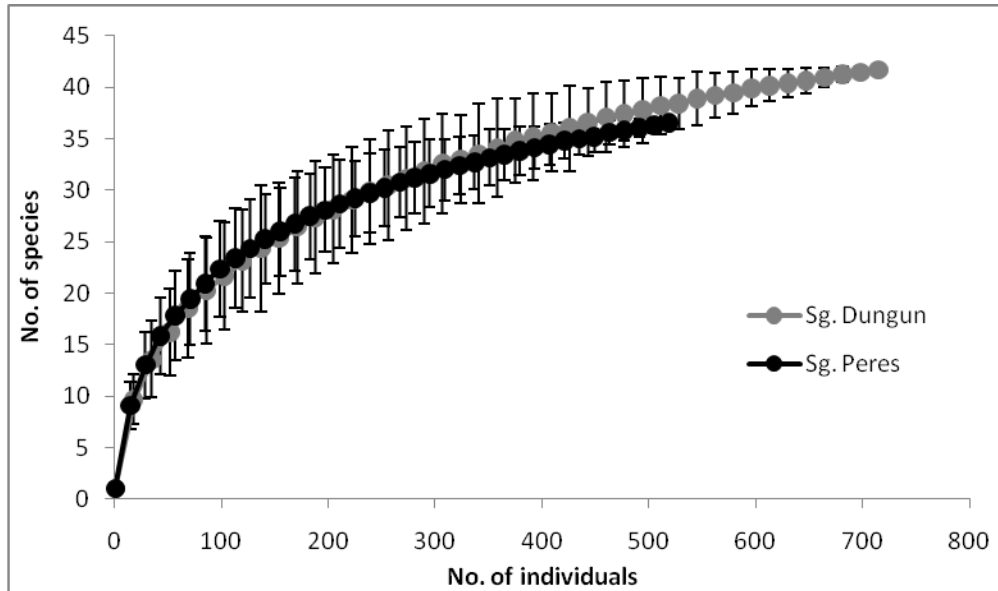


Figure 2.8. Abundant-based rarefaction curves for Sg. Peres and Sg. Dungun data sets.

Nine (24.3%) singletons and three (< 1%) doubletons were recorded from Sg. Peres with nine (21.4%) singletons and 10 (23.8%) doubletons recorded from the tributaries of Sg. Dungun. Unique and duplicate species at Sg. Peres numbered 11 (29.7%) and nine (24.3%) respectively, while 17 (40.5%) unique and six (14.3%) duplicate species recorded were recorded from Sg. Dungun. Most of these were considered rare due to the small number of individuals collected. Within this study, rare species were narrowly-defined as species totalling less than 0.5% of accumulated abundance at each study site.

PCA analysis (Figure 2.9) of the rare fish species inhabiting small streams within the two systems signified that they can be grouped into four categories based on their biological and ecological traits (Appendix 2.5): 1. Fast swimming species: large-bodied, predatory fishes dominated by piscivores; 2. Non-migratory, benthophagous species: usually solitary and feeding on aquatic insects; 3. Benthopelagic, potamodromus species: strong seasonal abundance, usually feeding on plant materials; 4. Slow swimming species: with relatively small body sizes, relatively inactive predatory fishes feeding on allochthonous invertebrates.

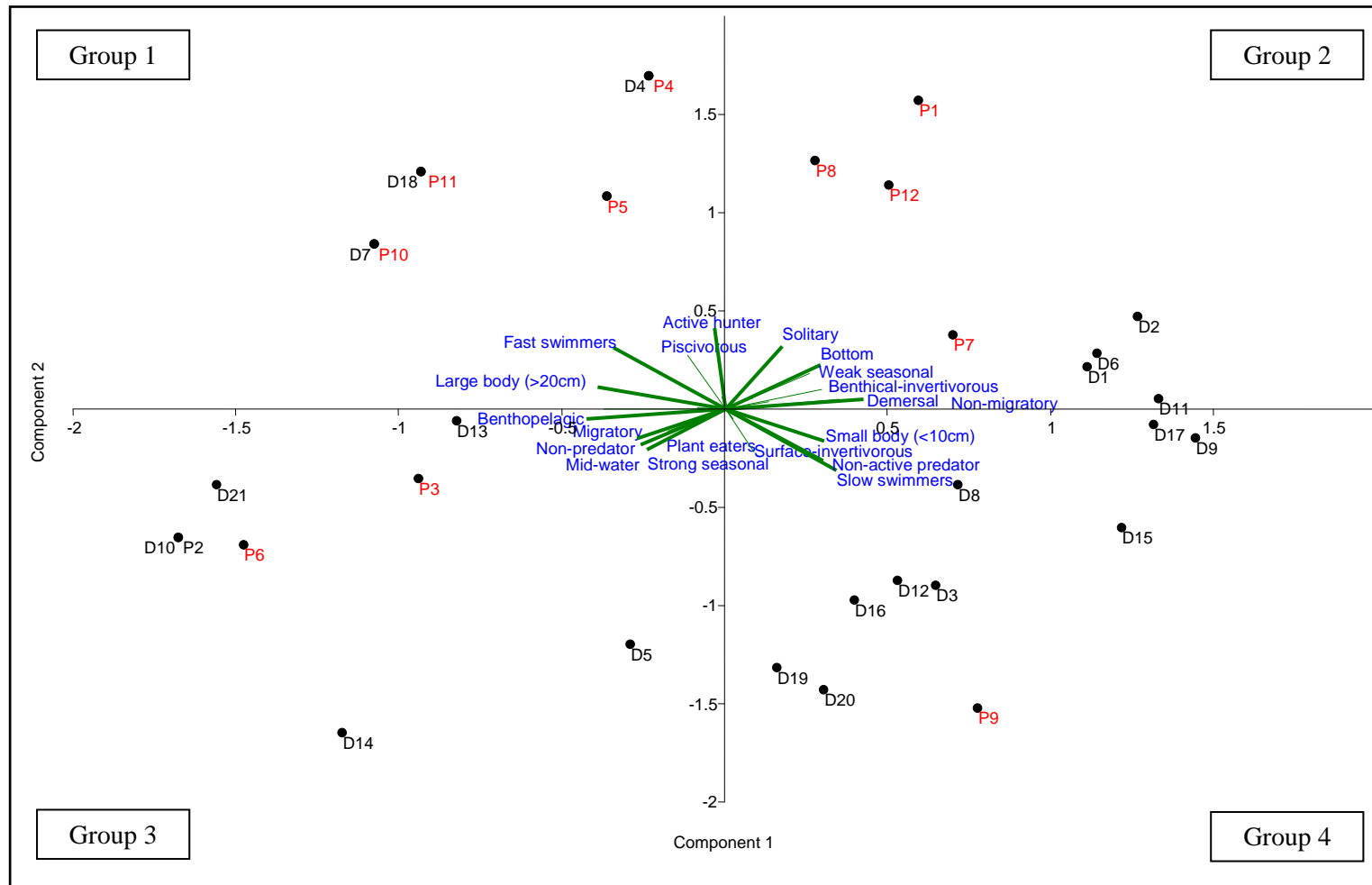


Figure 2.9. Distribution of rare species with respect to biological trait variables, identified by principle component analyses (PCA) for component 1 and component 2. Some traits were removed for clarity of the figure. See Appendix 2.6. (Table A2.3) for details.

Group 1 fishes consist mostly large-bodied, piscivorous species usually common to river and lakes except *Channa melasoma* which is more often confined to small streams but rarely collected. Most group 2 fishes (except akysiid catfish) were collected in large number streams and rivers of all sizes. This group typically comprises solitary, bottom-dwelling fishes feeding upon small invertebrates but utilising different microhabitats from shallow, rocky environments to those with deep, sandy substrates or containing submerged logs in deeper water. Fishes group 3 is largely composed of gregarious, herbivorous, mainly potamodromous species which are frequently found at middle depth ranges in main river channels and lakes. The exception was *Crossocheilus oblongus* which is a bottom-dweller and frequents fast-flowing stretches of small streams. All of these rare species belong to the family Cyprinidae. Group 4 included fishes of small body size, which may be passively, or non-predatory, often feed on allochthonous invertebrates and in this study included an amalgam of species from several families, most of which were demersal and/or slow swimmers. The majority of this latter group were rarely recorded from the Sg. Dungun tributaries a few were present in the Sg. Peres, where they were not rare.

Of the 37 fish species recorded at Sg. Peres, 12 were defined as rare based on relative abundance (those contributing less than 0.5% of total abundance), and this grouping included all single and doubletons. Twenty one species recorded from tributaries of the Sg. Dungun were considered rare using these criteria, and also included trios (species for which three individuals were recorded). The rare species assemblages inhabiting the two stream systems exhibited few similarities with only four species occurring in both streams, *i.e.* *Hampala macrolepidota*, *Labiobarbus leptocheilus*, *Raiamas guttatus* and *Channa melasoma*. Four rare species, *Crossocheilus oblongus*, *Mystus castaneus*, *Hemirhamphodon pogonognathus* and *Channa lucius*, were recorded only from the Sg. Peres whereas 11 rare species were present only in the Sg. Dungun tributaries (see Appendix 2.2). Four species that were rare at Sg. Peres, *Osteochilus waandersi*, *Homaloptera parclitella*, *Acantopsis dialuzona* and *Hemibagrus nemurus*, were present in relatively large numbers at Sg. Dungun, while six species that were rare at Sg. Dungun, *i.e.* *Tor tambra*, *Homaloptera ogilviei*, *H. zollingeri*, *Glyptothorax siamensis*, *Macrogathus maculatus* and *Pristolepis grootii*, were relatively common at Sg. Peres.

2.4 Discussion

Since neither richness estimators nor observed species accumulation curves attained an asymptote, my sampling efforts were far from sufficient to accurately estimate the number of fish species inhabiting these drainages. According to my results, a minor, lowland stream (Sg. Peres) contains a relatively similar number of species to an entire, complex system of tributaries (Sg. Dungun). However, rarefaction analyses showed that the latter harbours a more diverse fish species when equal numbers of individuals were compared. Diversity indices of the Sg. Peres data were higher illustrated that fish community structure was more diverse and evenly distributed compared to Sg. Dungun.

In both stream systems, similar fish groups dominated catches. Dominance percentages for the three most abundant species recorded were 41% in the Sg. Peres, 48% in tributaries of the Sg. Dungun thus demonstrating that only a handful of species contribute greatly to total abundance. Despite lower sampling intensity during field work the Sg. Peres had a smaller adjusted estimate range, thus indicating that variations in estimated values were smaller than from the Sg. Dungun. Further, fishes from the Sg. Dungun tributaries were better sampled than Sg. Peres as indicated by higher values for sampling effort. On the other hand, the number of doubletons recorded was far higher for the Sg. Dungun than the Sg. Peres.

2.4.1 Estimation of species richness

The comparative performance of species richness estimators is always subject to the definition of performance being employed (Walter & Morand, 1998), and usually interpreted using species richness curves. Although there are inconsistencies and performance varies (Glowacki & Penczak, 2005), reliable and accurate estimates of total species richness are important to researchers in various fields (Walter & Morand, 1998). As expected, direct species observation techniques undoubtedly underestimated species richness in both stream systems of the present study (Figure 2.4 and 2.5). Since sampling was nowhere near exhaustive (*i.e.* the species accumulation curve failed to asymptote), the estimation tools were very useful and probably represent the most powerful statistical method available in terms of generating comparable and reliable estimates of species

richness in ecology and biodiversity assessment and monitoring. Since there exists no right or wrong outcome to the number of species generated by the richness estimators, the results can be used to determine whether they over- or underestimated the species number (Glowacki & Penczak, 2005).

Species richness estimators that asymptote accurately and early with smaller sample sizes can be considered 'good' estimators (Colwell & Coddington, 1994). In the present study, none of the estimators used reached an asymptote for either data set. Other studies have shown that species accumulation curves fail to asymptote (Paller, 1995; Hughes *et al.*, 2002) as additional species are captured with increasing sampling effort (Kanno *et al.*, 2009). However, in this study, the nonparametric estimator of Chao 2 for Sg. Peres and Chao 1 for Sg. Dungun provided the best overall performance. These stabilised relatively quickly as more individuals were added to the data sets, and were in accordance with Toti *et al.* (2000) as 'good' estimators since they reached (or at least closely approached) a stable asymptote with fewer samples than were required for the observed species accumulation curve to reach the same (Figure 2.4 and 2.5 respectively). Even though Chao 2 returned an estimated value among the highest of all estimators used, the value was generally acceptable. However, for the Sg. Dungun tributaries data set, Chao 1 performed better and yielded an estimate that was lower but slightly different from the other estimators used. In both cases, the estimators were able to provide a close-to-reasonable visual extrapolation of the observed species accumulation curve asymptote. In both data sets, richness estimator curves seemed to coalesce with species accumulation curves as sample sizes increased. This suggests that the estimation of 51 species at Sg. Peres and 46 species at upper Sg. Dungun by Chao 2 and Chao 1 respectively may represent quite reliable predictions.

At Sg. Peres the species accumulation curve did not approach an asymptote. However, only the Chao 2 estimator displayed a potential sign of convergence should sampling have been continued. For the Sg. Dungun data sets, the species accumulation curve also failed to reach asymptote and in fact was still rising, but the Chao 1 and Chao 2 curves suggest a tendency to plateau and seem to converge with the S_{obs} value. The number of singletons in the sample was declining, implying that continued sampling would have resulted in the capture of fewer additional species from those tributaries. This infers that species richness in the tributaries of Sg. Dungun was within the range suggested by the richness estimators.

Thus, the estimated values can be considered accurate and reliable, at least for Chao 1. Chao 2 also exhibited a downwardly-orientated curve, and therefore the possibility to converge with S_{obs} .

Chao 2 is known to perform better for various data sets and is usually regarded the best estimator (Colwell & Coddington, 1994; Chazdon *et al.*, 1998) for incidence data as opposed to Chao 1 (but see Walter & Morand, 1998) that is usually perform well for occurrence data set. As an abundance-based estimator Chao 1 performs better in samples with large number of specimens (Sorensen *et al.*, 2002), and this was demonstrated in the present study in which more specimens were collected from tributaries of Sg. Dungun than Sg. Peres (740 v. 547 specimens). However, even when all 740 individual collected from Sg. Dungun were included the curve was far from converging with S_{obs} . At low sample sizes Chao 1 underestimates true species richness (Hughes *et al.*, 2001) and only considers sampling complete when all species are represented as doubletons or greater (Coddington *et al.*, 1996). In contrast, Chao 2 performs well at small sample sizes and is relatively insensitive to sample density and species patchiness (Longino *et al.*, 2002; Magurran, 2007). This was demonstrated here by the Sg. Peres data set for which Chao 2 performed relatively well compared to the other estimators. According to Coddington *et al.* (1996) Chao 2 considers the inventory complete when the number of duplicates in a given samples begins to decrease.

Several studies have demonstrated that discontinuous distribution of species over a large spatial scale (Kanno *et al.*, 2009) slows species accumulation and influences its shape (Chazdon *et al.*, 1998) which in turn affects estimated species totals, and sporadic distribution of fish species may be caused by specific habitat preferences. Stream fishes are known to associate with certain habitat types (*e.g.* pools and riffles, Eros *et al.*, 2008) and in many cases, not all microhabitat-types are present in all stream sections. Such discontinuous species distribution may explain the high number of singletons recorded in this study in both stream systems (Kanno *et al.*, 2009, see below).

The final inventory in this study apparently sampled between 67 to 89% and 65 to 91% of fish species richness in the Sg. Peres and upper catchment of the Sg. Dungun, respectively. Sampling in the Sg. Dungun produced more favourable estimations of species richness because sampling was close to completion *i.e.* the singletons curve was declining

(Magurran, 2007). The number of observed species is always an underestimate of total species richness when sampling is not exhaustive (Walter & Morand, 1998). It has also been noted that in general richness estimators are highly influenced by the number of rare species present (Bossart *et al.*, 2006) and that both S_{obs} and estimated species richness tend to diverge considerably if the ratio of singletons to doubletons (or unique to duplicates) is greatly skewed. A high proportion of rare species will also escalate estimates of species diversity (Coddington *et al.*, 1996). When species abundance distribution is highly skewed and species number is inadequate, Chao estimators generally provide accurate estimates of species richness from small sample sizes (Gimaret-Carpentier *et al.*, 1998).

2.4.2 Species assemblages

The number of fish species recorded from Sg. Peres was slightly less than that recorded from Sg. Dungun (37 vs. 42 species, Table 2.2). Even though the number of species in the Sg. Peres was comparatively less with respect to species abundance, both diversity indices measuring relative abundance of the fish communities sampled indicated that Sg. Peres was more diverse than Sg. Dungun. Shannon's H' value for Sg. Peres was higher and attained a stable value (2.75) but for tributaries of Sg. Dungun it failed to level off even after all individuals were added to the data set (Figure 2.6). Diversity index curves for both Shannon's H' and Simpson's $1/D$ stabilised more rapidly for Sg. Peres than Sg. Dungun. This showed that species richness of Sg. Peres was more rapidly determinable, and from a lesser number of fish specimens collected. Consequently, less effort was required to determine the number of species inhabiting Sg. Peres than Sg. Dungun. However, greater variance was displayed by Simpson's $1/D$ mean for Sg. Peres, showing that the individual samples collected from Sg. Peres contained a greater variety of species number compared to those from Sg. Dungun. The evenness values for the two streams indicate a more even distribution of relative abundance both within and between fish species in Sg. Peres than Sg. Dungun.

Diversity indices show how species abundance is dispersed among the different species which comprise a given population (Gimaret-Carpentier *et al.*, 1998), whereas diversity measures such as Shannon's H' are weighted by relative abundance of the most abundant species (Krebs, 1985), and are more sensitive to sample size (Gimaret-Carpentier *et al.*, 1998) and equality of species distribution. The Simpson reciprocal diversity index did not

deviate greatly for either stream system sampled in this study and failed to attain a constant value (Figure 2.7). However, the value of $1/D$ approached a constant figure once the data set exceeded 500 sampled individuals in the Sg. Peres. This index was sensitive to the high occurrence of rare species and consequently achieved asymptote only after dominant species were included in the sample (Gimaret-Carpentier *et al.*, 1998). The evenness value for Sg. Peres was slightly higher than for the 12 streams of the upper Sg. Dungun (Table 2.2) though the difference was hardly noticeable and therefore insignificant. Shannon's index was more sensitive to sample size and thus perpetually underestimated species diversity in the study areas.

Both communities were dominated by a few very abundant species and the vast majority of specimens were of these few predominant species. In a diverse community where species are more equally represented, randomly encountered individuals are more likely to represent different taxa (Purvis & Hector, 2000). In the present study, diversity indices demonstrated that the fish community in Sg. Peres was richer than that of Sg. Dungun but interestingly, rarified richness values for the lowest number of individuals collected from the two communities confirmed that there were more species at the upper drainage of Sg. Dungun than that at Sg. Peres when quantified as a single measure of diversity. This was consistent with theoretical expectations of species-area relationships *i.e.* that species richness increases concurrently with area sampled, with larger areas tending to support more species compared to smaller areas. However, the species accumulation curves in both stream systems failed to level off indicating that sampling was not complete.

In this study, the inventory obtained was approximately 67 to 89% and 65 to 91% of fish species richness expected to occur at Sg. Peres and the upper catchment of Sg. Dungun, respectively. Sampling effort was appropriate, and sampling over a short distance in the Sg. Peres resulted in five fewer species being recorded than at the upper catchment of the Sg. Dungun (where streams were considered more adequately sampled). Several authors have suggested that 90-95% capture of observed species is considered sufficient for a given sampling location (Hughes *et al.*, 2002; Dauwalter & Pert, 2003). Here, the number of species recorded for a small stream (Sg. Peres) was relatively high despite the short sampling distance, which was considerably less than recommended by many researchers (more than 20-85 mean stream width, MSW; Paller, 1995; Hughes *et al.*, 2002; dos Anjos & Zuanon, 2007; Hughes & Herlihy, 2007).

Studies on fish diversity within single stream sections are lacking for Peninsular Malaysia meaning detailed comparison of the number of species obtained at Sg. Peres with other stream systems is not possible, plus sampling effort was slightly dissimilar among investigators. However, Samat *et al.* (2005) reported 24 species from two sections of the Sg. Rengit in the Krau Wildlife Reserve, Pahang which comparatively equivalent to the size of Sg. Peres. For a single stream section, Sg. Peres definitely harboured relatively high species richness compared to relatively similar stream system such as studied by Samat *et al.* (2005).

The number of fishes inhabiting the upper reaches of Sg. Dungun was slightly higher than in Sg. Peres, and comparable to the findings of similar studies of multiple stream reaches in Peninsular Malaysia. Lim *et al.* (1990) recorded 47 species of freshwater fishes from streams and rivers of the Endau-Rompin drainage, Johor-Pahang, Peninsular Malaysia. Zakaria-Ismail (1993) recorded 54 species of fishes from montane and lowland streams within the Krau Game Reserve, Bukit Rengit, Pahang, and Zakaria-Ismail & Lim (1995) 23 species of fishes caught from four tributaries in Temenggor reservoir, Perak. Similarly, Samat *et al.* (2005) reported 29 species from two stream reaches of the Sg. Rengit, Pahang, Mohd-Sham *et al.* (2005) 45 species from five streams in Sungkai Wildlife Reserve, Perak and Ambak & Zakaria (2010) 36 species from five streams of the upper Kelantan River, Peninsular Malaysia. A survey conducted by Watson & Balon (1984) in a tributary of the Baram River, Sarawak recorded 57 species while Martin-Smith & Tan (1998) reported 47 species from the upper Segama River, eastern Sabah, in Malaysia after intensive sampling over a period of two years. However, in the latter survey sampling effort was greater than in the present study, the rivers involved were larger and in the case of the upper Segama, sampling was conducted over a much longer period. Although sampling intensity (individuals : species) for both stream systems in my study was basically not exhaustive, I am convinced the number of species obtained was accurate and reliable. This was supported by the low adjusted estimate ranges (sums of all estimator values : S_{obs}) which suggest that the estimated values do not varies greatly in both data sets.

In many community censuses, the number of species initially accumulates quickly as the commonest are collected, but then increase more slowly as rarer, infrequently captured taxa are added (Gotelli & Colwell, 2001; Kanno *et al.*, 2009). Since both rarity and

frequency of species occurrence have been known to affect the reliability of species richness estimates and comparisons between assemblages (Foggo *et al.*, 2003; Gotelli & Colwell, 2001), it was worthwhile here to further examine the natural history of the rare species recorded from the two stream systems. Longino *et al.* (2002) used the term “edge” when referring to rare ant species in their study and grouped these into two assemblages, which they termed “methodological” and “geographic” edge species (See Appendix 2.6).

In the current study, several geographically rare species, *i.e.* those that are strongly seasonal and potamodromous, *i.e.* migrated from large river to small stream (group 3) were rare but not unique. When in season *i.e.* breeding, they can be collected in large numbers from small tributaries which they enter to spawn, usually during the rainy season (pers. obsv.). Fishes often undergo seasonal movements (Matthews, 1998) between different reaches of specific streams (downstream-upstream movement) *e.g.* Sg. Peres, or move from one part of a river system to another (Glowacki & Penczak, 2005) *e.g.* Sg. Dungun. Most of the species reported as rare during this study were either solitary or in-group, frequently small-bodied and living over or within the substrate (Figure 3.9, Group 2 and 4). Repeat sampling at different times of year or the simultaneous application of several different data collection methods should therefore be sufficient to overcome or eliminate such episodes of rarity.

Novotny & Basset (2000) acknowledged several factors that define a species as rare: solitary species can be so due to low population density, while in-group species may be rare because their preferred habitat is lacking within the areas sampled. Sampling equipment may also contribute to the purported rarity of some species if not designed to adequately capture them. For example, fish species inhabiting woody debris on the streambed will not be collected *via* electrofishing. However, the general pattern of a species assemblage comprising few, common and many, rare species is repeated in many communities and across various taxa (Magurran & Henderson, 2003).

Of the 33 species collected from the two study sites, which may be considered rare, probably one-third were in fact not rare (demonstrating a high total abundance when the two data sets were combined). However, of the 15 species for which total abundance remained low (singletons and doubletons), at least five were ‘group 3’ fishes and one group 4, and these could potentially be removed from the list of rare species if sampling

was repeated at different times of the year. All the remaining six rare species were singletons belonging to two specialised groups and inhabiting limited ecological niches. The *geographically rare* and *global unique* species included a bagrid catfish (*Mystus castaneus*, family Bagridae) and a fighting fish (*Betta stigmosa*, family Osphronemidae). *Mystus castaneus* has a wide distribution in Peninsular Malaysia but it is seldom collected in large numbers (see *Material examined* in Ng, 2002). The type series of *Betta stigmosa* was obtained from Sg. Peres (see Tan & Ng, 2005), but in this study not a single specimen was collected there. This species has a limited distribution in Peninsular Malaysia but was previously collected in relatively large numbers (see *Material examined* in Tan & Ng, 2005) from the type locality. Both *Acrochordonichthys rugosus* and *A. septentrionalis* (family Akysidae) are rarely found in Peninsular Malaysia (see Ng & Ng, 2001), though the former was more frequently recorded (*methodologically rare*) compared to the latter (*geographically rare*) (see *Material examined* in Ng & Ng, 2001 for both species). Another *geographically rare* species was a silurid catfish (*Ompok siluroides*, family Siluridae) that can usually be found in standing waters of lakes, swamps, slow flowing rivers and heavily-obstructed pools in small streams and has never been recorded to occur in large numbers in small stream habitats of Peninsular Malaysia. The slender loach (*Pangio piperata*, family Cobitidae) was another *methodologically rare* species recorded at Sg. Peres. It can easily be collected from leaf litter and woody debris using a hand-held push net and was previously common here (pers. obsv., but see also *Material examined* in Kottelat & Lim, 1993), but electrofishing was probably not an efficient sampling method meaning its presence in the sample was unexpected.

Tolerant species demonstrate a greater ability to adapt to habitat degradation or utilise a wider range of habitat than some restricted species. All resident fish species of two small streams were successfully recorded in this study with a few composing the majority of species collected. Of the six commonest species (>5% total abundance), only five, all frequenting small, fast-flowing headwater streams, were present in both communities. A carp-like species, *Neolissocheilus soroides* (family Cyprinidae), was locally abundant at Sg. Dungun but not recorded from Sg. Peres, though this was likely because the sampling plots at Sg. Peres were not extended above a waterfall further upstream, where *N. soroides* was probably more abundant. Five of the commonest species were members of the family Cyprinidae, the most widespread family of freshwater fishes in Peninsular Malaysia (Mohsin & Ambak, 1983). Most of these species were relatively tolerant and utilised a

wider variety of resources and habitat with the exception of *N. soroides* which is an obligate dweller of pristine, fast flowing streams. All five are “open spawners” normally considered to display effective dispersal and an efficient mode of breeding. Likewise, these species are characterised by traits inferring a degree of resistance to habitat alteration and deterioration, *i.e.* they are generalists in terms of resource utilisation, meaning they are expected to occur in numbers in many small streams of Peninsular Malaysia.

2.5 Conclusion

Species diversity values, which were measured by both observed and estimated species richness were generally variable – observed species richness always provided an underestimate of true species richness while the result varied among species richness estimators depending on the type employed. Observed species richness was directly affected by species abundance and correlated positively with sample size (McCabe & Gotelli, 2000) until sampling was close to exhaustive. Nonparametric estimators proved to be a powerful and effective alternative (Brose *et al.*, 2003) for assessments of total species richness as they reduced bias (to a certain degree) and were independent of sample size (above a given minimum). In this study, sampling effort was considered adequate for the species accumulation and estimate curves to converge. For the Sg. Peres data sets, the proportion of rare species was low, Chao 2 performed best and displayed signs of convergence with the species accumulation curve. For the Sg. Dungun data set, Chao 1 performed best with the proportion of rare species over samples predominant. In summary, sampling effort was far from sufficient to accurately estimate species richness in either stream system.

Most of the species richness estimators used was highly influenced by the number of rare species recorded. The presence of a large number of singletons compared to doubletons in the sample was responsible for the significant degree of divergence between observed and estimated species richness curves. Performance graphs indicate that asymptotic species richness estimator curves may not always be reliable estimates of true diversity. Data sets for which observed and estimates curves coalesce regardless of the estimators employed may indicate that true species richness has been exemplified by the sampled community. Therefore, separation of these curves in the current study illustrated the possibility that additional species may have been recorded with additional, more intensive sampling. The extrapolation method appears capable of producing accurate and reliable estimates of species richness (Brose *et al.*, 2003) and proved very useful under constraints of time and cost. It therefore shows potential for further application in biodiversity research, and in particular inventory-based studies.

The majority of rare species recorded in this study can be regarded as artefacts of both methodological and geographic edge effect rather than actual rarity (Longino *et al.*, 2002). Seasonally abundant species, which mostly consisted of potamodromous species, made up a significantly proportion of the rare species inventory. Other species were apparently rare because sampling was not extended to cover different times of year as well as the limited capture methods employed. Several species for which only a small number of individuals were collected in this study could therefore have been reversed had alternative methods been utilised. However, it should be noted that several genuinely rare species well-known to have limited distributions in Peninsular Malaysia were captured at the two study sites in small numbers. The common species *i.e.* resident population of these communities were thoroughly recorded, meaning that electrofishing can be regarded as an effective tool for rapid fish collection and population assessment, plus generation of viable, trustworthy data to estimate the species richness of small streams in Peninsular Malaysia.

CHAPTER 3

THE EFFECT OF DISTURBANCE ON DIVERSITY AND COMMUNITY STRUCTURE OF SMALL STREAM FISHES IN PENINSULAR MALAYSIA

3.0 Abstract

Prior assessment studies regarding the impact of anthropogenic disturbances on freshwater fishes in Malaysia are not only limited in number but also traditionally performed in large rivers associated with dams as stipulated by Environmental Impact Assessment (EIA) regulations. In this chapter, I therefore consider the effects linked to small-scale, localised alterations of varying magnitude on fish communities inhabiting nine small stream systems in Peninsular Malaysia. Rarefaction analyses indicated that fish species richness was relatively similar at all selected sites, but fish abundance appeared to decrease when disturbances were apparent. Rank-abundance plots suggested that all communities were typified by a handful of common fishes occurring alongside numerous relatively rare species. Moreover, the identities of such locally dominant taxa at disturbed sites (*e.g.* *Crossocheilus oblongus*, *Poropuntius smedleyi* and *Cyclocheilichthys apogon*) differed slightly from those present at more intact localities (*e.g.* *Devario regina*, *Glyptothorax major* and *Rasbora elegans*). That said it remains premature to conclude that the latter are explicitly sensitive and thus their potential utility as bioindicators of disturbance-influenced community changes remain to be confirmed. Diversity index (Shannon H') estimates were comparatively uniform with little differentiation between disturbed and undisturbed fish communities. Changes in community assemblage structures were not clearly noticeable either, as Morisita-Horn index and mean rank shift values for each community were fairly identical. Moreover, it was not possible to separate pristine and disturbed sites using community classification, and taxonomic composition were similar for both years. These findings suggest that maintenance practises being applied to small streams modified for recreational usage were not imposing detectable negative consequences, at least across the sites sampled in this study.

3.1 Introduction

Under normal circumstances, ecological patterns and processes are determined by biotic interactions, abiotic (environmental) constraints and habitat disturbance. Previous studies have shown that both natural phenomena and the activity of humans can inflict significant negative impacts on biological diversity. Magurran & Dornelas (2010) stated that anthropogenic changes directly threaten biodiversity while Mace *et al.* (2010) found that localised declines in species range and abundance were more strongly linked to environmental degradation caused by human interference than ecological or biological determinants. Using a simulation model, Dornelas (2010) predicted that disturbances influencing carrying capacity were likely to have the most serious ramifications for species richness in isolated communities.

3.1.1 Modification, species diversity and community structure of small streams

Freshwater fish diversity and community structure can be adversely affected by various disturbance types including acidification (Heard *et al.*, 1997; Warren *et al.*, 2010), drought (Davey & Kelly, 2007; Pires *et al.*, 2010), habitat alteration (Eros *et al.*, 2003; Eros *et al.*, 2008; Holcik, 2003; Wang *et al.*, 2001) and fragmentation (Poulet, 2007), impoundment of streams and rivers (Herbert & Gelwick, 2003; Quinn & Kwak, 2003; Hoeinghaus *et al.*, 2009), reduction in habitat and water quality (Walter & Post, 2008; Vila-Gispert *et al.*, 2002; Benejam *et al.*, 2010), introduction of exotic species (Cambray, 2003; Olden *et al.*, 2010) and overfishing (Allan *et al.*, 2005). Localised species extinction is promoted by habitat loss and fragmentation with the latter is exaggerated by urbanisation (Wang *et al.*, 2001; Quinn & Kwak, 2003) and extensive agriculture, especially large-scale monoculture plantations that lead to removal of the riparian zone (Pusey & Arthington, 2003). Table 3.1 includes some examples of natural and anthropogenic impacts on species richness and community structure.

Table 3.1. Previous studies on the effect of disturbance on species richness and community structure in streams and rivers.

Reference/attribute	Type of disturbance	Response
<u>Natural disturbance</u>		
Heard <i>et al.</i> (1997)	Acidification	Reduced community structure
Warren <i>et al.</i> (2010)	Stream pH	Lower pH decreased community structure
Eros <i>et al.</i> (2003)	Habitat patchiness	Disconnected habitat reduced diversity
Lake (2003)	Drought	Loss of habitat connectivity; decreased
Franssen <i>et al.</i> (2006)	Flood	Increased colonisation
Davey & Kelly (2007)	Drought	Species responded differently to drying
Pires <i>et al.</i> (2010)	Drought	Fish refuges to pool during drought
<u>Anthropogenic – stream alteration</u>		
Chang <i>et al.</i> (1999)	Building dam	Reduced connectivity and species diversity
Wang <i>et al.</i> (2001)	Urbanization-impervious	Reduced fish species richness and habitat
Herbert & Gelwick (2003)	Impoundment	Varies discharge influencing fish
Holcik (2003)	Large scale modification	Abrupt declined in fish fauna
Quinn & Kwak (2003)	Impoundment	Reduced species richness and diversity
Morgan & Cushman (2005)	High urbanization	Decreased fish abundance and richness
Freeman & Marcinek (2006)	Water withdrawal	Declining in species richness
Poulet (2007)	Weir	Strong impact on fish communities,
Eros <i>et al.</i> (2008)	Bank embankment	Increased fish biological traits
Walter & Post (2008)	Water diversion	Reduced fish size
Benejam <i>et al.</i> (2010)	Water abstraction	Reduced fish assemblages
Kanno & Vokoun (2010)	Water withdrawal	Changed species composition
<u>Anthropogenic – others</u>		
Cambay (2003)	Introduced species	Impacted biodiversity
Vila-Gispert <i>et al.</i> (2002)	Pollutions	Polluted areas reduced fish assemblage
Cambay (2003)	Recreational fisheries	Impacted biodiversity

Natural and anthropogenic disturbances can cause a reduction in overall habitat health, with decreases in vegetation diversity and quality among the most commonly-encountered impacts alongside others such as increases in the number of introduced species and chemical pollutants, all of which may lead to a decline in breeding capacity of certain species. Recent studies have shown that desiccation (Lake, 2000; 2003; Davey & Kelly, 2007; Bond *et al.*, 2008; Pires *et al.*, 2010) and episodic acidification events (Heard *et al.*, 1997) not only cause a reduction in stream fish diversity but also impinge upon species composition. In his review, Lake (2000) stated that drought-related disturbances in streams bring about destruction and fragmentation of favourable habitat, meaning species that may not otherwise inhabit such pools (*e.g.* riffle specialists) congregate there during drought periods as such biotopes offer the most suitable conditions and greater structural

complexity (Pires *et al.*, 2010). Eros *et al.* (2003) concluded that fish community structure correlates positively with the habitat continuum, while reductions in pH have been reported to be associated with a decrease fish biomass (Warren *et al.*, 2010) in headwater streams of the northeastern United States.

Biological invasions are an additional, well-examined threat to local species richness and community assemblages (Garcia-Berthou & Moreno-Amich, 2000; Cambray, 2003). In the Iberian Peninsula, a discernible upturn in localized extirpation events coupled with a strong downturn in native species populations has been largely attributed to the rapid establishment and expansion of exotic species in the region (Garcia-Berthou & Moreno-Amich, 2000). Cambray (2003) demonstrated that introduction of invasive fishes for sport fishing has caused considerable disruption to native ecosystems in many countries.

Higher habitat heterogeneity has been associated with increased species richness (Arunachalam, 2000) in streams of the Western Ghats, India, and temporal, heterogeneous climatic characteristics, chemical or environmental constituents associated with such habitats are another important factor influencing resident fish communities (Jackson *et al.*, 2001). According to Beamish *et al.* (2006) fish species abundance in streams across central Thailand decreased correspondingly with water discharge while richness was affected inversely by habitat breadth and positively by ambient oxygen and alkalinity values.

Many authors agree that land use over the macro-scale is the primary negative influence on streams across the globe (Matson *et al.*, 1997; Iwata *et al.*, 2003), although other forms of land-cover such as agriculture and urbanisation also typically create detrimental repercussions for both terrestrial and aquatic ecosystems. Nevertheless, some studies have proposed that disturbance does not necessarily induce significant negative change (Wolda, 1987), and may even facilitate an upturn in community diversity (Hill *et al.*, 1995, Hamer *et al.*, 1997; Spitzer *et al.*, 1997). Increases in species richness are often driven via invasion of disturbed areas by generalist and/or widely distributed species, and the resultant, ongoing homogenisation of the world's biological communities is among the major threats to biodiversity maintenance at the global scale. The chief environmental impacts of natural and anthropogenic disturbances on streams can thus be summarised as: (1) increase in habitat loss and/or fragmentation; (2) simplification in habitat complexity; (3) lower discharge rate and water level; (4) deterioration of water quality.

3.1.2 Intermediate Disturbance Hypothesis and community stress

The concept known as the "intermediate disturbance hypothesis" (Figure 3.1) was first proposed by Connell (1978) and based on the assertion that "*the highest diversity is maintained at intermediate levels of disturbance*". The environmental stress model (ESM, see Menge & Sutherland, 1987) made similar predictions. The former presents considerable practical implications (Townsend *et al.*, 1997) in terms of biodiversity maintenance, within which species richness is the most basic component, since it essentially predicts that species diversity should be highest when under intermediate disturbance pressures. The bases of the theory are that minor habitat disruptions allow superior competitors to dominate resources (Dornelas, 2010), while intensive modifications inhibit the ability of less resistant species to flourish, with reduced diversity the result in both cases.

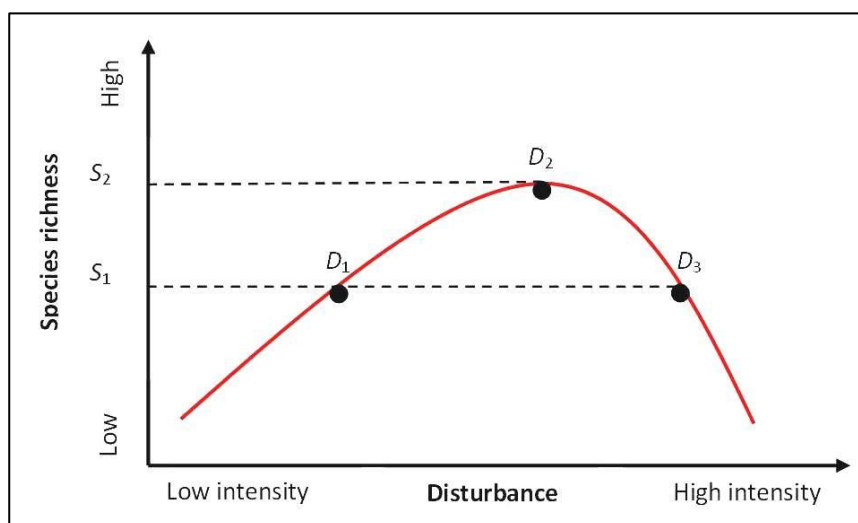


Figure 3.1. Schematic presentation of the intermediate disturbance hypotheses (IDH). S_1 and S_2 are species richness and D_1 , D_2 and D_3 indicate the different levels of disturbance. At an intermediate level of disturbance (D_2) IDH predicts that there are more species (S_2) than at both low and high disturbance levels (D_1 and D_3).

There exists much evidence to suggest that intermediate disturbance imposes only minor negative consequences on species richness (Fox, 1979; Molino & Sabatier, 2001; Bertrand *et al.*, 2004). Fox (1979) demonstrated that cyclone-disturbed forest on the north coast of Kolombangara Island, SW Pacific, exhibited greater species diversity than the 'pristine'

west coast. Bertrand *et al.* (2004) found that algal community structure conformed to the intermediate disturbance hypothesis.

Flowing streams are highly dynamic systems exposed to perpetual natural disturbances and can thus be classified as relatively harsh habitats characterised by extreme, unpredictable environmental conditions. In such ecosystems, fish assemblages are thought to be primarily structured by abiotic factors as such anthropogenic disturbances can readily impose detectable, negative consequences on their integrity and native aquatic communities. However, the specific effect(s) of anthropogenic disturbances on fishes in small streams has never been thoroughly investigated in Peninsular Malaysia or indeed throughout much of tropical Southeastern Asia. Small stream fishes are under increasing pressure from human activity around the world due to a variety of stresses including habitat modifications, overfishing, land-based pollution and eradication of juvenile microhabitats or feeding grounds. It is clearly essential to understand how aquatic biological communities respond to anthropogenic disturbances in order to better manage the ecosystems and their associated resources.

Small streams comprise a significant proportion of Peninsular Malaysia's terrestrial landscape. Many are exploited by local residents for a variety of reasons including in some cases household and agricultural water supply or recreation. The fishes inhabiting them are seldom regarded as an important fisheries resource hence their diversity is not widely reported nor fully understood. Moreover, tropical freshwater fish communities are typically diverse with up to 35 species recorded from even moderately-sized streams (Inger & Chin, 1962; Watson & Balon, 1984; Martin-Smith, 1998b) and representing a number of important taxonomic groups (Martin-Smith, 1998c).

In Malaysia, concern over the large-scale conversion of primary tropical forest for agriculture and the resultant side-effects on aquatic ecosystems, particularly the comparative response of fish communities to such intensive alteration, has been investigated in the past (*e.g.* Martin-Smith, 1998b), but for general review, see Blackie *et al.* (1980) or Campbell & Doeg (1989). Although the consequences of logging with regard to the physical and biological properties of forest streams are conspicuous and thus well-researched, the increasingly prevalent influences applied by localised disturbances such as utilisation of particular stretches for recreation, short-stream channelization, removal of

overhanging or riparian vegetation and woody debris on fish communities are not well-documented. Since there are usually no immediately quantifiable signs of degradation, minor habitat alterations are thus often overlooked and neglected in terms of appropriate research.

Tropical freshwater fish assemblages are typically diverse and many native species of which the majority are dependent on pristine streams to some extent (Sutton & Collins, 1991). When compared with invertebrate groups native to Peninsular Malaysia fishes are more easily visible and their taxonomy is well-known. Stream fauna, including fishes, are likely to be particularly affected by artificial disturbances - yet relatively few studies have focussed on them despite their dominance of the stream faunal community in terms of species richness, abundance and biomass. Fishes are therefore appropriate subjects to be used as representative model organisms in impact studies of altered aquatic ecosystems.

This study therefore aims to assess the nature and extent of effects caused by habitat alterations on fish community structure and species diversity in small streams of Peninsular Malaysia. The impact of anthropogenically-controlled disturbances on these characteristics is described and discussed in the context of earlier, complementary studies conducted throughout the tropics. The baseline hypothesis, which predicts that non-natural disturbances (often associated with direct, physical modifications to the stream or the surrounding terrain) reduce biointegrity within a given ecosystem and lead to detrimental shifts in species diversity and assemblage structure, is used as a frame of reference throughout interpretation of results.

3.2 Methodology

3.2.1 Study sites and sampling

The climate of Peninsular Malaysia is relatively stable and characterised by a principal wet season between November and February plus a shorter one in June and July, with sporadic, torrential rainfall events occurring throughout the year. Annual precipitation varies from 2000 to 4000 mm, and all small streams are therefore subjected to a degree of natural disturbance. In order to reduce the likelihood of disproportionate fish species distribution adversely influencing results, plots representing ‘undisturbed’, ‘moderately disturbed’ (referred to herein as ‘intermediate’), and ‘disturbed’ were selected within each stream system sampled (see Appendix 3.1). Throughout this study, ‘disturbance’ is broadly defined to represent any form, factor or other alteration associated with anthropogenic influence, *e.g.* modification of particular stream stretches, artificial stabilisation of banks, removal of riparian vegetation, *etc.*

Field data collections (Figure 3.2) were conducted over two periods between the months of August to September 2008 and May to July 2009 using multiple-pass electrofishing. At each site, such sampling was performed on three 25 m plots chosen to represent both fast and slow-flowing stream stretches exhibiting varying degrees of anthropogenically-influenced disturbance. Plots were isolated using 3 mm block-nets at up- and downstream extremities in order to prevent escapes and maximize catch efficiency. A minimum of two passes were made with a backpack electrofisher at each plot, and all stunned fish specimens were collected by two assistants using long-handled scoop-nets. In each case, external observation involving walking the length of the plot or when necessary snorkelling was employed immediately after the final pass in order to collect specimens snagged among boulders or other submerged structures. In total nine small, lowland foothill streams comprising three stream sections located within each of the northwest, south and eastern biogeographical regions of Peninsular Malaysia, respectively, and featuring varying degrees of disturbance, were sampled. Fish individuals were identified to the most basal taxon possible, and their standard length and weight recorded. The majority were returned to the water with voucher specimens of all species logged in the University Malaysia Terengganu Ichthyological Collection (UMTIC).

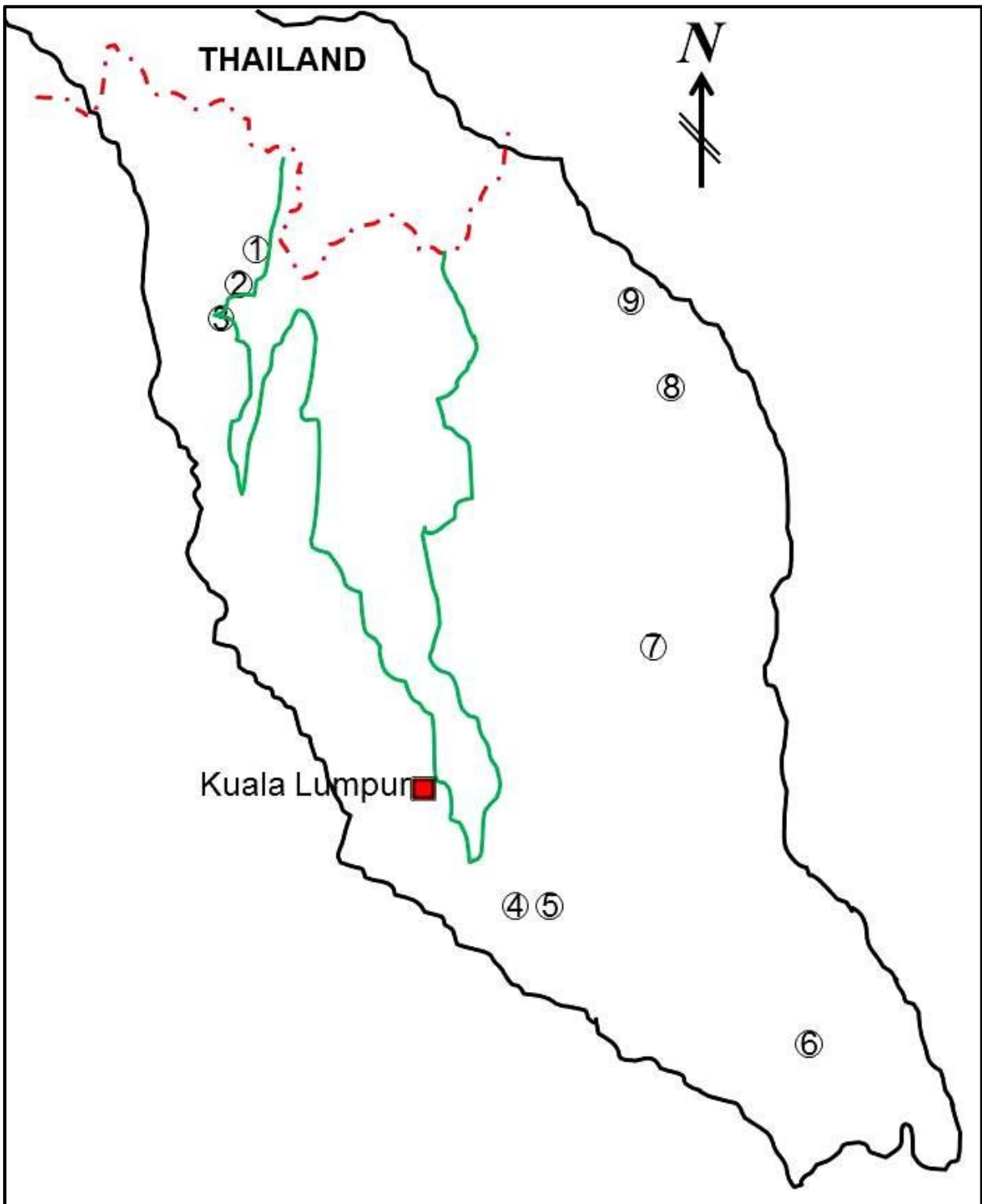


Figure 3.2 Map of Peninsular Malaysia showing the approximate locations sampled in this study. Green line denotes Banjaran Titiwangsa, the mountainous range extended south from Peninsular Thailand. Sites no. 1 = Chepir, 2 = Bayu, 3 = Hijau, 4 = Bendul, 5 = Tengkek, 6 = Berlumut, 7 = Berkelah, 8 = Peres and 9 = Belatan, respectively.

3.2.2 Data analysis

Species richness and assemblage composition

The diversity of resident fish species assemblages was assessed in a number of ways. Initially, simple species richness (number of species) was determined for each plot. Sample sizes were standardised *via* rarefaction statistics provided by the *EcoSim* program (Gotelli & Entsminger, 2003) and computed to 100 iterations and independent sampling of randomly chosen individuals from the total species pool in each plot. To assist in the process, data sets from plots considered to exhibit comparable disturbance levels were pooled, and species richness subsequently expressed as the number of species occurring within equal sub-sample sizes (this corresponding to a total of 10 identified species among 13 specimens collected from an undisturbed plot in 2008). Interpretation of results was based on simulated 95% confidence intervals again generated by *EcoSim* (Gotelli & Entsminger, 2001; McCabe & Gotelli, 2000). A standard two-way ANOVA was used to determine differences between plots representing the three classes of disturbance and supplemented by a post hoc test using PASW for Windows 2009 in cases where outcomes appeared to denote marked dissimilarities.

Species diversity

In order to ascertain the extent to which relative abundance of fish species is affected by habitat alteration, rank-abundance plots were constructed for each community using combined data for streams of comparable disturbance level. The relative abundance of each species was additionally plotted on a logarithmic scale against the species' abundance ranking, the latter arranged in a graded fashion from most to least abundant (Magurran, 2007).

An index of diversity (Shannon's H') using \log_e was also computed for each fish community to present a simple measure of alpha diversity for all sites, and chosen for its recognised stability across many spatial distributions and insensitivity to changes in rare species abundance (Ludwig & Reynolds, 1988; Pires *et al.*, 1999). In addition, the Morisita-Horn index (Wolda, 1981; Magurran, 2007) was employed to estimate beta diversity. The Morisita-Horn index was selected because it takes account of species

abundances, and although the estimate is influenced by the most abundant species in a given sample (Magurran, 2007), it is not constrained by sample size or overall diversity (Magurran, 2007) and thus offers an acceptable mechanism by which to compare community structure over the two study years. Diversity indices were enumerated by the Multivariate Statistical Package, (MVSP shareware 2.0). The mean rank shift calculation was utilised to evaluate variations in community structure as per Collins *et al.* (2008). This latter formula measures relative fluctuations in species rank abundance over time and can be used to portray temporal changes in species abundance.

Species community structure

A Venn diagram was drafted to examine species overlap between the three communities across both years. Fish census data were then analysed to assess among-site discrepancies in disturbance intensity using non-metric multidimensional scaling (nMDS) ordination based on the Bray–Curtis similarity measure (Clarke, 1993), an index frequently applied in ecological surveys (Clarke & Gorley, 2001; Ellingsen, 2002). A forth-root transformation of abundance figures was carried out using PRIMER6 software (Clarke & Gorley, 2001), allowing it to be visualised in a reduced set of dimensions. In order to present accurate descriptions of the patterns observed, nMDS ordinations exhibiting high stress values (> 0.2) were included only after comparison with less stress-sensitive cluster analyses of the same data. Cluster analysis was also utilised in order to artificially visualise relationships between plots and streams of differing disturbance amplitude. Assessments of concurrence between all possible pairs of plots and streams were conducted using the Bray-Curtis similarity index, and in this case clustering was carried out using Ward’s method based on a single linkage by employing Euclidean distances to the Bray-Curtis results.

A major prediction of this study was that disturbance would induce clear alterations in fish assemblage structure. In order to corroborate this hypothesis, average taxonomic distinctness ($AvTD$, Δ^+), a measure of taxonomic relatedness was calculated for all communities (Clarke & Warwick, 1998). $AvTD$ is a non-parametric measure based on presence/absence data and quantified using PRIMER6 (<http://www.primer-e.com>) software. The six level (Phylum, Class, Order, Family, Genus and species) system of classification utilised by Bhat & Magurran (2006) was followed with the additions of

Superorder, Subdivision and Division in order to more accurately clarify the degree of taxonomic relatedness of species assemblages inhabiting each plot.

3.3 Results

3.3.1 Species composition and richness

Within each of the nine selected stream drainages three plots, all approximately 25m long, were chosen to represent examples of pristine (undisturbed), partially (intermediate) and disturbed fish communities, respectively. Sampling was conducted during 2008 and 2009 and a total of 3754 fishes representing 69 species and 18 families recorded (Appendix 3.2., Table A3.2). The dominant family was Cyprinidae which contributed 26 species followed by Balitoridae with eight and Bagridae seven. Among these the three most common taxa were the cyprinids *Crossocheilus oblongus* (of which 386 individual specimens were collected over the two years fieldwork), and *Poropuntius smedleyi* (335 specimens) plus the sisorid catfish *Glyptothorax major* (327 specimens). A greater number of specimens were collected in 2009 than 2008, although fish abundance was not significantly different ($F_{1, 53} = 0.25$, $p > 0.05$). In both years fish abundance was greater for less-disturbed than disturbed communities but not significantly different ($F_{2, 53} = 3.03$, $p > 0.05$), and there was similarly low divergence between mean values of fish abundance and species richness.

Rarefaction analyses of entire communities across both years were performed to provide a standard of correlation for selected data subsets and facilitate comparison between sites at which sampling efficiency differed. On a rarefied sub-sample of 438 individuals (corresponding to the smallest sample size), fewer species were recorded from the less-disturbed communities in both 2008 and 2009 (Table 3.2). Further, when rarefaction analyses of species abundance were applied to the entire data set the communities designated as undisturbed could not be distinguished from those inhabiting modified environments (Figures 3.3a and b), and the number of fish species collected from disturbed communities falls within the 95% confidence intervals for pristine habitats. Similarly, when rarefaction analyses were applied to selected sample data sets from both years, species richness results for unimpacted communities were not significantly divergent from those disturbed to some extent disturbed ones (Appendix 3.3., Figure A3.1). The rarefied values of species abundance (when species richness is standardised to 13 individuals) also failed to detect any noteworthy dissimilarity between communities ($F_{2, 53} = 0.01$, $p = 0.98$).

Table 3.2. Comparison of fish community statistical results between sites of differing disturbance intensity (n=9). U, I and D refer to undisturbed, intermediate and disturbed communities, respectively.

	2008			2009		
	U	I	D	U	I	D
Total no. of	657	717	438	780	602	560
Mean rel.	73.00±41.91	79.67±50.87	48.67±29.79	86.67±32.20	66.89±34.99	62.22±14.91
Rarefied no.	42.02±2.52	40.65±2.87	43	42.76±2.82	44.08±1.34	45.30±1.39
No. of species	46	45	43	47	46	47
Mean rel.	11.60±3.55	11.10±5.77	9.56±3.43	12.60±4.59	12.30±4.48	11.44±4.72
*Standardized	6.57±2.01	6.11±1.62	6.19±2.08	5.77±1.40	6.19±1.45	6.29±2.13
Singletons	10	9	11	7	6	7
Unique	17	18	20	17	20	18

Note. * Rarefaction analyses was performed based on the smallest number of fish specimens collected at a single locality, *i.e.* 13 individuals at an undisturbed site in 2008, in order to standardise species richness at each community. Singletons are species with only one specimen recorded and unique represent a species that was found only once in the sample.

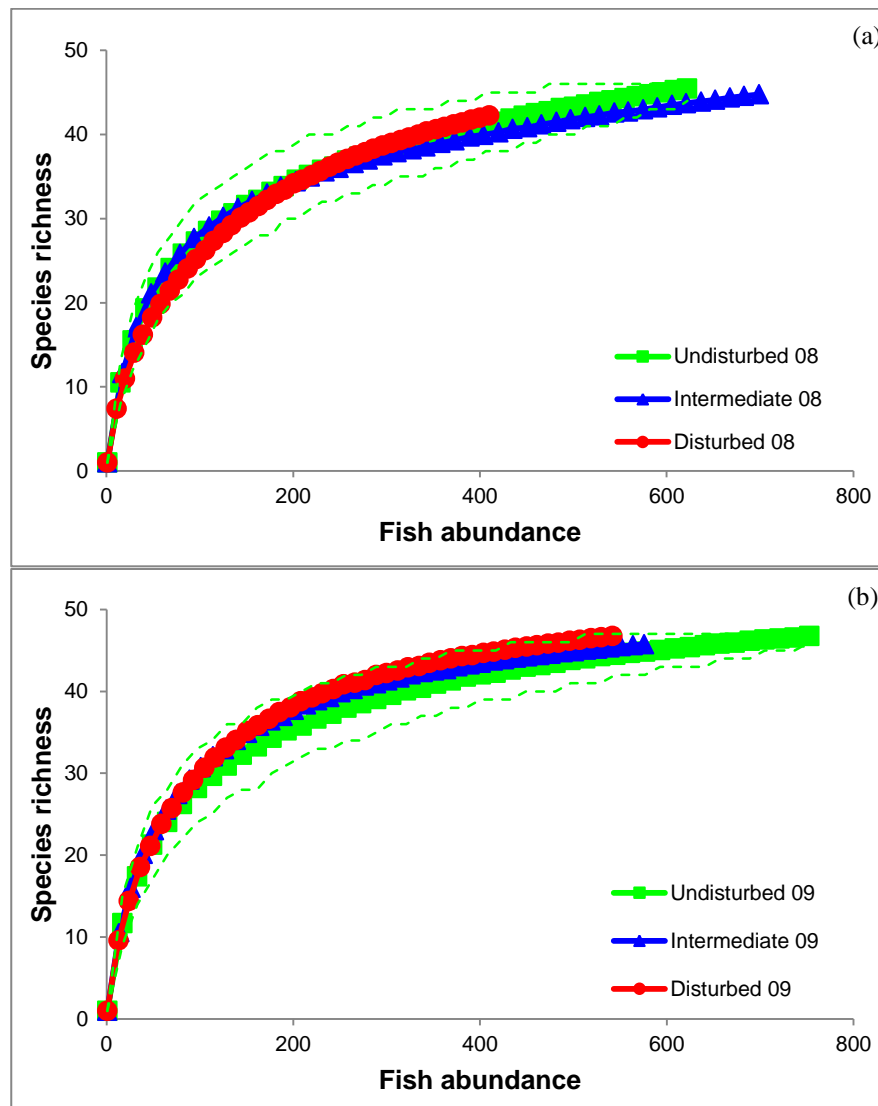


Figure 3.3. Rarefaction curves of fish communities based on the entire data set for each disturbance intensity level in 2008 (a) and 2009 (b). Only the 95% confidence intervals for the undisturbed community in 2009 are also shown to provide additional clarity.

In 2008 a total of 46 species were recorded at the undisturbed community versus 43 at the disturbed whereas in 2009 both were equally diverse with 47 species recorded from each. There was a substantial range of species overlap among the three communities in both years (Figure 3.4, see Appendix 3.4 for species identity), although such instances were more frequent in 2009 than 2008 (36 vs. 33), and in general only a handful of taxa were restricted to a single community (Appendix 3.4).

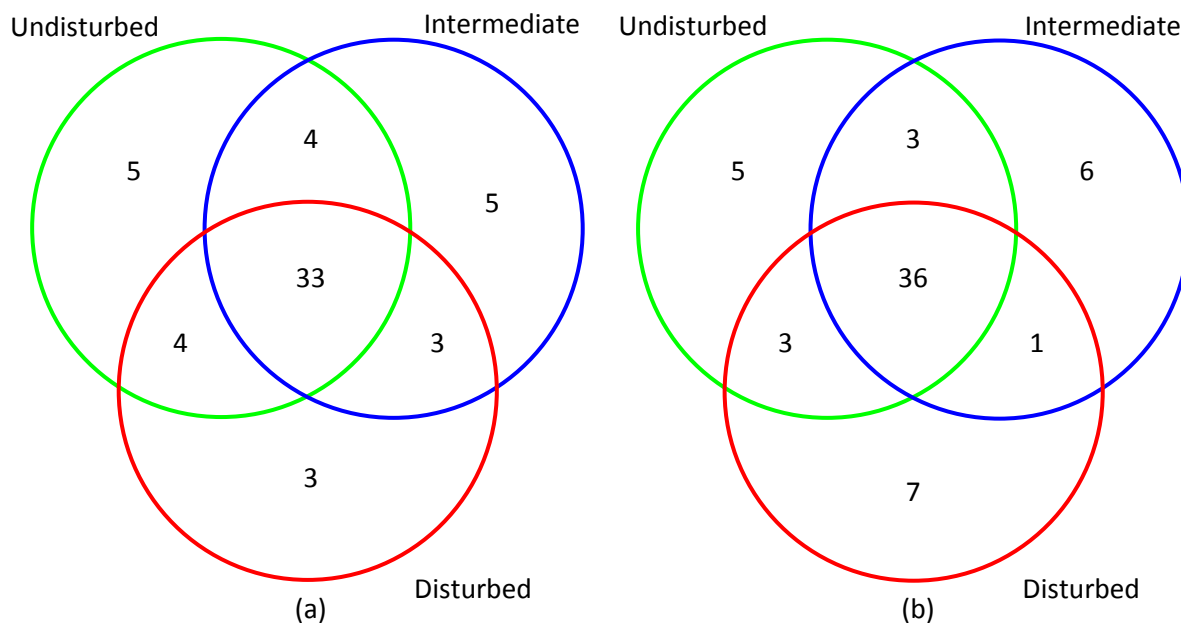


Figure 3.4. Species overlap among the three communities illustrated by Venn diagram and representing the number of species recorded in (a) 2008 and (b) 2009.

In 2009 a greater number of species were observed in disturbed communities than in 2008, while occurrences of those apparently confined to pristine and partially-disturbed communities were more or less equivalent throughout the study. The results obtained here also suggest that species richness does not necessarily correlate positively with the numbers of individuals present in a given habitat (Figure 3.5). Analyses of variance (ANOVA) were performed on species richness data for each community and revealed a lack of substantial distinctions between them ($F_{2, 53} = 0.49, p = 0.62$).

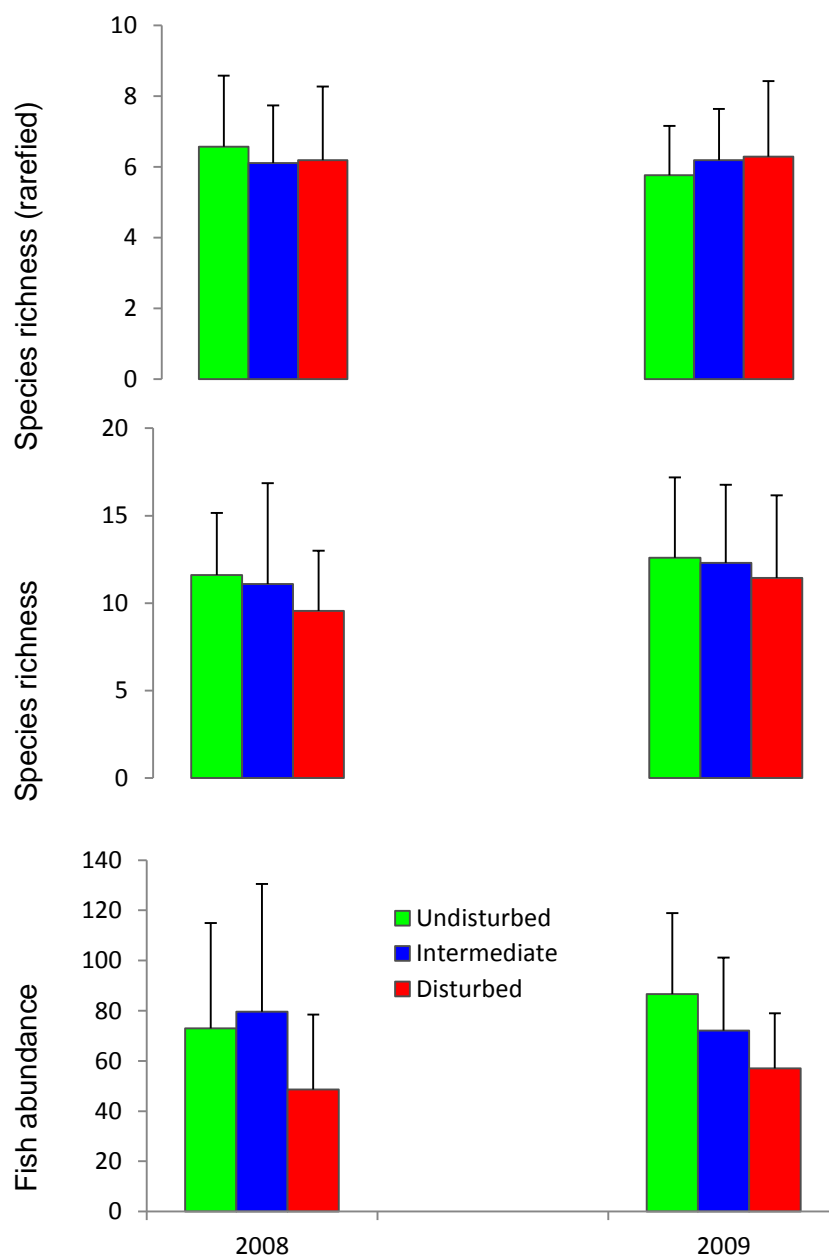


Figure 3.5. Fish assemblage characteristics for sites of differing disturbance intensity (n= 9) in Peninsular Malaysia. Note the relative similarity between species richness and the rarefied species richness.

3.3.2 Species diversity

Shannon's diversity index (H') values were generally lowest when applied to the 2009 data set compared with 2008 (Figure 3.6). The pattern of results for less-disturbed communities did not conform to the rarefied species richness analyses since the values obtained were slightly higher than that in disturbed community-types in both 2008 and 2009. Several outliers were also observed in the data set with the smallest H' value recorded from the

disturbed plot at Ulu Bendul in 2008. The basic implication is thus that the various communities measures do not differ significantly from one another ($F_{2, 53} = 0.22$, $p = 0.81$).

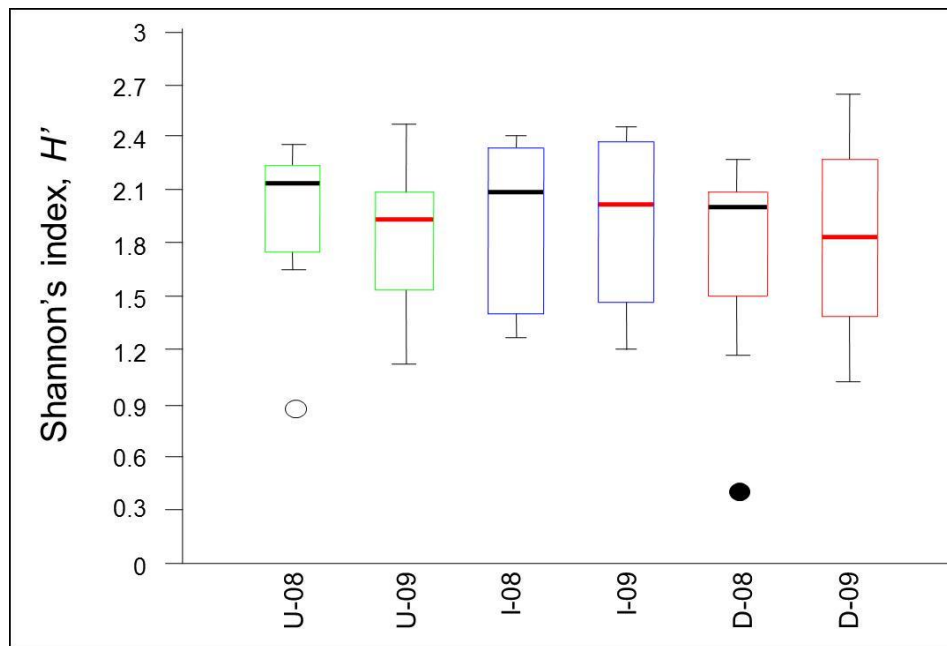


Figure 3.6. Mean alpha-diversity (generated via Shannon's H' index) for all communities in both 2008 and 2009, expressed as box-plots. The thick horizontal bars indicate median values of Shannon diversity index for each community. The circles indicate the outlier values with the solid circle a significantly low value in D-08.

The quantitative measures of beta-diversity (Morisita-Horn) between years indicate that pristine and less-disturbed communities were more comparable than that of the more disturbed community. The disturbed habitats displayed greater overall beta-diversity but Morisita-Horn index values were not markedly different (Figure 3.7). No conspicuous swings in mean rank of fish abundance for the various communities were observed, nor when the community types themselves were compared (Figure 3.8).

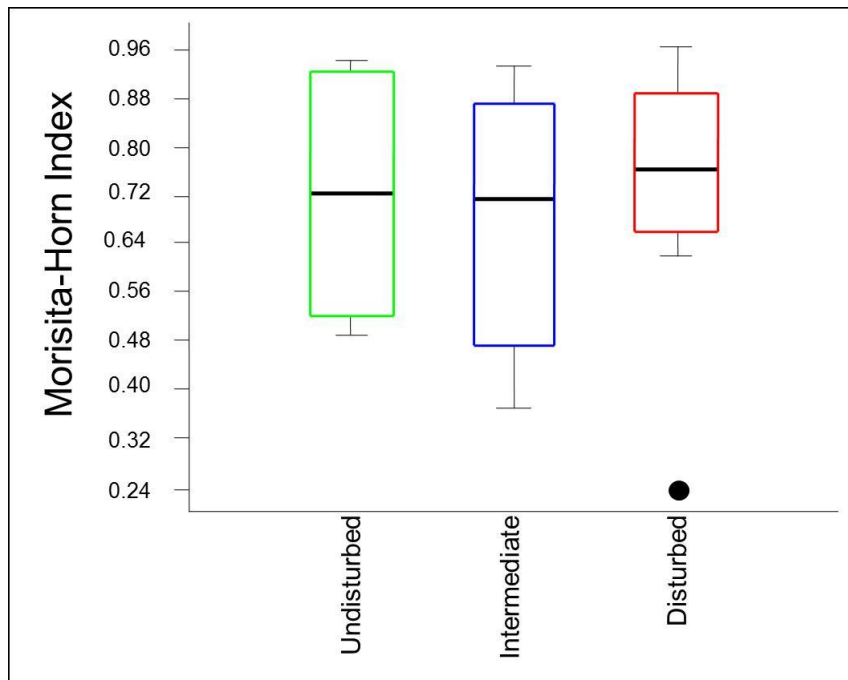


Figure 3.7. Box-plots depicting the Morisita-Horn index for three difference community-types in 2008 and 2009 based on species abundance. The thick horizontal bars indicate median values for each community and the solid dot represents the outlier.

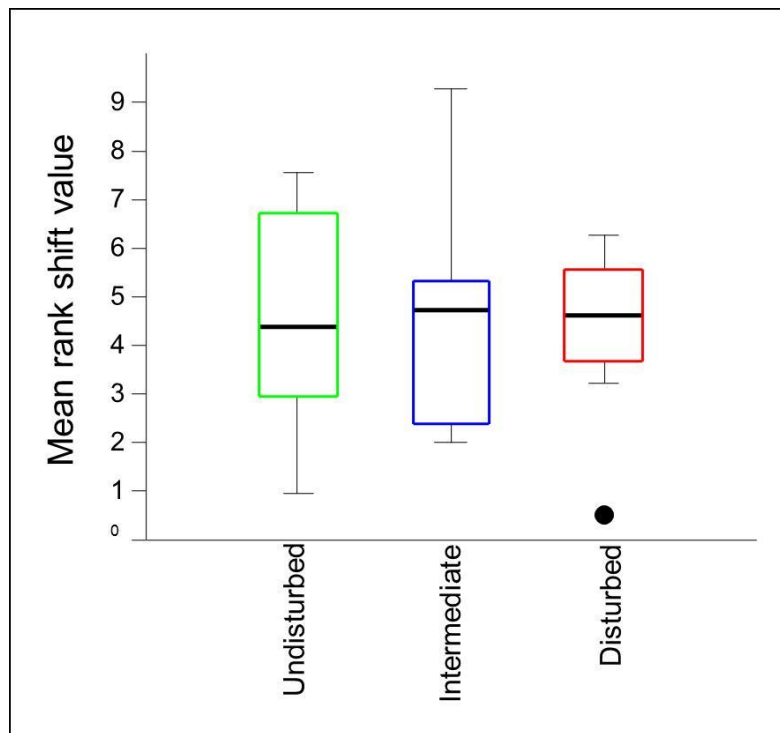


Figure 3.8. Box-plots depicting mean rank shift for three difference communities based on fish species abundance in 2008 and 2009. The thick horizontal bars indicate the median mean rank shift values for each community and the solid dot represents the outlier.

3.3.3 Species community structure

Numerous rarely-occurring species (Figures 3.9a and b) were recorded in both study years. The two-dimensional nMDS ordination based on the Bray-Curtis similarity matrix was generated after the fourth root transformation and resulted in a final configuration with a stress value of 0.17 for the 2008 data set and 0.16 for 2009 (Figure 3.10).

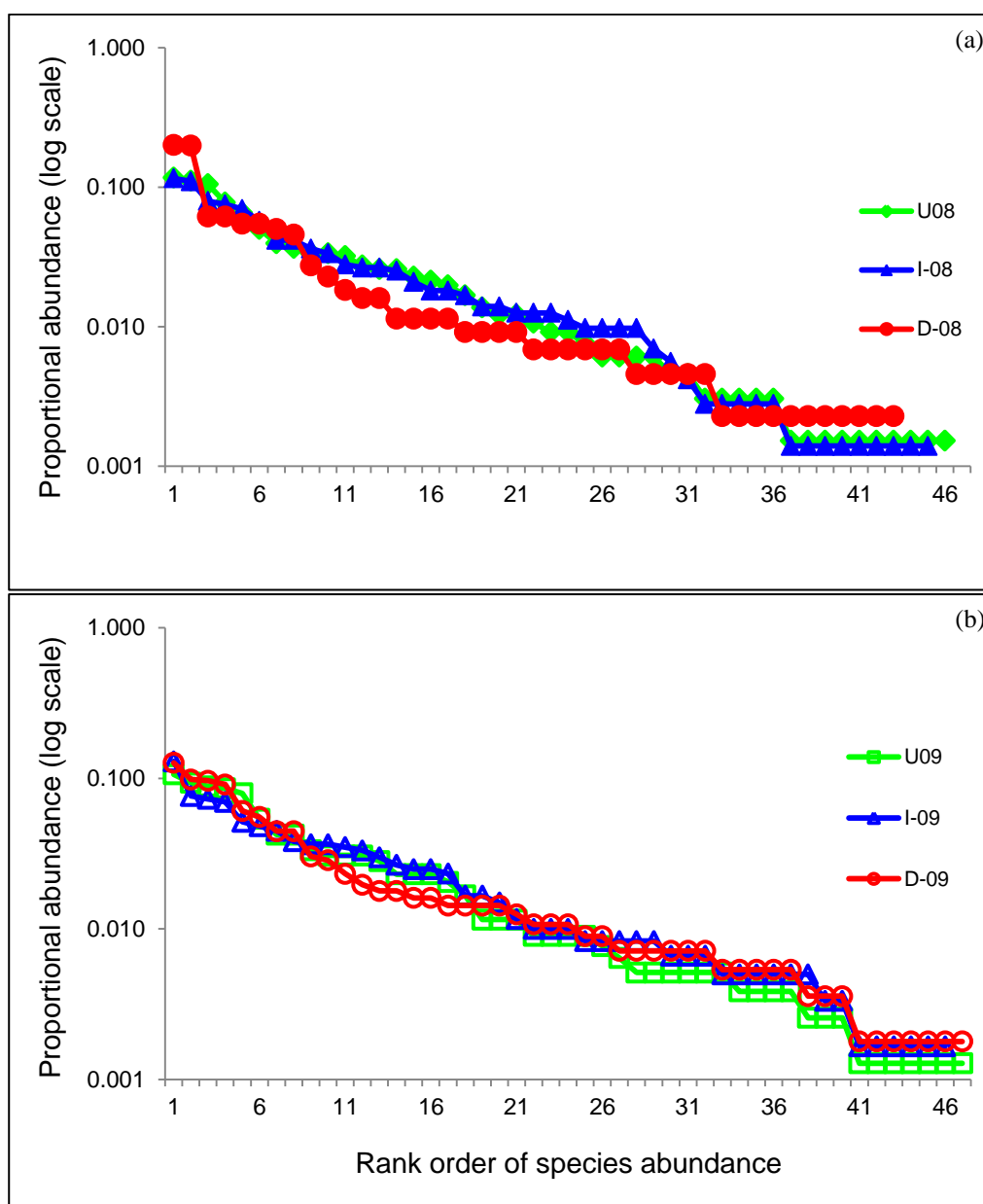


Figure 3.9. Rank-log abundance curves for fishes collected from nine small streams in Peninsular Malaysia (a. 2008 sampling, and b. 2009 sampling). Fish species from three communities differing in disturbance intensity are ranked according to their proportional abundance in undisturbed (U), intermediate (I) and disturbed (D) community.

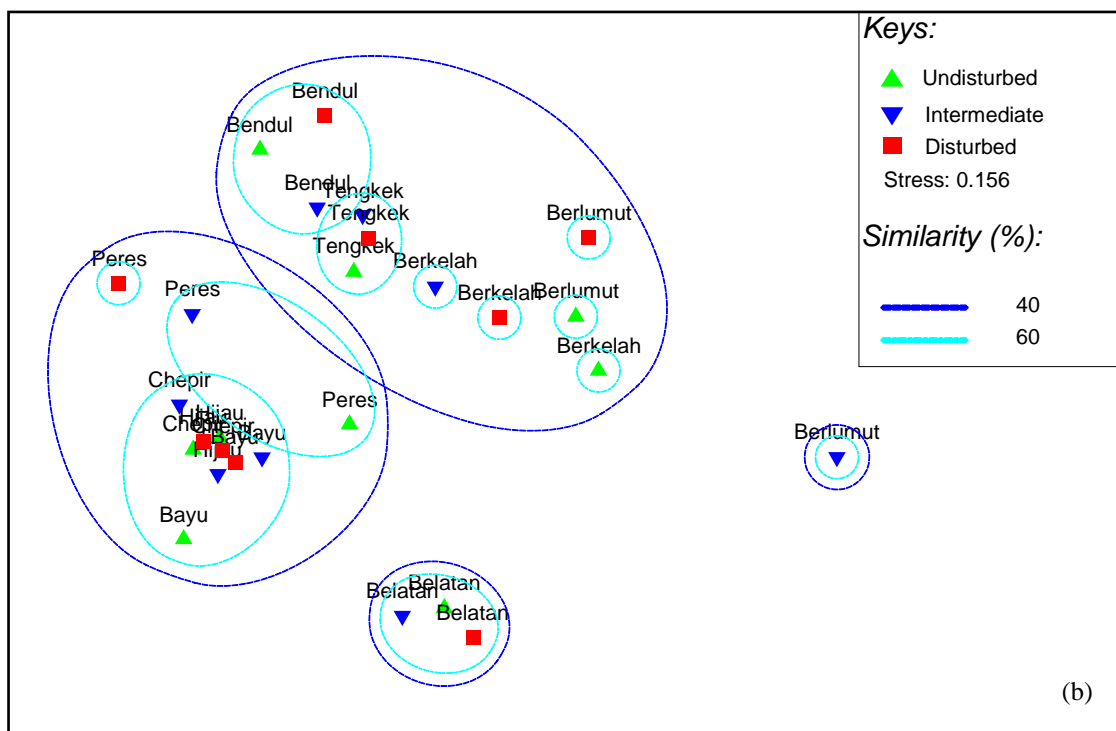
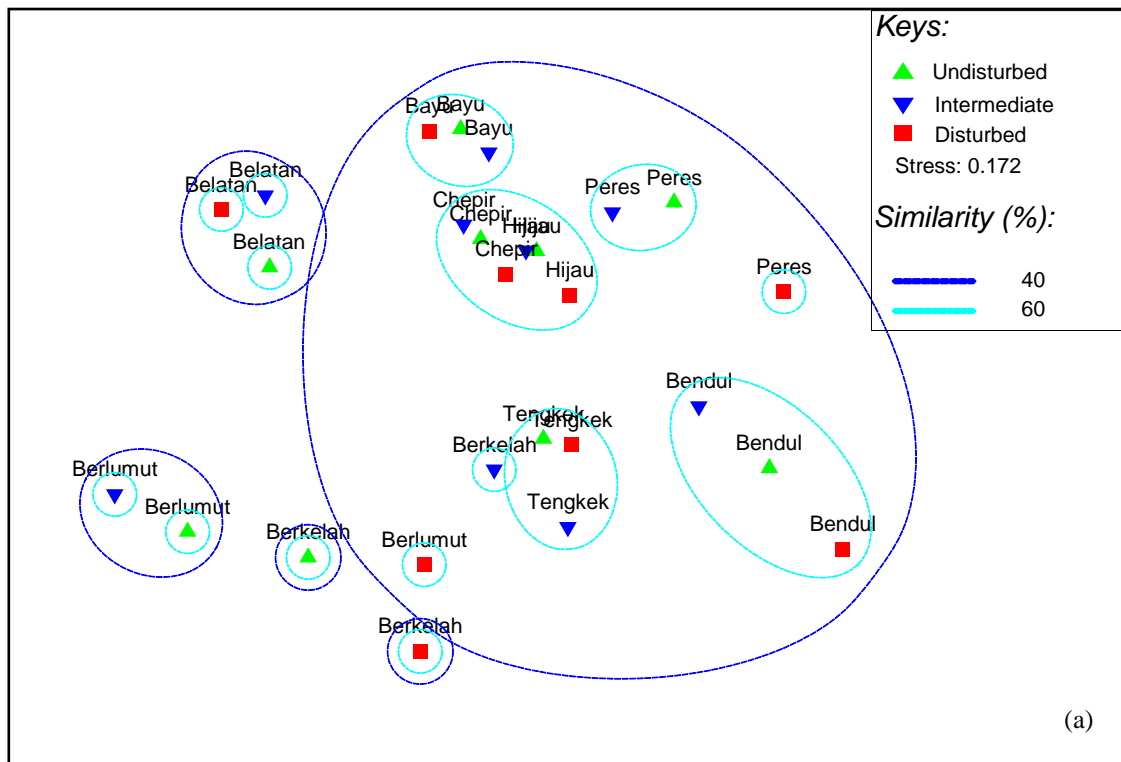


Figure 3.10. Two-dimensional nMDS configuration with superimposed clusters at similarity levels of 40% (dark blue line) and >60% (light blue line) for (a) 2008 sampling, and (b) 2009.

Despite these figures amounting to less than 0.2, the cluster results were superimposed onto a 2D-nMDS ordination (Clarke & Warwick, 2001) (Appendix 3.5. Figure A3.2a and b) from which it is inferred that species similarity between the sampled communities was governed chiefly by the relative proximity of sites to one another as opposed to the degree of disturbance. Furthermore, the results did not support the hypothesis that taxonomic composition is influenced by the extent of habitat modification, at least in the cases discussed here. Analysis of taxonomic distinctness based on hierarchical, Linnaean classification also indicated that all communities were similar to one another (Figure 3.11).

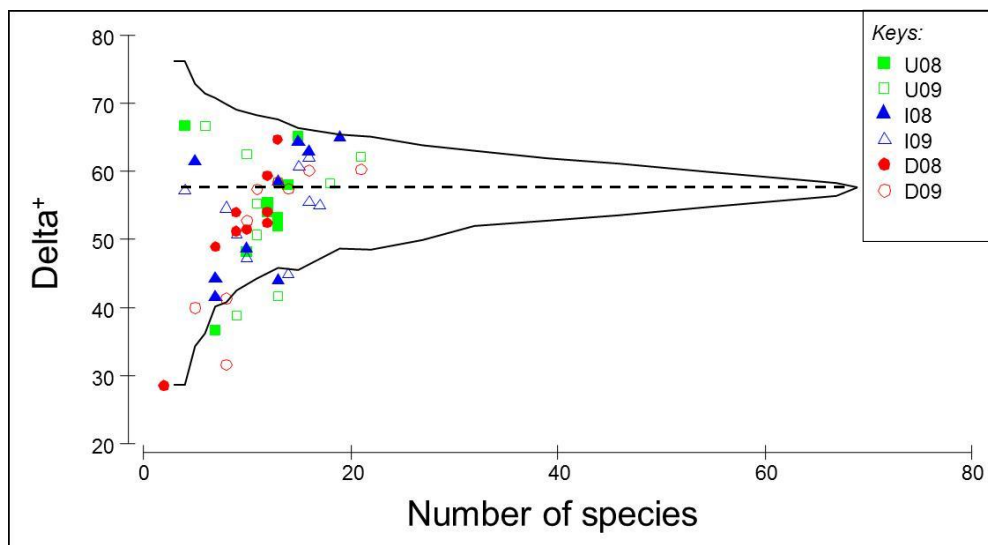


Figure 3.11. Confidence funnel representing the average taxonomic distinctness (delta^+) of fish communities sampled in 2008 (solid symbols) and 2009 (empty symbols) for localities across Peninsular Malaysia. The funnel plot demonstrates the 95% probability limits of delta^+ for every value of the number of species. The dotted line represents the average taxonomic distinctness which is independent of species richness.

3.4 Discussion

Previous studies have established that the native freshwater fish fauna of Peninsular Malaysia is both rich and diverse (Mohsin & Ambak, 1983; Zakaria-Ismail, 1994; Abell *et al.*, 2008). In the present work a total of 69 primary freshwater fish species were recorded of which the Order Cypriniformes, particularly representatives from the family Cyprinidae, proved the dominant grouping, followed by the Order Siluriformes. In this study, total species richness varied between communities, numbering 40 to 45 species, whereas the number of species found per plot sampled was relatively even with five to six species typically present after standardization using rarefaction analysis. While more fish species were recorded in 2009 there was no statistically significant trend in temporal diversity. Although community structure and taxonomic arrangement of fishes were roughly comparable in both disturbed and undisturbed habitats, rarefaction analysis demonstrated that when sampling effort was equal there were slightly more species present in the former. In general however, fish communities were comparably diverse across all study sites in both years with numerous species occurring at multiple sites and only a handful restricted to a particular environment or community. One clear disparity was that species confined to less disturbed communities were more diverse (14 taxa) than those encountered only in disturbed habitats (three taxa in 2008, seven in 2009).

Nonetheless, values generated via Shannon's (H') diversity index when applied to the entire data set indicate that species diversity was roughly equal at all communities, and there was a concurrent degree of conformity in fish species abundance with no substantial shift in similarity index between 2008 and 2009. These results suggest that neither the precise arrangement of member species within fish assemblages nor their relative taxonomic distinctness is linked to disturbance – at least at the disturbance levels investigated here - and that the extent of heterogeneity is in fact most strongly influenced by the respective proximity of one site to another.

3.4.1 Species composition and richness

It has been well-documented that artificial modification of aquatic habitats can contribute to decreased ecological heterogeneity. Freshwater fish communities tend to exhibit conspicuous dissimilarities depending on the degree of alteration, especially in terms of habitat complexity which correlates negatively with disturbance in the majority of circumstances and thus exerts repercussive effects on the diversity, structure and population dynamics of the resident fish fauna (Karr *et al.*, 1986). Such conclusions were not supported by the present study, however, the data showed a trend that is consistent with the intermediate disturbance hypothesis. Fish species richness and community composition were relatively uniform across all sites sampled indicating that the number of fish species collected was independent of disturbance, and conflicting with earlier works which concluded that species diversity was greatest in less-disturbed environments, *e.g.* Casatti *et al.* (2006). The results obtained from 2009 are particularly notable since they imply that a number of species conventionally regarded as habitat specialists *i.e.* restricted to a defined biotope-types were unexpectedly most abundant in disturbed communities, therefore implying that a moderate grade of disturbance may sometimes impart genuine advantages for certain resident fish species.

Among vertebrates inhabiting aquatic ecosystems, fishes are by far the most ubiquitous with results obtained here further verify the extraordinary diversity of species inhabiting small streams in Peninsular Malaysia. More extensive surveys would likely reveal the presence of numerous additional taxa given that species richness curves plotted using the data obtained here failed to reach asymptote (curves not shown, but see also Figure 3.2). The mean relative proportion of species per site was practically identical and a standardised estimate of species richness using 13 specimens (corresponding to the lowest measure of species abundance recorded throughout the study) exposed few differences (Table 3.2) between communities. This result is important and interesting at least in the case of small stream fishes in Peninsular Malaysia but since no other equivalent studies have been conducted in Peninsular Malaysia, a meaningful comparison cannot currently be made. Rarefaction curves did not plateau as the number of individuals or sample size increased (Figure 3.2), and though the precise number of species, *i.e.* species richness, present in each community was not estimated, observed species richness did not vary either between years or among communities. There exists a clear requirement to conduct

more extensive investigations including additional stream systems in order to more accurately assess the effects of habitat disturbance on fish species and community richness.

Species assemblages in an ecological community are defined as occurring together in a spatial and/or temporal sense together and utilising the available resources in different ways. The resultant taxonomic associations are known to be determined by a combination of biotic (*e.g.* competition, predation, *etc.*) and non-biotic relationships *i.e.* patterns of co-existence are structured randomly by intrinsic, species-specific traits which in some cases enable them to endure biotope modification (Ricklefs & Schluter, 1993). Many small, lowland streams in Peninsular Malaysia have undergone various forms of anthropogenic perturbation with subsequent shifts in local physico-chemical and hydrological parameters in turn influencing biotic and abiotic characteristics, (Vannote *et al.*, 1980) particularly flow regime, temperature and dissolved oxygen content. Prior to this study the expectation was that such ‘*ecosystem remodelling*’ should exert noticeable impacts on fish diversity and community composition. However, the results obtained suggest that species richness within the disturbed communities was not significantly reduced, an outcome most clearly illustrated by comparison with figures obtained from less disturbed sites (Figure 3.2).

Rarefaction analyses performed on data sets for both study years (2008 and 2009) likewise indicate that species richness of the three respective communities were more-or-less commensurate with each other. Previously, studies focussed on terrestrial fauna (*e.g.* butterflies – Hogsden & Hutchinson, 2004) had suggested otherwise, but the outcomes presented here fail to support the IDH theory, in which species richness is said to exhibit natural, generalised progress towards climax community (CC) status and peak at sites under ‘intermediate’ disturbance which may harbour greater diversity than the CC itself (Connell, 1978). Although the extent of disturbance in this study is probably very modest, a bit more disturbance could have shown an effect to fish community. Unfortunately, more data are needed on these systems to ascertain the level of disturbance on the low-to-high disturbance continuum.

In Peninsular Malaysia, small tropical streams are under the perpetual influence of seasonal climatic events such as rapid increases in depth and flow following heavy precipitation that can provoke losses in both availability and diversity of suitable habitat. Such natural events may also bring about detectable impacts on the abundance and

distribution of both resident and immigrant fish species (Lowe-McConnell, 1975). At the disturbed study sites sampled here human-induced habitat simplification was expected to impose negative consequences upon fish community composition and species richness but in fact no significant differences were observed, with only species abundance among the three communities displaying negligible variance (Figure 3.5). However, a larger number of individual specimens were collected from less disturbed communities in both 2008 and 2009 (Figure 3.5) which may serve to illustrate that pristine environments possess a greater carrying capacity in terms of fish abundance. At any rate no clear conclusions regarding the precise effect(s) exerted by habitat modification on community composition (Karr *et al.*, 1985; Copp, 1990) can be deduced from the results obtained, though it seems reasonable to surmise influence both relative abundance and species richness of particular organisms to differing extents depending on a range of biotic and abiotic variables (Schiemer *et al.*, 2001; Eros *et al.*, 2008).

3.4.2 Species diversity

The variety and arrangement of species recorded plus the indices of diversity values obtained signify that the sampled communities exhibited low dominance and a comparatively even distribution of species (Figure 3.9). The observed pattern of few common and many rare taxa comprising a given community is near-universal (Magurran, 2007) and it is also typical that most species were present in low densities (Mendonca *et al.*, 2005), and in this case the fact that sites considered to be disturbed only displayed relatively mild habitat modification may also have played a part. It may also prove notable that in general the same fish species dominated the disturbed communities in both 2008 and 2009 whereas in the undisturbed communities the dominant taxa differed between years. These phenomena are not well-recognised nor studied meaning additional investigation is recommended and may yield interesting results. Without exception all fish species considered 'abundant' in the disturbed communities were small, open-water, obligate dwellers of flowing streams and typically sensitive to high water temperatures and low dissolved oxygen content (Beamish *et al.*, 2006; 2008).

In the past a series of species richness and diversity indices, alongside measures of equitability such as Shannon's index and evenness, have been used in combination in order to assess the effects of habitat degradation in aquatic environments (Fausch *et al.*, 1990).

In the present study, diversity indices failed to diagnose any coherent pattern of arrangement in fish community structure when under the influence of habitat disturbance, and the expected decrease in species richness was not detected with an increase in the presence of ubiquitous species representing the unique quantifiable observation. Moreover, community evenness did not fluctuate a great deal across all study sites which may have obscured any reduction in species richness. Overall, therefore, the three sampled communities demonstrated very little disparity both within and between study years (Figure 3.7). Similarly, the Morisita-Horn index failed to reveal any significant discrepancies in fish community structure when applied to the entire data set, and there was only a negligible change in taxonomic inventory between the two years (Figure 3.7.), with a similar assortment of species documented at all sites (Figure 3.4). The disturbed communities also exhibited extensive species overlap, encompassing more than 76% of the species encountered at all three sites. The implication of these results thus appears to be that localised habitat alterations do not exert detectable impacts on resident fish communities, despite the conclusions of several earlier studies which stated that artificial disruption of flow regimes and other physical stream features will bring about negative consequences for native biota (Bunn & Arthington, 2002; Kanno & Vokoun, 2010).

3.4.3 Species community structure

Freshwater ecosystems have already undergone a greater degree of modification and contamination than any other. Kennard *et al.* (2005) stated that modified stretches of rivers and streams are additionally susceptible to invasion of exotic species but all taxa recorded in the present study were representatives of the primary, native fish fauna. Prior to fieldwork and results analysis, the expectation was that habitat alteration should facilitate a decrease in species richness since such activities are known to reduce habitat heterogeneity and decrease availability of essential resources. As a general rule fish groups which have evolved specialisations to particular environments are understood to be most susceptible to such modifications, but in this study all communities were composed of a largely similar range of species. Moreover, the specific ecological traits of those species which were entirely absent from the disturbed communities *e.g.* *Barbus diabolica*, *Hemibagrus gracilis*, *Silurichthys hasseltii* and *Doryichthys martensii* are not well-understood meaning that in these cases non-acute disturbance did not appear to prompt a

reduction in species diversity, although species abundance may have been abbreviated slightly.

Marked changes in the structure and dynamics of fish communities inhabiting disturbed environments has been reported by several authors (*e.g.*, Bain *et al.*, 1988; Dynesius & Nilsson, 1994; Freeman *et al.*, 2001; Eros *et al.*, 2008). Other studies (*e.g.*, Roger *et al.*, 1999; Davey & Kelly, 2007) have demonstrated that these communities often comprise a much smaller taxonomic range of species compared to those occupying pristine habitats, but in the present case there was no discernible decrease in species richness of disturbed communities over a two year period. Community ordination (nMDS) of the data obtained for three pre-defined levels of disturbance likewise failed to disclose any clear differentiation related to disturbance in either year (Figure 3.10). There were no distinctive patterns to indicate that sites of similar disturbance types ‘naturally’ group together, with geographic proximity apparently playing a more influential role in this respect. The groupings depicted on the nMDS plots for both years cannot be defined by disturbance level but were instead determined by site proximity, perhaps most simply expressed by the fact that adjacent sites sharing similar taxa always clustered together. Previous work has also demonstrated that a reduction in habitat quality associated with diminished stream discharge exerts a profound effect on the resident biota (Kanno & Vokoun, 2010) *e.g.* declining fish density and population conditions (Hakala & Hartman, 2004).

Despite the degree of disturbance observed during fieldwork for this study, habitat quality did not appear to be significantly affected, possibly because the water quality remained unaffected throughout the year. The fact that measures of taxonomic distinctness do not depend on sample size or effort (Clarke & Warwick, 2001) must also be taken into account. Fish species recorded in the three communities deviated slightly from the overall mean of taxonomic diversity (master list) (Figure 3.11) with taxonomic membership generally very similar. If habitat alteration is applying any effect on these communities it may therefore be minimal, applicable only to individual species or obscure particular ecological traits (Wenger *et al.*, 2008). However, Kanno & Vokoun (2010) cautioned that single-species approaches might not be beneficial in terms of highlighting the broader consequences of environmental degradation.

Species groupings based on ecological traits have sometimes been used to understand the impact of environmental disruption on fishes (Wenger *et al.*, 2008), and Kanno & Vokoun (2010) emphasised that this is an appropriate method to evaluate the ramifications of water extraction. In general, fish communities inhabiting small, fast-flowing streams are not equipped to withstand severe fluctuations in temperature and dissolved oxygen and can be categorised into two distinct groups as follows: 1. Ubiquitous, locally abundant species that able to tolerate habitat modification and 2. Less adaptable species that tend to seek conditions that are more suitable when their habitats are altered. In disturbed communities members of group 1 (*e.g. Crossocheilus oblongus, Poropuntius smedleyi* and *Cyclocheilichthys apogon*) are typically present in proportionately greater numbers than in pristine biotopes where more group 2 members (*e.g. Devario regina, Glyptothorax major* and *Rasbora elegans*) are generally found in abundance.

Disturbances resulted in decreased tree canopy cover and greater penetration of sunlight favours abundance of herbivores and algae grazers, while increased densities of submerged woody structures provide ideal habitat for certain cryptic species. Unfortunately, the results obtained here do provide any definitive conclusions regarding species-specific responses to given levels of disturbance, but the ubiquitous presence of substrate-dwelling specialists adapted to inhabit fast-flowing, cool waters with a high proportion of dissolved oxygen in all three communities throughout the study may infer that many forms of habitat modification do not impact detrimentally resident fish assemblages. Martin-Smith (1998b) reported that selective timber harvesting had only a minor negative effect on stream fish communities, with such assemblages largely able to tolerate less intensive habitat alterations be they permanent or temporary.

3.5 Conclusion

It is typical for artificially-modified habitats to suffer a loss of integrity associated with human activities, usually alongside concurrent, often profound, impacts on local species richness (Jackson *et al.*, 2001). However, the outcomes of the present study suggest an alternative circumstance whereby in a continuous system such as a small stream, natural succession and turnover of fish species may be maintained between disturbed and undisturbed habitats when local diversity and stocks are high. If the latter are not consistently replenishable the re-establishment of fish communities in perturbed habitats may be restricted with negative consequences more apparent and easily-detectable, though. The results obtained here also infer that when disturbance is localised, and does not inhibit water quality or excessively modify entire stretches of stream, it may be less destructive and an increase species richness may actually be favoured. In the small stream drainages of Peninsular Malaysia examined here, a moderate degree of anthropogenic disturbance has imposed no measurable deterioration in fish community composition or species richness, instead appearing to facilitate an overall increase in diversity.

The results have some generality in that modest human impacts are not necessarily detrimental to small stream fish community. The precise ramifications of anthropogenic habitat disturbance on freshwater fish communities and associated species richness are not readily definable and much depends on unpredictable factors such as the nature, history, scale and intensity of the interference plus the fish community itself which will be subject to natural, spatial and temporal variations. Though inappropriate to form judgements based on the results of a single study, there evidently exists a requirement for integration of detailed, reliable methods of overview into the design of conservation strategies for such valuable, diverse habitats. Moreover, extensive, long-term monitoring programs must be implemented as soon as possible because despite the often negligible short-term effects of human-induced ecological disturbances on fish communities, recovery of species is much more difficult when diversity decreases over longer periods (Iwata *et al.*, 2003).

The conservation value of a biological community is not only contingent on richness and diversity, but also relative rarity and endemism of its constituent taxa, and the ability of those species to maintain viable populations under pressure of disturbance. This research is

thus relevant to conservation managers conducting future appraisals of freshwater fish diversity, particularly those pertaining to small, disturbed, stream ecosystems in species rich region such as Peninsular Malaysia. The existence of protected areas and nature reserves offers inestimable protection to both aquatic and terrestrial biota in addition to maximising within-stream connectivity (Pringle, 2001); this is critical since within larger ecosystems small streams are normally among the habitats to most rapidly exhibit any negative consequences associated with land modification. It is hoped that this study will provide a practical addition to current knowledge regarding the results of habitat modification, despite the apparently minimal effect recorded in small stream fish communities of Peninsular Malaysia.

CHAPTER 4

MODIFICATION OF SMALL STREAMS REACHES AND FRESHWATER FISH DIVERSITY IN PENINSULAR MALAYSIA

4.0 Abstract

Human-influenced modification of lowland, headwater stream habitats in Peninsular Malaysia is common and often exemplified by the creation of pools in stretches of rapids and riffles. I predicted that such alterations would have detectable influences on the species diversity, and structure of the stream fish community relative to natural pools. My results suggest that both modified and natural pools have similar community structure, but modified pools have higher species richness than expected. Estimated species richness, generated using nine species richness estimators, ranged from 26 – 44 for modified pools compared to 17 – 28 for natural pools although observed richness was markedly less (23 and 16, respectively). Rarefaction statistics standardise sampling effort and allowed a fair comparison of ‘pool’ types. On a rarified sub-sample of 393 individual fish specimens when equivalent numbers of individuals were randomly drawn from modified pool samples, the average estimated species richness value (20.6 ± 1.71 species) was higher than that in natural pools (16 species). I therefore conclude that species richness is higher for modified pools even after making adjustments to account for sampling differences. Values of average taxonomic distinctness (Δ^+) were almost identical for species assemblages inhabiting both modified and natural pools, thus indicating that pool-type has little influence on fish community structure. These findings suggest that local habitat modification does not necessarily cause a decrease in freshwater fish diversity, with only minor negative consequences for other community variables recorded in this study, and therefore raise interesting issues regarding conservation.

4.1 Introduction

Profound habitat modification in aquatic ecosystems is increasingly common. Poulet (2007) recognised that habitat fragmentation is one of the most severe and extensive consequences of human disturbance. The pressures exerted on fishes by large infrastructure projects such as navigation canals (Wolter, 2001; Wolter & Arlinghaus, 2003) and dams (Glowacki & Penzak, 2000; Roberts, 2001; Kruk & Penczak, 2003) are well-documented. In Southeast Asia, the building of dams on major river courses has led to drastic changes in the aquatic environment, and by extension fish communities (Dudgeon, 2000; Roberts, 2001). Associated impoundments (Roberts, 1993; 2001) and weirs modify the food resources available and have caused stream fish populations to decline in many cases (Herbert & Gelwick, 2003; Holcik, 2003; Quinn & Kwak, 2003; Freeman & Marcinek, 2006; Poulet, 2007; Kanno & Vokoun, 2010). Damming a river or stream also causes perturbations to the behavioural patterns of migratory fish species by disturbing the natural flow regime and acting as an additional physical barrier (Roberts, 2001).

Other human activities such as water abstraction for agriculture also affect species richness (Benejam *et al.*, 2010). Water withdrawal and stream impoundment are known to negatively impact fluviially-dependent, pelagic and benthic invertivorous fishes (Kanno & Vokoun, 2010). Diversion of water courses reduces discharge with corresponding detrimental effects on fish body mass (Walter & Post, 2008) and species assemblage complexity (Freeman & Marcinek, 2006). Urbanisation also has an impact on small stream environments; Wang *et al.* (2001) reported that construction of impervious surfaces reduced fish species richness and in the study of Morgan & Cushman (2005) measurable declines in both fish abundance and community richness were wholly attributable to intensive urbanisation.

In another study, Poulet (2007) confirmed that permanently modified habitats favour integration of introduced species. Vila-Gispert *et al.* (2002) documented a decrease in fish biomass and species abundance as water quality deteriorated in the Terri River, Spain, while in the upper Manyame River, Zimbabwe exotic predators did not reduce species richness, rather exerting an effect on relative abundance of fishes (Gratwicke *et al.*, 2003).

Recreation also has an impact on wildlife (Pomerantz *et al.*, 1988). The outcome may be more variable than from other impact factors but it can nevertheless prove harmful to particularly sensitive areas or endangered species (Leung & Marion, 2000). However, previous studies assessing the impacts of recreational activities on local wildlife have inclined towards terrestrial fauna (see Knight & Gutzwiller, 1995) or aquatic mammals, *e.g.* manatee (O'Shea, 1995). Leung & Marion (2000) recognised five direct and three indirect factors related to water recreation including "composition changes". However, research assessing the environmental consequences of water-based recreation on aquatic habitats is more limited. Activities such as motorboating can alter both physical and chemical aspects of aquatic habitats (Cole & Landres, 1995), which in turn affects the resources available to resident organisms and thus species distribution (Buisson *et al.*, 2008).

Lush tropical forests containing small, freshwater streams are typical of lowland foothills in Peninsular Malaysia. The latter provide suitable places for water-related recreational activities and local residents have been using them as such for decades. Since such streams generally have little-to-no fisheries value (Lyons, 2006), the diversity of their resident ichthyofauna is poorly known. Fish fauna in small streams in Peninsular Malaysia is diverse (see also Chapter 2) but under threat from human-related activities such as profound habitat modification. Other studies have demonstrated that small streams and rivers in Peninsular Malaysia do in fact harbour a rich ichthyofauna (Zakaria-Ismail, 1993; Ng & Tan, 1999; Mohd-Sham *et al.*, 2005).

Although the destructive, large-scale impacts that river and stream alteration impose on native fish species in many countries have been adequately documented (Roberts, 2001; Dudgeon, 2000; Kottelat & Whitten, 1996), much less is known about the effects of small-scale habitat modification on species richness and community structure in small lowland streams, *e.g.* in Malaysia of which many have been affected to some extent (see Chapter 3). Particularly prevalent are alterations to channel morphology *via* stabilisation or strengthening of the banks from erosions, scaled-down diversions *via* channel construction using concrete, rocks or sandy bricks, reduction of pool depth by the addition of rocks and removal of submerged, in-stream structures and elimination of riparian vegetation.

However, perhaps the most commonly-seen modification is the creation of recreational pools in rapidly-flowing stream sections (Figure 4.1a-c).



Figure 4.1. Profound small-scale habitat modification in small lowland streams in Peninsular Malaysia, a. Creation of permanent recreational pools in rapidly-flowing stream sections, b. Temporary pools along the stream section and c. Stabilisation or strengthening of the banks from erosions.

The effects of these modifications on Peninsular Malaysian stream biota are not well-documented. In fact I am unaware of any research conducted in Peninsular Malaysia which evaluates the consequences of creating such pools in terms of species richness, composition and the functional structure of fish assemblages in small streams. In this chapter, I specifically examine the consequence of stream reach modification on fish communities in small, lowland streams in Peninsular Malaysia. Fieldwork was conducted in three small streams in eastern Peninsular Malaysia, an area where neither fish diversity nor human and/or environmental impacts on stream habitats are well-reported. Fish samples from modified and natural pool were compared to examine the effects of stream modification on species richness and fish assemblages. I predict that such habitat alteration will exhibit a detectable influence on fish community structure in modified pools in contrast with natural pools. I ask how these two habitats differ in regard to species richness and community structure and hypothesise that species richness and fish communities in modified pools will differ from natural pools. I further predict that modified pool communities are more likely to represent subsets of the naturally-occurring pool species, and that the two habitat-types will display a significant degree of divergence in terms of fish species richness and community composition.

4.2 Methods

4.2.1 Study areas

All field study took place in the state of Terengganu, eastern Peninsular Malaysia, where 25 pools in three small, lowland streams draining into the South China Sea were surveyed between July and December 2004 (Figure 4.2). An unnamed second-order stream near Kertih, south of Kuala Terengganu (hereafter referred to as ‘Air Menderu’) was a small, relatively low gradient biotope compared to the other two, more steeply-orientated streams which were both third-order streams known as ‘Sg. Peres’ and ‘Sg. Bubu’, respectively. All streams in this part of Peninsular Malaysia are characterised by slightly acidic, poorly-conductive but well-oxygenated water, with the three surveyed in this study are all less than a few kilometres in length and flowing under forest cover along boulder-strewn courses. Substrates were mainly composed of sand, pebbles and boulders with open bedrock prevalent further upstream. The typical vegetation type in this region is classified as lowland dipterocarp forest with the surveyed catchments located within protected forest reserves and representing popular picnicking spots for local residents. Terrestrial anthropogenic disturbances were therefore limited to small-scale clearing of ground vegetation and some leaf litter removal.

A series of naturally-occurring (Figure 4.3) plus permanent pools and modified pools (Figure 4.4) were selected at random along the course of each stream. A pool was considered ‘natural’ when created by a naturally-occurring feature such as a riffle or cascade and no external modification had been made to water flow, *i.e.* there was no evidence of human interference in terms of structures, obstructions, or rocks being removed to deepen the water and decrease current. Such habitats included plunge-pools and bank under-cuts. Conversely, ‘modified’ pools were created using rock barricades and removing parts of the stream bed to increase depth and reduce flow. All pools were mostly shallow (water depth less than 1.0 m). Modified pools usually have limited microhabitats; a few large boulders may remain at newly-created sites but small, liftable rocks are removed. Submerged woody structures such as twigs, snags and logs were usually absent, while decomposing leaves were limited to shallower zones. During periods of low water

the modified pools are partially isolated from the main stream channel but connection is restored when the water level rises once more.

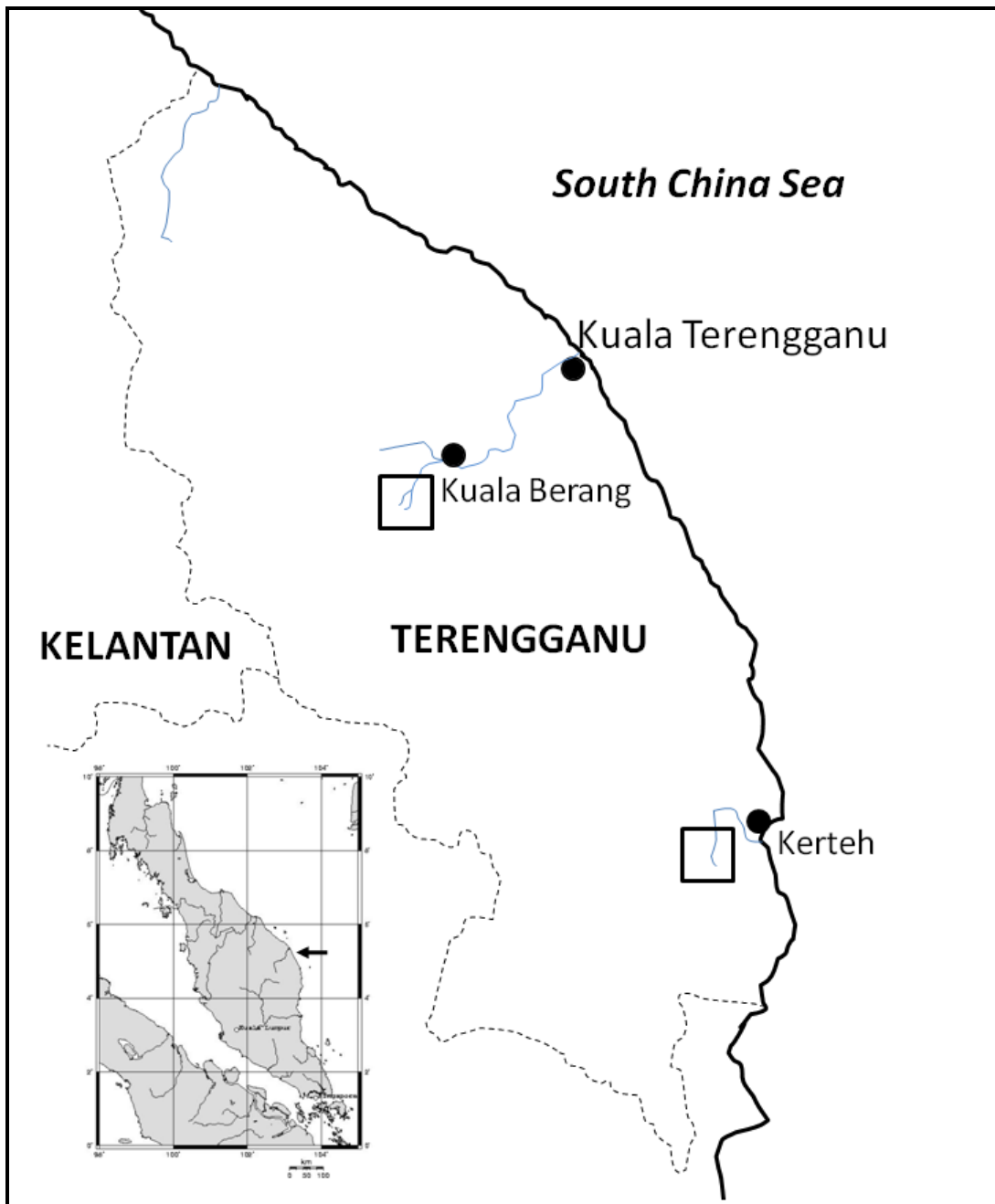


Figure 4.2. A map of Terengganu showing the approximate locations of sites sampled in this study (squares). Inset is a general map of Peninsular Malaysia. Arrow shows the location of Terengganu state.

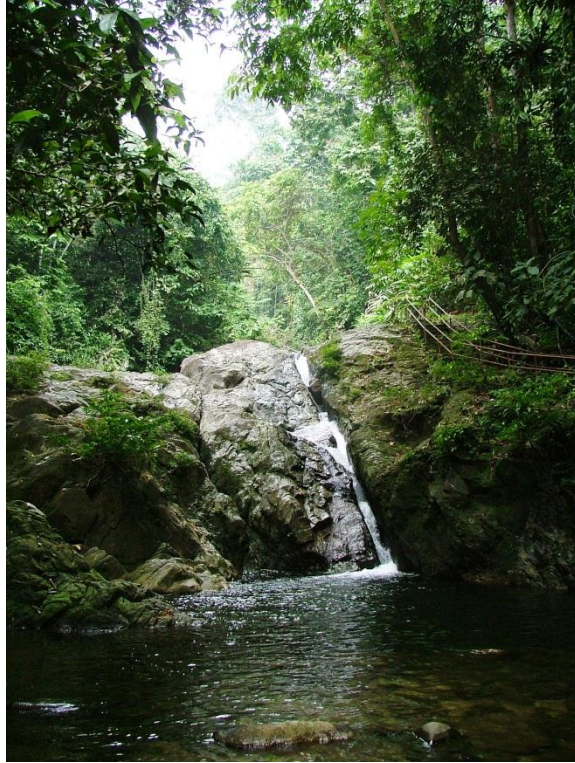


Figure 4.3. A natural pool below the waterfall is one of the most common pools found in small stream.



Figure 4.4. A 'modified' pool was created using rock barricades and removing parts of the stream bed to increase depth and reduce flow.

4.2.2 Fish collection

Fish samples were obtained using a generator-powered (Honda model EX350) backpack electro-shocker (Smith-Root model 15-D). Between four and seven passes were performed once at each site during low-water period to account for potential variations in water flow and volume that may have otherwise affected catches. The duration of each pass was about 1 minute, and the final pass usually resulted in no fish. Additionally, each pool was checked using snorkel and mask after the final pass. All specimens were classified and identified using the taxonomic keys of Alfred (1969), Roberts (1989), Kottelat *et al.* (1993), Rainboth (1996), Ng & Ng (1998), Ng & Kottelat (2000) and Kottelat (2005) and counted, before being released.

4.2.3 Data analysis

Fish assemblages

Data were analysed using various software packages freely available on the World Wide Web. Species diversity was expressed as simple species counts (species richness). Regression analyses were employed to examine the relationship between species richness, abundance and water surface area. Fishes from each pool type (modified and natural pool) were combined to plot a dominance diversity (species abundance) curve and tested for differences using Mann-Whitney *U*-test. Diversity indices integrating species richness and evenness into a single measure were useful in an attempt to define overall heterogeneity at a site. Diversity (Shannon and Simpson), evenness and similarity (Bray-Curtis and Sorenson) indices were calculated for each pool type. These indices were robust and easily interpreted, although no diversity index was considered a perfectly unified measure (Magurran, 2007). In addition to the two similarity indices, percentage complementarity (a measure of community differences) was calculated following Toti *et al.* (2000) to compare the taxonomic composition between the two types of pool community.

Sampling effort

Sampling intensity representing the ratio of total individual caught to total number of species obtained in the sampling (see Toti *et al.*, 2000; Bonaldo *et al.*, 2007) was computed

for each pool type and for the whole data set. Inventory completeness index (*i.e.*, the percentage of species that are not singletons) was calculated based on Toti *et al.* (2000). In addition, I also measured “inventory completion” (or completeness) as suggested by Scharff *et al.* (2003). This is an inventory partition defined as the ratio of observed species richness (S_{obs}) to the Chao 1 species richness estimator (see below) value for that partition and provides a broader comparison of sampling completion within a given habitat besides indicating how efficient sampling has been performed within a particular community. Adjusted estimate range was calculated using the values of all the species richness estimators used in this study (see below), and divided by the observed number of species (S_{obs}). This was computed to further emphasise inventory effort (Toti *et al.*, 2000).

Since sampling effort was difficult to standardize, and species abundance between the two samples rarely equal, I use rarefaction to overcome these shortcomings. Rarefaction is a robust statistical method (Bossart *et al.*, 2006) and is applied to calculate the number of expected species for a sub-samples selected at random from the total community (Gotelli & Colwell, 2001; Koellner *et al.*, 2004) – in this case from the total samples collected. Estimates for pools with larger sample sizes were interpolated to those with smaller by pre-specifying the number of individuals to be drawn (Bossart *et al.*, 2006). Similarly-sized sub-samples were then compared across all sites. To assess differences in species richness between the two pool types, observed species richness was rarefied in order to standardise deviations in sample sizes between pool types. Rarefaction analyses producing abundance-based curves were generated using the computer program EcoSims version 7.0.0 (<http://homepages.together.net/~gentsmin/ecosim.htm>). 95% confidence intervals (CI) were estimated for both pool types using the same software (Gotelli & Entsminger, 2003). Rarefied estimates of species richness were calculated after 1000 iterations.

Species richness estimation

Data on fish abundance were combined regardless of pool type in order to estimate overall richness of species inhabiting the surveyed environments. Then, abundance data for modified and natural pools were analysed separately to compare and estimate community composition and species richness of each pool type. Nine species richness estimators comprising seven non-parametric estimators (ACE, ICE, Chao 1, Chao 2, first order jackknife, second order jackknife, bootstrap – see Chapter 2 for explanation of each

species richness estimator; see also Toti *et al.*, 2000, Longino *et al.*, 2002, Sorensen *et al.*, 2002) and two accumulation curve models (Michaelis-Menten runs and Michaelis-Menten means) (see Walther & Morand, 1998) were applied to estimate species richness with calculations performed using *EstimateS* version 8.2.0 community analysis software (R. K. Colwell – <http://purl.oclc.org/estimates>). The coverage-based estimator (ACE and ICE) calculations were carried out using the *EstimateS* default “cut-off level” of 10 as suggested by Lee & Chao (1994).

A further pair of parameters that were examined as indicators of inventory completeness (Longino *et al.*, 2002) were the number of “unique” species (those known only from a single collection) and “duplicate” species (those known from only two samples), of which the results were obtained from *EstimateS*. Walther & Morand (1998) were followed in assuming that the total species richness of the community had been successfully determined if (1) the last 5% of values in the accumulation curve were equal (i.e. the curve had reached the horizontal asymptote) and (2) the last 50% of values in the accumulation curve were within 5% of the final value of the accumulation curve.

Taxonomic diversity

I predicted that pools with taxonomically similar fish species would be distinguished from those containing taxonomically diverse species when taxonomic distinctness (Δ^+), a taxonomic relatedness based index (Clarke & Warwick, 1998), was used to measure the phylogenetic relatedness of species assemblages between the two habitat types. Δ^+ is a non-parametric measure based on incidence data and was quantified using PRIMER Version 6.1 (<http://www.primer-e.com>) software. I follow Bhat & Magurran (2006) in using six levels of classification (Phylum, Class, Order, Family, Genus and species) and additionally, I used Superorder, Subdivision and Division in order to clarify the measurement of taxonomic distance between species assemblages inhabiting each pool.

4.3 Results

4.3.1 Fish assemblages

A total of 25 modified and natural pools were sampled during this study with the water surface area (pool size) varying between 26.26 m² to 64.05 m² and 25.41 m² to 53.67 m² respectively. There were weak correlations between pool surface area and number of individuals (N : modified pools $R^2 = 0.293$, natural pools $R^2 = 0.294$), and number of species (S : modified pools $R^2 = 0.275$, natural pools $R^2 = 0.253$) (Appendix 4.1. Figure A4.1). Although species abundance was generally greater in modified pool habitats, the statistical outcomes did not differ significantly from the results for undisturbed pools (Mann-Whitney U -test, $p < 0.05$). In both cases, there was a greater proportion of infrequently-occurring species (relative abundance is less than 10%) than ubiquitous species (Figure 4.5). In general, a relatively narrow range of ubiquitous species plus a wider array of less pervasive species characterized pool communities.

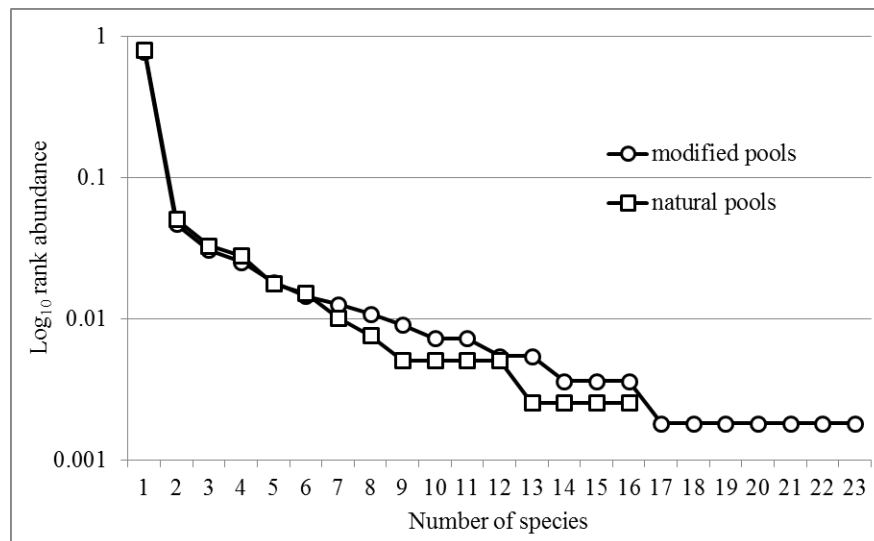


Figure 4.5. Dominance-diversity curve for the sampled fish communities, where \log_{10} rank abundance is plotted against species rank from most to least abundant.

A total of 944 fish specimens comprising 12 families and 26 species were collected and identified from 25 modified and natural pools in three small lowland streams of Terengganu, Peninsular Malaysia (Table 4.1). In general, similar fish families and species dominated both habitat types. The three dominant fish species, i.e. *Poropuntius smedleyi*,

Puntius lateristriga and *Hemirhamphodon pogonognathus* contributed more than 86% of the total catches. The family Cyprinidae (Order Cypriniformes) was most dominant with nine species, followed by Mastacembelidae (three species) and Bagridae, Balitoridae and Nemacheilidae represented by two species each. The most dominant species was *Poropuntius smedleyi* (Cyprinidae) contributing more than 78% of the total specimens collected. Eight species were classed as singletons (with only a single specimen recorded) and three species were doubletons (two specimens recorded).

Table 4.1. The relative abundance of fishes (%) of modified and natural pools.

Species	Modified pools	Natural pools
	% rel. abund.	% rel. abund.
Cyprinidae		
<i>Garra cambodgiensis</i> (Tirant 1884)	0.73	0.51
<i>Hampala macrolepidota</i> Kuhl & van Hasselt 1823	0.18	3.31
<i>Neolissochielus soroides</i> (Duncker 1904)	-	0.25
<i>Osteochilus waandersii</i> (Bleeker 1852)	-	0.51
<i>Puntius banksi</i> Herre 1940	1.27	1.78
<i>Puntius lateristriga</i> (Valenciennes 1842)	3.09	5.09
<i>Poropuntius smedleyi</i> (de Beaufort 1933)	78.22	80.66
<i>Rasbora notura</i> Kottelat 2005	2.54	1.53
<i>Tor tambra</i> (Valenciennes 1842)	0.18	-
Balitoridae		
<i>Homaloptera nebulosa</i> Alfred 1969	0.18	-
<i>Homaloptera zollingeri</i> Bleeker 1853	-	0.25
Nemacheilidae		
<i>Nemacheilus masyae</i> Smith 1933	0.18	-
<i>Nemacheilus selangoricus</i> Duncker 1904	0.54	-
Amblycitidae		
<i>Amblyceps foratum</i> Ng & Kottelat 2000	0.73	0.51
Siluridae		
<i>Silurichthys hasseltii</i> Bleeker 1858	0.91	1.02
Bagridae		
<i>Hemibagrus nemurus</i> (Valenciennes 1840)	1.45	0.25
<i>Leiocassis poecilopterus</i> (Valenciennes 1840)	1.09	0.76
Hemiramphidae		
<i>Hemirhamphodon pogonognathus</i> (Bleeker 1853)	4.72	-
Belonidae		
<i>Xenentodon canciloides</i> (Bleeker 1853)	0.18	-
Synbranchidae		
<i>Monopterus albus</i> (Zuiew 1793)	0.18	-
Mastacembelidae		
<i>Macrogathus maculatus</i> (Cuvier 1832)	0.36	0.51
<i>Macrogathus circumcinctus</i> (Hora 1924)	1.81	2.80
<i>Mastacembelus favus</i> Hora 1924	0.36	-
Pristolepitidae		
<i>Pristolepis grootii</i> (Bleeker 1852)	0.36	-
Osphronemidae		
<i>Betta pugnax</i> (Cantor 1849)	0.18	-
Channidae		
<i>Channa lucius</i> (Cuvier 1831)	0.54	0.25
Total number of fish	551	393

Note, that “-” indicates zero relative abundance/biomass.

Table 4.2. Summary of composition, diversity and similarity indices values for modified and natural pools communities. Percentage complementarity, sampling intensity, inventory completeness index and adjusted estimate range were calculated follow Toti *et al.* (2000). Percentage inventory completion was calculated following Scharff *et al.* (2003).

Pool	All	Modified	Natural
No. pool sample	25	15	10
No. individual	944	551	393
No. species observed	26	23	16
No. singletons	8	7	4
No. doubletons	3	3	4
No. uniques	11	10	7
No. duplicates	1	1	6
% Dominance (3 species)	86	86	89
Diversity index			
Shannon (\log_e), H'		1.09	0.93
Simpson, $1/D$		1.62	1.53
Evenness, J'		0.35	0.34
Similarity index			
Bray-Curtis	0.79		
Sorensen	0.70		
Percentage complementarity	42.31		
Sampling intensity	36.31	23.96	24.56
Inventory completeness index	69.23	69.56	75.0
% Inventory completion	56	82	94
Adjusted estimate range	0.995	0.742	1.241

Note: For the three most dominant species, see Table 4.1.

The Shannon's diversity index (H') score was higher for modified than natural pools (Table 4.2) but can be considered low for these habitat types. Modified pool communities were not only characterised by higher species diversity but also had a slightly more even spread of individuals across component taxa.

4.3.2 Sampling effort

Overall, sampling intensity was low suggesting that the sampling process may not have been sufficiently rigorous (Table 4.2). Inventory completeness index, an indication of how well a community has been sampled (Toti *et al.*, 2000) was somewhat high (close to 70%) for the total pool community overall indicating that there were relatively small proportion of singletons present in pool community recorded in this study. Percentage of inventory

completion for the whole pool community was small (56%). The value of adjusted estimate range for the whole pool community was high (close to 1), indicate that sampling was not thoroughly enough to obtain good species richness estimation for fish community inhabiting the pool environment. Sampling intensity at both communities (modified v. natural pools) in general was low (less than 50%), but they were equally sampled. The inventory completeness index was slightly lower for the modified pools (69.6%) than natural pools (75%) and the similar trend was shown by the percentage of inventory completion (81.4% vs. 93%). Adjusted estimate range scores for both pool types differ greatly, the value was much higher in natural pool habitat than modified pool (Table 4.2).

Sample-based (not shown) and abundance-based rarefaction curves (Figure 4.6) exhibited a similar pattern of species richness for the sampled pools of both types. The abundance-based curves for modified pools increase exponentially with number of individuals and indicate that there were more species present in modified than natural pools. On a rarified sub-sample of 393 individuals (corresponding to the total number of fish specimens in the smallest sample, *i.e.* natural pool samples), when equivalent number of individuals were randomly drawn from modified pool, the average estimated diversity value (20.6 ± 1.71 species) was higher in modified than natural pools (16 species).

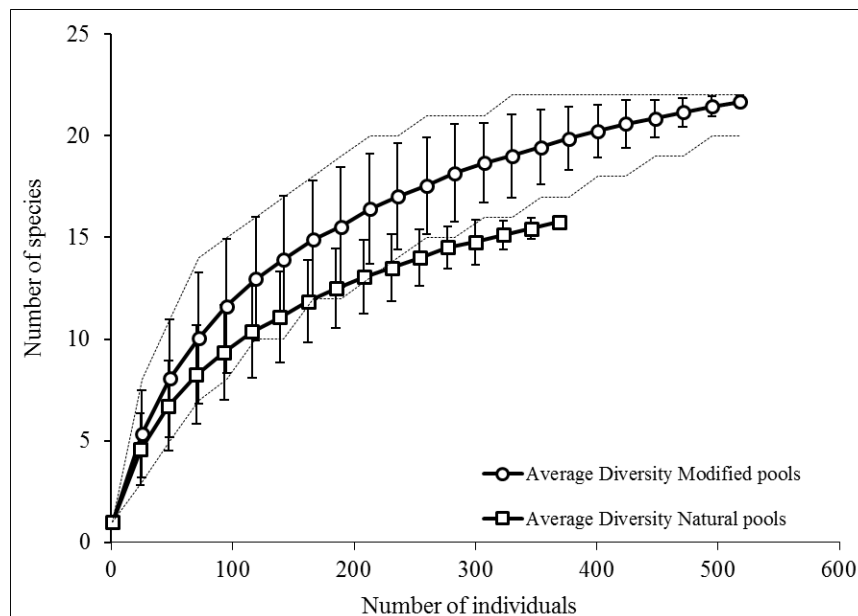


Figure 4.6. Abundance-based rarefaction curves for modified and natural (\pm SD) pools with their respective 95% confidence interval lower and upper bound. The x-axis depicts number of individuals (based on the number of sample chosen) and the y-axis the number of species sampled. Curve outside the CI is significant different to the scale above.

4.3.3 Species richness estimation

Species richness values generated by nine estimators varied considerably (Table 4.3) with the mean and observed species accumulation curves failing to reach an asymptote for any of the three data sets included, *i.e.* modified pools, natural pools, modified pools plus natural pools (Figure 4.7a). Considering all data together, the overall species richness ranged from 30 species (bootstrap) to 56 species (Chao 2). Among the nine estimators, Chao 2 give the highest estimate with 56.2 ± 28.64 and bootstraps estimates the lowest with 30.4 species.

Table 4.3. Richness estimates values for modified and natural pool communities. Each richness estimate represents the mean (and, for some estimators, the SD) for 50 randomizations of sample order.

	All	Modified	Natural
Richness estimates			
S_{obs}	26.00 \pm 3.70	23.00 \pm 3.93	16.00 \pm 1.73
ACE	35.65	29.57	19.34
ICE	37.00	32.89	28.47
Chao 1	46.25 \pm 20.19	28.25 \pm 5.38	17.20 \pm 1.84
Chao 2	56.25 \pm 28.64	44.00 \pm 18.11	18.70 \pm 2.91
Jack 1	36.56 \pm 3.94	32.33 \pm 4.86	22.30 \pm 3.56
Jack 2	44.92	40.20	23.63
Bootstrap	30.38	26.93	19.09
MM runs	33.62	41.31	37.05
MM means	31.88	31.98	24.30

The curves reflecting natural pool data more closely approach an asymptote than do those of the corresponding modified pool data sets (Figure 4.7b and 4.7c, respectively). For natural pool communities, all estimators except bootstrap and the two Michaelis-Menten estimators approach the asymptote (Figure 4.7b). In contrast none of the estimators flatten out for modified pool communities (Figure 4.7c). In no case did the last 5% of values along a given accumulation curve consist of equal values, and neither were the values between 50-100% along any curve within 5% of the final estimated value. In this study, species richness tools estimated fish assemblages inhabiting sampled sites between 26-44 species for modified pools and 17-37 species for natural pools. Observed richness during fieldwork was 23 species for modified and 16 for natural pools, indicating that modified

pool fish communities potentially comprise a greater number of species than those found in natural pools.

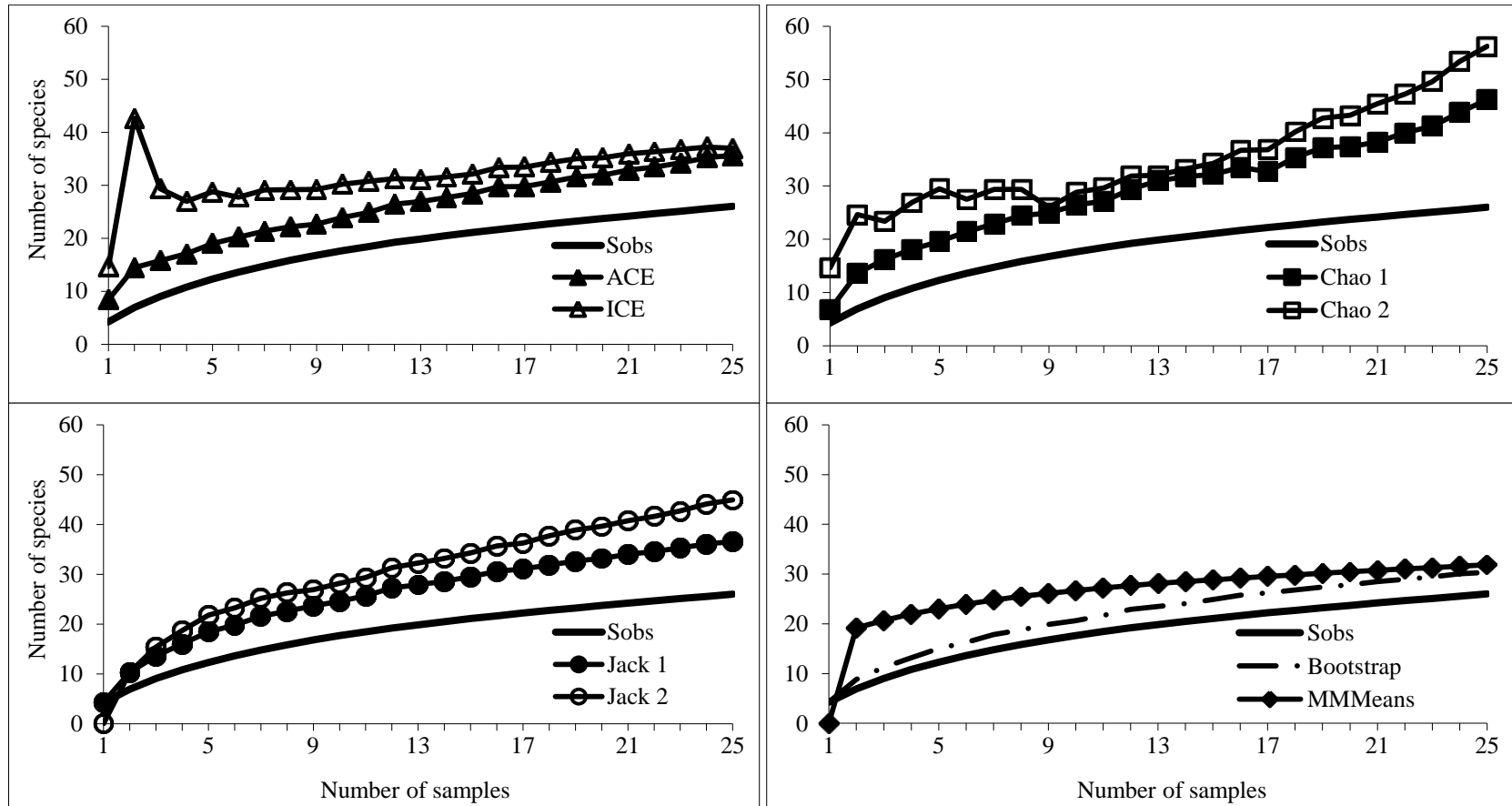


Figure 4.7a. Species richness accumulation curves for all data sets. S_{obs} (Mao Tau) (\pm SD range) is the observed number of species, ACE and Chao 1 are abundance-based estimators, and ICE, Chao 2, Jack 1, bootstrap and the two Michaelis-Menten (MMMeans and MMruns) are incidence-based estimators. To improve clarity of the figures plots of MMRuns for all three data sets are omitted.

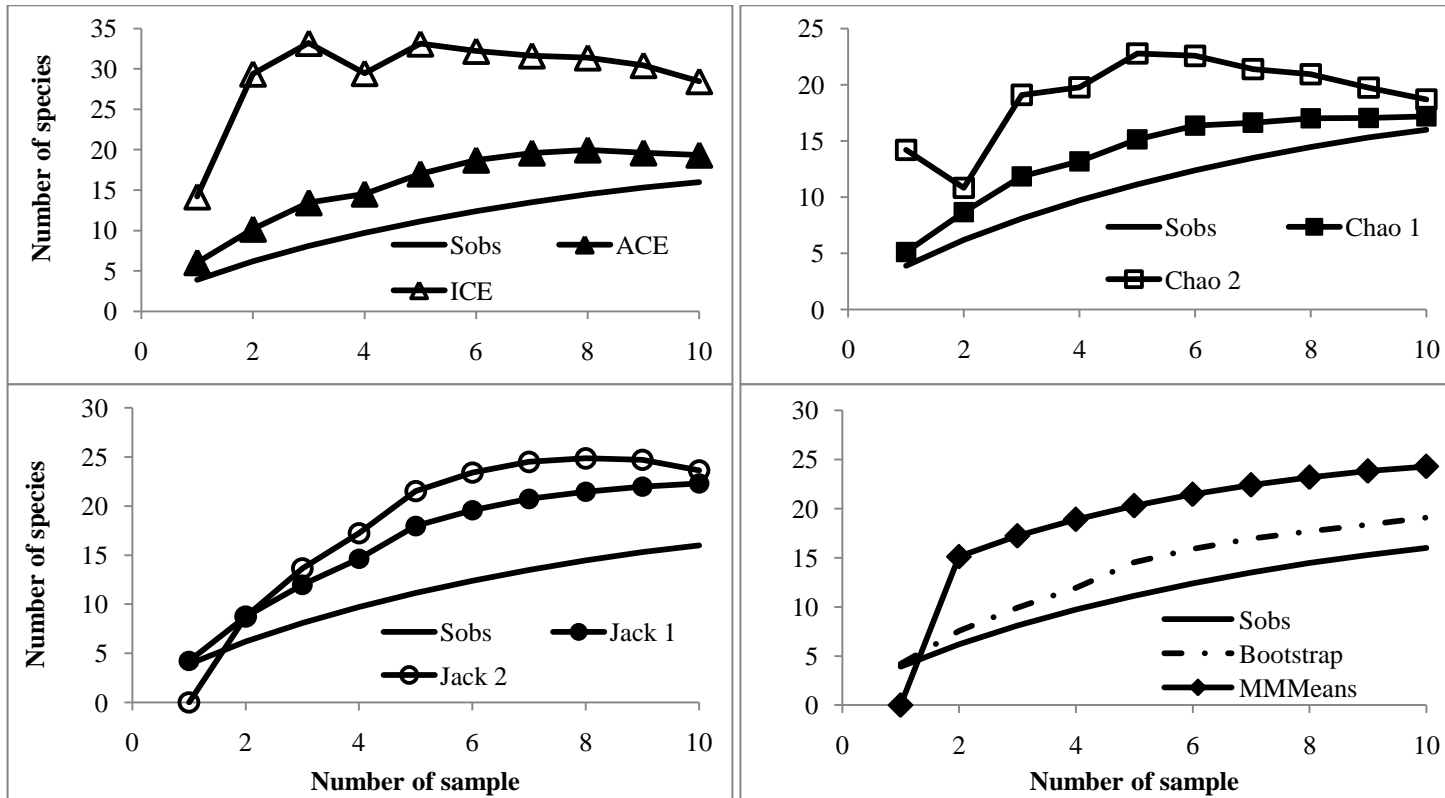


Figure 4.7b. Species richness accumulation curves for natural pools. S_{obs} (Mao Tau) (\pm SD range) is the observed number of species, ACE and Chao 1 are abundance-based estimators, and ICE, Chao 2, Jack 1, bootstrap and the two Michaelis-Menten (MMMeans and MMruns) are incidence-based estimators. To improve clarity of the figures plots of MMRuns for all three data sets are omitted.

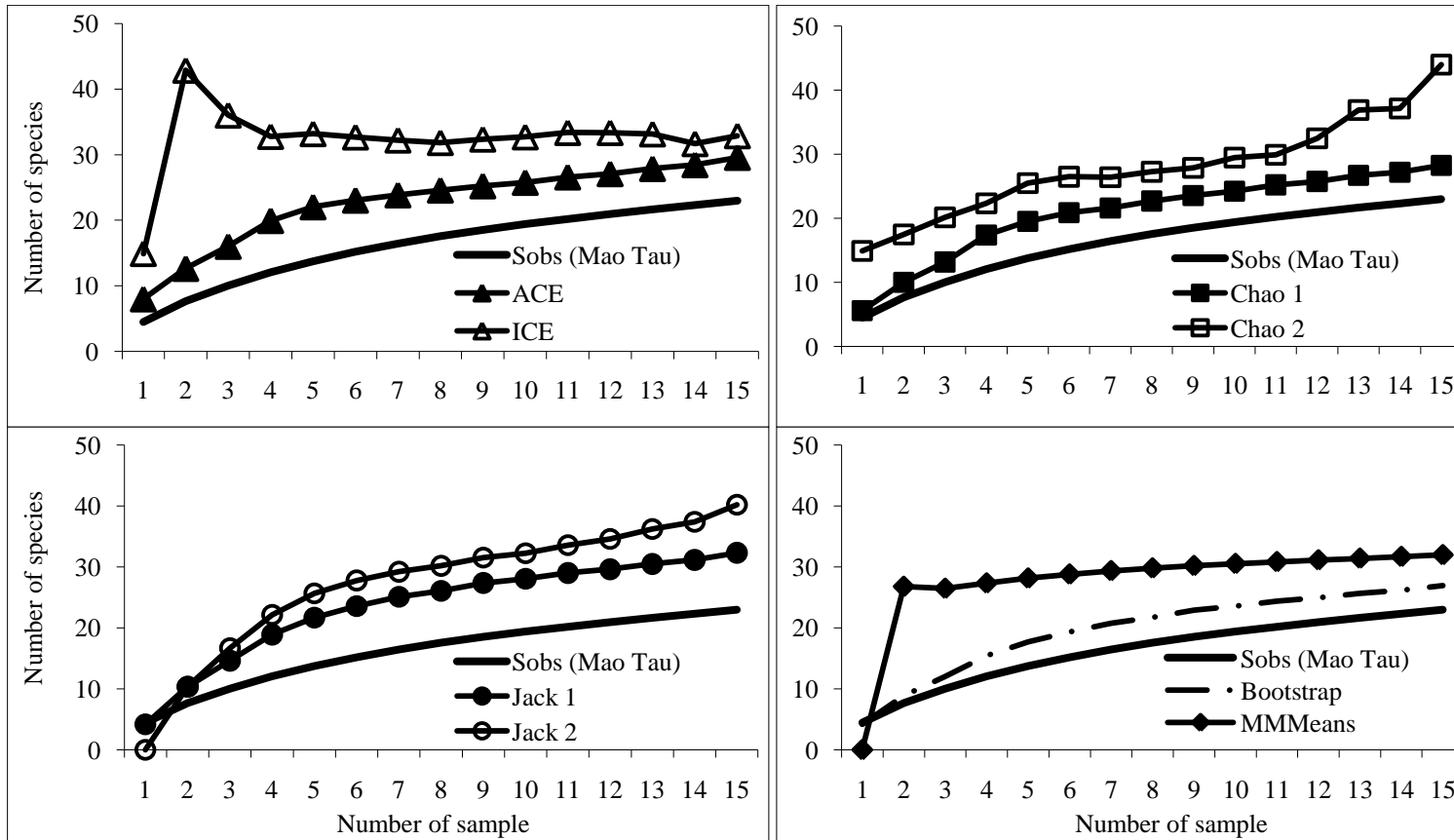


Figure 4.7c. Species richness accumulation curves for modified pools. S_{obs} (Mao Tau) (\pm SD range) is the observed number of species, ACE and Chao 1 are abundance-based estimators, and ICE, Chao 2, Jack 1, bootstrap and the two Michaelis-Menten (MMMeans and MMruns) are incidence-based estimators. To improve clarity of the figures plots of MMRuns for all three data sets are omitted.

4.3.4 Taxonomic diversity

Scores for non-parametric taxonomic diversity indices (average taxonomic distinctness, Δ^+), were almost identical for both assemblage types, and the funnel plot for all sampled pools can be seen in Figure 4.8. The mean Δ^+ fluctuated slightly at small sample sizes became constant once sample size increased. The 95% probability limits become increasingly divergent as sample size decreases, thus limiting the capacity of the test to detect changes in distinctness. The distributions of Δ^+ values are skewed to the left for pools in which low numbers of species were recorded. Taxonomic variance between pool fish communities was less conspicuous, however the average distinctness value for five modified and four natural pools are close to that of the master list mean Δ^+ , while eight pools have average distinctness values below the mean Δ^+ . Five pools displayed significantly reduced average distinctness and fell outside the 95% simulated Δ^+ values.

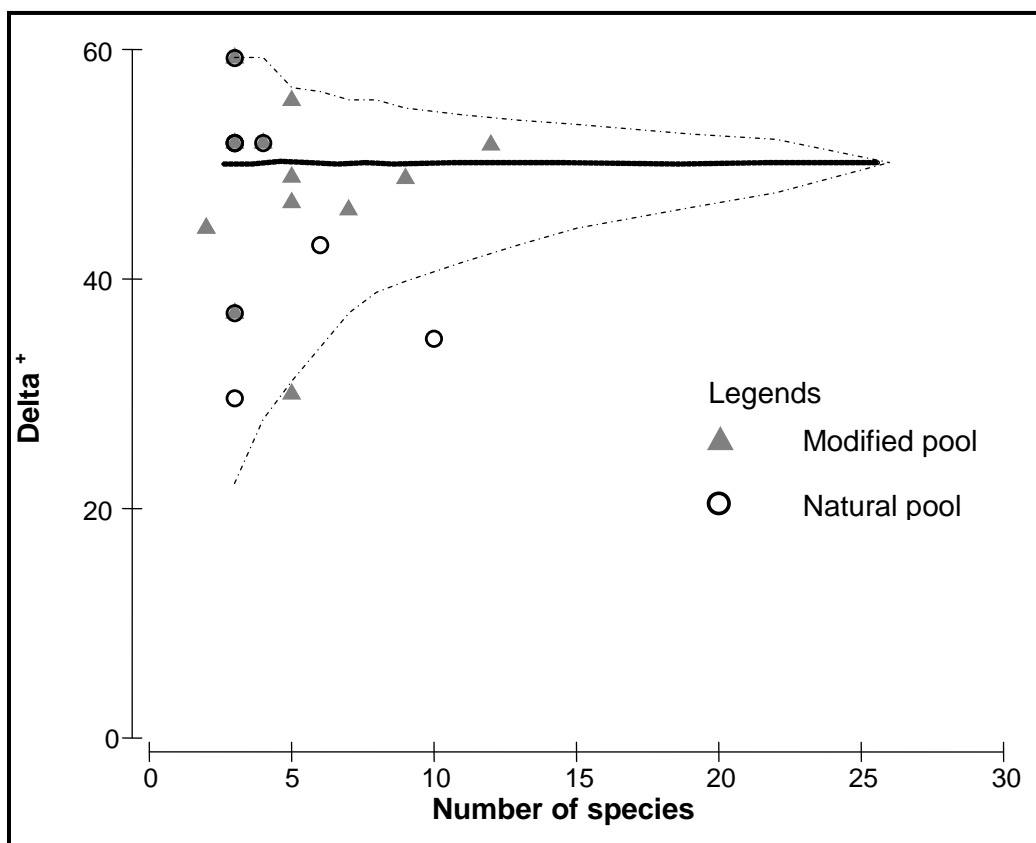


Figure 4.8. Confidence funnel to show average taxonomic distinctness (AvTD, Δ^+) (based on presence/absence data) plotted against observed number of species for both modified and natural pools, and then combined in relation to the pattern for localities of samples. Dashed lines indicate limits within which 95% of the simulated Δ^+ value lies and the solid horizontal line within the funnel indicate the mean Δ^+ value.

4.4 Discussion

Fishes are often the most conspicuous fauna inhabiting aquatic environments. They occupy a diverse array of biotopes and are arguably the easiest choice of study organism in stream environments. The results of this study showed that fish assemblages in sampled pools were dominated by a handful of locally-abundant species comprising the majority of individuals in each community, and there were several rare species. Modified pools generally contained more species than natural pools but the differences in community structure were negligible. Sampling intensity and inventory completeness indexes were relatively modest but sufficient to provide a reasonable estimate of fish species richness as demonstrated by the strong inventory completion percentages for each habitat but not when all pools were combined. The applied estimators of richness returned variable results with none achieving an asymptote, thus implying the presence of species additional to those recorded. Rarefaction analysis indicated that species richness in modified pools was higher than in natural pools when sampling effort was equal. The ichthyofauna in all sampled communities was taxonomically similar.

4.4.1 Fish assemblages

Fish assemblages in this study exhibited a right-skewed frequency of distribution (Figure 4.5) comprising a low proportion of abundant species and relatively high proportion of uncommon ones (Williams, 1964). In both modified and natural pools a single fish species, *Poropuntius smedleyi*, dominated the catch and can thus be considered a specialist in pool habitats (Table 4.2). This species has a discontinuous distribution in Peninsular Malaysia, being absent in streams of the northern states, viz. Perlis and Kedah. When present in other areas, it is normally abundant, however.

Characteristic features of small, high gradient stream in the tropics include pools interconnected by riffles. These two habitat-types exhibit marked differences in flow regime and habitat complexity, therefore the patterns and processes driving the composition of their respective fish communities are not the same (Gelwick, 1990). The present study shows that fish community in pools were dominated by several dominant species, mainly from the family Cyprinidae. The family Cyprinidae can be considered a

highly-diverse group of fishes in Peninsular Malaysia (Herre, 1940b); in this study almost 40% of species recorded were cyprinids, and similar reports exist from elsewhere (Mohsin & Ambak, 1983; Zakaria-Ismail, 1994). Cyprinid abundance is typical in Southeast Asia with the family also reported to be both common and diverse in Thailand (Beamish *et al.*, 2006), Borneo (Inger & Chin, 1990; Watson & Balon, 1984; Roberts, 1989) and indeed throughout the region (Howes, 1991).

Studies comparing fish species diversity, community composition and assemblage structure in habitats typified by slow, stable flow rates (*e.g.*, pools) with those featuring rapid/turbulent flow have been conducted by several researchers, but conclusions have tended to differ (Angermeier & Karr, 1983; Angermeier & Schlosser, 1989; Gelwick, 1990; Aadland, 1991; Taylor, 2000; Langeani *et al.*, 2005). Habitat complexity and environmental factors are known to exert significant influences on species richness and total abundance (Angermeier & Karr, 1983; Beamish *et al.*, 2006). This has been demonstrated in birds communities (MacArthur, 1964) which increased in parallel with vegetation complexity. The relatively poor diversity of fishes reported in this study was expected since habitat complexity is typically limited in pools of small streams. Both biotic and abiotic factors play major roles in dictating species distribution and abundance (Brown, 1984; Taylor *et al.*, 1993).

Pools sampled in this study generally contained a less diverse ichthyofauna than has been reported in other surveys of comparably-sized stream catchments or entire drainage systems in Peninsular Malaysia (*e.g.*, Endau drainage: Ng & Tan, 1999; Krau Game Reserve: Zakaria-Ismail, 1993; Sungkai: Mohd-Sham *et al.*, 2005). This is unsurprising given the limited area and number of habitats sampled. This is also consistent with the theoretical expectation of species-area relationships, which shows that larger geographical areas are able to support greater numbers of species (Angermeier & Schlosser, 1989).

Human-influenced disturbances stream catchments in Peninsular Malaysia are manifold, the most common of which in the study area was the creation of pools for recreational purposes in swiftly-flowing stretches. Such modifications have caused remodelling of habitat structure and complexity which may in turn alter fish species richness, composition and community structure. Habitat modification is known to be one of the most important factors governing biodiversity (Karr *et al.*, 1985; Eros *et al.*, 2008) in aquatic ecosystems,

and typically causes an overall reduction in fish diversity (Karr *et al.*, 1985; Copp, 1990) with a negative influence on community structure (Schiemer *et al.*, 2001; Eros *et al.*, 2008). Prior to this study, however, such research in Peninsular Malaysia was limited and data regarding fish species diversity in modified vs. naturally created pools were also lacking.

The overall ichthyofauna inhabiting both types of pool was very similar and illustrates that the two habitats share many common features. Although a greater number of fish species were recorded from the modified pools, the difference in species richness compared with natural pools was not significant. In fluvial environments, habitat complexity can also be referred to as in-stream complexity, with the number of substrate types a useful predictor of species richness (Angermeier & Schlosser, 1989). Research has shown that reducing habitat complexity applies a negative effect to fish diversity and community composition (see Chapter 3 but see also Table 3.1).

Aquatic fauna such as fishes are able to utilise all the aquatic environment in three dimensions (Gorman & Karr, 1978) thus flow regime, substrate complexity and availability of food are all influencing species richness. The negligible differences observed in both taxa and guild composition between species assemblages in the two pool types were not entirely unexpected considering they also share similarities in habitat structure and complexity. Post-modification, a stretch of water which previously flowed swiftly may acquire certain characteristics of a natural pool e.g. reductions in substrate complexity and flow rate could make modified habitats more suitable for pool specialists. Since the number of sample data sets (pools) was limited in the current study, these findings can only be considered on a preliminary basis and their application limited to small streams in Peninsular Malaysia.

4.4.2 Sampling effort

Electrofishing can be considered an adequate technique for sampling of stream fishes (Meador *et al.*, 2003; Reynolds *et al.*, 2003). Coddington *et al.* (1991) remarked that a sampling intensity (the ratio of total abundance to total number of species recorded) score of 10 would prove inadequate for accurate a survey result but Coddington *et al.* (1996) found that value to be insufficiently low for sampling spider fauna. The results obtained in

this study, *i.e.* 36.3 for overall community, approximately 24 and 25 for modified and natural pool habitats respectively, was bigger than that suggested by Coddington *et al.* (1991) and comparable to the value obtained by Toti *et al.* (2000), for spider assemblages indicate that sampling effort was relatively unsatisfactory. The conclusion was further substantiated by high adjusted estimate range scoring that fell close to 1 for all data sets and more than 1 for natural pool habitat suggesting inventories were further from complete (Toti *et al.*, 2000).

Sampling intensity in this study was relatively low but sampling effectiveness (as measured by inventory completeness index = the percentage of species that is not singletons; Borges & Brown, 2003) was reasonably high, indicates sampling was relatively thorough, therefore an acceptable inventory completeness index was obtained for the pool community and both pool types. The results also indicate a fairly complete inventories were achieved for the modified pools as smaller adjusted estimate range but not natural pools (Table 4.2) suggesting that the former communities had been better sampled than the latter. In general, percentage inventory completion was high implying a shortfall in sampling (Scharff *et al.*, 2003) especially when the pool community were treated separately. Inventory completion is weighted on Chao 1 estimator value. Chao 1 is based on proportion of singletons and doubletons (species represented respectively by one and two individuals in the sample). These results confirmed that the proportion of singletons and doubletons in overall pool community and in modified pool community was higher than that in natural pool community. The high proportion of singletons to doubletons in the sample will reduced the value of inventory completion percentage, demonstrating that sampling was not adequately completed. There is a need to extend the investigation to encompass a wider area and greater number of both habitat types in order to more accurately assess the diversity of fish species inhabiting pools in small streams of Peninsular Malaysia.

In this study, the ratio of singletons and doubletons was considerably larger in modified pools compared to natural pools, and of a similar proportion when all-pools were combined. If the ratio of singletons and doubletons (or unique and duplicate) in a given community is large, observed and estimated richness should diverge significantly (Bossart *et al.*, 2006). This may have caused species richness for modified and all-pools curves were far from achieving asymptote. During fieldwork sampling bias was unlikely and

equipment limitation should not have affected results because almost all fish specimens were collected from the pools during sampling. The equipment was effective on a wide range of fish sizes (from small to large).

To compare species richness in a strict sense (Bonaldo *et al.*, 2007) and account for discrepancies in sampling effort between study sites (Gotelli & Colwell, 2001) it was necessary to use rarefaction analyses. These can be beneficial since they offer a more precise estimation of richness than conventional diversity indices (Eros *et al.*, 2008) in which sample size can often prove difficult to standardise (Gotelli & Colwell, 2001). Rarefaction statistics thus allowed accurate comparisons of pool types that had been sampled with similar efficiency. When applied to my study, I found that modified and natural pools possessed similar species richness, although a difference between rarefied sample and abundance curves was observed. Both curve types clearly show that modified pools were more diverse in fish species, but there was no significant difference in shape between abundance or sample-based curves which suggests that sampling effect was low. In conclusion, species richness was found to be higher for modified pools even after adjustments to account for discrepancies in sampling had been made.

4.4.3 Species richness estimation

Observed richness is a strongly biased measure of species richness (Walther & Morand, 1998; Brose *et al.*, 2003) and highly correlated to sample size (sampling effort) and study area. In total 26 species were recorded across the entire set of sampled pools, with modified pools containing seven more species than natural pools. However, in this study total diversity was unknown meaning observed richness was undoubtedly an underestimate of true species richness (Bossart *et al.*, 2006) because sampling was not complete.

Non-parametric richness estimators are known to be effective tools in assessing total species richness (Brose *et al.*, 2003) because they reduce bias and function independently of above a stated minimum sample size (Colwell & Coddington, 1994). In the current study, these non-parametric estimators generated total species estimates between 30 (bootstrap) and 56 (Chao 2) species for the combined data set of all sampled pools. In modified pools, total richness was estimated to fall between 26 (bootstrap) and 44 (Chao 2) species and in natural pools between 17 (Chao 1) and 37 (MMRuns) species (Table 4.3). In

many previous cases, ICE and Chao 2 estimators have been recommended because they function well at small sample sizes and are relatively uninfluenced by sample density and species patchiness (Chazdon *et al.*, 1996; Longino *et al.*, 2002; Magurran, 2007). In this study, ICE returned slightly better results than Chao 2 for modified pool and combined data sets but in results for the natural pool data set Chao 2 appears to be converging with the observed species curve. I do not believe these figures to be overestimated, therefore they represent a satisfactory estimate of fish diversity in small streams in Peninsular Malaysia, particularly in areas where modified pools are commonplace. However, because sampling intensity was less than 50% and species inventory incomplete, the estimates obtained using the data from the total sample must be interpreted with caution.

Actual species diversity in the sampled streams thus remains unknown. The estimated richness, based on the combined total pools abundance is overestimated somewhat and was probably skewed by the limited sample size (number of pools). None of the species accumulation curves reached an asymptote, further suggesting that sampling was not complete. However, despite a relative lack of sampling intensity, I do not believe the values generated by the richness estimators to be extreme. This is because asymptotic level could never be achieved in any sampling. Furthermore, fish species inhabits small streams are constantly moving and migrating from one stream to the other within the same drainage, as well as upstream and downstream, so there will be a constant inflow and outflow of species (Anne E. Magurran, personal communication). In this study, sampled streams were considerably smaller and shorter than those surveyed by earlier authors (see above), and fish species diversity was therefore predictably low. The results can however be used to predict how many fish species are found in pools communities of small stream environments in Peninsular Malaysia.

These results also allow me to assess estimator performance and evaluate the usefulness of species richness estimators (Colwell & Coddington, 1994). Even with the small sample size (number of pools) some estimators returned more accurate results value than others. Toti *et al.* (2000) listed the characteristics of the ‘good’ estimators and the values generated from the nine estimators in the current study were close to reasonable visual extrapolations of the asymptote of the observed species accumulation curve (Toti *et al.*, 2000; Williams *et al.*, 2007). The results suggest that the species inventory recorded for natural pools was closer to being complete than that for modified pools inventory as in

some cases the estimator species curves appear to coalesce with observed species curves. Although sampling effort was roughly equivalent at all sites, the data set for natural pools yielded estimated species richness curves that more closely approach asymptote with smaller discrepancies between the observed and estimated curves (Toti *et al.*, 2000). However the interval between the most conservative and exaggerated richness estimates was not markedly divergent between the two pool types. It is clear that additional sampling at both pool types would be required to determine whether any of these tools provide a meaningful estimate of species richness for pool fish assemblages.

When sampling any fish community, the common, abundant species tend to be collected quickly and most easily with rarer, infrequently-captured species requiring more effort (Gotelli & Colwell, 2001). In the current study the number of singleton and unique species in natural and modified pool habitats failed to decline (Appendix 4.2., Figure A4.2.i and ii) as sample size increased meaning that when all sampled pool data were combined (Appendix 4.2., Figure A4.2.iii) sampling appeared somewhat incomplete. Since ‘rare’ species (in this case singletons and uniques) are highly influential in estimations of richness (Longino *et al.*, 2002; Bossart *et al.*, 2006) and play a major role in generating results, I examined the ecological and natural history of those recorded in this study. The ‘rarity’ of a species in a given sample was not a function of sampling method but because it was physically scarce in the sampled community.

Most of the singleton species encountered (seven in modified pools and four in natural pools) are common in other aquatic habitats of the region but less abundant in small streams. For example, *Xenontodon canciloides* and *Monopterus albus* are regularly recorded in much bigger stream and river systems plus the latter often collected in other habitats such as swamps and irrigation channels. For many singletons species inhabits modified pools, they were usually collected in large numbers in other small streams, except *Monopterus albus* and *Betta pugnax* that were not so abundant particularly in relatively fast flowing water. A combination of environmental factors, such as abiotic factors (Peres-Neto, 2004) and biological attributes (Jackson *et al.*, 2001) may cause this sporadic distribution of species in stream.

In the natural pools, singleton species mostly comprised of common but less abundant species. The occurrence of *Homaloptera zollingeri* in one natural pool was surprising since

this species normally prefers fast-flowing water (*e.g.*, Beamish *et al.*, 2008), so its absence from modified pools was therefore a little unexpected but not entirely surprising given modified pools typically contain few rocks – the typical habitat of this species. In their study, Beamish *et al.* (2008) found that fishes from the family Balitoridae were absent in low-flow location, and recognised the important of hard substratum for the fish to hold-on during feeding. Many balitorid loaches (family Balitoridae) are obligate dwellers of riffles and rapids with substrates of boulders, rocks and gravel and simply vanish when such habitats are modified to form pools due to associated flow reduction and substrate removal (Beamish *et al.*, 2008).

Further, some of the recorded singletons may not be permanent occupants of small streams and were probably transient artefacts, highlighting the patchy distribution of fish species in small streams. Juveniles of some species, *e.g.*, *Hampala macrolepidota* and *Tor tambra* utilising small streams as nursery. Adult individuals of both species naturally migrate to larger pools in main river channels so are unlikely to be found in smaller tributaries. These were powerful swimmers which could feasibly escape the investigator prior to sampling but may also be intolerant of habitat modification and therefore scarce in many small streams with profound alteration.

4.4.4 Taxonomic diversity

Taxonomic distinctness (TD) is a measure of diversity used to determine the taxonomic relatedness of an assemblage (Clarke & Warwick, 1998; 1999). Taxonomic distinctness has been successfully utilised in numerous studies of marine communities (Clarke & Warwick, 1998; 1999) but has rarely been applied to freshwater organisms despite its considerable potential for environmental assessment and conservation (Bhat & Magurran, 2006). By using TD, Warwick & Clarke (1998) were able to show that marine nematode populations inhabiting degraded locations along the coastlines of UK and Chile were impoverished compared to those at relatively pristine locations.

Prior to field work involved in this study, I hypothesised that any dissimilarities observed in species richness between the two pool types may be related to habitat complexity, resource availability and the ability of fishes to perceive the investigator during sampling and escape (Eros *et al.*, 2008). However when scores for average taxonomic distinctness

(Δ^+) were used to compare fish community composition in the pools based on taxonomic relatedness, no significant disparities were observed (Figure 4.8), *i.e.* the two pool types contained more-or-less analogous fish communities. In spite of various precautions taken during sampling, there is insufficient evidence to suggest that fish communities inhabiting these pools are distinctive.

The results of this study raise interesting implications for conservation. I believe fish species diversity and assemblage structure exhibit differing responses to habitat disturbance depending on various factors. Detailed assessment of how species diversity is maintained on a local scale is still limited and among the foremost challenges for community ecologists (Bruno *et al.*, 2003; Kimbro & Grosholz, 2006). I do not have data from before and immediately after the modified pools were created, so am unable to quantify any repercussions of such disturbances with regard to species richness, but I believe the modified pools sampled in this study exhibit intermediate levels of disturbance enabling the coexistence of different species and trophic guilds.

Likewise, I am unable to conclude that habitat modification has caused detrimental changes in composition and structure of fish species communities in small streams sampled in this study. At a glance, the modified pools appear to contain a higher diversity of fish species than previously thought. The results obtained show that while modified pools appear richer in terms of species by number, they do not differ significantly from natural pools. These findings apparently show that local habitat modification does not necessarily lead to a decrease in fish biodiversity and has only minor negative consequences for other community variables. However the assumption that an assemblage is similar to another or otherwise based on a simple species checklist or abundance data can be misleading since in some cases comparisons are best expressed via a combination of diversity measurements (Lewis & Whitfield, 1999). It could even be said that modification has facilitated an increase in biodiversity of fast-flowing stream sections although this can only be considered a preliminary finding despite its potential influence.

4.5 Conclusion

In many small streams in Peninsular Malaysia, localised anthropogenic disturbances in stream watersheds, such as the modification of swiftly-flowing stretches to form pools, were common. Such modified pools tended to be shallower and smaller than similar, naturally-occurring features, making them ideal for recreational usage by local residents. From a biological stand point (data collection/generation of information) sampling of fish species from a given stream section which contains one or more modified pools will provides similar species richness results to those recorded for natural pools. From a conservation perspective the results presented here suggest that modified pools may play an equally significant role in maintaining fish diversity as do natural pools provided modification is within an acceptable scale. Since before and after data for the modified stream sections were unavailable, the findings of this study can only be viewed as preliminary and must therefore be interpreted with some caution. However the checklist recorded will provide valuable reference material for future researchers working on fish diversity of small streams, particularly in Peninsular Malaysia. Although this study was far from comprehensive due to the small sample size, the standardised sampling technique employed add further value to the results, as do the habitat preference details for the species recorded.

Habitat heterogeneity between modified and natural pools in some streams of Peninsular Malaysia did not appear to exert a significant influence on resident fish assemblages. These habitats not only shared noteworthy similarities in fish community structure, but were also highly comparable in terms of species diversity and composition. Modified pools in natural stream sections were shown to support more fish species than similar habitats in unaltered stretches. Given that modifications of this kind are increasingly common in Peninsular Malaysia, these findings may provide some insight regarding fish distribution and community composition in such newly created habitats. The conclusion of the present study is that modification of rapid stream stretches does not necessarily decrease biodiversity and apparently has few negative consequences for other community variables, thus some interesting questions regarding conservation are raised. At the least we can assume that low-intensity, localised habitat modification seems less likely to change fish diversity in small stream environments. On the contrary, the creation of cleverly-designed

artificial pools in stretches of fast-flowing water may in fact promote fish diversity and complexity of assemblage structure in freshwater streams of Peninsular Malaysia.

CHAPTER 5

BETA DIVERSITY AMONG SMALL STREAMS FISH ASSEMBLAGES IN PENINSULAR MALAYSIA

5.0 Abstract

The rich diversity of tropical stream environments is the result of both within-habitat (alpha) diversity and between-habitat (beta) diversity. Here I examine the contribution of beta-diversity to the biological diversity of stream fish communities in Peninsular Malaysia. I predict that beta diversity will increase with isolation and in response to stream heterogeneity. To test this idea I used a standardised sampling scheme to investigate a series of streams that has originated from different land mass and from different ichthyogeographic regions. A total of 75 species were recorded, 63 in 2008 and 64 in 2009. Of these 75 species, 23% occurred at low frequency and 36% had a narrow range. The results showed that there was substantial beta diversity particularly amongst sites that are geographically separated from one another. Moreover, there was a marked temporal shift in the pattern of beta diversity between sites and regions. A few contiguous sites displayed low beta diversity (less than 50% similarity) but several non-contiguous showed significantly high similarities based on 2008 sampling. On the contrary, the lowest beta diversity values were portrayed by contiguous sites and non-contiguous pairs demonstrated marked dissimilarity in species composition for 2009 data set. Eleven and five pairs exhibited total variation recorded in 2008 and 2009 respectively, and many of which involving Ledang which did not shared any fish species with many streams. Species assemblages among the regions did not show any distinct similarity but east and north regions were measurably more similar, at least based on 2008 data set. Such irregular dispersal is not wholly unsurprising. Stream fish assemblages are influenced by numerous spatial and environmental variables and to a lesser degree occurrence of locally endemic species with restricted natural distributional ranges. Fish species also exhibit discontinuous patterns of distribution within the specific range studied. These results show that previously published hypotheses that divide Peninsular Malaysia into three distinct ichthyogeographic regions may be in need of re-evaluation. Conservation managers should therefore place particular emphasis on small streams since localities in close proximity to one another can exhibit surprisingly high beta diversity, meaning that partial or small-scale habitat protection may prove insufficient.

5.1 Introduction

High species richness in the tropics is related to exceptional within-habitat (alpha) diversity, combined with high beta diversity to give high regional (gamma) diversity (Magurran, 2007). The expectation is that an increase in environmental dissimilarity plus spatial separation of areas leads to high beta diversity between localities (Harrison *et al.*, 2011: see Figure 1).

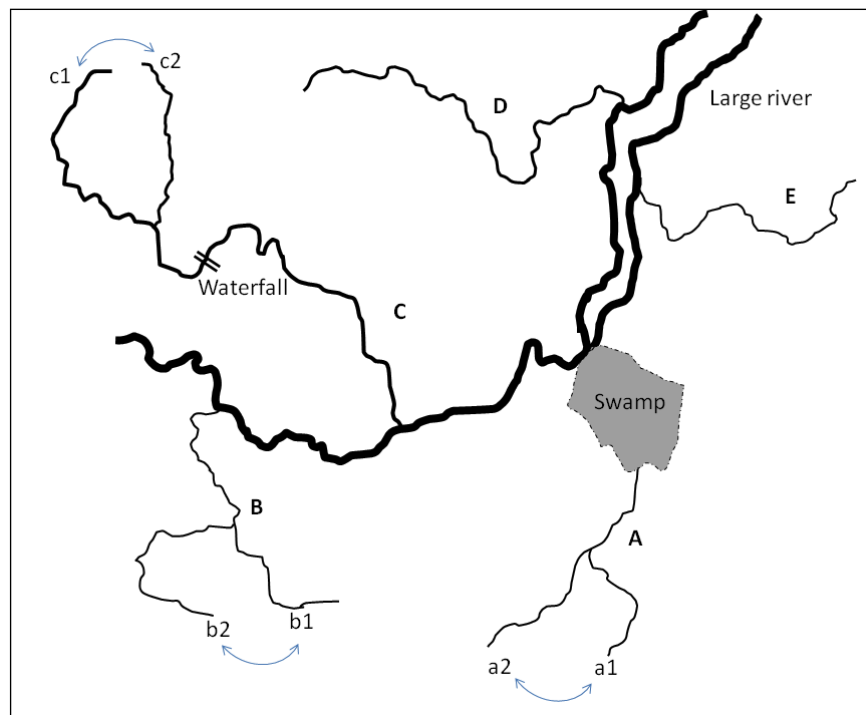


Figure 1. A schematic diagram of the river and streams to demonstrate the variation (*sensu* Anderson *et al.*, 2011) in beta diversity between a pair of stream in relation to other pairs. Stream a1-a2, b1-b2, and c1-c2 are expected to share similar species between them and relatively dissimilar between each pair, but variation of species assemblage (beta diversity) is expected to be greater among stream A, B, C D and E.

The dispersal of obligate aquatic fauna such as fishes is largely dictated by the environment they inhabit (Abell *et al.*, 2008). In many rivers and streams today, including those in the tropics, the latter was determined during the last Ice Age (Lowe-McConnell, 1987; Yap, 2002; McConnell, 2004; Abell *et al.*, 2008), when fishes were commonly confined to a single river or lake basin due to the presence of natural barriers or lack of connectivity between adjacent basins (Schonhuth *et al.*, 2011). Even in tropics, unless a natural means of connection is formed or humans transported fishes to new areas, drainage basins act as distinctive natural entities linking various ecosystem components (Hornung &

Reynolds, 1995). This is especially true in the context of small stream fishes for which physical and geological features can more easily act as connectivity barriers (Jacquemin & Pyron, 2011). For example, changes in landscape topology or elevation can result in the formation of waterfalls or cascades and restrict upstream dispersal or migration events (Robinson & Rand, 2005) or large river channels may hinder cross-colonisation between tributaries draining into opposite banks. As a result, the resident fish fauna of tributary drainages within larger river systems can differ, this being particularly true for small, benthic species (Kottelat & Whitten, 1996).

Species diversity and community structure – a combination of different species at a specific time and place (Magurran, 2007) is strongly influenced by several large scale factors including climatic and hydrological patterns, soils type, habitat heterogeneity and structure, combination of topographic factors, species immigration rate and habitat disturbance plus time scale at the evolutionary and ecological level (Gaston, 1996; De Troch *et al.*, 2001). General diversity over a defined set of geographical units or *inventory diversity* (Magurran, 2007) can be categorised as follows: point diversity, alpha (α -) diversity, beta (β -) diversity, gamma (γ -) diversity, delta (Δ -) diversity and epsilon (ϵ -) diversity (Magurran, 2007; Tuomisto, 2010). Over a macro scale, *e.g.* an entire ecosystem, total species richness is referred to as gamma diversity (Whittaker, 1960), while diversity of species within a specific habitat is normally termed alpha diversity (Whittaker, 1960; Magurran, 2007). Between-habitat diversity is also known as beta diversity (Magurran, 2007; Anderson *et al.*, 2011).

In their review on navigating the diverse meanings of beta diversity, Anderson *et al.* (2011) provide an insightful path for ecologist interested in the research of beta diversity. They separate beta diversity into two main concepts: ‘turnover’ that is *directional* (or ‘structured’, *sensu* Harrison *et al.*, 2011) and ‘variation’ which is *non-directional* (or ‘unstructured’, *sensu* Harrison *et al.*, 2011). In essence, viewing beta diversity as *turnover* means computing the variation in species assemblage from one survey to the other along a spatial, temporal or environmental gradient (Anderson *et al.*, 2011). According to the Anderson *et al.* (p. 20), “a specific gradient of interest with directionality” need to be characterised for turnover, and they give examples of the rate of turnover in “an east-west direction” which could be dissimilar from that “in a north-south direction”. The second idea of beta diversity, in contrast, is *variation* in species assemblage among samples as in

Whittaker's β_w *i.e.* "variation in the identities of species among units" (Anderson *et al.*, 2011: pg. 20). In both cases various measures of beta diversity can be employed such as $\beta = \gamma/\bar{\alpha}$, (Whittaker, 1960), Jaccard and Bray-Curtis dissimilarity indices.

A community in a given habitat comprises a subset of taxa inhabiting the larger, surrounding landscape (Rocha *et al.*, 2008). The regional species pool (gamma diversity) can thus be regarded as a source for immigration of species to local communities (Thompson & Townsend, 2006) with the speciation process responsible for creating new individuals or replenishing populations at the regional level. The degree of similarity between species inventories for different regions can be affected by both speciation and dispersal limitations (Harte, 2003) therefore distribution of individual taxa is rarely continuous (Robinson & Rand, 2005). Further, dispersal capacity differs between species. Both natural dispersal barriers and replacement of individuals may therefore influence the diversity of a site by immigration or speciation. In addition, responses to localised ecological conditions may be important, as put forward by Tilman (2004) in his 'niche' theory. It is thus reasonable to expect that unconnected (Harte, 2003) as well as sites in close proximity will harbour discrete communities.

Tropical regions have high ichthyofaunal diversity (Lowe-McConnell, 1987; Kottelat & Whitten, 1996). The alpha diversity of tropical stream fish assemblages tends to be pronounced (Lowe-McConnell, 1987). Kottelat & Whitten (1996) noted that the distribution of many species is determined by specific habitat requirements, *i.e.* environmental heterogeneity (Goettsch & Hernandez, 2006). Consequently, different tributary drainages within a larger river basin may exhibit different species composition, which is further limited by dispersal capacity and breadth of tolerance to differing environmental conditions (Goettsch & Hernandez, 2006).

Number of species, or species richness, is a key measure of alpha diversity (Gotelli & Colwell, 2001; Magurran, 2007). Localised variation in species richness between individual sites by means of random extinction events or temporal substitution of species (Thompson & Townsend, 2006) promotes beta diversity. Harrison *et al.* (2011) stated that beta diversity is not only linked to environmental heterogeneity, but is also promoted by habitat specialization (Fine *et al.*, 2008), stochastic processes (Condit *et al.*, 2002; Chase,

2010) deterministic effects (Chase, 2003; Clark & McLachlan, 2003), and other factors (*e.g.* altitudes, latitudes, productivity, *etc.*).

To my knowledge, beta diversity patterns displayed by freshwater fish communities in Peninsular Malaysia have never been investigated, although numerous studies of species taxonomy, enumeration and diversity *per se* have been conducted. In this study, alpha diversity is defined as the richness of fish species within a single tributary/stream and beta diversity is the difference in diversity between assemblages. I predict that beta diversity will be highest amongst study sites that are geographically distant. I am interested in both *turnover* and *variation* in beta diversity *sensu* Anderson *et al.* (2011). Habitat and physio-chemical heterogeneity may also affect beta diversity but are out of the scope of this study. My study therefore aims to: 1. Evaluate both alpha and beta diversity; 2. examine species turnover and its relationship with inter-site distance; 3. Correlate species diversity and species turnover with distance; and 4. Assess species' range via measurement of species distribution.

5.2 Methodology

5.2.1. Study area

Fish samples were collected from small lowland and foothill streams throughout Peninsular Malaysia (Figure 5.2) in August 2008 and May 2009 at 13 and 10 individual localities, respectively. Peninsular Malaysia has a relatively stable climate with two annual rainy periods (the most important falling between November and February with a second, shorter spell in June and July) with annual precipitation varies from 2000 to 4000 mm. During the study periods, torrential rainfall occurred sporadically especially in the afternoon.

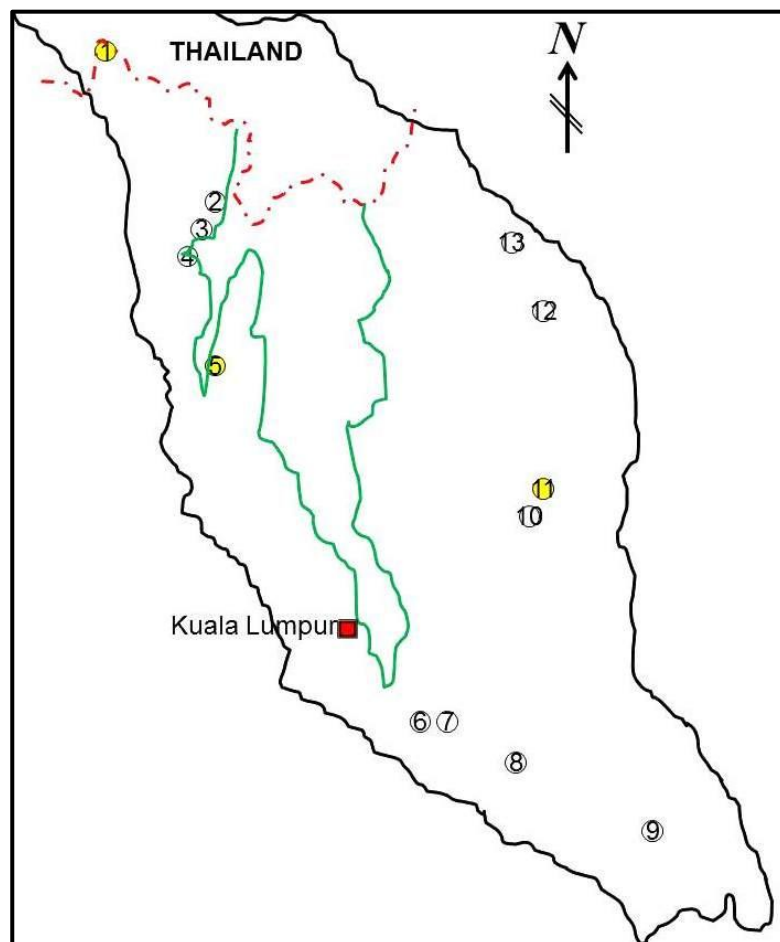


Figure 5.2. Map of Peninsular Malaysia showing the approximate sites sampled in this study (see Table 5.1 for site name corresponding to each number). Green line denotes Banjaran Titiwangsa, the mountainous range extended south from Peninsular Thailand. Filled circles indicate sites that were not visited in 2009.

Most streams are situated within protected forest reserves so riparian vegetation tended to be reasonably pristine, while in all cases water flow was perennial and some streams are utilised by locals for recreational activities such as picnicking. Based on Horton's index, the majority of these streams could be classified as second order stream, and were no more than 10 m wide with substrates generally composed of sand, gravel and boulders. Only a handful of localities were located within the same drainage basin as one another, *e.g.* the Bayu, Chepir and Hijau all empty into the Muda River system while the Tengkek and Bendul are tributaries of the Muar River system, which ultimately drains into the Straits of Malacca. Table 5.1 shows the sampling sites with their respective drainage basin plus the condition of each stream based on human usage. Approximate distances between sites are given in Table 5.2 and sites less than 50 km are considered a contiguous site.

Table 5.1. Sites sampled in 2008 and 2009 and their main river systems, plus remarks on the general usage of each stream by local residents during sampling. No quantitative measurements of stream usage were taken.

Site name, state	Main drainage	Remarks
		Recreational usage level
1. Tasoh, Perlis*	Sg. Perlis	Us low; Ds low
2. Bayu, Kedah	Sg. Muda	Us high; Ds low
3. Chepir, Kedah	Sg. Muda	Us, moderate; Ds low
4. Hijau, Kedah	Sg. Muda	Us moderate, Ds low
5. Kenas, Perak*	Sg. Perak	Us, Ds moderate
6. Bendul, N. Sembilan	Sg. Muar	Us high, Ds high
7. Tengkek, N. Sembilan	Sg. Muar	Us, Ds moderate
8. Ledang, Johor	Sg. Kesang	Us low, Ds moderate
9. Berlumut, Johor	Sg. Endau	Us, Ds moderate
10. Berkelah, Pahang	Sg. Pahang	Us moderate, Ds high
11. Jin, Pahang*	Sg. Kuantan	Us, Ds moderate
12. Peres, Terengganu	Sg. Terengganu	Us high, Ds low
13. Belatan, Terengganu	Sg. Kluang Besar	Us low, Ds high

Note. Asterisk (*) indicates sites not sampled in 2009. Us and Ds denote upstream and downstream, respectively.

Table 5.2. Approximate distance (in kilometres) between sites. Boxed values indicates sites in close proximity (< 50 km) to one another.

	North-western region					Southern region			Eastern region (incl. Belatan)			
	Tasoh*	Bayu	Chepir	Hijau	Kenas**	Tengkek	Bendul	Ledang	Berlumut	Berkelah	Jin**	Peres
Bayu	125											
Chepir	114	16										
Hijau	143	25	41									
Kenas	231	114	130	91								
Tengkek	473	350	363	331	248							
Bendul	482	360	373	340	254	20						
Ledang	548	424	437	404	323	76	74					
Berlumut	630	506	518	390	414	175	177	105				
Berkelah	447	325	335	314	256	130	150	160	197			
Jin	433	312	321	302	250	151	171	184	219	24		
Peres	360	252	256	250	235	247	266	293	330	136	115	
Belatan	288	196	196	202	216	310	327	365	412	215	193	87

Note. Asterisks (*) denote sites for which permission to conduct sampling was not granted by the local authority and ** denotes sites that were not sampled in 2009 due to heavy precipitation.

Sampling sites were grouped into eastern, southern and northwestern regions on the basis of the zones of ichthyogeographic similarity in Peninsular Malaysia as proposed by Mohsin & Ambak (1983) and my own personal knowledge of the system. By my definition, the ‘north-western’ region extends from the northern tip of Peninsular Malaysia to the southern limit of the Sg. Perak drainage, this representing one of the main river systems within this area alongside the Sg. Muda, Sg. Kedah and Sg. Krian. The ‘southern’ region encompasses river basins located south of the Sg. Perak, to the south and west of the Endau-Rompin drainages and eastward to the southern periphery of the mainland. The most important rivers in this zone include the Sg. Bernam, Sg. Selangor and Sg. Muar, all draining into the Straits of Malacca, plus the Sg. Endau and Sg. Rompin systems, which flow into the South China Sea. My ‘eastern’ region includes all northeastern drainages with its southern boundary the Sg. Pahang basin. Major rivers here comprise the Sg. Golok, Sg. Kelantan, Sg. Terengganu, Sg. Dungun, Sg. Kuantan and Sg. Pahang. The central Titiwangsa mountain range (Banjaran Titiwangsa) acts as a natural barrier separating each region.

5.2.2. Data collection

Fishes were collected from representative 25 m stretches of stream or plot in triplicate fashion. Plots were at least 50 to 100 m apart and isolated using 3 mm block-nets at both upper and lower extremities in order to prevent fish escaping and maximize catch. At each plot, a minimum of two to five passes were made with a battery-powered backpack electrofisher (model LR-24 Smith-Root), depending on the size of the stream (*e.g.* only two passes made at Sg. Ledang). This was deemed sufficient following Angermeier & Schlosser (1989) who demonstrated that 80% of species and individuals recorded after five such passes were normally captured within the first two. All stunned fishes were collected using dip nets or from the downstream block net and placed into a collapsible holding net or bucket. After the final pass a snorkel and mask were employed in each case to perform an observatory check for individuals trapped among boulders and other submerged structures. Collected fishes were identified to species level, counted and returned to the water immediately after sampling. Voucher specimens of all species were deposited in the ichthyological collection at the University Malaysia Terengganu (UMTIC).

5.2.3. Data analysis

Fishes recovered at each plot within a single stream were pooled together to evaluate species richness and frequency of occurrence (the ratio of species occurrence compared to total number of sampling sites for each year) across Peninsular Malaysia. Variations (*sensu* Anderson *et al.*, 2011) in species assemblage composition were analysed using beta diversity measurements. Traditional studies have tended to consider beta diversity as the ratio of alpha (within habitat) to gamma (within landscape) diversity *i.e.* $\beta = \gamma/\bar{\alpha}$ (Whittaker, 1972). In my case, pairwise dissimilarity metrics were used as a proxy for beta diversity measures (Chase, 2010). This constituted a measure of species variation between a given pair of sites calculated for both study years based on Bray-Curtis's (dis)similarity index [1-Bray-Curtis's (abundance-based)] (See Box 1 for the worked examples) and were calculated using the software *EstimateS* 8.0.0 (R. K. Colwell – <http://purl.oclc.org/estimates>). In order to complement these beta diversity measurements, Jaccard's index of similarity was also computed and the resultant values subtracted from 1 [1-Jaccard's (incidence-based)] to obtain dissimilarity values. Dendrograms were then plotted using the *R* computer program (*pvclust*) and Euclidean distance was calculated

based on Ward's method to examine turnover in community structure. p -value (95%) was given as 'Approximately Unbiased' (AU) from the *R* package but 'Bootstrap Probability' (BP) was also given (shown as AU/BP in the diagrams). Clusters with AU over 95% are shown as red rectangles, and are significantly supported by data. Taxonomic similarity (Δ_S), an index derived from taxonomic separation of species, was determined using binary (presence/absence) data from across the three regions via the method described by Izsak & Price (2001), based on the most common representative of freshwater fishes in the region (*i.e.* Cypriniformes) and Whittaker's beta-diversity [$\beta = (\gamma/\bar{\alpha}) - 1$] using Paleontological Statistics (PAST), version 2.0.1 (Ø. Hammer & D. A. T. Harper, <http://folk.uio.no/hammer/past>) software was calculated for each individual region to measure turnover (*sensu* Anderson *et al.* 2011).

5.3 Results

5.3.1. Species richness and fish assemblage

Thirteen streams were sampled in 2008 and 10 in 2009. 5640 fish specimens representing 75 taxa were recorded overall with annual totals of 63 and 64 species, respectively (Table 5.3, but see also Appendix 5.1., Table A5.1). Cypriniformes was the most abundant order, with 36 (57% of total) member species documented in 2008 and 35 (54%) in 2009, within which Cyprinidae was the most speciose family contributing 24 (38%) and 25 (39%) species. In contrast, nine families were represented by only a single species during the course of sampling in 2008 and eight in 2009, while 11 species were catalogued solely in 2008 and 12 in 2009. Eight species were classified as singletons (represented by a single individual) in 2008 as were 11 in the following year. The five most abundant species for both years combined contributed more than 45% of the overall total recorded and were also dominated by the family Cyprinidae (Appendix 5.1., Table A5.1).

Table 5.3. Summary of fish species composition collected from all sites in 2008 and 2009

Order	No of family	No of genus	No of species
Beloniformes	2/2	2/2	2/2
Cypriniformes	4/4	21/21	36/35
Gasterosteiformes	1/-	1/-	1/-
Perciformes	5/4	5/4	7/6
Siluriformes	5/6	10/12	13/17
Synbranchiformes	2/2	3/3	4/4
Total (08/09)	18/18	42/42	63/64

Note. X/Yvalue = 2008/2009; - = absent

In both sets of fieldwork, *Glyptothorax major* was the most wide-ranging species being recorded from 10 sites in 2008, 8 sites in 2009 and displaying a near-continuous pattern of distribution (Appendix 5.2., Table A5.2 and Appendix 5.3., Table A5.3). Thirteen species were recorded from more than six streams in both years of which eight (*Glyptothorax major*, *G. siamensis*, *Hemibagrus nemurus*, *Homaloptera zollingeri*, *H. parclitella*, *Macrogathus maculatus*, *Mastacembelus favus* and *Neolissocheilus soroides*) can be considered the most common fish inhabiting small streams of Peninsular Malaysia. However, the majority of fishes exhibited discontinuous distribution e.g. *Devario regina* and *Rasbora notura*; the former were common in the north-western region and the latter

were common in the eastern region but absent elsewhere. *Batasio fluviatilis* (a small bagriid catfish), *Monopterus albus* (a swamp eel) and *Lobocheilos rhabdoura* (a cyprinid) were recorded more often in the north-west than the south and east regions but were not considered regionally endemic. Similarly, *Silurichthys schneideri* and *Homaloptera nebulosa* were collected with greater frequency towards the north-west but the former was also recorded in the east region during 2009, whereas *Nemacheilus masyae*, a small sand dwelling loach, appeared mainly in eastern inventories but was also recorded from Tengkek in the south during 2008. Most of the species reported at just a single locality (unique species) were from the east or south, and between 15 and 23 species were regarded as extremely restricted.

5.3.2. Beta diversity: Variation in community structure

This study shows that spatial factors influence beta diversity. Beta diversity values for all pairs of contiguous and non-contiguous were calculated and the results for both years presented in Tables 5.4 and 5.5, (see Figure 5.3). In all cases, these were greater than zero (0), indicating a general dissimilarity in fish community composition between sites. For the 2008 survey, the plot between the Berkelah-Berlumut and Belatan-Berlumut returned the lowest beta diversity value of 0.04, followed by the Peres-Berlumut (0.06). None of these is contiguous sites. In contrast, in 2009 the lowest values were for the Hijau-Chepir (0.31), Chepir-Bayu (0.40), and Hijau-Bayu (0.46) which all are contiguous pairs. The lowest values among contiguous sites sampled in 2008 were for the Hijau-Chepir (0.40), Hijau-Bayu (0.47) and Ledang-Bendul (0.47). Eleven and five pairs of sites demonstrated total variation in 2008 and 2009, respectively (Tables 5.4 and 5.5). Many streams did not have fish similarity with Ledang. Nonetheless, many sites in both years showed high variation in beta diversity particularly between non-contiguous pairs of site.

Table 5.4. Beta diversity (1-Bray-Curtis, lower diagonal) and Jaccard's (dis)similarity values (upper diagonal) for sites sampled in 2008.

		Jaccard's (dis)similarity values												
		Tasoh	Bayu	Chepir	Hijau	Kenas	Tengkek	Bendul	Ledang	Berlumut	Berkelah	Jin	Peres	Belatan
Beta diversity (1-Bray-Curtis)	Tasoh		0.72	0.87	0.92	0.93	0.96	1.00	1.00	0.92	0.91	0.94	0.94	0.77
	Bayu	0.77		0.52	0.52	0.67	0.74	0.87	1.00	0.88	0.82	0.72	0.66	0.74
	Chepir	0.67	0.52		0.32	0.60	0.74	0.76	1.00	0.90	0.83	0.79	0.69	0.74
	Hijau	0.84	<u>0.47</u>	<u>0.40</u>		0.60	0.74	0.76	1.00	0.90	0.80	0.82	0.69	0.74
	Kenas	0.97	0.81	0.82	0.84		0.72	0.86	1.00	0.67	0.68	0.74	0.76	0.79
	Tengkek	1.00	0.91	0.85	0.78	0.57		0.71	0.93	0.80	0.70	0.84	0.75	0.92
	Bendul	1.00	0.96	0.92	0.93	0.94	0.91		0.83	1.00	0.89	0.88	0.83	0.93
	Ledang	1.00	1.00	1.00	1.00	1.00	1.00	<u>0.47</u>		0.94	0.96	0.92	0.96	1.00
	Berlumut	0.99	0.94	0.92	0.95	<u>0.47</u>	0.70	1.00	1.00		0.66	0.72	0.82	0.84
	Berkelah	0.99	0.92	0.86	0.86	0.68	0.76	0.96	0.98	<u>0.04</u>		0.68	0.74	0.77
	Jin	0.99	0.82	0.90	0.88	0.81	0.95	0.64	<u>0.45</u>	<u>0.36</u>	0.84		0.69	0.72
	Peres	0.98	0.68	0.75	0.71	0.80	0.73	0.94	0.94	<u>0.06</u>	0.85	0.82		0.77
	Belatan	0.88	0.75	0.82	0.83	0.86	0.94	0.96	1.00	<u>0.04</u>	0.84	0.77	0.86	

Note: 1. Values in bold indicates total dissimilarity, 2. Italicised values in bold at the upper diagonal indicates pairs of sites with high similarity, 3. Boxed values at the lower diagonal indicates close proximity sites with low beta diversity, 4. An underlined value indicates additional sites with low beta diversity

Table 5.5. Beta diversity (1-Bray-Curtis, lower diagonal) and Jaccard's (dis)similarity values (upper diagonal) for sites sampled in 2009.

		Jaccard's (dis)similarity values									
		Bayu	Chepir	Hijau	Tengkek	Bendul	Ledang	Berlumut	Berkelah	Peres	Belatan
Beta diversity (1-Bray-Curtis)	Bayu		0.32	0.38	0.78	0.75	0.96	0.86	0.80	0.66	0.74
	Chepir	<u>0.40</u>		0.30	0.78	0.86	1.00	0.96	0.81	0.73	0.81
	Hijau	<u>0.46</u>	<u>0.31</u>		0.70	0.77	1.00	0.96	0.82	0.67	0.78
	Tengkek	0.90	0.78	0.78		0.50	1.00	0.85	0.78	0.81	0.92
	Bendul	0.93	0.91	0.96	0.80		0.92	0.89	0.80	0.83	0.91
	Ledang	1.00	1.00	1.00	1.00	0.52		0.85	0.89	0.93	0.97
	Berlumut	0.96	0.99	0.99	0.79	0.98	0.99		0.81	0.88	0.94
	Berkelah	0.88	0.80	0.82	0.64	0.92	0.97	0.67		0.82	0.83
	Peres	0.65	0.76	0.76	0.85	0.78	0.82	0.97	0.83		0.82
	Belatan	0.81	0.90	0.91	0.96	0.95	1.00	0.89	0.88	0.93	

Note: 1. Values in bold indicates total dissimilarity, 2. Italicised values in bold at the upper diagonal indicates pairs of sites with high similarity, 3. Boxed values at the lower diagonal indicates close proximity sites with low beta diversity, 4. An underlined value indicates additional sites with low beta diversity

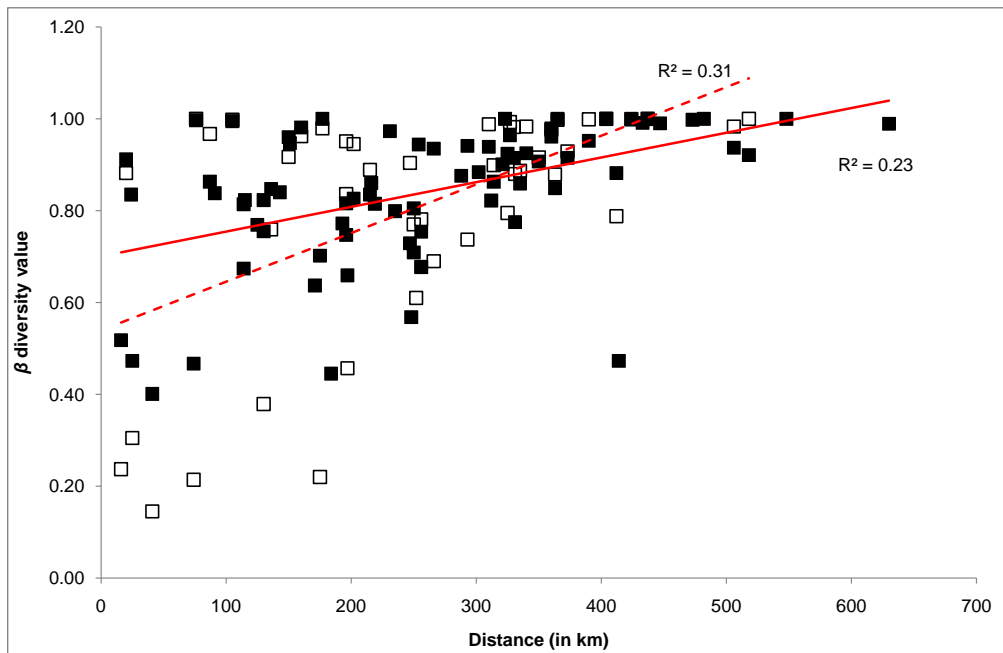


Figure 5.3. Relationship between beta diversity values (Bray-Curtis dissimilarity) and site distance based on fish abundance in 2008 (filled squares) and 2009 (empty squares) with respective linear regression lines (solid line for 2008 and dashed line for 2009, respectively). Geographically separated pairs of sites display less similarity than adjoining sites.

Interestingly, in the 2008 results set, the lowest variation in beta diversity value was derived from non-contiguous sites whereas the opposite was true in 2009. In some cases, geographically disparate pairs of streams also expressed surprisingly low variation, presumably indicating some environmental and/or geomorphological similarities between them. The lowest value (0.40) for contiguous sites (obtained by pairing the Hijau and Chepir) in 2008 was far higher than that for non-contiguous sites *e.g.* the Berkelah-Berlumut (197 km apart, $\beta = 0.04$) and Belatan-Berlumut (412 km apart, $\beta = 0.04$).

As far as the analysis of contiguous sites is concerned, only a handful of site pairs in the northwestern region displayed lower beta diversity values than that of the other regions in both years. A number of distantly-separated sites displayed total dissimilarity, *i.e.* no overlap in species composition, in which $\beta = 1$ (see Tables 5.4 and 5.5), but some southern localities in relatively close proximity to one another (*e.g.* the Ledang-Berlumut and Tengkek-Ledang) exhibited significant species variation in both years. The Berlumut-Bendul was another incongruous site pair within that region, at least for samples taken during 2008.

In this study, fish community structure was predominantly related to the extent of geographical separation between streams (Figure 5.3). This was evidenced by a detectable positive correlation between beta diversity value and site separation distance, plus a correspondent positive correlation with dissimilarity value (*i.e.* beta diversity, $R^2 = 0.23$ and $R^2 = 0.31$ for 2008 and 2009, respectively). My data sets for both years demonstrate that fish communities in small streams tend to differ between northern, southern and eastern regions in Peninsular Malaysia, with locally contiguous habitats generally containing more analogous ichthyofaunal communities.

5.3.3. Ichthyofaunal dissimilarity: Turnover in species assemblages

Ichthyofaunal similarity between sites for each region and year was evaluated using Jaccard's dissimilarity (see Tables 5.4 and 5.5) and dendrograms were plotted based on Euclidean distance calculated using Ward's methods (Figures 5.4 and 5.5). Jaccard's similarity values were consistently above zero (0), denoting that none of the habitat pairs were entirely similar for either year. In 2008, the lowest dissimilarity values based on species composition between contiguous sites were $IS_{J\beta} = 0.32$ for the Chepir-Hijau and $IS_{J\beta} = 0.52$ for the Bayu-Chepir and Bayu-Hijau. With the exception of a few north-western localities, the majority of site-pair comparisons performed show great dissimilarities, with those in the same region often notably heterogeneous in terms of species composition, *e.g.* the Bendul-Berlumut in 2008 and Ledang-Tengkek in 2009 (Tables 5.4 and 5.5). Many site pairs exhibited comprehensive disparity in both years.

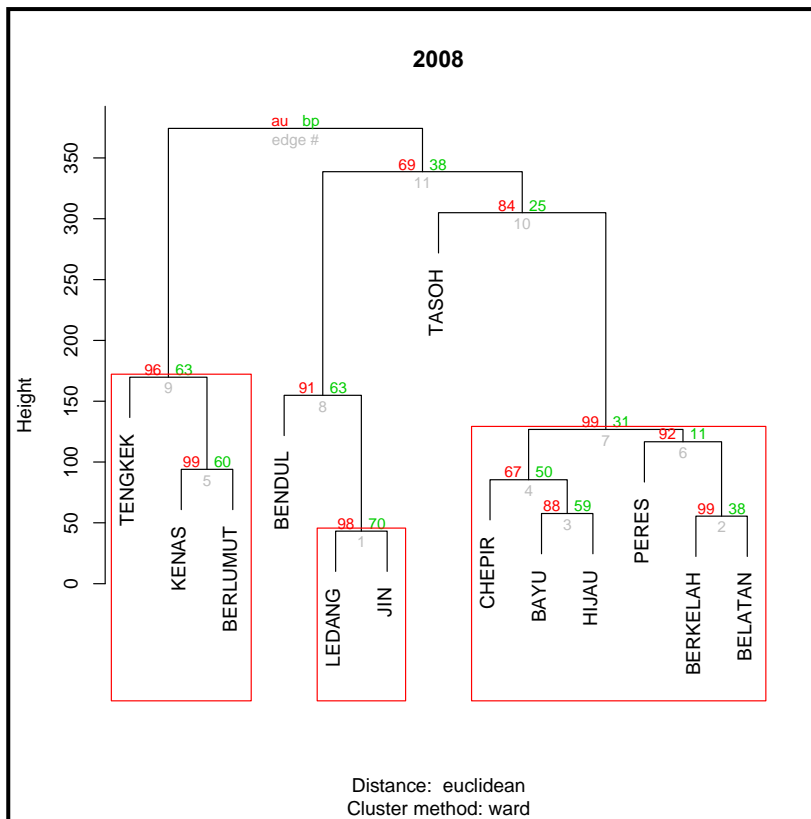


Figure 5.4. Dendrogram derived from Ward's methods for sites sampled in 2008.

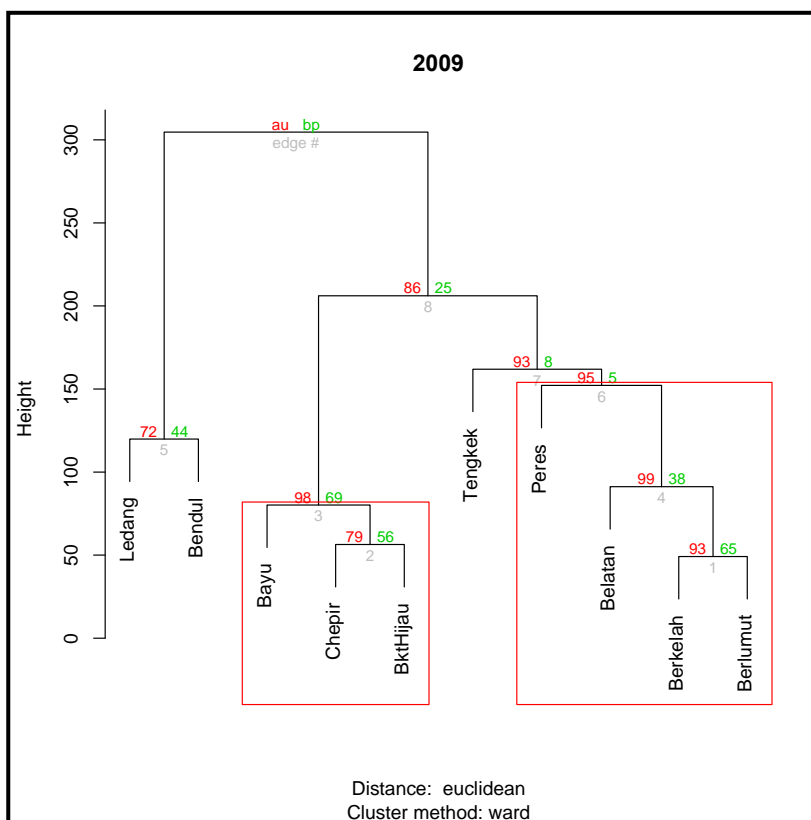


Figure 5.5. Dendrogram derived from Ward's methods for sites sampled in 2009.

Through examination of the dendrogram, it was possible to establish that areas where streams are located in close proximity to one another do not necessarily contain similar species assemblages, although in some instances this was the case. Cluster analyses of streams sampled in 2008 (Figure 5.4), based on Euclidean distance matrix and using Ward's methods, resulted in sites being grouped into three clusters that were significantly different from one another (see Figure 5.4). The northwestern (the Chepir and Bayu-Hijau) and eastern regions (the Berkelah-Belatan and Peres) were strongly linked together to form a cluster that significantly differ (AU *p-value* 99%) from the Ledang-Jin pair (second cluster) and Kenas-Berlumut and Tengkek cluster which significantly dissimilar between each other (AU *p-value* = 98% and 96%, respectively). Two sites displayed deviations in community composition compared with others in the northwestern region, with the Tasoh drainage somewhat isolated from the other localities sampled and the Kenas system unexpectedly more allied (AU *p value* = 99%) to streams in the southern region. The eastern region formed a sub-cluster together with the northwestern localities except one site (the Jin) which seemed isolated in terms of species composition. Nevertheless, the southern sites are clearly separated into two groups – the Tengkek-Kenas-Berlumut and the Bendul-Ledang-Jin which considerably dissimilar (AU *p-value* = 96%).

Sites also formed three clusters for 2009 (Figure 5.5). However, only two clusters were radically distinct – these were where the northwestern localities diverged greatly from the eastern sites. Northwestern streams mostly clustered (except the Berlumut which is the southern site), with those in the eastern region plus the Tengkek which was somewhat isolated from other southern localities, however this separation was not significant. Northwestern sites tended to group together more strongly but those of the southern region were clearly divided into two clusters. Species composition in the Berlumut drainage was regarded as being more similar to the northwestern (2008) and eastern (2009) regions than other southern region sites. The Tengkek system was more comparable to others than to the Ledang and Bendul but significantly similar (AU *p-value* = 96%) to Berlumut (in 2008) or its group (in 2009). These two southern streams were generally distinctive from all other sites as evidenced by the low values for Jaccard's index of similarity (see Table 7 and 8) signifying an increase in turnover among assemblages.

5.3.4. Within region taxonomic similarity

Taxonomic similarity results, expressed as Δ_S , an index derived from taxonomic spread of species, was determined using incidence-based data and based on the presence of fishes from the order Cypriniformes collected at every site over the entire study were analysed separately. The outputs are summarised in Table 5.6. In regional comparisons, performed using Δ_S and Whittaker's β_W the southern region displayed the greatest beta diversity in both surveys. Beta diversity was also more pronounced in the northwestern than eastern region when expressed as Δ_S , and inverse values calculated using Whittaker's β_W formed similar patterns. The overall ichthyofauna of streams in the same given region was more similar in 2009 than 2008, and fish communities of the eastern region were the most homogeneous whether (artificially) composed only of the most common group (Order Cypriniformes) or all species combined. Sample variance was very high (noticeable in Whittaker's β_W measurements) for streams of the southern region across both years.

Table 5.6. Statistical summary for taxonomic similarity (Δ_S) applied to fishes of the order Cypriniformes (presence/absence) and Whittaker's β -diversity for all fishes recorded during 2008 and 2009, respectively.

	2008			2009		
	North	South	East	North	South	East
Taxonomic similarity, Δ_S (based only on the presence of Cypriniformes fishes)						
Mean	0.466	0.440	0.653	0.507	0.475	0.680
Sample Variance	0.007	0.035	0.004	0.000	0.011	0.008
Range	0.230	0.370	0.140	0.020	0.230	0.180
Whittaker, β_W (based on total data for both years)						
Mean	2.984	12.163	1.561	2.534	7.566	1.401
Sample Variance	1.115	165.056	0.056	0.227	25.127	0.003
Range	2.727	27.794	0.530	0.952	10.667	0.091

5.4. Discussion

The key findings of this study are that (1) several species show non-continuous distributional patterns, and (2) variation and turnover of species assemblages is positively related to distance. Seventy-five species of primary freshwater fishes were recorded during this study with relatively equivalent species richness figures recorded in both years. Sixty-three species were recorded from 13 sites sampled in 2008 and 64 species from 10 sites in 2009. This diverse ichthyofauna was primarily dominated by fishes of the family Cyprinidae as is common in many parts of Southeast Asia. A handful of taxa were widely distributed but many were restricted to a few localities or endemic to a particular region, the latter group including such species as *Devario regina* (north-western region) and *Rasbora notura* (eastern region). A greater number of species were recorded from the eastern than the northwestern and southern regions.

The results of this study also suggest that contiguous habitats tend to accommodate more similar fish species assemblages than non-contiguous ones, whereas beta diversity is most often higher between pairs of the latter. Most assemblages within a given region were more similar to those in the same region. The turnover degree of community structure in eastern region exhibiting is lesser than that in the northwestern or southern regions. In addition, the southern ichthyofauna displayed more notable localised variations than the northwestern or eastern equivalents, which in turn were most alike to each other.

5.4.1. Species richness and fish assemblages

Taking the data sets individually, the number of fish species recorded in both years was almost identical despite fewer streams being sampled in 2009. The taxonomic composition of the surveyed fish communities was consistent with earlier censuses of freshwater habitats in Peninsular Malaysia (Zakaria-Ismail, 1993; 1994; Samat *et al.* 2005). Species of the family Cyprinidae dominated the catch in both years, of which those recorded in more than 50% of sites were considered widespread. Despite the abundance and success of cyprinids throughout the study regions, the most widely distributed species was in fact *Glyptothorax major*, a hill-stream sisorid catfish.

A minority of species were found to be sparsely distributed and restricted to a few particular stream systems. The Queen danio, *Devario regina*, was recorded only in the northwestern region and absent elsewhere, for example, though this was not entirely unexpected since it was already thought confined to that area (Zakaria-Ismail & Lim, 1995; Ahmad & Lim, 2006) with a wider distribution in Peninsular Thailand. Likewise, *Rasbora notura* was not found outside the eastern region, this agreeing with Kottelat (2005) who stated that it is endemic to streams in eastern Peninsular Malaysia. Despite their relatively limited patterns of distribution, both species were locally abundant and found to occur in numerous drainages within their respective regions.

More than a quarter of the fish species recorded in 2008 can be regarded as localised in terms of their distribution, this figure rising to almost half for 2009. Further, some of these occur only in a small number of streams and some as singletons, within their specific distribution range. Eastern streams contain more 'unique' species than the others, thus supporting the proposal of Abell *et al.* (2008) who demonstrated the anomalous nature of that region. Their 'Malay peninsula eastern slope' (Abell *et al.*, 2008) includes the southern region as referred to here, an apparently legitimate theory based on the current findings since the Berlumut drainage fish communities returned low beta diversity values when compared with eastern assemblages (Table 5.4). However, the results of 2009 sampling were not in consistence with previous findings.

5.4.2. Beta diversity: Variation in community structure

The beta diversity values of localities in close proximity to one another were not necessarily lower than those of more geographically-distant sites, and all pairs of sites displayed a degree of heterogeneous species composition. For example, several pairs of non-contiguous sites returned unexpectedly low beta diversity results including the Berkelah-Berlumut ($\beta = 0.04$), Belatan-Berlumut ($\beta = 0.04$), Peres-Berlumut ($\beta = 0.06$), Jin-Berlumut ($\beta = 0.36$) and Kenas-Berlumut ($\beta = 0.47$). Such exceptions can probably be explained by the presence of similar fish species at each site, and are presumably indicative of some shared environmental and/or geomorphological aspects driving community structure.

Eastern sites were indisputably more allied to those of the southern than northwestern region, thus signifying an existent degree of connectivity (Hooper & Kennedy, 2002) between their respective ichthyofaunas as mentioned in earlier studies related to the biogeography and distribution of fauna in Southeast Asia (*e.g.*, Rainboth, 1996; Voris, 2000). McConnell (2004) ascertained that exchange of aquatic fauna in Southeast Asia occurred as early as the Pleistocene glacial maxima *via* the great Sunda Rivers, which flowed across the Sunda shelf. During the Pleistocene to late Pleistocene, many streams in the eastern region drained into the Siam River, or extended Chao Phraya, which then comprised a single system. Rainboth (1996) and Voris (2000) discussed the likelihood that streams and rivers of eastern Peninsular Malaysia were previously connected to the same river system that once drained the southern region. The conspicuous degree of similarity observed between the ichthyofauna of the Berlumut system and many streams of the eastern region can be taken as extant proof of this ancient link. The enormous Pleistocene river systems may therefore have been largely responsible for shaping the current distribution patterns of freshwater fishes in Peninsular Malaysia (McConnell, 2004).

The comparative beta diversity values of contiguous site pairs, *e.g.* the Bayu-Hijau ($\beta = 0.47$) and Hijau-Chepir ($\beta = 0.40$) were unsurprising since these streams are tributaries of the same river system and therefore expected to contain near-identical species assemblages (Thompson & Townsend, 2006). The degree of conformity was more profound for the 2009 data sets although unfortunately none of the non-contiguous site pairs exhibiting low beta diversity values in 2008 were revisited in 2009. Hooper & Kennedy (2002) suggested that taxonomic composition is unrelated to the distance between sites and instead more strongly influenced by environmental gradients which may offer an explanation as to why some contiguous site pairs did not accommodate comparable fish assemblages *e.g.* the Bendul-Tengkek (2008 and 2009) or Jin-Berkelah (2008).

Several well-separated site pairs displayed a complete turnover of resident species between 2008 and 2009, evidenced by beta diversity values reaching 1. For example, data in 2008 shows that the Tasoh did not share any species with the Tengkek, Bendul and Ledang systems, nor did the Ledang with the Bayu, Chepir, Hijau, Kenas, Tengkek, Berlumut or Belatan. The Bendul-Berlumut site pair was also dissimilar in species composition despite their relatively proximity, which suggests a lack of connectivity and thus species exchange, between the two systems during the last glacial maxima as demonstrated by

Rainboth (1996) and Voris (2000). Assemblage structure in the Ledang basin was comparatively distinct from many of the other sites in 2009, while the Berlumut displayed complete species turnover compared with the north-western Hijau and Chepir drainages, only sharing a few species with the Bayu in that region and Peres in the east. The apparent lack of similarity between the Berlumut and Peres in the present study was probably influenced by severe precipitation during fieldwork, which may have adversely affected sampling. The mobility of animals is also known to impact on beta diversity (Hewitt *et al.*, 2005), and minor similarities between site pairs were expected because habitat generalists with extensive ranges naturally infiltrate many streams.

During the analysis of contiguous site pairs in close proximity to one another, those returning relatively high beta diversity values were the Bayu-Chepir ($\beta = 0.52$, 2008), Bendul-Tengkek ($\beta = 0.91$, 2008; 0.88, 2009) and Jin-Berkelah ($\beta = 0.84$, 2008). Of these, the result for the Bayu-Chepir was high in 2008 as heavy precipitation caused an increase in water level and resultant complications in sampling, meaning that when revisited in 2009 the beta diversity value was a little lower ($\beta = 0.40$). The Bendul and Tengkek were also typified by high beta diversity values, which might be explicable by the contrasting impact of human activities on these sites. The Bendul is located close to a main road and has proven very popular as a picnicking spot with a number of artificially-modified pools created for swimming, *etc.* along certain stretches, whereas the Tengkek is less accessible and relatively undisturbed. It is therefore unsurprising that this pair contained contrasting species assemblages.

The Jin and Berkelah systems also produced high beta diversity figures, but in these cases species arrangement was more likely influenced by variations in biotope physical characteristics *i.e.* microhabitat structure. The Jin is relatively smaller than the Berkelah and in its upper reaches substrates consist of pebbles, a few small boulders and exposed granite bedrock. Downstream submerged snags and fallen branches were common and there were numerous stretches of open water. The upper Berkelah has a sandy base substrate with many boulders and the lower section, though similar to the Jin, features less woody material and open water. Ellingsen & Gray (2002) illustrated how habitat heterogeneity can influence ecological relationships within a specified area, and correspondingly the Jin site contributed a greater variety of not only pelagic species but others favouring sheltered habitats, such as snags, than the Berkelah. These included

Rasbora paucisqualis, *Xenentodon canciloides*, *Parachela oxygastroides*, *Pristolepis grootii* and *Rasbora argyrotaenia*, all of which are also surface feeders preying chiefly on allochthonous invertebrates, whereas the majority of species recorded only from the Berkelah were specialised inhabitants of rocky environments feeding on benthic invertebrates.

Beta diversity values for non-contiguous pairs of sites were, as expected, high except in a handful of cases. The 2008 data for the Berlumut, in particular, returned very modest beta diversity results when paired with the Kenas, Berkelah, Jin, Peres or Belatan but 2009 values were markedly higher. Reduced beta diversity between geographically distant pairs may pertain to relative occurrence of common, alimentary generalist species frequenting fast-flowing water in less disturbed surroundings, and comparable factors may have been responsible for the Tengkek-Berkelah and Tengkek-Berlumut results in 2009. Pairing of the Bendul and Ledang unsurprisingly yielded low beta diversity values for both years' data sets ($\beta = 0.47$, 2008; $\beta = 0.52$, 2009), almost certainly because both sites are popular recreational spots (the Ledang slightly less so), and only a small number of highly tolerant, headwater-dwelling species occupied both streams. In less speciose ecosystems such as these, a single species can influence beta diversity even when shared between sites, which in this case is expressed as an increase in similarity (IS_J value = 0.50). The results obtained here thus exemplify both niche and neutral theories, whereby it is difficult to prove that similarities in fish community structure displayed by specified sites are primarily determined by localised ecological parity (Thompson & Townsend, 2006), and increased geographical separation apparently reduces the extent of such analogies between sites (Hooper & Kennedy, 2002).

5.4.3. Ichthyofaunal similarity: Turnover in species assemblages

On the whole, ichthyofaunal diversity across the study sites was high but unevenly distributed. Streams of the northwestern region exhibited close similarities but there were some marked differences between contiguous pairs in the south and east with some, such as the Ledang having a different composition from almost all other sites in both 2008 and 2009. Several streams in close proximity to one another contained dissimilar fish assemblages, *e.g.* the Tengkek-Bendul in 2008, and dendrograms derived from Ward's

methods illustrate that very few of the closely-affiliated stream pairs (distance less than 50 km) were similar, *e.g.* the Bayu-Hijau.

These findings suggest that species occurrence and abundance patterns correlate with spatial arrangement of stream habitats as well as prevailing environmental conditions (Thompson & Townsend, 2006). In 2008, clustering analyses using Ward's methods demonstrate that the streams can be grouped into three distinct clusters. The first contains two sub-clusters representing northern and eastern streams, respectively. When results were combined these were found to share more fish species with second cluster streams, leaving the Tengkek, Kenas and Berlumut to comprise a different cluster. When sampling was repeated the following year, contrasting results were obtained; although the northern sites still clustered together, those of other regions did not with the exceptions of the Ledang and Bendul. In fact, the results of the 2008 sampling efforts appear to disclose that fish assemblages do not exhibit a clear northwestern/southern/eastern segregation as suggested by Mohsin & Ambak (1983) but rather correspond to Abell *et al.* (2008) who proposed a simpler east-west segregation.

Streams in the east and south regions harbour a greater number of unique species than those in the north-west (Tables 5.4 and 5.5). The existence of this division is further supported by results obtained in 2009 in which the Berlumut grouped with the eastern cluster and Tengkek. When the two least diverse streams *i.e.* the Bendul and Ledang are omitted from results, the southern region displays marked similarities to the east but is noticeably disassociated from the north-west. In summation, these outcomes infer that modern patterns of connectivity between streams and rivers within Peninsular Malaysia derive from great ancient rivers, which additionally shaped the distribution of aquatic fauna. These findings agree with the conclusions of Abell *et al.* (2008) in that freshwater ichthyofauna of the Malay peninsula is dissociated into two, clearly delineated (eastern and western) geographical entities rather than the single territory proposed by Zakaria-Ismail (1994) and Yap (2002) or three regions as per Mohsin & Ambak (1983).

5.4.4. Within region taxonomic similarity

In both study years, fish communities were dominated by members of the Order Cypriniformes (barbs, carps and loaches), these constituting more than 50% of species

recorded. In recent years, the use of taxonomic similarity (TS) indices derived from taxonomic distance (TD; computed from species incidence data) have come to represent a popular means of comparing site similarity based on species occurrence (Bacaro *et al.*, 2007; Bacaro *et al.*, 2009; Hooper & Kennedy, 2002; Izsak & Price, 2001; Terlizzi *et al.*, 2009). In the present study, TS was used to evaluate homogeneity between streams, based on relative abundance of cypriniforme fishes, in order to more clearly define the inter-relationships existing within fish assemblages at the regional level. The resultant figures were considerably higher for streams in the eastern region than the north-west and south for both years, thus indicating a greater degree of species conformity there than in other regions. Contrastingly, beta diversity across the entire dataset, based on Whittaker's β_w , was more extreme for northwestern and southern regions, this coinciding with the TS results for cypriniforme fishes.

Izsak & Price (2001) suggested that extensive, widely disconnected areas may be relatively homogeneous in terms of species composition, hence alterations due to 'localised' extinction or migration events are unlikely to cause total loss of a species due to its likely occurrence elsewhere. It was also expected that an overall prominent degree of species similarity and TS (*i.e.*, low beta diversity) would be observed when a large area is sampled. However, these assumptions were not fulfilled in the present study, in which the average distance between sites was largest in the eastern region (128.3 km and 146 km for 2008 and 2009, respectively). Instead, species inhabiting streams of the eastern region demonstrated closer phylogenetic relatedness to each other than in the north-west or south, which may indicate the existence of a more homogeneous series of ecological factors in that area and thus support niche theory (Thompson & Townsend, 2006). On the other hand, fish assemblage composition in streams of the south was more heterogeneous than in the north-west and consequently returned low TS and high beta diversity values (Table 5.4). Since the average distance between streams was greater in the south than the north-west, neutral theory appears to be favoured in this case (Thompson & Townsend, 2006).

Though derived from a partial dataset, the TS results obtained complement those for beta diversity perfectly, indicating that species-rich genera with widely distributed representatives can offer potentially useful comparison between habitats. Small sites of the north-western region in close proximity to one another were typified by relatively high TS and low beta diversity values (see Table 5.5 for 2009 results), indicating that spatial

heterogeneity is suppressed when all streams are tributaries of the same river. The findings of this study indicate that distance correlates positively with community homogeneity (Caterino, 2007).

TS is not strongly influenced by sampling effort (Izsak & Price, 2001) as unlike conventional measures it does not depend on relative occurrence of shared species. An additional practical advantage when compared with conventional similarity indices is the fact that robustness is retained when species misidentification is likely. Comparisons of TS (or other similarity indices) between different habitats or environments are therefore simple to comprehend and can be used in conjunction with other graphical representations such as dendrograms or multidimensional scaling (MDS) plots (Bacaro *et al.*, 2007).

5.5. Conclusion

This study presents the first extensive evaluation of ichthyofaunal turnover within and between small freshwater streams in Peninsular Malaysia, a major component of the natural landscape. My findings prove that such habitats contain highly distinctive species assemblages not necessarily replicated in the broader environment. It was also demonstrated that there is more support for two (western and eastern) ichthyogeographical divisions in Peninsular Malaysia, as per Abell *et al.* (2008), rather than three (Mohsin & Ambak, 1983) or one (Zakaria-Ismail, 1994; Yap, 2002) as previously hypothesised.

Faunal variation and turnover is positively correlated with distance (Thompson & Townsend, 2006) and habitat heterogeneity (Hewitt *et al.*, 2005; Caterino, 2007). In this study, the comparatively large rate of ichthyofaunal variation and turnover over distances of less than 100 km offers valuable insights regarding the scale over which conservation managers must consider aquatic diversity in terms of effective planning for a biodiverse region. There is also an incontrovertible need for additional, intensive investigation of such habitats in order to obtain a more comprehensive understanding of small stream biota in general. Obligate aquatic organisms, such as freshwater fish species, have a restricted ability to re-colonise new areas (Abell *et al.*, 2008), are prone to localised extirpation and frequently overlooked in conservation management proposals.

While many of the habitats sampled here lie within protected reserves, it is clear that anthropogenic influences may cause alterations to fish habitats with resultant imbalances in species richness and abundance. Furthermore, beta diversity is affected by habitat heterogeneity (Hewitt *et al.*, 2005) which is likely increased *via* extensive scale habitat modifications. The high proportion of unique and rare species recorded at the local scale here should incite ramifications regarding effective management of designated small-scale reserves, for which current practices do not usually involve protection of entire streams and therefore (from results obtained here, at least) may not accurately reflect regional diversity (Hooper & Kennedy, 2002). Although this study focussed primarily on similarity and variation of localised ichthyofauna, and provides pivotal information regarding such assemblages, it additionally offers suggestions as to why species diversity differs so

greatly between small streams in different regions and how significant a contribution they impart to freshwater fish diversity and conservation in Peninsular Malaysia.

Box 1.

a. Bray–Curtis dissimilarity

Bray-Curtis dissimilarity is used as a proxy for beta diversity (BC_β) calculation (Chase, 2010). Bray-Curtis dissimilarity is obtained after subtracting the value of Bray-Curtis coefficient from 1 [$1 - \text{Bray-Curtis's (abundance-based)}$]. Bray-Curtis coefficient is one of the most commonly used similarity measures in ecology (Clarke & Warwick, 2001). It is computed using some simple formula:

$$BC_{jk} = \frac{\sum_{i=1}^p 2\min(y_{ij}, y_{ik})}{\sum_{i=1}^p (y_{ij} + y_{ik})}$$

Where,

BC_{jk} = the similarity between the j th and the k th,

y_{ij} = the entry in the i th row and j th column for the i th species in the j th sample ($i = 1, 2, \dots, p; j = 1, 2, \dots, n$)

y_{ik} = the count for the i th species in the k th sample,

$|\dots|$ represents the absolute value of the difference, and

$\min(.,.)$ = the minimum of the two count. The separate sums in the numerator and denominator are both over all rows (*i.e.* species) in the matrix.

Worked example:

i. Calculation of Bray-Curtis coefficient.

Sample- j	6	15	9	0	0
Sample- k	0	3	12	5	3

$$BC_{jk} = \frac{2[0 + 3 + 9 + 0 + 0]}{6 + 18 + 21 + 5 + 3} = 0.4528$$

ii. Calculation of Bray-Curtis dissimilarity (BC_β) index.

$$BC_\beta = 1 - 0.4528 = 0.5472$$

b. Jaccard's dissimilarity index

Jaccard's dissimilarity index is applied as a surrogate for beta diversity ($IS_{J\beta}$) calculation (Chase 2010). The value of $IS_{J\beta}$ is obtained after deducting the value of IS_J coefficient from 1 [$1 - \text{Jaccard's (incidence-based)}$]. Jaccard's index is a similarity index (IS_J) that is also known as Jaccard similarity coefficient that use the presence-absence (binary) data for comparing the similarity of a pair of samples. The index takes into account the resemblance between the two samples. The total number of shared species between a pair of samples is divided by the total number of attributes present in either of the samples (Real, 1999; Southwood & Henderson, 2000). It can be expressed as follows:

$$IS_J = \frac{c}{a + b + c}$$

Where,

c = the total number of species shared between the two samples,
 a and b = is the number of species present in sample A and B, respectively.

Worked example:

i. Calculation of Jaccard similarity coefficient.

Sample A	1	1	1	0	1
Sample B	0	1	1	1	1

$$IS_J = \frac{3}{3 + 4 + 3} = 0.3$$

ii. Calculation of Jaccard dissimilarity ($IS_{J\beta}$) index.

$$IS_{J\beta} = 1 - 0.3 = 0.7$$

Beta diversity is the opposite concepts of similarity (Goettsch & Hernandez, 2006). Therefore, beta diversity value increased when value of the paired similarity decreased (Figure 6). The Bray–Curtis and Jaccard dissimilarity indices values are bound between 0 (low) and 1 (high), where 0 denotes a pair of sites have the similar assemblage, meaning that the two sites share all the species), and 1 imply that the two sites do not have any similar species.

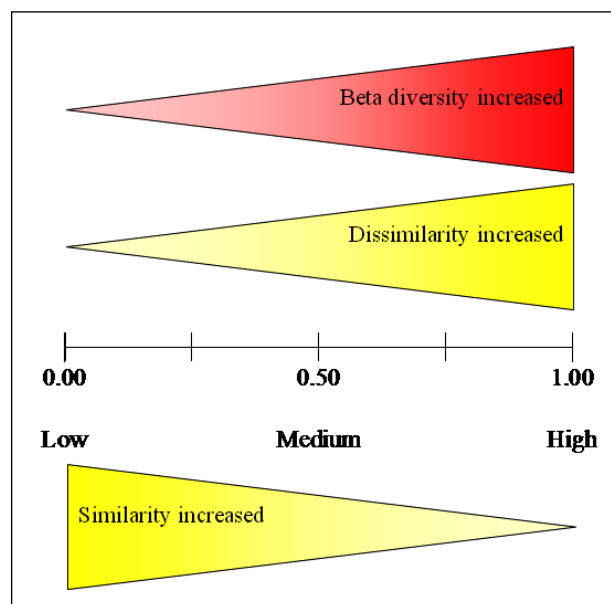


Figure 6. The concept of beta diversity and similarity showing the benchmark for beta diversity values.

CHAPTER 6

PATTERNS OF RARITY AMONG STREAM-DWELLING FISHES IN PENINSULAR MALAYSIA

6.0 Abstract

Patterns of species richness, distribution and comparative rarity of fishes were investigated in small stream habitats of Peninsular Malaysia. 50 such biotopes were selected with species richness (α -diversity) ranging between 4 and 44. Overall there were 103 recorded taxa, largely dominated by representatives of the family Cyprinidae. Species richness estimates were approximately 12% (calculated via Chao 1) and 10% (Chao 2) greater than the observed number suggesting the existence of numerous 'unseen' species. Many fishes exhibited discontinuous patterns of distribution and were considered to be rare while only a handful were widely distributed and abundant. Ordination based on the relative resemblance of fish communities to one another support the existence of two distinct ichthyogeographic divisions in Peninsular Malaysia. In addition, a degree of dissimilarity between regions was observed in terms of species richness and 'diagnostic' species, despite frequent species overlap between some regions. It was possible to assign the species recorded to all seven of Rabinowitz's categories of rarity, with at least 10 restricted to a single stream and locally scarce, although not all of these could be described as hyper-endemic. It is recommended that a sizeable augmentation of the existing protected areas is needed to safeguard Malaysia's exceptionally diverse stream-dwelling fauna of which fishes are simply the most well-known inhabitants.

6.1 Introduction

6.1.1 Ichthyogeographic province in Peninsular Malaysia

Species richness is known to correlate positively with habitat heterogeneity and environmental complexity, some of which factors may vary over space and time thus affecting their occurrence and beta diversity. Obligate freshwater-dwelling fishes are by definition unable to disperse via saline waters. When interference from humans is absent, fish dispersal is thus highly dependent on historical dispersal connections (Rosenfield, 2002) such as the establishment of new downstream connections between river basins during marine regressions or geomorphological events like orogenesis which allow ‘river capture’ and creation of new stream networks connecting adjacent basins (Reyjol *et al.*, 2007). The current dispersal of fish species within small stream tributary systems of larger river basins can be attributed to multiple biotic and abiotic factors (Jackson *et al.*, 2001) and further restricted by the specific hydrogeographical networks within each drainage (Reyjol *et al.*, 2007).

Disparities observed in the geographical ranges of abundant and rare species in nature can possibly be attributed to differences in speciation rate and/or extinction rate experienced by a particular group of species in a given region (Stephens & Wiens, 2003; Domínguez-Lozano & Schwartz, 2005; Lobo *et al.*, 2008). Mittlebach *et al.* (2007) postulated that the age of tropical environments relative to temperate ones allows for more diversity to build up during the lengthier ‘effective’ period (*i.e.*, ‘time-for-speciation effect’; Stephens & Wiens, 2003; Davies & Buckley, 2011). Given longer time-for-speciation, *i.e.*, ‘evolutionary’ time, the species richness of an area will increase. Historical climatic episodes and geological events are known to induce both isolation and connection of water bodies (Hugueny & Lévêque, 1994; Mittlebach *et al.*, 2007). Drainage basins that were created via drawn out or repeated exposure to such episodes often exhibit unique characteristics (Hornung & Raynold, 1995).

In the past, several attempts to separate Peninsular Malaysia into distinct ichthyogeographic regions have been made based on sparse, and sometimes anecdotal, information relating to the presence and distribution of fish species. In terms of fish species, Mohsin & Ambak (1983)

divided Peninsular Malaysia into north-western, north-east and central and southern regions (see Chapter 1, Figure 1.2) although many subsequent workers (*sensu* their figures – Kottelat, 1989: Figure 1; Zakaria-Ismail, 1994: Figure 1; Rainboth, 1996: p. 150; Yap, 2002: Figure 1) have tended to regard the ‘Malay Peninsula’ as a single biogeographic entity running contiguously southwards through Peninsular Thailand from the Isthmus of Kra which also including the northern half of Sumatra plus Singapore (Note: in this study Peninsular Malaysia is defined by its existing political boundaries and so encompasses the area also known as West Malaysia).

Abell *et al.* (2008) more recently suggested that the Malay peninsula should be considered in terms of two principal ecoregions, incorporating the Malay peninsula eastern slope and northern Sumatra-Western Malaysia respectively, essentially splitting Peninsular Malaysia down the centre. Since fishes inhabiting small stream habitats frequently demonstrate discontinuous natural ranges, the unconfirmed existence of smaller, detectable ichthyogeographic regions in Peninsular Malaysia would appear to be a reasonable hypothesis. This chapter therefore attempts to investigate the soundness of this assumption via analysis of data collected recently during field surveys.

6.1.2 Forms of species rarity

Some species are typically encountered in high abundance wherever they are found while others always occur in low densities (Preston, 1948; 1962a; 1962b; MacArthur & Wilson, 1967; Hughes *et al.*, 2001; Magurran, 2007). As a result, some habitats display high equitability of species whereby a significant percentage of resident species have similar chances of being caught during surveys (Thompson *et al.*, 2003) whereas many rare species are difficult to encounter throughout their entire range (De Troch *et al.*, 2001). Main (1982) proposed that in the biological perspective, rare species can be defined as those that are (i) widespread but patchily distributed, (ii) locally abundant but with a very narrow range or (iii) locally scarce with an exceptionally limited range (*i.e.* locally endemic and with a low number of individuals).

Other definitions of rarity include (iv) common species that are only observed occasionally within a specified range (geographical edge species (Longino *et al.*, 2002)), (v) transient individuals passing through an area that they do not usually inhabit, (vi) species that are difficult to catch using standard equipment ('methodological edge' species (Longino *et al.*, 2002)), (vii) known across a relatively wide range but never common ('globally rare' species (Longino *et al.*, 2002)) and (viii) endemic species (globally unique species (Longino *et al.*, 2002)). Rare species are therefore generally limited in numbers and range (Gaston, 1994; Mace & Kershaw, 1997), exhibit restricted range sizes (Manne *et al.*, 1999), are specialised to a particular biotope, display low reproductive rates (Purvis *et al.*, 2000), and are often of large size (Owen & Bennets, 2000) and positioned high in the local food chain *e.g.* apex predators.

Table 6.1. Forms of rarity used to describe various organisms which are equivalent to what is used by Longino *et al.* (2002).

Form of rarity	Equivalent
common species that are only observed occasionally within a specified range	geographical edge
transient individuals	
species that are difficult to catch using standard equipment	methodological edge
known across a relatively wide range but never common	globally rare
endemic species	globally unique

Species considered to be rare are conventionally regarded as prone to extinction (Manne & Pimm, 2001). The existence of such taxa in field samples is sometimes 'inevitable' but can equally be random or accidental depending on local conditions (Cunningham & Lindenmayer, 2005). During sampling itself there are inevitably 'missing' species which are simply not present in the habitat but in many cases the absence of a particular taxon is random or unintentional due to deficient sampling methods. Alternatively, some species may be impossible to detect whether they form part of the natural community or not due to removal by predators or localised extinction events (Cunningham & Lindenmayer, 2005).

6.1.3 Species classification into forms of rarity

Several researchers have defined various forms of rarity relating to certain organisms (Rabinowitz *et al.*, 1986; Yu & Dobson, 2000; Caiafa & Martins, 2010). However, an exception can still be found in some organisms such as fishes. Rabinowitz *et al.* (1986) diagnosed relative rarity based on three traits, (1) geographic range, (2) habitat specificity and (3) local abundance of species, and the fish species recorded in the present study are categorised following these criteria. All are heavily influenced by continuous variables (Rabinowitz *et al.*, 1986) which can be dichotomised into an eight-celled (A-H) matrix in which cell A represents widespread, abundant, non-habitat specialists normally referred to simply as ‘common’ species. Cells B – H represent escalating degrees of rarity with Cell H the most extreme (Caiafa & Martins, 2010).

An organism may be abundant or occur in low numbers over a restricted area (*i.e.* rare) within its natural range. The term ‘extensive’ is applied to widespread species occurring in multiple geographical regions and ‘restricted’ to those found only in a single region. In terms of fishes inhabiting small stream environments, some are restricted to a particular habitat type while others are able to utilise a broader spectrum of non-specific biotopes, with these referred to as ‘stenoecious’ and ‘euryecious’ (*sensu* Caiafa & Martins, 2010), respectively.

Field work for the present study was conducted in several small streams of Peninsular Malaysia, the majority of which are situated in a forest reserve frequented by local people for picnicking and other recreational activities. Water quality and habitat structure are relatively pristine and intact throughout the area, with a limited amount of artificial modification observed at all sites surveyed. The principal aims were: (1) investigation and assessment of ichthyofaunal diversity, (2) corroboration of the ichthyoprovinces existing in the country as identified by previous authors, and (3) identification and evaluation of the commonness and relative rarity (*sensu* Rabinowitz *et al.*, 1986) of the resident fish species. Measures of species richness were thus employed during data analysis with both cumulative (observed) and extrapolated (estimated) richness (Chao 1 and Chao 2) determined using *EstimateS*. The faunistic distance between study sites was computed based on Euclidian distance with Ward’s

method used to plot a hierarchical cluster analysis in order to explore the number of recognisable clusters (*i.e.*, ichthyogeographic provinces/sub-provinces) present within the dataset and display the relationships between them. Classification, presented as a dendrogram, was implemented and a community table constructed to highlight which particular species assemblages distinguish distinct stream groups. All species recorded were additionally grouped according to geographic range, habitat specificity and local population size into the eight categories of rarity (*sensu* Rabinowitz *et al.*, 1986).

6.2 Methodology

6.2.1 Study sites

The total dataset obtained during field work between 2004 and 2009 can be depicted as a 103 (species) \times 50 (streams/sites) fish species matrix. Sampling sites were grouped according to their location into three ichthyogeographic regions (Figure 6.1) following a slightly-modified version of the model proposed by Mohsin & Ambak (1983) (see Chapter 1: Figure 1.2). Fifty 40-100 meter stretches of 1st to 3rd order streams were sampled throughout Peninsular Malaysia with the majority of this work conducted during the dry season base flow between June to September. This decision was taken in order to avert short-term fish displacement which occurs more frequently when water level are high during rainy periods and also because sampling is easier to accomplish and more reliable when less water is present.

All study sites exhibited the three principal physical characters associated with streams *i.e.* pools, riffles and glides, and the length of the study plots was considered adequate to ensure both reliable estimations of raw species richness and community structure (Oberdoff *et al.*, 2001; Tedesco *et al.*, 2007). When sites were revisited, sampling always took place at the same location. Most sites displayed the suite of characters conventionally associated with small, lowland, headwater streams with upstream localities typified by fast-flowing water and substrates chiefly composed of boulders, gravels and cobbles, while downstream water flow was generally slower with a greater proportion of glides or runs and sandy substrates. Pools tended to form underneath the bank's cut and were usually replete with coarse woody debris, logs and fallen riparian vegetation.



Figure 6.1. The map of Peninsular Malaysia showing the sampling sites which were grouped according to their location into three ichthyogeographic regions (yellow = northern, blue= southern and red = eastern) following a slightly-modified version of the model proposed by Mohsin & Ambak (1983) (see Chapter 1: Figure 1.2). Large circles signify location with more than one site within an area.

6.2.2 Sampling

Streams stretches with contrasting morphology representing different channel types (*i.e.* pools, riffles, runs) were selected for sampling via electrofishing between 2004 and 2009. In most cases multiple, orderly passes were made using a portable, backpack electroshocker (Smith-Root model LR-24 with pulsed direct current) in an upstream-downstream direction (Davies & Nelson, 1994), except at a handful of sites at which the width measured 3-5 m several

unidirectional, short-duration passes (*c.* 5-10 s) were made. Stop nets with 3 mm mesh were installed at both extremes of each site to prevent fish from entering or escaping during sampling and maximise catch efficacy. Smaller specimens were transferred into an aerated bucket whereas larger individuals were placed into a loop-net in the stream itself until sampling was completed.

All specimens were anaesthetized with an aqueous, buffered tricaine methanesulfonate (MS-222) solution, identified to species level, measured (total length to the nearest millimetre) and weighed prior to release. Voucher specimens were fixed in a 10% formalin solution and after two weeks transferred to a 70% ethanol solution for long-term preservation and in the case of doubtful identifications, additional diagnosis before being deposited in the ichthyological collection at the Department of Biological Sciences, University Malaysia Terengganu (UMTIC), Malaysia.

6.2.3 Data analysis

Community species richness was initially calculated by a simple count of the number of species collected during field work, and ‘true’ species richness was approximated via the nonparametric Chao 1 and Chao 2 estimators using the *EstimateS* freeware. Chao 1 employs abundance-based data to quantify rarity (Toti *et al.*, 2000) based on the number of singletons and doubletons, and therefore does not necessitate repeat sampling (Scharff *et al.*, 2003). Chao 2 is an incidence-based tool that takes into account the number of unique and duplicate species so is consequently less-biased, more efficient and robust (Colwell & Coddington, 1994; Walter & Martin, 2001; Scharff *et al.*, 2003) although it does entail repeat sampling to function effectively. Randomisation of the sample order was set at 250 runs without replacement and achieved using *EstimateS*.

A Venn diagram was prepared to examine overlapping species occurrences in the three ichthyofaunal regions, and species rank-abundance distributions plotted to evaluate species evenness. $\log_{10} p_i$ where p_i represents the frequency of the i th species in the sample (Lennon *et al.*, 2004) was determined for all taxa recorded and compared with the corresponding

relative rank values (Bossart *et al.*, 2006). Similarities in species equitability among regions are evident from the differences in share and steepness of the curves of different regions (Southwood & Henderson, 2000; Magurran, 2007).

To determine true species richness species sampling must be complete and sampling effort exhaustive, although rarefaction techniques which compute statistical probability (Koellner *et al.*, 2004) from a reiterated re-sampling of all pooled sampling units (González-Oreja *et al.*, 2010) can be used to estimate the definite number of species at an equivalent number of samples. Rarefaction was also utilised in order to standardise observed species richness (Bossart *et al.*, 2006) for sites at which sampling effort was unequal (Gotelli & Colwell, 2001). The predicted number of species at the specific abundance for a given sample site when sampling effort was the lowest was enumerated using the computer program *EcoSim* (Gotelli & Entsminger, 2003) after 1000 iterations.

Fish community composition was appraised in an attempt to demonstrate which species groups characterised particular streams or groups of streams. A dendrogram was generated using the *pvclust*, package a free statistical software package written in 'R' language and downloaded from <http://www.statmethods.net/advstats/cluster.htm>, and Euclidean distance measured based on Ward's method to examine community ordination structure. The resultant *p*-value (95%) was 'Approximately Unbiased' (AU) according to the *R* package but 'Bootstrap Probability' (BP) was also displayed (shown as AU/BP in the diagrams). Clusters of streams with an AU value in excess of 95% are rendered as red rectangles, denotes significantly supported clusters by data set.

A uniqueness value (*sensu* Stohlgren *et al.*, 2005) was calculated for each stream within a region and taken to represent the mean frequency value of every species within a 'plot' divided by the species richness of that plot (Stohlgren *et al.*, 2005). The equation employed thus follows Dapporto & Dennis (2008) in which the 'rarity' of a species = $[1 - (\sum_{i=1,j} p_i / S)]$ where p_i is the proportional frequency of a species in a given stream calculated as the stream number for *i*th species (n_i) divided by the total number of streams (N), and S is the species richness value. The range of values runs from 0 to 1 with higher uniqueness values indicating

less equality between streams (Dennis *et al.*, 2000). A stream containing species with more restricted distributions (unique species) will therefore present small p_i and high uniqueness scores. Inter-regional discrepancies in uniqueness were also analysed using ANOVA.

Both common and rare species were grouped according to geographic range, habitat specificity and local population size and referred to one of eight categories of rarity (*sensu* Rabinowitz *et al.*, 1986). The definition of 'geographic range' is here limited to apply to the presence of fish species at each locality surveyed and the cut-off between 'extensive' and 'restricted' is as given above. Habitat specificity was taken to be 'euryecious' when a species was present in many streams within a region and 'stenoecious' if recorded only at a single locality. The overall population size of a given species is considered 'abundant' when the tallied number of specimens was greater than 10 and 'scarce' when less than 10.

6.3 Results

6.3.1 Species composition: Peninsular Malaysia

A total of 103 fish species were identified from 15181 specimens collected from 50 streams throughout Peninsular Malaysia, with members of the family Cyprinidae predominant (Appendix 6.1. Table A6.1). The majority of those recorded were native to Peninsular Malaysia but two (*Esomus metallicus* and *Trichopodus pectoralis*) were introduced species. 12 singletons and six doubletons species were recorded, 22 species were unique and 11 were considered duplicates species. The nonparametric estimators Chao 1 and Chao 2 performed better than the species accumulation curve (S_{obs}) (Figure 6.2). The predictions derived from both estimators did however appear to correspond with S_{obs} , since all three tools suggested the presence of 10 to 12 additional species which were not encountered during field surveys.

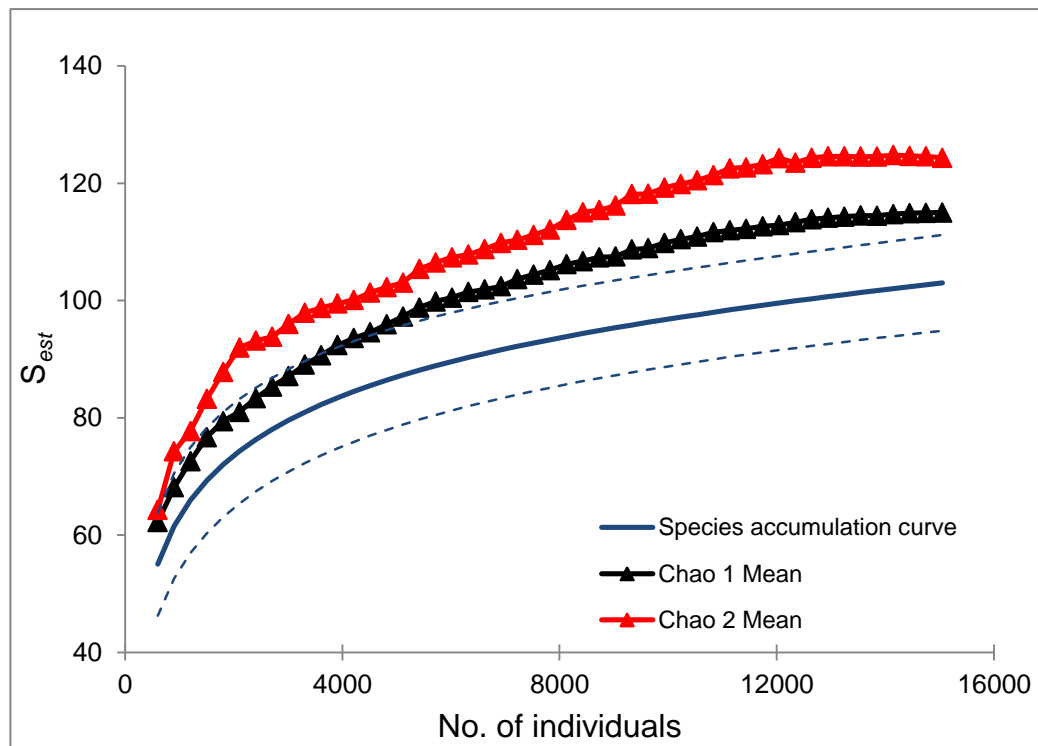


Figure 6.2. Species accumulation curve (solid continuous line), 95% confident intervals (CI) (thin dashes) and estimated species richness curves (Chao 1 and Chao 2) of stream-dwelling fishes in Peninsular Malaysia. The accumulation curve exhibits no indication of plateau but the two estimator curves are beginning to reach an asymptote as the number of individuals increases.

The most abundant species were *Poropuntius smedleyi* (Family Cyprinidae), *Devario regina* (Family Cyprinidae) and *Crossocheilus oblongus* (Family Cyprinidae) while *Glyptothorax major* (Family Sisoridae), *Mystacoleucus marginatus* (Family Cyprinidae) and *Hemibagrus nemurus* (Family Bagridae) were the most widespread. Twenty-five (25.3%) species occurred in all three ichthyogeographic regions (Figure 6.3). The northwestern and eastern regions shared a significant number of species (53 or c. 51%), with 33 species shared between southern and eastern regions. 34 taxa appear restricted to the eastern region whereas the northwestern and southern regions contributed seven and one unique species, respectively.

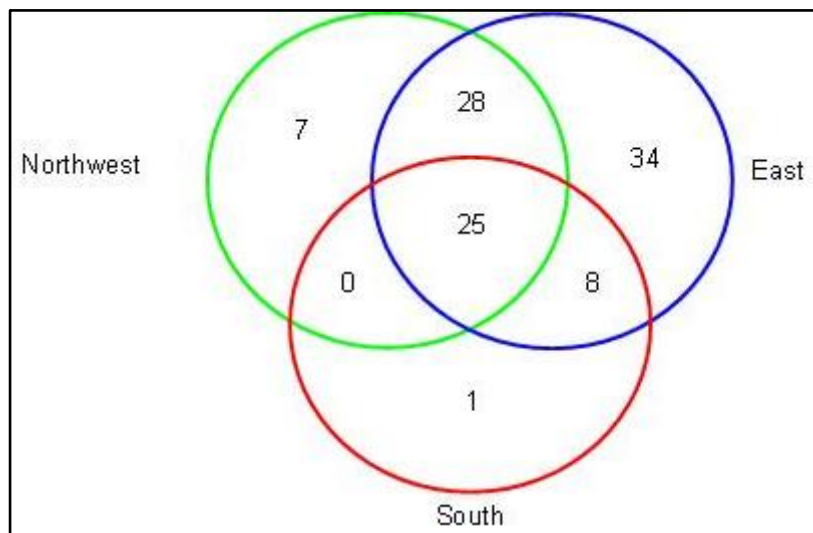


Figure 6.3. Species overlap between the three purported ichthyogeographic regions illustrated using a Venn diagram representing the number of species recorded throughout the survey.

The results obtained here imply that only a handful of stream-dwelling fish species can be considered abundant in Peninsular Malaysia with the remainder exhibiting varying degrees of rarity (Figure 6.4). Similarly, very few taxa are widely distributed with the majority either restricted somehow and/or patchily distributed throughout their range. Most of the latter were also uncommon even when present in a habitat, meaning that they were never recorded in high densities.

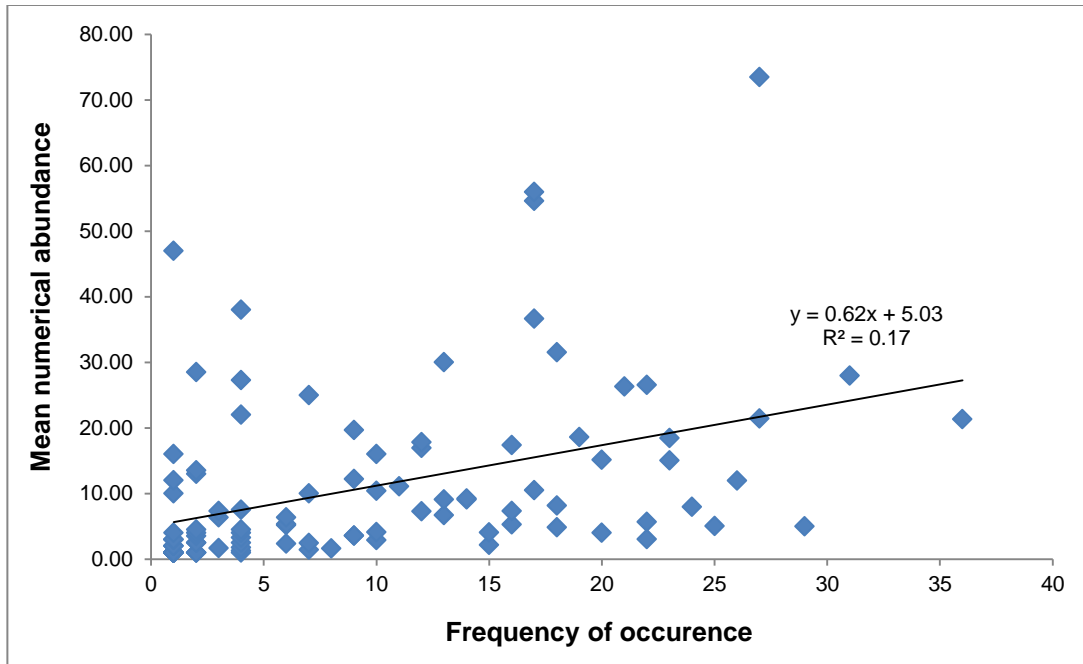


Figure 6.4. The relationship between mean species abundance and distribution of fishes in 50 small streams of Peninsular Malaysia. A positive correlation is obtained when the mean numerical abundance of fish species is plotted against the number of streams inhabited. Many species are scarce and very few widespread species are abundant in small streams.

6.3.2 Species composition: Regional

The combined rank-abundance plot for the three regions formed a distinctive pattern (Figure 6.5) whereby the southern region resembles a log series and differs from the other two regions, which are more similar to a log normal distribution. The slope of the eastern region more extensive and lower thus indicating the presence of a more profuse array of fish species displaying a more even distribution of abundance than the southern and northwestern regions. The eastern region contained the greatest number of species recorded (95) followed by the northwestern (60) and southern (34) regions.

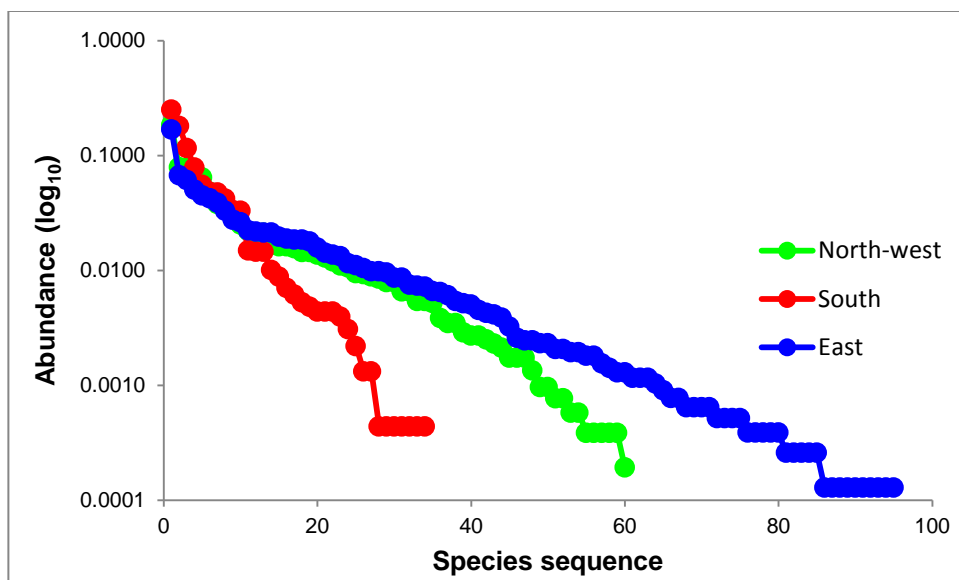


Figure 6.5. Rank/abundance plots for stream-dwelling fishes in Peninsular Malaysia. The gradients of the graphs are indicative of a log series distribution, and the steeper incline shown for the southern region indicates that it is the least even assemblage.

Only one singleton and five doubletons were recorded among the 60 species documented in the northwestern region, while eight were unique and a dozen duplicates. The most abundant species were *Devario regina*, *Puntius binotatus* and *Rasbora paviana* of which the first two were also the most widespread followed by *Glyptothorax major* and *Hampala macrolepidota*. In the south, seven singletons and no doubletons were recorded with almost half of the total (15) unique and nine duplicates. The most abundant species in this region were *Poropuntius smedleyi*, *Crossocheilus oblongus* and *Puntius banksi* while the most frequently encountered were the latter pair plus *Rasbora elegans*. From a total of 95 species collected in the eastern region, ten were singletons and five doubletons, twenty-four species were unique and ten were duplicates. The most abundant species here were *Poropuntius smedleyi*, *Mystacoleucus marginatus* and *Osteochilus waandersii*, while the most extensively distributed were *Glyptothorax major* followed by *Poropuntius smedleyi* and *Mystacoleucus marginatus*.

The rarefaction curves plotted for the three regions escalate steeply as the number of specimens increases (Figure 6.6), with that of the northwestern region apparently stabilising most rapidly, thus illustrating that sampling effort in this region was sufficient to provide a reliable species richness estimate. All regions exhibited noteworthy dissimilarities in species richness with the 95% CI's plotted for each failing to overlap. When rarefaction analysis was

performed on the smallest sample size collected during field work (2274 individuals), between 54 to 60 (57 ± 1.99) and 76 to 86 (81 ± 6.81) species would theoretically be present in equally-sized samples from the northwestern and eastern regions. When species richness values for the eastern and northwestern regions were compared for a similar number of specimens (5179), the eastern region contributed a greater number of taxa, *i.e.* 87 and 94 (91 ± 2.99) species. There were more species can be expected at the eastern region than that from the northwestern and southern regions.

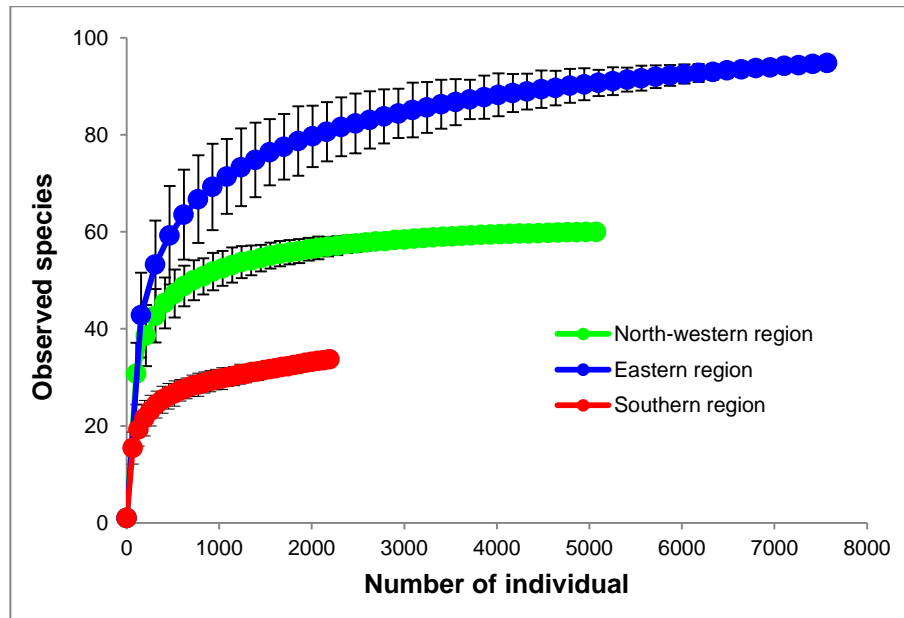


Figure 6.6. Rarefaction curves (and 95% CIs) used to compare species richness between different sample sizes. The three curves do not overlap one another indicating that species richness among the regions is dissimilar.

6.3.3 Ichthyofaunal division

Cluster analyses of the data suggest the existence of two generalised ichthyogeographic regions in Peninsular Malaysia (Figure 6.7). The dendrogram generated by *pvclust* and based on Euclidean distance using Ward's methods denotes that streams were clustered randomly based on their commonly shared species rather than the proximity of sites to one another. Although several clusters of streams show some grouping, these were clearly not based on their regional positioning. A minor degree of separation between eastern and western sites is

evident but cannot be considered significant. Results for the most southerly-located sites of the 'eastern slope' (Figure 6.7 – left branch) deviated considerably from those in the rest of the region, instead appearing more analogous with some northern sites (*i.e.*, Jerangkang, Belimbing and Berkelah). In addition, several eastern streams (*i.e.*, Pasu, Bakar and Linang) were most comparable to those of the 'northwestern slope'. In general, streams were clustered into groups depending on incidence of shared species, notwithstanding distance between sites.

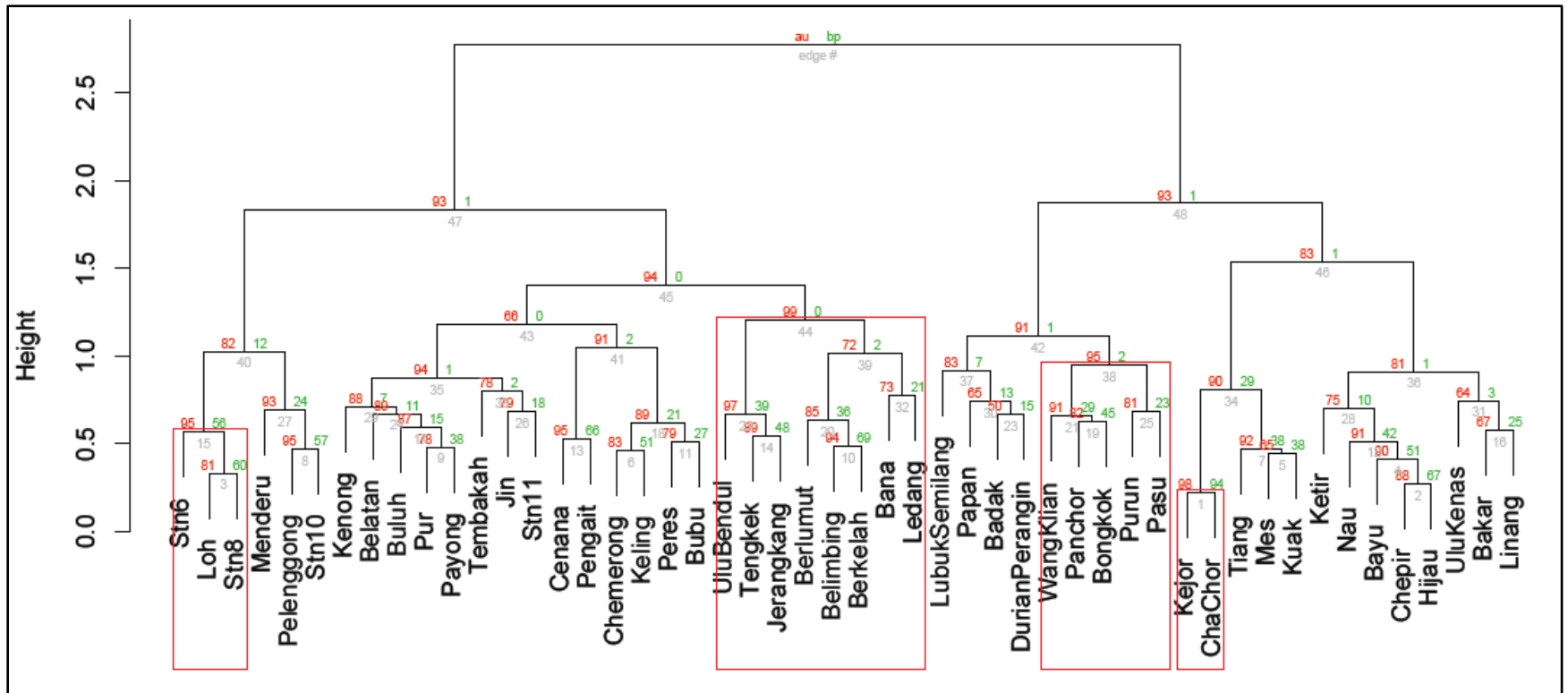


Figure 6.7. Similarities in the composition of fish species among 50 small streams in Peninsular Malaysia. Dendrogram obtained following Ward's method using Euclidean distance. Values in red are p -values and the red rectangles represent significant clusters.

Stream uniqueness can be predicted and represented by a value between 0 and 1 (extremely unique in term of species presence at the location compared to others), and such values for the northwestern region varied wildly in the present study. The overall uniqueness scores for individual streams ranged between 0.54 and 0.79. Values for streams of the southern and eastern regions fall between those for the northwest with ranges of 0.55 to 0.69 and 0.56 to 0.74, respectively. The mean uniqueness figure of northwestern sites (0.64 ± 0.06) did not diverge significantly from southern (0.63 ± 0.06) or eastern (0.65 ± 0.05) ones ($p\text{-value} > 0.05$) (Figure 6.8), while the greatest uniqueness values were derived from streams in the east which had higher median values than in the other two regions (0.66 vs. 0.63 and 0.62).

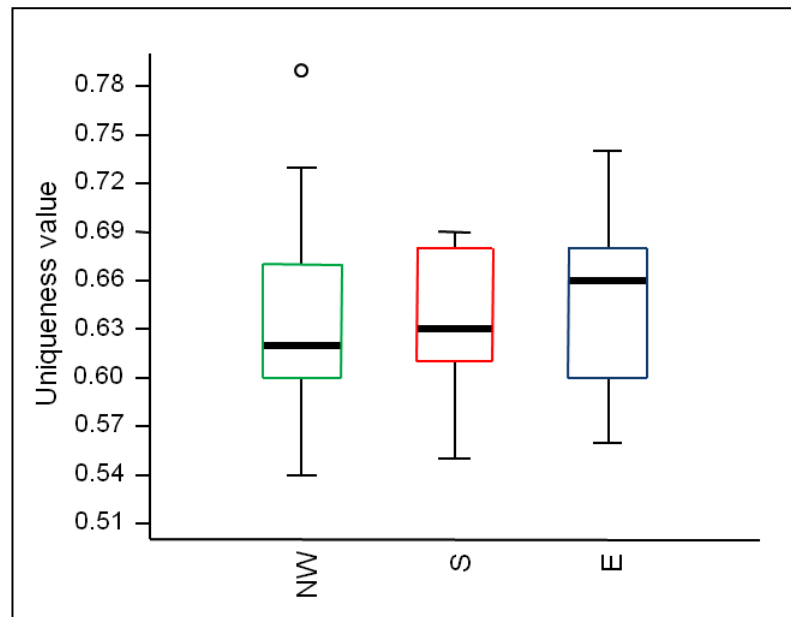


Figure 6.8. Variations in uniqueness value between sites within each region portrayed as a box and whiskers plot, a nonparametric analysis indicating the degree of dispersion and skewedness in data sets, with range indicated by the top and bottom bars. The 25th and 75th percentiles are represented by the box, the median value by the black horizontal bar and the outlier by the open circle. The median value for the eastern region is slightly higher than that of the other two regions but the difference is not significant ($F = 0.23$, $df = 2$, $p > 0.05$).

6.3.4 Patterns of rarity

The classification of species richness based on the eight categories of rarity varies markedly. Approximately 54% of the 103 species documented can be termed abundant in

that they were represented by more than 10 specimens in the samples (Table 6.2), with the remainder considered scarce. Almost 60% of species evidenced a naturally wide distribution range and were recorded in more than two regions, while approximately 40% were highly restricted and found only at a single locality so can be adjudged unique within the region where they were recorded. In excess of 75% of all species were recorded from more than a single stream and thus designated euryecious, while around 23% were only recorded once and therefore deemed stenoecious.

Table 6.2. Forms of rarity of fishes in small stream in Peninsular Malaysia based on categories after Rabinowitz *et al.* (1986). Rarity is assessed based on abundance data of small stream fishes collected since 1998 to present. Shaded values represent grouping of species based on their occurrences and placed in the cell comparable to classification as suggested by Rabinowitz *et al.* (1986), where ‘a’ = ≥ 25 sites, ‘b’ 20 – 24 sites, ‘c’ = 15-19 sites, ‘d’ = 10 – 14 sites, ‘e’ = 5 – 9 sites, ‘f’ = 3 – 4 sites, ‘g’ = 2 sites and ‘h’ = 1 site. Category ‘h’ consists of the ‘rarest’ species subdivided into two subcategories, ‘h₁’ and ‘h₂’ which the former contains two to 10 specimens and the latter have singleton species recorded in this study.

Habitat specificity (U)	Distribution range (R)			
	Extensive (2 or more regions)		Restricted (within a single region)	
	Euryecious	Stenoecious	Euryecious	Stenoecious
Population size (N)	[A]	[C]	[E]	[G]
	34 species 33.01%	1 species 0.97%	10 species 9.71%	11 species 10.68%
	[a]	[c]	[e]	[g]
	7 species 6.80%	13 species 12.75%	13 species 12.75%	11 species 10.79%
	[B]	[D]	[F]	[H]
	25 species 24.27%	1 species 0.97%	9 species 8.74%	12 species 11.65%
[b]	[d]	[f]	[h]	
9 species 8.82%	13 species 12.75%	14 species 13.73%	23 species 22.55%	
			[h ₁ = 11 sp] [h ₂ = 12 sp]	

When classification of rarity based on species occurrence (distribution range) was attempted, entirely different values were obtained. For example, when number of sites at which each species was present was used, category ‘a’ (equivalent to the ‘common’ category in Rabinowitz *et al.*, 1986) comprised just seven species with the vast majority

regarded as rare. Category 'h' contained the most representatives with 23 species consisting of two subgroups of which 'h₂' contained the rarest species (singletons).

In terms of categorising relative rarity, a total of 34 common species can be assigned to category A, this figure representing a little over 33% of the total species recorded. All other taxa (69 species) were somewhat rare and classified variously among the seven divisions of rarity proposed by Rabinowitz *et al.* (1986). Species that were scarce everywhere (the small 'n' category) comprised roughly 45% of the total. Euryecious species represented by 75.73% was far more common than stenoecious species and there were more widely (59%) than narrowly distributed species found in the present study.

Approximately 12% of taxa were both scarce and stenoecious (the small 'n' and 'u' categories) and almost 12% scarce, stenoecious and restricted (the 'nur' category), including both introduced species. *Rasbora caudimaculata* was the only locally abundant species, wherever encountered, and was collected in two regions is rare due to its unique habitat which was recorded from only in one stream at each region (category C or 'NuR'). The congener *Rasbora bankanensis* was however locally uncommon and, of all species documented in this study, uniquely assigned to category D or the 'nuR' group. A total of 19 species were restricted to a single region (small 'r' category) but found at multiple localities (capital 'U' category) in opposition are those species that are unique in their geographic distribution. In contrast, categories G (Nur) and H (nur) contain those species with unique patterns of distribution, here incorporating 21 species, with category H epitomising the most restrictive form of rarity according to Rabinowitz *et al.* (1986).

Table 6.3. Forms of rarity of fishes in small stream in Peninsular Malaysia based on categories after Rabinowitz *et al.* (1986). Rarity is assessed based on data of small stream fishes collected since 1998 to present.

Species abundance (N)	Habitat specificity (U)	Geographic range (R)	Description
Abundant (N)	Euryecious (U) (NUR)	Extensive (R)	Species is abundant in a community, widespread and occurs in a wide range of habitats (and therefore cannot be considered rare)
34 species (33.01%) Category A			
Abundant (N)	Euryecious (U) (NUr) Category E	Restricted (r)	Species is abundant in a community, occurs over a widespread area but highly restricted in distribution range and found in few places where it occurs
10 species (9.71%)			
Abundant (N)	Stenoecious (u) (NuR)	Extensive (R)	Species is abundant in a community, but occurs in limited habitat and is common in places where it occurs
1 species (0.97%) Category C			
Abundant (N)	Stenoecious (u) (Nur)	Restricted (r)	Species is abundant in a community, but occurs in limited habitat and highly restricted in distribution range and found in few places where it occurs
11 species (10.68%) Category G			
Scarce (n)	Euryecious (U) (nUR)	Extensive (R)	Species is scarcely found in a community, but occurs over a widespread area and is common in places where it occurs
25 species (24.27%) Category B			
Scarce (n)	Euryecious (U) (nUr)	Restricted (r)	Species is scarcely found in a community, but occurs over a widespread area and but highly restricted in distribution range and is restricted in places where it occurs
9 species (8.74%) Category F			
Scarce (n)	Stenoecious (u) (nuR)	Extensive (R)	Species is scarcely found in a community, but occurs in limited habitat and is common in places where it occurs
1 species (0.97%) Category D			
Scarce (n)	Stenoecious (u) (nur)	Restricted (r)	Species is scarcely found in a community, but occurs in limited habitat and highly restricted in distribution range and is restricted in places where it occurs
12 species (11.65%) Category H			

6.4 Discussion

Among 15 181 specimens collected during field work, 103 fish species were identified, the majority of which were natives with just two exceptions, *i.e.* *Esomus metallicus* and *Trichopodus pectoralis* that were introduced species. Of the native species, 12 were singletons and six doubletons. The abundance-based species richness estimator Chao 1 predicted an overall total of 115 species, and the incidence-based estimator Chao 2 113 for small streams in Peninsular Malaysia. Both estimations seem to concur with the species accumulation curve although Chao 2 performed slightly better in terms of accuracy.

The most abundant (number of individuals) species recorded were not necessarily the most widespread (measured as number of sites present); with fishes from the family Cyprinidae most abundant over the entire data set whereas a sisorid catfish was the most widespread individual species. At the regional level, the relationship between species abundance and distribution differs slightly. Species overlap in the northwestern and eastern regions was significant with a high number of shared species. The greatest number of species was recorded from the eastern region and the least in the southern region. Rarefaction analysis confirmed that ichthyodiversity in the eastern region was significantly higher compared to the northwestern and southern regions.

‘Rare’ species were more frequent than ‘common’ throughout this study, and similarly many species exhibited restricted distribution whereas only a few could be considered widespread. Cluster analyses determined the existence of an eastern/western ichthyogeographic division in Peninsular Malaysia. Population size (number of individuals per species recorded at a given site) is a major influence in determining rarity but distribution contributes significantly as well.

6.4.1 Species composition

As currently-recognised there are around 300 freshwater fish species native to Peninsular Malaysia (*pers. obs.*). The results of the present study demonstrate that small stream

habitats contribute approximately 1/3rd of this total, a significant proportion. Species richness estimators employed during data analysis performed well with both approaching an asymptote early, thus exemplifying the high diversity of fishes within the field samples. Moreover, more than 20% of species recorded were encountered at just a single locality among the selected study sites, and roughly 10% were singletons (species with a single representative). The presence of such high percentages of unique and singleton species among a data set naturally exerts a profound effect on species richness (Colwell & Coddington, 1994; Coddington *et al.*, 1996) as demonstrated by the curves in Figure 6.2, both of which tend to reach an asymptote. The abundance-based estimator Chao 1 predicted fewer species than the incidence-based Chao 2 although both appeared to provide a relatively reliable estimate of true species richness.

The majority of fish species recorded during this study were barbs and carps from the family Cyprinidae (Order Cypriniformes), thus supporting previous studies (*e.g.* Beamish *et al.*, 2006; Mohsin & Ambak, 1983; Kottelat *et al.*, 1993; Zakaria-Ismail & Lim, 1995). The same pattern was repeated at the regional (ichthyogeographic regions within Peninsular Malaysia) level (see Table A6.1) although species identity differed. The most abundant species also belonged to the family Cyprinidae but these were not the most widespread, with two representatives of the Order Siluriformes among the three commonest species and recorded at more than 50% of study sites. At the regional level, several species were considered widespread including the cyprinids *Devario regina* (northwestern region) and *Crossocheilus oblongus* (southern region) and the sisorid *Glyptothorax major* (eastern region).

There was frequent species overlap between regions (Figure 6.3), and despite the mountainous Main Range forming a natural barrier between their respective catchment areas many species were shared between the northwest and east. Woodruff (2003) proposed that the Isthmus of Kra Seaway, an ancient marine seaway that divided the Thai-Malay peninsula (see Figure 2 in Woodruff [2003], Figure 1 in de Bruyn *et al.* [2005] and Figure 6.9), may have facilitated the dispersal of species between the two regions, and this concept appears to be upheld by the results obtained here.

The observed pattern of few common and many rare species (Figure 6.4) has been demonstrated previously in both animals (*e.g.* Jones *et al.*, 2002; Magurran & Henderson, 2010) and in plants (*e.g.* Stohlgren *et al.*, 2005; Lennon *et al.*, 2011). The abundance of rare species in the field samples can be attributed to sampling error (Preston, 1948; Magurran, 2007). This leads to a disproportionate detection of rare species in many studies (*e.g.*, Gu & Swihart, 2004; MacKenzie *et al.*, 2005; MacNeil *et al.*, 2008). Under ideal circumstances sampling should therefore be extended over time with the anticipation that as sampling time increases, the relative proportion of rare species within an assemblage ought to decrease. Instances of localised species abundance as depicted in the rank-abundance plots (Figure 6.5) ratify the eastern and northwestern regions to be substantially dissimilar from the southern region, with more species recorded and more even community structure. These discrepancies were validated by rarefaction analyses (Figure 6.6) which indicated that species richness in the southern region is comparatively limited, although continuous sampling over an extended timeframe could potentially result in more species being recorded (Magurran *et al.*, 2011) because distribution is an inconstant variable.

6.4.2 Ichthyofaunal divisions

This study demonstrates that Peninsular Malaysia can be divided into two principal ichthyogeographic regions – the eastern and northwestern slopes, corresponding to the hypothesis of Abell *et al.* (2008), and this finding take precedence over previous work, *e.g.* Mohsin & Ambak (1993). Johnson (1967) stated that there is no disparity in fish distribution between eastern and western regions of Peninsular Malaysia, and those dissimilarities between the north and south is a consequence of edaphic and climatic factors. Moreover, Yap (2002) suggested that resemblances exhibited by the ichthyofauna of different regions can be attributed to concurrent similarities in geomorphology between catchment areas, the latter derived from movement of tectonic plates, in conjunction with the other events such as glaciations, river capture and other orographic processes.

Despite a paucity of information concerning water chemistry and other parameters for the streams visited in this study, the perceived relationship between southern and eastern sites implies the existence of ancient connectivity between them (Rainboth, 1996; Voris, 2000). Dodson *et al.* (1995) proposed that affinities between freshwater fishes of Southeast Asia are the result of sea-level changes on the Sunda Shelf during the Pleistocene which in turn influenced species dispersal processes occurring at the time. The congruity observed between the eastern and southern regions of Peninsular Malaysia in the present study may be related to the fact that they are derived from the same Laurasian plate (Figure 6.9), whereas the western slope was part of the Sibumasu tectonic division which separated from Gondwana during the Devonian period (Metcalf, 2001; Woodruff, 2003; Metcalfe, 2011). These contrasting geomorphic histories are thus likely to have exerted profound impacts in terms of species dispersal and colonisation (Yap, 2002).

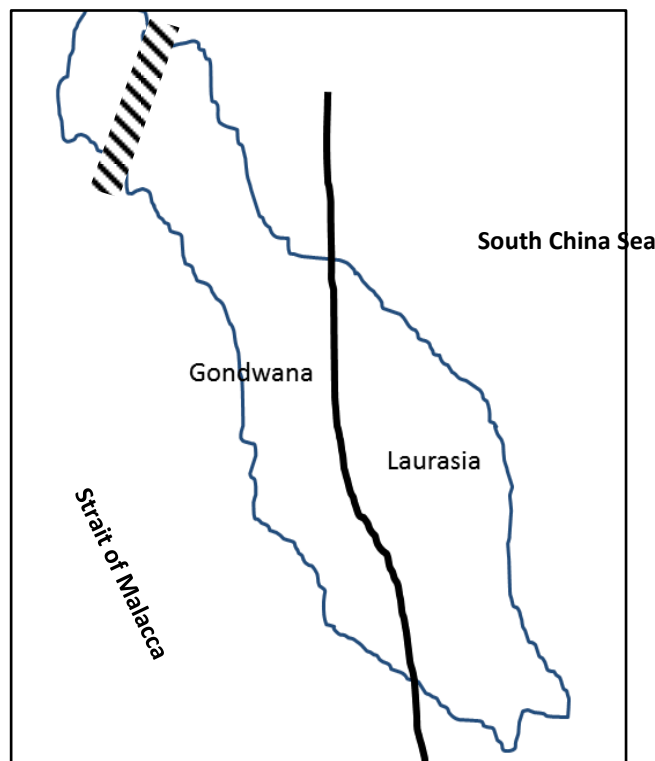


Figure 6.9. Outline map indicating the positioning of tectonic plates forming the landmass of the Malay Peninsula. The thick black line running north/south indicates the Bentong-Bengkalis suture, and the shaded area indicates the location of an ancient seaway that may once have divided the Isthmus of Kra (see also de Bruyn *et al.*, 2005).

A 'uniqueness' value can be assigned to a given stream in order to denote how 'distinctive' it is in terms of resident ichthyofauna. These ranges between 0 (ordinary) to 1 (unique) with those streams surveyed in the present study all rating between 0.54 and 0.79. The mean uniqueness values for each region were somewhat high but did not differ significantly from one another, illustrating that the study sites were equally unique. Highly unique sites are, logically, more likely to harbour endangered native species in need of preservation (Stohlgren *et al.*, 2005) and it is essential to minimise threats by any means possible. The primary implications are thus: (1) parity between sites reduces bias when comparing them to one another; and (2) such information could be employed during environmental impact assessment when the aim is to establish the probable effects of habitat degradation and potential for extinction of resident species (Arita, 1993).

6.4.3 Patterns of species rarity

The number of species in each category varied markedly with those classified as common (category A) representing about $1/3^{\text{rd}}$ of the total recorded based on Rabinowitz *et al.* (1986). The remainder were considered rare to some degree with 12 displaying the full suite of conditions – small population, limited habitat and restricted distribution range. Based on comparative incidence, more species were rare than common. 23 can be ranked among the rarest of all species, comprising those of the scarce, stenoeious and restricted species ('n', 'u' and 'r' categories). Formal classification of rarity has changed somewhat in recent years, with greater emphasis being placed on the known distribution (presence/absence) of a given species (*i.e.* qualitative information), rather than more customary numerical (quantitative) methods (Flather & Sieg, 2007). This shift in contemporary opinion was driven by the theory that when attempting to systemise species rarity abundance data should be treated with caution since it may result in overrepresentation of common species (Pritt & Frimpong, 2010).

There is only a negligible difference between the aggregated numbers of species considered 'abundant' (combined total of categories A, C, E and G, comprising 47 species) and 'scarce' (categories B, D, E and H; 59 species). Approximately half of all

species recorded can be regarded 'rare' on account of small population size (those included in categories B, D, E and H) or limited geographic range (categories b, d, f and h), and even in the absence of immediate threat the latter in particular tend to be naturally vulnerable to unexpected habitat alteration (Arita, 1993). Common species should have their populations maintained at a particular level in order to avoid excessive depletion. However, both sets of species (rare and common) are equally important environmental characters.

The system of rarity classification employed in this study therefore draws attention to fish groups which should be prioritised in terms of conservation efforts. It should be noted, though, that certain species assigned to categories G (Nur) (*e.g. Puntius lineatus*, *Syncrossus beauforti* and *Mystacoleucus chilopectus*) and H (nur) (*e.g. Clarias meladerma*, *Oxyeleotris marmoratus* and *Monotretete palembangensis*) were considered rare, even among the rarest recorded in some respects, they can in fact be regarded as of least concern since they are only sporadic or vagrant visitors to the type of small stream habitats investigated for this study. Nevertheless, several species recorded here are obligate dwellers of particular, often narrow, ecological niches and are thus deserving of special attention (Caiafa & Martins, 2010), *e.g. Acrochordonichthys rugosus*, *A. septentrionalis*, *Akysis hendriksoni* and *Pangio filinarius* in group H. There existed little prior information regarding the latter group of species, but the results obtained here suggest them as priority candidates for future conservation projects, *Acrochordonichthys rugosus* and *A. septentrionalis* were examined further in Chapter 2.

Rabinowitz's method of classifying relative rarity is essentially based on a combination of local abundance, geographic distribution and habitat specificity. Although it generally requires little effort and can be beneficial in determining appropriate conservation measures, it is prudent to appreciate that such variables do not remain constant for a given species and therefore results may differ depending on when field work is conducted (Pitman *et al.*, 1999; Caiafa & Martins, 2010). In the results presented here, habitat specificity proved a notably predominant factor in rarity classification, an outcome supported by Caiafa & Martis (2010) in their study of the Brazilian Atlantic rainforest.

Nonetheless, additional information in respect of species incidence, biology and habitat uniqueness should be incorporated when attempting to categorise rarity and preclude the inclusion of sporadic and/or vagrant species. This more-exhaustive approach has already been employed to effectively identify less populous, restrictedly-distributed or otherwise scarce species with greater potential to be adversely affected by habitat destruction (Pritt & Frimpong, 2010).

As things stand, none of the species classified within category H here are known to be endangered but on going population monitoring could help prevent future issues and provide benefits to other resident species, particularly those ranked 'scarce widespread' and 'scarce restricted' (Manne & Pimm, 2001). Species falling outside category A may also require increased attention since in some cases they were both endemic and regionally-restricted *e.g.* *Neolissocheilus hendersoni* and *Rasbora notura* plus some populations exhibit marked variations in morphology and may even represent distinct taxa (Zemlak *et al.*, 2009).

6.5 Conclusion

In tropical regions, exponentially-increasing habitat loss and degradation have exerted adverse effects on many freshwater fish species of which some case now exist only in a few small, widely-separated locations (Kottelat *et al.*, 2006). The tropics are among the most rapidly developing parts of the world and in Peninsular Malaysia, small streams are weakly-protected except at source in the majority of cases. Tropical streams are known to house diverse fish species assemblages but may also conceal hitherto undescribed taxa, such as *Nemacheilus paucimaculatus* (see Bohlen and Šlechtová, 2011), discovered and described recently from southern Peninsular Malaysia. Unfortunately, a consistent, intensive demand for new agricultural land has resulted in extensive forest clearing and consequent devastation of aquatic habitats in recent decades. While human development will inevitably persist, the establishment of a diligently-managed network of protected areas is clearly required in order to ensure long-term preservation of Peninsular Malaysia's native aquatic fauna while the opportunity to do so still remains.

Freshwater fishes are valuable for numerous economic and recreational purposes (Magurran *et al.*, 2011), and are among the commonest fauna in aquatic ecosystems, yet they tend to lack conservation priority regardless of rarity. Instead, greater attention tends to be given to mammals and birds (May, 2002; Magurran *et al.*, 2011), particularly those 'flagship' species with which the public are able to more easily identify. Clear evidence of this is presented here in that not a single one of the species identified as rare in this study are officially-protected or have even been evaluated in terms of conservation status. It is hoped that successful implementation of a simple method by which to classify freshwater fish species into categories of relative rarity, as demonstrated in this study, will compel conservation managers to develop urgently-required strategies for safeguarding the diverse ichthyofauna inhabiting small streams of Peninsular Malaysia.

CHAPTER 7

GENERAL DISCUSSION

7.1 Summary

This thesis set out to investigate and evaluate the species richness, community composition and assemblage structure of freshwater fish populations inhabiting small stream environments in Peninsular Malaysia. The results obtained will not only enhance understanding of these questions but assist in developing best practice for conserving such biodiverse habitats.

Small stream ichthyodiversity at both the local and regional scales was examined (Chapters 2 and 6) since numerous authors have stated that accurate appraisal of species richness is important in terms of ecological research and biodiversity conservation (Lu *et al.*, 2007). But something that is exceptionally difficult to achieve, especially when the presence of cryptic species is likely. In this study small streams in Peninsular Malaysia were found to contain a highly diverse ichthyofauna although the number of species recorded varied depending on locality. For example, a total of 51 and 46 species are estimated to occur within the Sg. Peres system and headwater tributaries of the Sg. Dungun, respectively. These findings concur with previous stream fish inventories conducted in the region (see Chapters 2 and 6).

The total number of fish species inhabiting small streams within Peninsular Malaysia is reckoned to be between 112 and 115, slightly in excess of those recorded in this study (Chapter 6). The actual number of species recorded per study site rarely exceeded 30 although beta diversity was consistently high. In general streams located in different regions were more likely to exhibit dissimilarities in fish community composition than those within a single region (Chapter 5). Historic geomorphological events and physical distance between streams were among the factors contributing to the degree of homogeneity.

The current rate of habitat loss is increasing exponentially (Reid, 1992; Lindenmayer & Franklin, 2002; Lindenmayer & Burgman, 2005) and thus more rapidly than our ability to accurately document species occurrence records within specified ecosystems. However, moderate anthropogenic interference was found to exert only a negligible impact on fish species richness and community structure in the stream drainages surveyed which had

been subject to various forms of small scale disturbance (Chapter 3). Stream banks featuring dense growth of riparian vegetation favour the presence of different and more diverse fish assemblages than less complex grass or mud banks although habitats adjacent to grassy banks may in fact support greater abundance and richness of fish species (Growth *et al.*, 2003). The riparian zone thus unquestionably provides both food and shelter for fish communities and plays an important role in structuring species assemblages (Grenouillet *et al.*, 2002; Arthington *et al.*, 2006). In the present study ‘disturbed’ sites in particular were lacking riparian vegetation but supported a comparable number of species relative to sites considered less disturbed. Modest removal of the riparian plant community has therefore not significantly impacted fish species richness and assemblage composition in these cases. The relative lack of pelagic insectivores and other surface-feeding fish species recorded in this study (see Chapter 2) suggests that small streams in Peninsular Malaysia also support a less diverse surface-dwelling ichthyocommunity in comparison with other guilds as a consequence of which they may be less susceptible to changes in assemblage structure driven by removal of marginal vegetation. Small-scale management plans or disturbance events occurring within riparian zones therefore seem to impose only inconsequential effects on resident fish communities despite numerous earlier studies concluding otherwise (Paller, 2002; Casatti *et al.*, 2006).

Many small streams in Peninsular Malaysia are utilised for recreational purposes with stretches of rapids frequently modified to form bathing pools, but a comparison between fish species richness and community structure at such modified biotopes and natural pools returned broadly similar results (Chapter 4). It appears that when habitat modification is not extreme fish communities are able to adapt to minor changes in habitat structure. Increased exploitation or heavy modification are often associated with urbanisation or channelisation projects can of course provoke detrimental transformations in fish community structure, however (see Brasher, 2003; Ramirez *et al.*, 2011).

Artificial disturbances typically lead to reductions in habitat quality and quantity as secondary effects of changes in morphology and composition and often lead to alterations in fish community structure. However, although the results of the present study does not prove this as such, the intensity of habitat disturbance exerted upon the small streams surveyed here can be considered minimal with species richness at ‘impacted’ and

‘unimpacted’ sites comparable. More comprehensive studies including additional examples are recommended in order to understand the issue fully.

Among the fish species recorded in this study a greater proportion were rare species rather than common (Chapter 6), this conforming with the general pattern of few common and many rare species in freshwater fish communities worldwide. Sampling effort have been shown to be the most significant factor determining the dominance of rare species, *e.g.*, in studies of marine benthic assemblages (Gray *et al.*, 2005), and results of the present study appear to suggest that many Malaysian freshwater fish species have narrow natural ranges being restricted to a handful of sites or existing only in small populations . These data agree largely with Rabinowitz’ classification of rare species. An excess of rare species in field samples can also be related to continuous immigration and emigration which is common in natural systems (Gray *et al.*, 2005). This natural flux may temporarily amplify fish species richness in open ecosystems such as river drainages with the result that - unlike with tree communities, for example - it is almost impossible to tally all species no matter the scale at which sampling is conducted. This perpetual movement of species is often further supplemented by regular natural habitat modification via meteorological events which can affect the distribution of both small-bodied, anomalous species and large, usually migrant taxa that may not otherwise frequent a given habitat (Gray *et al.*, 2005).

7.2 Conclusion

Estimating species richness is frequently a primary objective in when compiling inventories of biodiversity or planning habitat conservation measures. Reliable quantitative sampling is therefore crucial in order to obtain the best possible projection of species numbers in a particular study area (Glowacki & Penczak, 2005). Although attaining a complete inventory is traditionally assumed to be unachievable a genuinely reliable estimate of species richness can be calculated using a combination of qualitative and quantitative methods. In this study, sampling was repeated several times along suitable sections of individual streams (*c.* 25 m) or multiple streams with a limited distance (*e.g.*, 100 m) using an electrofishing unit. Under certain conditions the efficiency of electrofishing is doubtful (Glowacki & Penczak, 2005) but in this case the data sets

returned were wholly suitable in terms of species richness estimation and appraisal of stream-dwelling fish communities. Since the use of rotenone for sampling fishes is banned in Malaysia as in many other places throughout the world, a combination of electrofishing and non-parametric species richness estimators offers an efficient, low cost method by which conservation managers can obtain reliable estimates of diversity within a short time frame.

Freshwater biotopes and the life forms they support are among the most threatened ecosystems in the world (Saunders *et al.*, 2002), with anthropogenic activity having induced a major, ongoing decline freshwater fish populations across the globe (Magurran, 2009). Habitat alteration and deterioration of water quality plus reduction of available water volume currently appear to represent the most significant threats alongside the increasing presence of invasive species and widely-anticipated climate change. Although the small stream systems sampled in the present study are incessantly subjected to human encroachment the impact is probably minimal and to date there appears no substantial threat to fish species richness and community structure. This implies that current management routines and highly-localised, small scale disturbances such as clearing of riparian vegetation, bank strengthening or creation of non-permanent pools are acceptable and have no detectable impact on resident fishes.

Rare species were more frequent accounted than common ones throughout the course of field work meaning a significant number exhibited restricted distributional ranges, are confined to a narrow ecological niche or have small population sizes (Magurran, 2009). This pattern has also been demonstrated to occur in other group of organisms including plants, birds and mammals and highlights the need for proper management and conservation of many species to ensure their continued existence. In terms of fishes those in category H (species that is scarcely found, occurs in limited habitat and restricted in distribution range; h_1 and h_2) are generally considered rarest and most in need of close monitoring. In order to conserve such species appropriate habitats should first be restored and officially-protected freshwater zones designated (Saunders *et al.*, 2002). Native fish species can subsequently be allowed to proliferate with introduction of conspecific specimens from closely-related populations a potential method to maintain genetic variability and enhance phenotypic traits, though it should be noted there exist a number of reasons why this is open for debate (Magurran, 2009).

7.3 Future research

Much additional research is required regarding the ecology and maintenance of diversity in fish populations inhabiting small, freshwater streams both within Peninsular Malaysia and throughout the tropics. The present study addresses some underlying aspects of small stream ecology and highlights the extraordinary biodiversity of these ecosystems, so future research should focus on:

- *Comparisons of watersheds vs. single streams.* This study is almost entirely based on data sets obtained from single stream sites with the exception of the upper Sg. Dungun where tributaries were sampled. However, it would be both preferable and more valuable to analyse fish species richness and community structure throughout each watershed since this would allow variance in species richness and community structure between different streams within each drainage basin to be compared. The results presented in this paper demonstrate that small streams are rich in ichthyofauna of which many species are somewhat rare, and larger scale comparisons should help determine if this pattern is replicated over the macro scale. There exists a deficit of information regarding freshwater fish diversity at this larger scale for Peninsular Malaysian watersheds and determining which populations are behaving as “source” or “sink” is worthy of investigation.
- *Anthropogenic impacts on longitudinal and lateral connectivity of small streams.* Changes in land use and urbanisation are currently increasing rapidly in many areas of rural Peninsular Malaysia yet the repercussions for stream-dwelling fauna are not well established. Structures such as road crossings or channelization can reduce longitudinal connectivity of small streams by fragmenting downstream water flow from headwaters. It is essential to quantify the consequences of diminished connectivity in terms of seasonal fish migrations between large river channels and smaller tributary streams, fish population dynamics, the lateral movement of fishes, fish biology and species richness.
- *The relationship between habitat and ichthyofaunal diversity.* Ichthyofaunal diversity is directly related to habitat heterogeneity and availability, *i.e.* the

quantity and quality of suitable habitat play key roles in fish species distribution. Although the concept that native faunal assemblages can be safeguarded by maintaining habitat connectivity is well-established, little is known regarding the specific habitat requirements of the indigenous fish fauna. Although details are available for certain group of fishes (*e.g.*, Beamish *et al.*, 2006; 2008) future efforts should focus on evaluating whether such information can help guide conservation efforts elsewhere in the tropics.

- Additional studies should also centre on the response of species richness and community structure to natural disturbances, *e.g.*, flash stream-water increase and elevated temperature in accordance with anticipated climate change. A further issue requiring attention is increased sedimentation which is typically caused by excessive land use. Although fish populations tend to react positively response to such disturbance over the long term (see Martin-Smith, 1998c) their immediate response is poorly documented not only in Peninsular Malaysia but throughout the tropics.

- Many earlier species assemblage studies on tropical freshwater fishes have been orientated towards ‘taxonomic’ assemblages with ‘functional’ diversity of tropical freshwater fishes almost unexplored to examine disparities between regions. With their highly diverse native fish fauna, tropical freshwater stream systems thus appear to represent an ideal environment for investigation of how functional diversity relates to ecosystem stability and other processes (Tilman, 2000).

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APPENDIX

Appendix 2.1

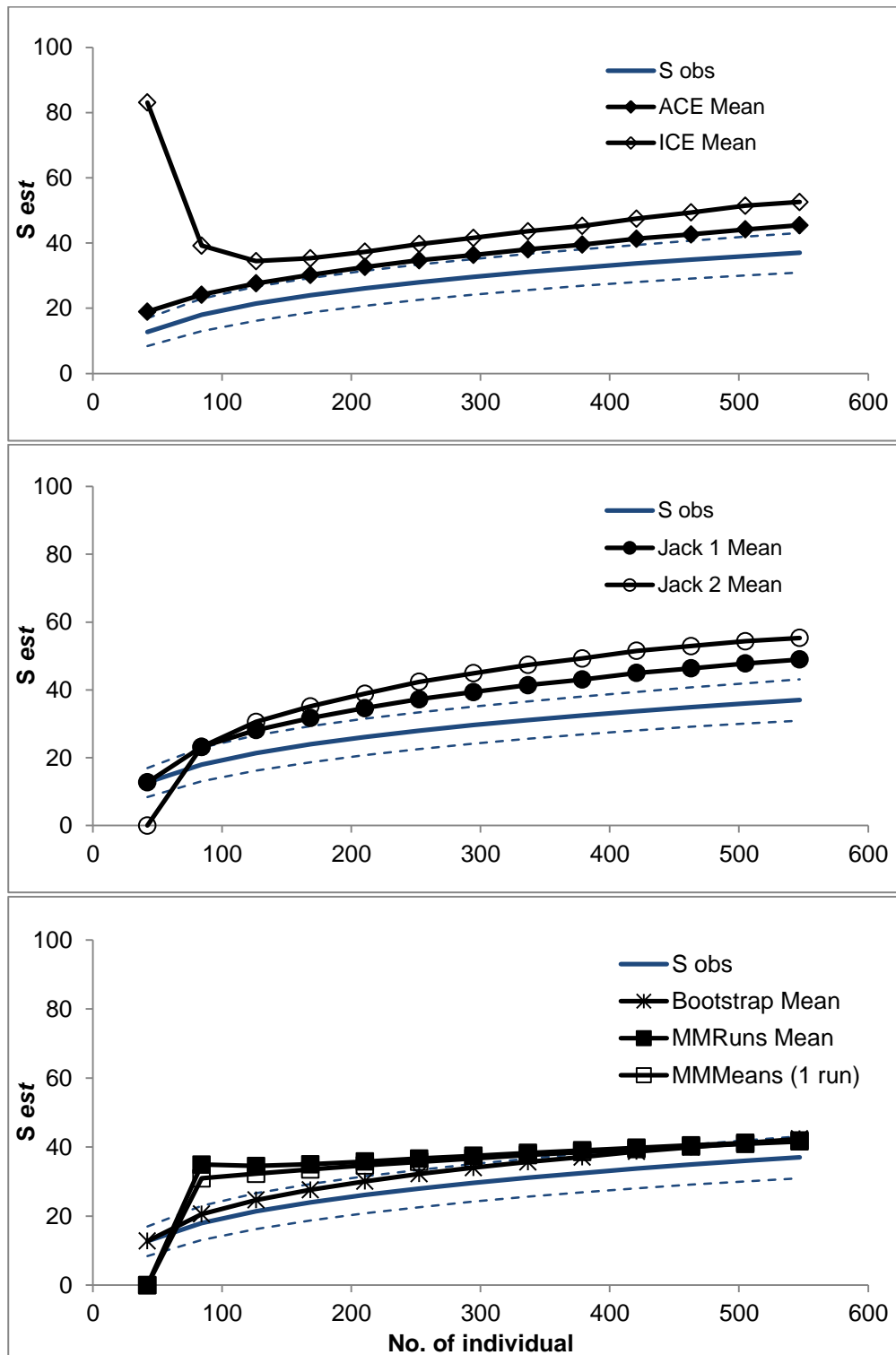


Figure A2.1. Observed and estimated number of fish species in small streams of the Sg. Peres, Terengganu versus number of individuals collected based on 250 randomised samples and patchiness of 0.5.

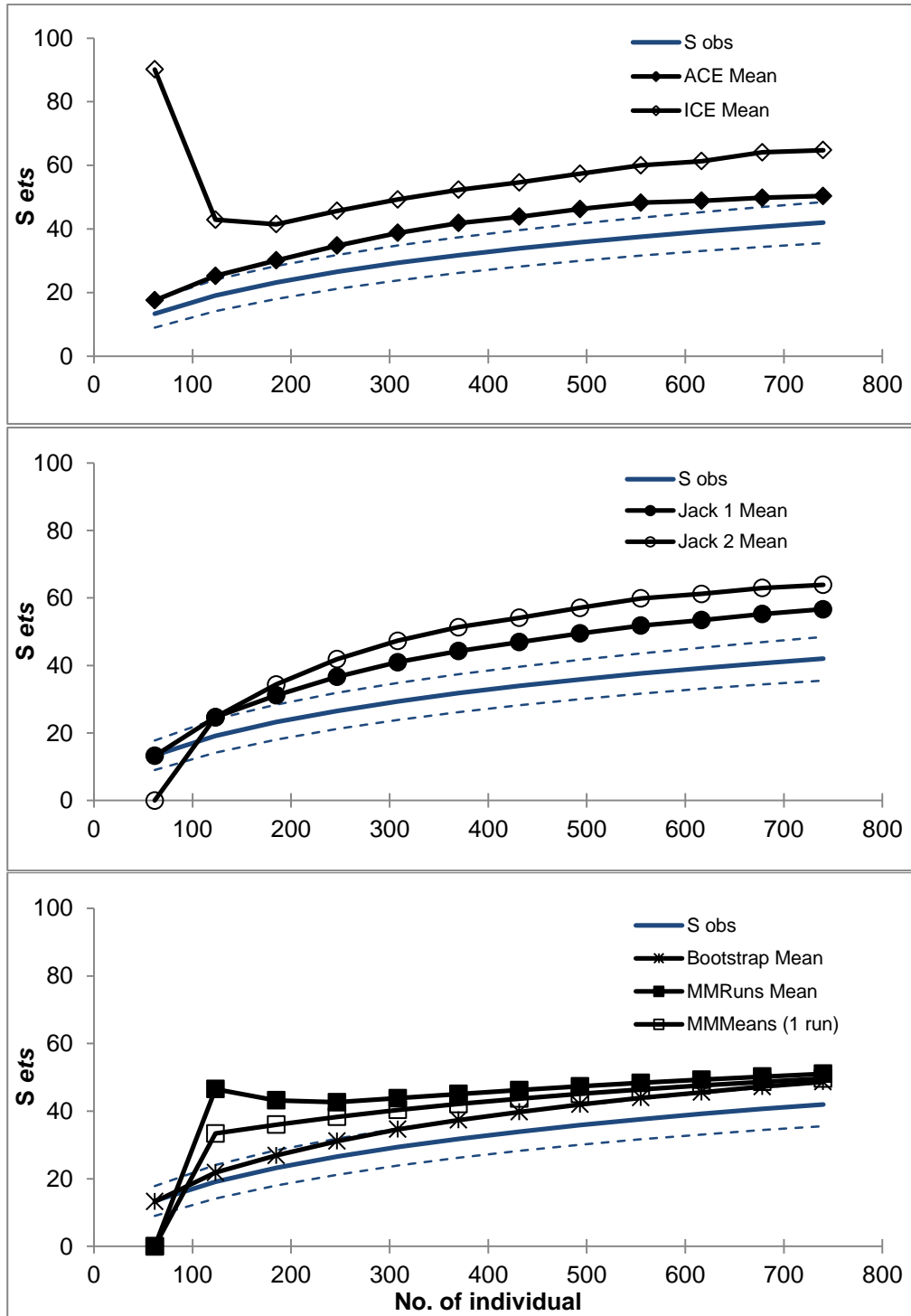


Figure A2.2 Observed and estimated number of fish species in small streams of the Sg. Dungun, Terengganu versus number of individuals collected based on 250 randomised samples and patchiness of 0.5.

Appendix 2.2

Table A2.1. Fishes collected at each site.

Family	Species	Sg. Peres	Sg. Dungun
Cyprinidae	<i>Crossocheilus oblongus</i> Kuhl & van Hasselt	1	9
	<i>Cyclocheilichthys apogon</i> (Valenciennes)	0	1
	<i>Garra cambodgiensis</i> (Tirant)	56	45
	<i>Hampala macrolepidota</i> Kuhl & van Hasselt	1	3
	<i>Labiobarbus leptocheilus</i> (Valenciennes)	1	1
	<i>Mystacoleucus marginatus</i> (Valenciennes)	27	106
	<i>Neolissocheilus soroides</i> (Duncker)	0	68
	<i>Osteochilus microcephalus</i> (Valenciennes)	3	0
	<i>Osteochilus scapularis</i> (Bleeker)	0	1
	<i>Osteochilus vittatus</i> (Valenciennes)	0	2
	<i>Osteochilus waandersi</i> (Bleeker)	1	5
	<i>Poropuntius smedleyi</i> (de Beaufort)	44	110
	<i>Puntius banksi</i> Herre	6	54
	<i>Puntius lateristriga</i> (Valenciennes)	13	12
	<i>Raiamas guttatus</i> (Day)	1	2
	<i>Rasbora elegans</i> Volz	0	2
	<i>Rasbora notura</i> Kottelat	22	140
	<i>Rasbora paucisqualis</i> Ahl	0	3
	<i>Tor tambra</i> (Valenciennes)	10	2
	Balitoridae	<i>Homaloptera ogilviei</i> Alfred	4
<i>Homaloptera parclitella</i> Tan & Ng		2	7
<i>Homaloptera tweediei</i> Herre		39	0
<i>Homaloptera zollingeri</i> Bleeker		50	2
Nemacheilidae	<i>Nemacheilus masyae</i> Smith	8	10
	<i>Nemacheilus selangoricus</i> Duncker	3	15
Cobitidae	<i>Acantopsis dialuzona</i> van Hasselt	1	14
	<i>Pangio piperata</i> Kottelat & Lim	0	1
Bagridae	<i>Hemibagrus gracilis</i> Ng & Ng	3	0
	<i>Hemibagrus nemurus</i> (Valenciennes)	1	17
	<i>Leiocassis poecilopterus</i> (Valenciennes)	40	5
	<i>Mystus castaneus</i> Ng	1	0
	<i>Pseudomystus stenomus</i> (Valenciennes)	3	0
Siluridae	<i>Ompok siluroides</i> La Cepède	0	1
	<i>Silurichthys hasseltii</i> Bleeker	0	36
Akysidae	<i>Acrochordonichthys rugosus</i> (Bleeker)	0	1
	<i>Acrochordonichthys septentrionalis</i> Ng & Ng	0	1
Sisoridae	<i>Glyptothorax major</i> (Boulegner)	130	15
	<i>Glyptothorax siamensis</i> Hora	5	2
Amblycipitidae	<i>Amblyceps foratum</i> Ng & Kottelat	21	23
Clariidae	<i>Clarias lieacanthus</i> Bleeker	0	5
Hemiramphidae	<i>Hemirhamphodon pogonognathus</i> (Bleeker)	2	0
Syngnathidae	<i>Dorichthys martensii</i> (Peters)	3	0
Mastacembelidae	<i>Macragnathus maculatus</i> (Valenciennes)	12	2
	<i>Mastacembelus favus</i> Hora	10	5
Pristolepidae	<i>Pristolepis grootii</i> (Bleeker)	6	2
Gobiidae	<i>Glossogobius giuris</i> (Hamilton)	4	0
	<i>Pseudogobius oligactis</i> (Bleeker)	0	2
	<i>Schismatogobius</i> sp. cf. <i>marmoratus</i>	10	0
Osphronemidae	<i>Betta stigmosa</i> Tan & Ng	0	1
Channidae	<i>Channa gachua</i> Hamilton	0	4
	<i>Channa lucius</i> (Cuvier)	2	0
	<i>Channa melasoma</i> (Bleeker)	1	2
Total individuals collected		574	740
Total number of species recorded		37	42

Appendix 2.3

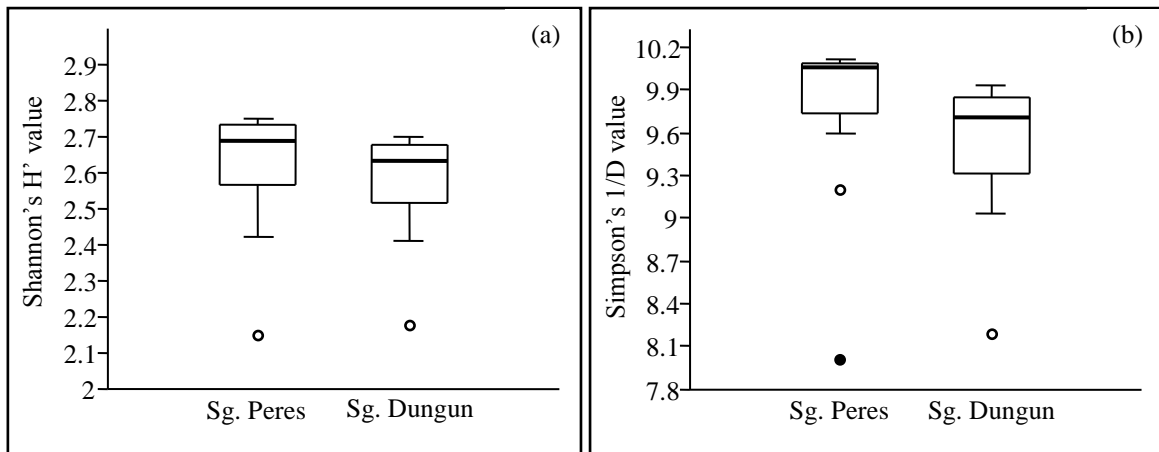


Figure A2.3. Means of Shannon's (H') diversity index and Simpson's reciprocal diversity index ($1/D$) for Sg. Peres and Sg. Dungun. Open and filled (lowest value) circles denote the outliers within the samples and thick horizontal bars within each box indicate the median for each diversity measure.

Appendix 2.4

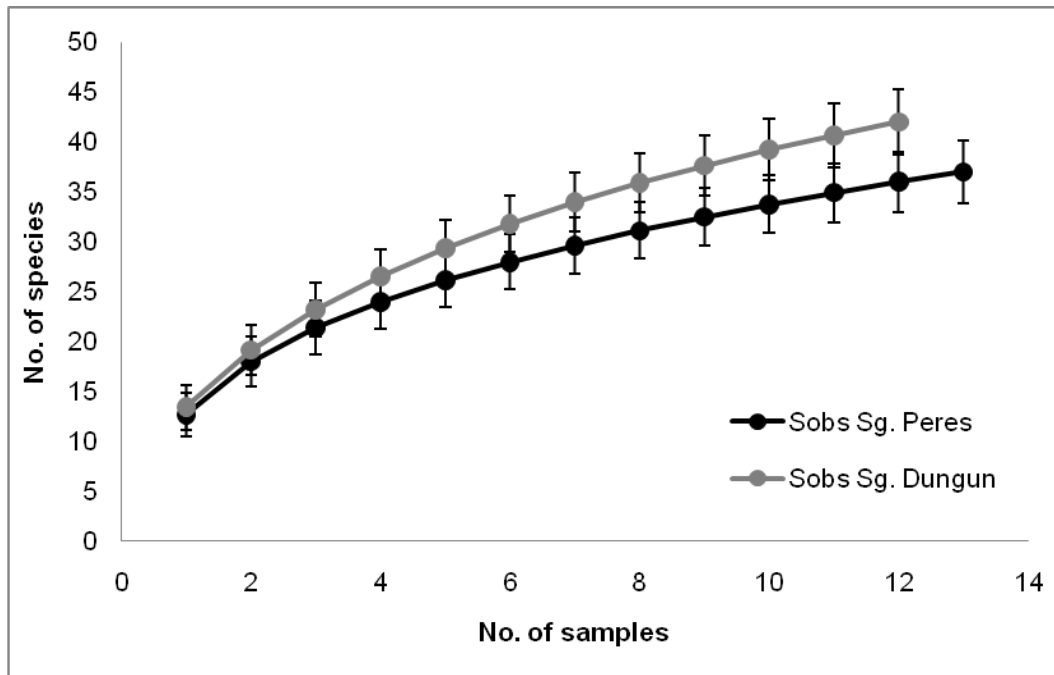


Figure A2.4. Species accumulation curve for Sg. Peres and Sg. Dungun, Terengganu.

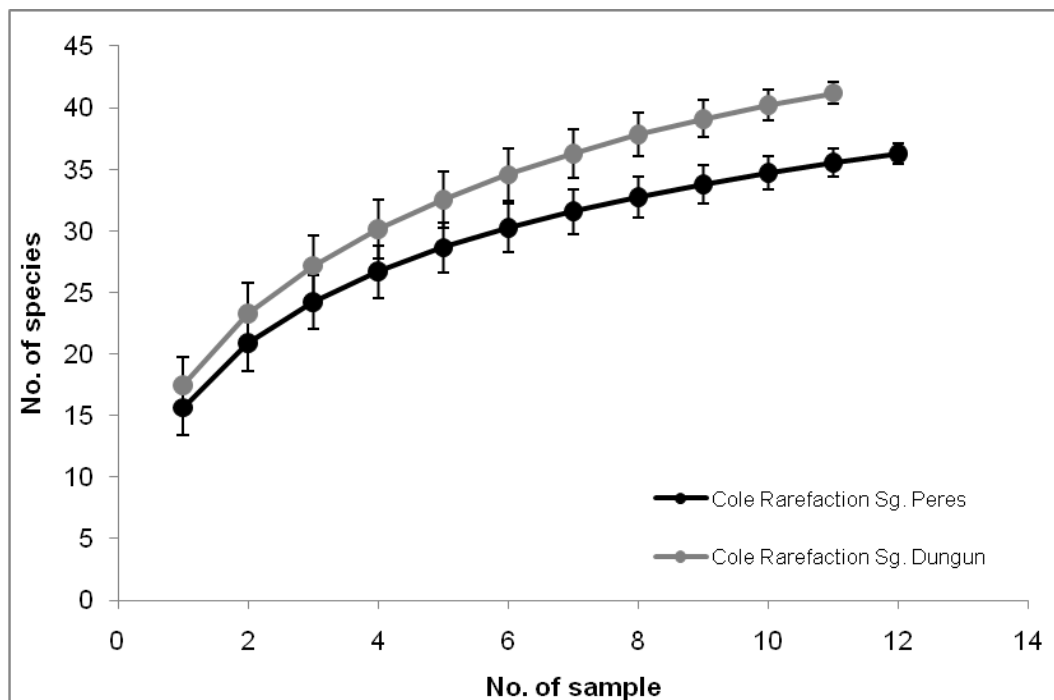


Figure A2.5. Coleman rarefaction curves (an individual-based rarefaction curve) for Sg. Peres and Sg. Dungun, Terengganu.

Appendix 2.5

Table A2.2. Biological traits generated from the natural history of rare species encountered. Letters “P” and “D” denote Sg. Peres and Sg. Dungun, respectively. See Appendix 2.6 (Table A2.3) for full list of species names.

		Sg. Peres												Sg. Dungun																					
Biological attributes		P1	P2	P3	P4	P5	P6	P7	P8	P9	P10	P11	P12	D1	D2	D3	D4	D5	D6	D7	D8	D9	D10	D11	D12	D13	D14	D15	D16	D17	D18	D19	D20	D21	
Habitat preferences: feeding	benthopelagic	0	1	1	1	1	1	1	1	0	1	1	0	0	0	1	1	1	0	1	0	0	1	0	0	1	1	0	1	0	1	1	1	1	
	demersal	1	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	1	0	1	1	0	1	1	0	0	1	0	1	0	0	0	0	
	pelagic	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
	plant eaters	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	1	1	0	0	0	0	0	0	0	1
Trophic preferences food	piscivorous	0	0	0	1	1	0	0	0	0	1	1	0	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	
	benthical-invertivorous	1	0	0	0	0	0	1	1	0	0	0	1	0	1	0	0	1	1	0	0	1	0	1	0	0	0	1	0	1	0	0	0	0	
	surface-invertivorous	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	1	1	0	
	large body (> 20 cm)	0	1	0	1	1	1	0	0	0	1	1	1	0	0	0	1	1	0	1	0	0	1	0	1	1	1	1	0	0	0	1	0	0	1
Life history: body size	medium body (10 - 20 cm)	1	0	1	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	
	small body (< 10 cm)	0	0	0	0	0	0	1	0	1	0	0	0	0	1	1	0	0	1	0	1	1	0	0	0	0	0	1	0	1	0	1	1	0	
Habitat preferences: vertical	bottom	1	0	1	1	0	0	1	1	0	0	0	1	1	1	0	1	0	1	0	1	1	0	1	0	1	0	1	0	1	0	0	0	0	
	mid-water	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	1	1	1	0	0	1	0	1	0	1	0	1	0	0	0	1	1	
	surface	0	0	0	0	1	0	0	0	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0
	gravel	0	0	1	0	0	1	1	0	0	0	0	0	1	1	0	0	0	1	0	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0
	coarse sand	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Habitat preferences: substratum	snag/vegetation	0	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	1	0	0	1	0	0	0	1	0	1	0	1	0	0	0	0	0	
	soft bottom	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
	shallow peripheral	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
	woody debris	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
	open space	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	1	1
Habitat preferences: latitudinal	pool	0	0	0	1	0	0	0	0	1	1	0	0	0	0	1	1	1	0	1	0	0	0	0	1	0	1	0	1	0	0	0	1	1	
	rapids	0	0	1	0	0	1	1	0	0	0	0	1	1	1	0	0	0	1	0	0	1	0	1	0	1	0	0	0	0	0	0	0	0	
	glide	1	1	0	0	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	1	0	1	1	1	1	0	0

Appendix 2.6

Table A2.3. Rare fish species recorded at each study site. Letters “P” and “D” denote Sg. Peres and Sg. Dungun, respectively.

Family	Legend	Species	Peres	Dungun
Cyprinidae	P3	<i>Crossocheilus oblongus</i>	1	0
	D5	<i>Cyclocheilichthys apogon</i>	0	1
	P10/D7	<i>Hampala macrolepidota</i>	1	3
	P2/D10	<i>Labiobarbus leptocheilus</i>	1	1
	D13	<i>Osteocheilus scapularis</i>	0	1
	D14	<i>Osteochilus vittatus</i>	0	2
	P6	<i>Osteochilus waandersii</i>	1	5
	P11/D18	<i>Raiamas guttatus</i>	1	2
	D19	<i>Rasbora elegans</i>	0	2
	D20	<i>Rasbora paucisqualis</i>	0	3
	D21	<i>Tor tambra</i>	10	2
	Balitoridae	D8	<i>Homaloptera ogilviei</i>	4
P7		<i>Homaloptera parclitella</i>	2	7
D9		<i>Homaloptera zollingeri</i>	50	2
Cobitiidae	P8	<i>Acantopsis dialuzona</i>	1	14
	D15	<i>Pangio piperata</i>	0	1
Bagridae	P12	<i>Hemibagrus nemurus</i>	1	17
	P1	<i>Mystus castaneus</i>	1	0
Siluridae	D12	<i>Ompok siluroides</i>	0	1
Akysidae	D1	<i>Acrochordonichthys rugosus</i>	0	1
	D2	<i>Acrochordonichthys septentrionalis</i>	0	1
Sisoridae	D6	<i>Glyptothorax siamensis</i>	5	2
Hemiramphidae	P9	<i>Hemirhampon poganognathus</i>	2	0
Mastacembelidae	D11	<i>Macrogathus maculatus</i>	12	2
Pristolepidae	D16	<i>Pristolepis grootii</i>	6	2
Gobiidae	D17	<i>Pseudogobiopsis oligactis</i>	0	2
Osphronemidae	D3	<i>Betta stigmata</i>	0	1
Channidae	P5	<i>Channa lucius</i>	2	0
	P4/D4	<i>Channa melasoma</i>	1	2

Appendix 3.1

Table A3.1. Degree of disturbance

Disturbance level	Remarks
Undisturbed	No or very minimal sign of human interference, riparian vegetation intact, substrate (<i>e.g.</i> , rocks and boulders) is not disturbed or being removed
Moderate	Human use of the stream section is visible, disturbance or alteration is limited to partially clearance of bank's vegetation but does not exposed the soil, minimal substrate disruption may present
Disturbed	Human use of the stream section is clearly marked, bank's vegetation is greatly regulated, in-stream substrate has been removed or stream being noticeably modified

Appendix 3.2

Table A3.2. Pooled results of fish abundance for each community in 2008 and 2009 collected from 25 m transects at nine sites in Peninsular Malaysia.

Family	Species	2008			2009		
		U	I	D	U	I	D
Cyprinidae	<i>Crossocheilus oblongus</i> Kuhl & van Hasselt	33	54	88	62	78	71
	<i>Cyclocheilichthys apogon</i> (Valenciennes)	0	0	2	1	1	8
	<i>Devario regina</i> (Fowler)	77	50	27	73	42	54
	<i>Garra cambodgiensis</i> (Tirant)	17	9	4	7	22	8
	<i>Hampala macrolepidota</i> Kuhl & van Hasselt	5	7	1	4	0	3
	<i>Labiobarbus fasciatus</i> (Bleeker)	1	19	0	18	6	6
	<i>Labiobarbus leptocheilus</i> (Valenciennes)	1	0	4	18	2	16
	<i>Lobocheilus rhabdoura</i> (Fowler)	4	7	7	7	20	5
	<i>Luciosoma setigerum</i> (Valenciennes)	1	0	3	1	0	0
	<i>Mystacoleucus marginatus</i> (Valenciennes)	15	30	10	69	10	5
	<i>Neolissochilus soroides</i> (Duncker)	69	30	22	24	18	34
	<i>Osteochilus scapularis</i> (Bleeker)	0	0	1	0	0	0
	<i>Osteochilus vittatus</i> (Valenciennes)	3	3	1	24	6	4
	<i>Osteochilus waandersi</i> (Bleeker)	14	41	4	67	29	10
	<i>Poropuntius smedleyi</i> (de Beaufort)	73	24	87	42	46	55
	<i>Puntius banksi</i> Herre	18	18	3	33	16	8
	<i>Puntius binotatus</i> (Valenciennes)	11	15	12	4	22	9
	<i>Puntius lateristriga</i> (Valenciennes)	6	2	3	7	5	6
	<i>Raiamas guttatus</i> (Day)	0	0	0	0	0	1
	<i>Rasbora bankanensis</i> (Bleeker)	0	0	0	0	3	0
	<i>Rasbora dusonensis</i> (Bleeker)	0	0	0	6	1	0
	<i>Rasbora elegans</i> Volz	13	2	2	9	1	3
	<i>Rasbora notura</i> Kottelat	1	0	5	0	0	6
	<i>Rasbora paucisqualis</i> Ahl	1	0	0	0	3	0
	<i>Rasbora paviana</i> Tirant	0	10	0	3	9	1
	<i>Tor tambra</i> (Valenciennes)	0	0	0	0	2	0
Balitoridae	<i>Barbucca diabolica</i> Roberts	2	0	0	0	0	0
	<i>Homaloptera leonardi</i> Hora	2	2	1	0	0	0
	<i>Homaloptera nebulosa</i> Alfred	17	20	5	33	31	17
	<i>Homaloptera ogilviei</i> Alfred	0	0	0	7	5	0
	<i>Homaloptera parclitella</i> Tan & Ng	2	83	0	4	4	9
	<i>Homaloptera smithi</i> Hora	8	9	20	1	14	4
	<i>Homaloptera tweediei</i> Herre	26	9	5	0	0	0
	<i>Homaloptera zollingeri</i> Bleeker	43	57	24	24	27	25
Nemacheilidae	<i>Nemacheilus masyae</i> Smith	0	13	3	5	6	4
	<i>Nemacheilus selangoricus</i> Duncker	6	1	1	9	4	4
Cobitidae	<i>Acantopsis dialuzona</i> van Hasselt	22	1	8	18	0	13
	<i>Lepidocephalichthys hasselti</i> (Valenciennes)	1	0	0	0	0	2
Bagridae	<i>Pangio piperata</i> Kottelat & Lim	0	0	0	0	1	0
	<i>Batasio fluviatilis</i> (Smith)	9	13	4	16	15	25
	<i>Hemibagrus gracilis</i> Ng & Ng	1	0	0	0	0	0
	<i>Hemibagrus nemurus</i> Valenciennes	8	4	2	4	3	4
	<i>Leiocassis poecilopterus</i> (Valenciennes)	4	8	1	0	5	0
	<i>Mystus castaneus</i> Ng	1	0	0	1	4	3
	<i>Pseudomystus leiacanthus</i> (Weber & de Beaufort)	0	0	0	3	1	0
Siluridae	<i>Pseudomystus stenomus</i> (Valenciennes)	0	0	1	2	1	1
	<i>Kryptopterus bicirrhis</i> (Valenciennes)	0	0	0	0	0	1
	<i>Ompok bimaculatus</i> (Bloch)	1	0	1	2	3	4
	<i>Silurichthys hasseltii</i> Bleeker	1	5	0	0	0	0
	<i>Silurichthys schneideri</i> Volz	7	10	3	13	7	8
Akysidae	<i>Akysis hendriksoni</i> Alfred	0	0	0	0	0	1
Sisoridae	<i>Glyptothorax major</i> Fowler	51	79	27	83	44	51
	<i>Glyptothorax siamensis</i> Hora	24	26	24	26	21	31

Table A3.2. Pooled results of fish abundance for each community in 2008 and 2009 collected from 25 m transects at nine sites in Peninsular Malaysia. (cont.).

Family	Species	2008			2009		
		U	I	D	U	I	D
Belontiidae	<i>Xenentodon canciloides</i> (Bleeker)	0	0	0	1	0	0
Amblycipitida	<i>Amblyceps foratum</i> Ng & Kottelat	21	19	7	22	23	10
Clariidae	<i>Clarias leiacanthus</i> Bleeker	0	1	0	0	0	1
	<i>Clarias meladerma</i> Bleeker	0	0	0	0	0	1
Hemiramphida	<i>Hemirhamphodon pogonognathus</i> (Bleeker)	3	1	1	4	0	2
Syngnathidae	<i>Doryichthys martensii</i> (Peters)	2	1	0	0	0	0
Synbranchidae	<i>Monopterus albus</i> Zuiew	4	1	2	3	3	2
Mastacembi	<i>Macrogathus maculatus</i> (Valenciennes)	22	12	5	9	15	7
	<i>Mastacembelus favus</i> Hora	4	7	3	4	5	11
	<i>Mastacembelus unicolor</i> Valenciennes	0	7	0	0	10	3
Nandidae	<i>Nandus nebulosa</i> (Gray)	0	1	0	1	0	0
Gobiidae	<i>Schismatogobius marmoratus</i> (Peters)	0	1	0	2	0	0
Osphronemida	<i>Betta pugnax</i> (Cantor)	2	1	2	0	0	0
Channidae	<i>Channa gachua</i> Hamilton	0	2	1	3	5	3
	<i>Channa lucius</i> (Cuvier)	0	2	1	0	3	0
	<i>Channa melasoma</i> (Bleeker)	0	0	0	1	0	0
Total individual caught		65	71	43	78	60	56

Appendix 3.3.

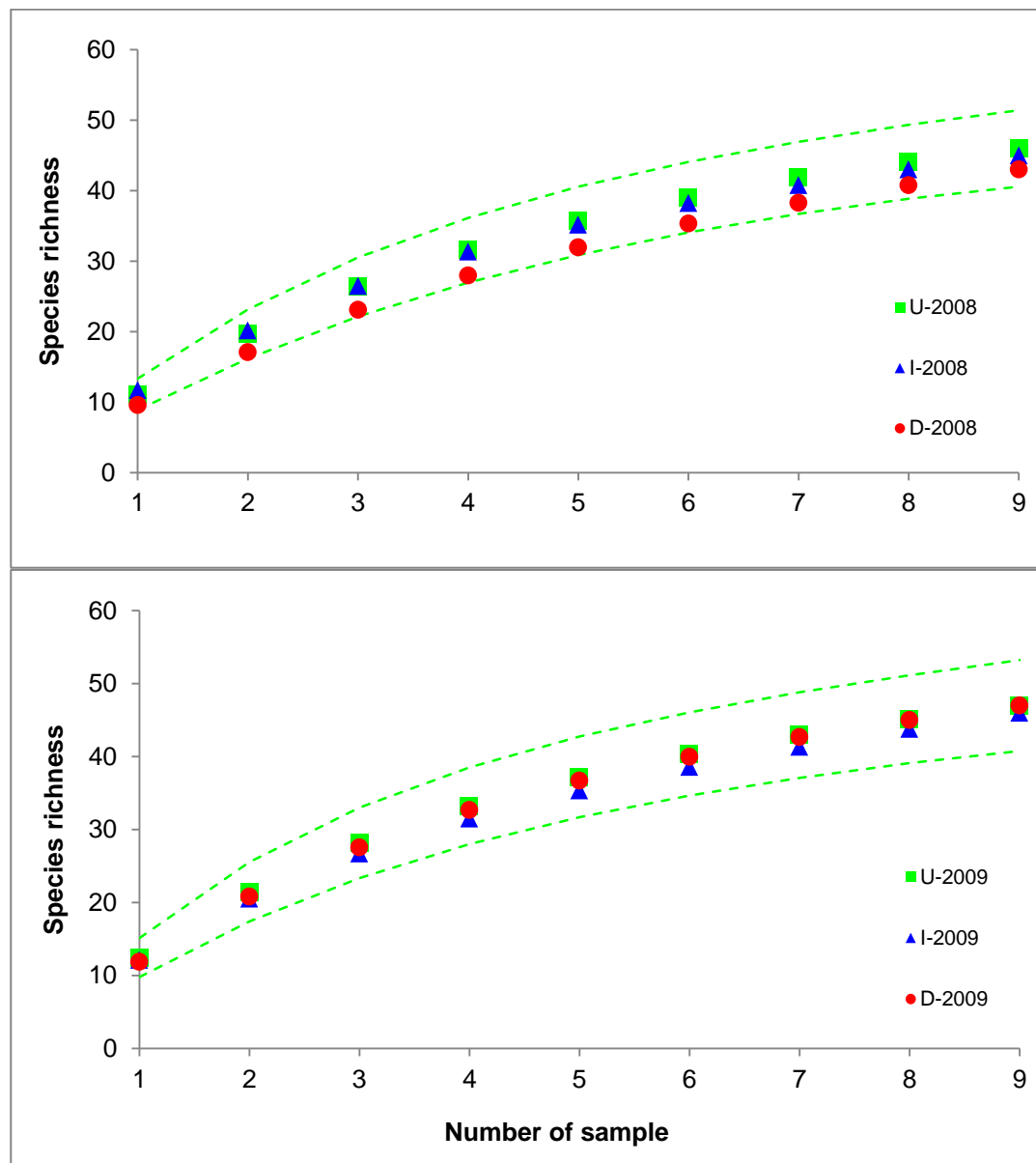


Figure A3.1. Sample-based rarefaction curves and 95% confidence intervals for fishes collected from nine streams in Peninsular Malaysia in 2008 (top) and 2009 (bottom) for undisturbed and disturbed communities.

Appendix 3.4.

Table A3.3. List of overlap species recorded in 2008 and 2009, respectively.

2008	2009
All streams	All streams
<i>Acantopsis dialuzona</i> van Hasselt	<i>Amblyceps foratum</i> Ng & Kottelat
<i>Amblyceps foratum</i> Ng & Kottelat	<i>Batasio fluviatilis</i> (Smith)
<i>Batasio fluviatilis</i> (Smith)	<i>Channa gachua</i> Hamilton
<i>Betta pugnax</i> (Cantor)	<i>Crossocheilus oblongus</i> Kuhl & van Hasselt
<i>Crossocheilus oblongus</i> Kuhl & van Hasselt	<i>Cyclocheilichthys apogon</i> (Valenciennes)
<i>Devario regina</i> (Fowler)	<i>Devario regina</i> (Fowler)
<i>Garra cambodgiensis</i> (Tirant)	<i>Garra cambodgiensis</i> (Tirant)
<i>Glyptothorax major</i> Fowler	<i>Glyptothorax major</i> Fowler
<i>Glyptothorax siamensis</i> Hora	<i>Glyptothorax siamensis</i> Hora
<i>Hampala macrolepidota</i> Kuhl & van Hasselt	<i>Hemibagrus nemurus</i> Valenciennes
<i>Hemibagrus nemurus</i> Valenciennes	<i>Homaloptera nebulosa</i> Alfred
<i>Hemirhamphodon pogonognathus</i> (Bleeker)	<i>Homaloptera parclitella</i> Tan & Ng
<i>Homaloptera leonardi</i> Hora	<i>Homaloptera smithi</i> Hora
<i>Homaloptera nebulosa</i> Alfred	<i>Homaloptera zollingeri</i> Bleeker
<i>Homaloptera smithi</i> Hora	<i>Labiobarbus fasciatus</i> (Bleeker)
<i>Homaloptera tweediei</i> Herre	<i>Labiobarbus leptocheilus</i> (Valenciennes)
<i>Homaloptera zollingeri</i> Bleeker	<i>Lobocheilos rhabdoura</i> (Fowler)
<i>Leiocassis poecilopterus</i> (Valenciennes)	<i>Macrognaathus maculatus</i> (Valenciennes)
<i>Lobocheilos rhabdoura</i> (Fowler)	<i>Mastacembelus favus</i> Hora
<i>Macrognaathus maculatus</i> (Valenciennes)	<i>Monopterus albus</i> Zuiew
<i>Mastacembelus favus</i> Hora	<i>Mystacoleucus marginatus</i> (Valenciennes)
<i>Monopterus albus</i> Zuiew	<i>Mystus castaneus</i> Ng
<i>Mystacoleucus marginatus</i> (Valenciennes)	<i>Nemacheilus masyae</i> Smith
<i>Nemacheilus selangoricus</i> Duncker	<i>Nemacheilus selangoricus</i> Duncker
<i>Neolissochilus soroides</i> (Duncker)	<i>Neolissochilus soroides</i> (Duncker)
<i>Osteochilus vittatus</i> (Valenciennes)	<i>Ompok bimaculatus</i> (Bloch)
<i>Osteochilus waandersi</i> (Bleeker)	<i>Osteochilus vittatus</i> (Valenciennes)
<i>Poropuntius smedleyi</i> (de Beaufort)	<i>Osteochilus waandersi</i> (Bleeker)
<i>Puntius banksi</i> Herre	<i>Poropuntius smedleyi</i> (de Beaufort)
<i>Puntius binotatus</i> (Valenciennes)	<i>Pseudomystus stenomus</i> (Valenciennes)
<i>Puntius lateristriga</i> (Valenciennes)	<i>Puntius banksi</i> Herre
<i>Rasbora elegans</i> Volz	<i>Puntius binotatus</i> (Valenciennes)
<i>Silurichthys schneideri</i> Volz	<i>Puntius lateristriga</i> (Valenciennes)
	<i>Rasbora elegans</i> Volz
	<i>Rasbora paviana</i> Tirant
	<i>Silurichthys schneideri</i> Volz

Table A3.3. List of overlap species recorded in 2008 and 2009, respectively (continue).

2008	2009
Undisturbed-Intermediate only	Undisturbed-Intermediate only
<i>Doryichthys martensii</i> (Peters)	<i>Homaloptera ogilviei</i> Alfred
<i>Homaloptera parclitella</i> Tan & Ng	<i>Pseudomystus leiacanthus</i> (Weber & de Beaufort)
<i>Labiobarbus fasciatus</i> (Bleeker)	<i>Rasbora dusonensis</i> (Bleeker)
<i>Silurichthys hasseltii</i> Bleeker	
Undisturbed-Disturbed only	Undisturbed-Disturbed only
<i>Labiobarbus leptocheilus</i> (Valenciennes)	<i>Acantopsis dialuzona</i> van Hasselt
<i>Luciosoma setigerum</i> (Valenciennes)	<i>Hampala macrolepidota</i> Kuhl & van Hasselt
<i>Ompok bimaculatus</i> (Bloch)	<i>Hemirhamphodon pogonognathus</i> (Bleeker)
<i>Rasbora notura</i> Kottelat	
Intermediate-Disturbed only	Intermediate-Disturbed only
<i>Channa gachua</i> Hamilton	<i>Mastacembelus unicolor</i> Valenciennes
<i>Channa lucius</i> (Cuvier)	
<i>Nemacheilus masyae</i> Smith	
Undisturbed only	Undisturbed only
<i>Barbucca diabolica</i> Roberts	<i>Luciosoma setigerum</i> (Valenciennes)
<i>Hemibagrus gracilis</i> Ng & Ng	<i>Channa melasoma</i> (Bleeker)
<i>Lepidocephalichthys hasselti</i> (Valenciennes)	<i>Nandus nebulosa</i> (Gray)
<i>Mystus castaneus</i> Ng	<i>Schismatogobius marmoratus</i> (Peters)
<i>Rasbora paucisqualis</i> Ahl	<i>Xenentodon canciloides</i> (Bleeker)
Intermediate only	Intermediate only
<i>Clarias leiacanthus</i> Bleeker	<i>Rasbora bankanensis</i> (Bleeker)
<i>Mastacembelus unicolor</i> Valenciennes	<i>Channa lucius</i> (Cuvier)
<i>Nandus nebulosa</i> (Gray)	<i>Leiocassis poecilopterus</i> (Valenciennes)
<i>Rasbora paviana</i> Tirant	<i>Pangio piperata</i> Kottelat & Lim
<i>Schismatogobius marmoratus</i> (Peters)	<i>Rasbora paucisqualis</i> Ahl
	<i>Tor tambra</i> (Valenciennes)
Disturbed only	Disturbed only
<i>Cyclocheilichthys apogon</i> (Valenciennes)	<i>Akysis hendriksoni</i> Alfred
<i>Osteochilus scapularis</i> (Bleeker)	<i>Clarias leiacanthus</i> Bleeker
<i>Pseudomystus stenomus</i> (Valenciennes)	<i>Clarias meladerma</i> Bleeker
	<i>Kryptopterus bicirrhis</i> (Valenciennes)
	<i>Lepidocephalichthys hasselti</i> (Valenciennes)
	<i>Raiamas guttatus</i> (Day)
	<i>Rasbora notura</i> Kottelat

Appendix 3.5

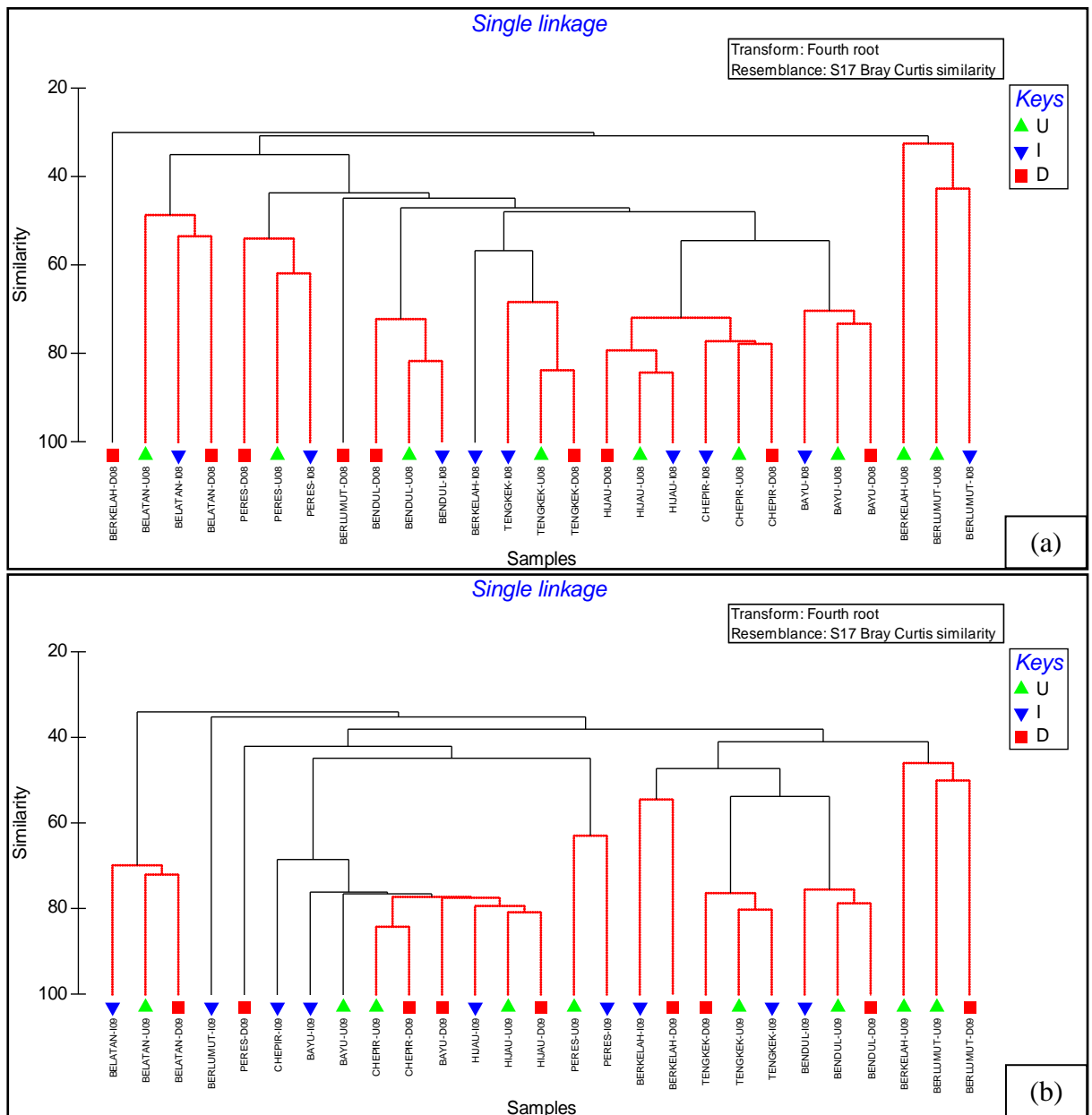


Figure A3.2. Dendrogram of the cluster analysis comparing the study sites, (a) 2008 and (b) 2009 in Peninsular Malaysia generated based on Bray-Curtis similarity resemblance. Letters U, I and D denote undisturbed, intermediate and disturbed stream section, respectively.

Appendix 4.1.

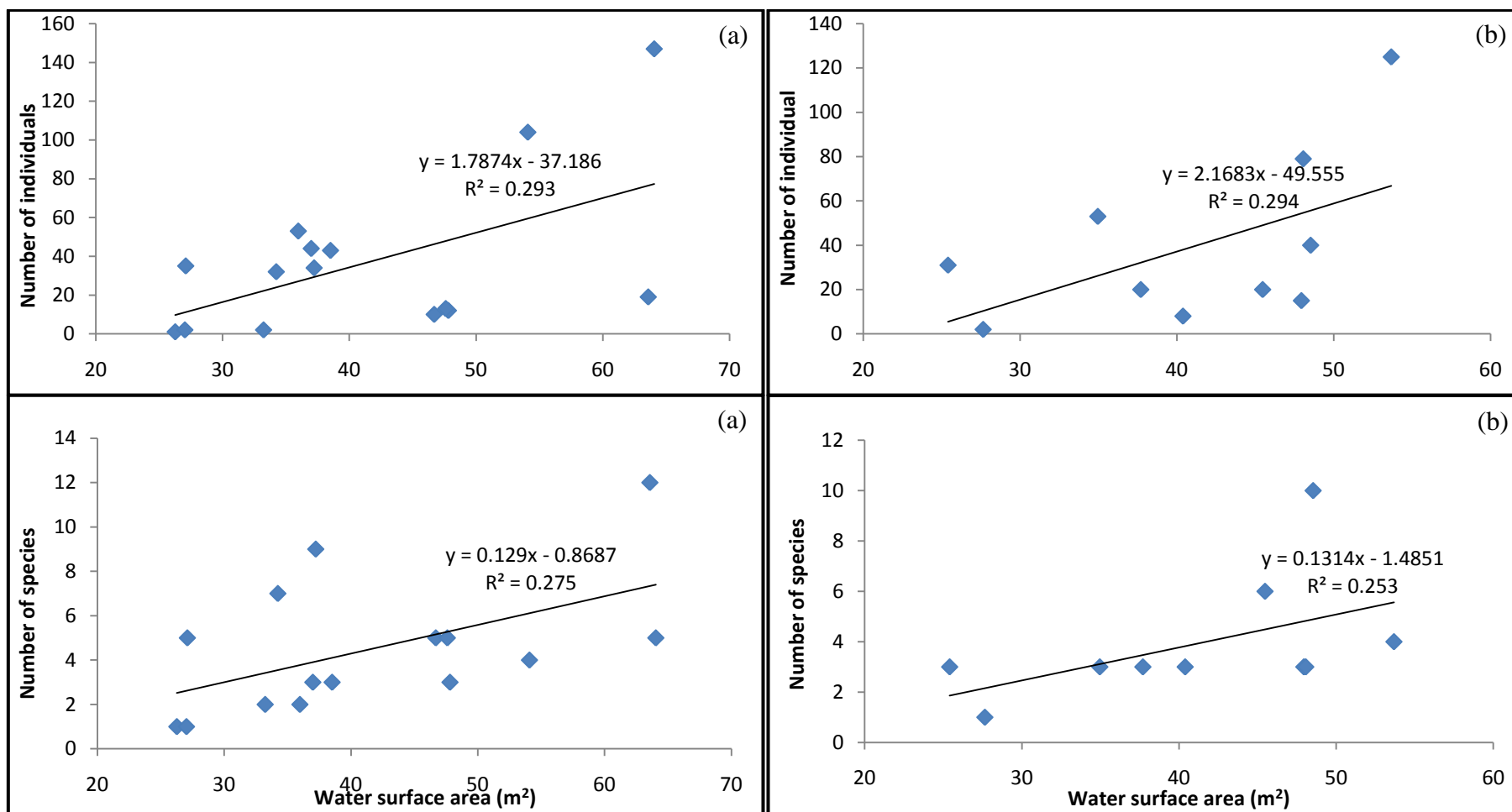


Figure A4.1. Relationships between faunistic variables and water surface area (m²): a) modified pools, and b) natural pools.

Appendix 4.2.

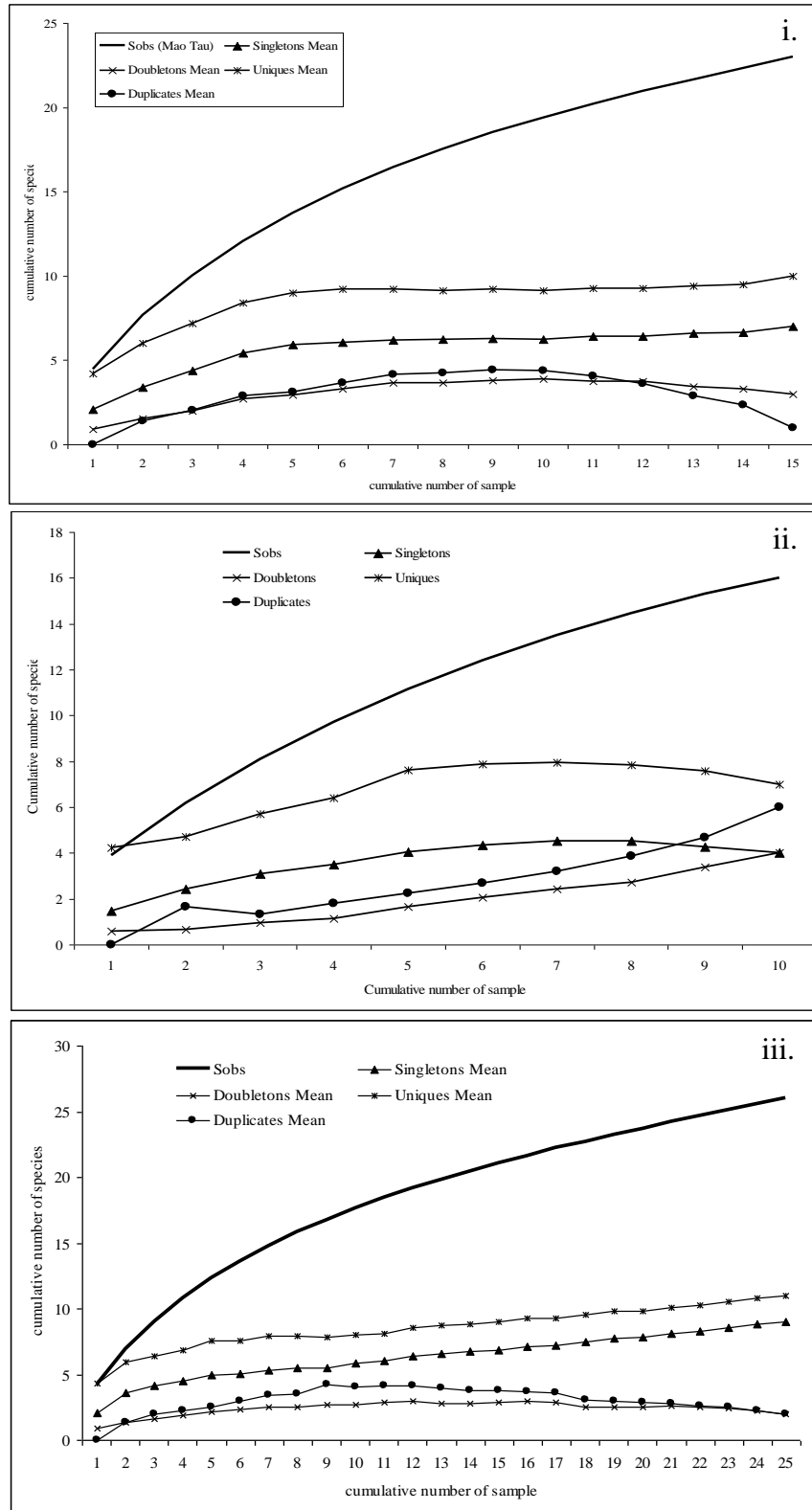


Figure A4.2. Observed number of species (S_{obs}): singletons, doubletons, uniques and duplicates curves for: i. modified pools, ii. natural pools, and iii. total pools.

Appendix 5.1

Table A5.1. Fish species and their frequency of occurrence in small streams in Peninsular Malaysia collected in 2008 (n=13) and 2009 (n=10) respectively.

Family	Species	Abundance	Frequency of occurrence (%)	
			2008	2009
Cyprinidae	<i>Crossocheilus oblongus</i>	604	30.77	40
	<i>Cyclocheilichthys apogon</i>	16	15.38	20
	<i>Devario regina</i>	576	38.46	30
	<i>Garra cambodgiensis</i>	94	38.46	50
	<i>Hampala macrolepidota</i>	24	15.38	40
	<i>Labiobarbus fasciatus</i>	56	7.69	20
	<i>Labiobarbus leptocheilus</i>	54	15.38	20
	<i>Lobocheilos rhabdoura</i>	77	38.46	40
	<i>Luciosoma setigerum</i>	7	15.38	10
	<i>Mystacoleucus marginatus</i>	194	61.54	50
	<i>Neolissochilus soroides</i>	218	46.15	60
	<i>Osteochilus scapularis</i>	3	15.38	-
	<i>Osteochilus vittatus</i>	46	38.46	20
	<i>Osteochilus waandersi</i>	243	38.46	40
	<i>Parachela oxygastroides</i>	2	7.69	-
	<i>Poropuntius smedleyi</i>	716	38.46	40
	<i>Puntius banksi</i>	119	30.77	50
	<i>Puntius binotatus</i>	229	46.15	30
	<i>Puntius lateristiga</i>	92	46.15	50
	<i>Raiamas guttatus</i>	1	-	10
	<i>Rasbora argyrotaenia</i>	12	7.69	-
	<i>Rasbora bankanensis</i>	3	-	10
	<i>Rasbora dusonensis</i>	7	-	10
	<i>Rasbora elegans</i>	64	30.77	20
	<i>Rasbora notura</i>	12	7.69	10
	<i>Rasbora paucisqualis</i>	8	15.38	10
	<i>Rasbora paviana</i>	87	15.38	10
	<i>Tor tambra</i>	2	-	10
Balitoridae	<i>Barbucca diabolica</i>	2	7.69	-
	<i>Homaloptera leonardi</i>	14	15.38	-
	<i>Homaloptera nebulosa</i>	219	23.08	40
	<i>Homaloptera ogilviei</i>	12	-	10
	<i>Homaloptera parclitella</i>	28	46.15	50
	<i>Homaloptera smithi</i>	75	46.15	10
	<i>Homaloptera tweediei</i>	49	30.77	-
	<i>Homaloptera zollingeri</i>	223	53.85	60
Cobitidae	<i>Acantopsis dialuzona</i>	62	15.38	30
	<i>Lepidocephalichthys hasselti</i>	3	7.69	10
	<i>Pangio filinaris</i>	1	7.69	-
	<i>Pangio piperata</i>	1	-	10

Table A5.1. Continue.

Family	Species	Abundance	Frequency of occurrence (%)	
			2008	2009
Nemacheilidae	<i>Nemacheilus masyae</i>	41	23.08	30
	<i>Nemacheilus selangoricus</i>	26	7.69	30
Bagridae	<i>Batasio fluviatilis</i>	127	38.46	40
	<i>Hemibagrus gracilis</i>	1	7.69	-
	<i>Hemibagrus nemurus</i>	34	61.54	50
	<i>Leiocassis poecilopterus</i>	25	30.77	10
	<i>Mystus castaneus</i>	10	7.69	20
	<i>Pseudomystus fumosus</i>	2	-	10
	<i>Pseudomystus leiacanthus</i>	4	-	20
	<i>Pseudomysus stenomus</i>	5	7.69	10
Siluridae	<i>Kryptopterus bicirrhis</i>	1	-	10
	<i>Ompok siluroides</i>	16	15.38	20
	<i>Silurichthys hasselti</i>	14	30.77	10
	<i>Silurichthys schneideri</i>	64	23.08	40
Akysidae	<i>Akysis hendriksoni</i>	1	-	10
Sisoridae	<i>Glyptothorax major</i>	393	76.92	70
	<i>Glyptothorax siamensis</i>	185	61.54	60
Amblycipitidae	<i>Amblyceps foratum</i>	135	46.15	40
Clariidae	<i>Clarias leiacanthus</i>	5	15.38	10
	<i>Clarias meladerma</i>	1	-	10
Belonidae	<i>Xenentodon canciloides</i>	4	15.38	10
Hemiramphidae	<i>Hemirhamphodon pogonognathus</i>	26	15.38	20
Syngnathidae	<i>Doryichthys martensii</i>	5	23.08	-
Synbranchidae	<i>Monopterus albus</i>	23	38.46	50
Mastecembelidae	<i>Macrognathus maculatus</i>	84	53.85	60
	<i>Mastacembelus favus</i>	54	53.85	50
	<i>Mastacembelus unicolor</i>	20	7.69	10
Nandidae	<i>Nandus nebulosa</i>	2	7.69	10
Pristolepididae	<i>Pristolepis grootii</i>	1	7.69	-
	<i>Pristolepis fasciatus</i>	2	7.69	-
Gobiidae	<i>Schismatogobius</i> sp. cf. <i>marmoratus</i>	3	7.69	10
Osphronemidae	<i>Betta pugnax</i>	36	38.46	10
Channidae	<i>Channa gachua</i>	28	23.08	30
	<i>Channa lucius</i>	6	15.38	10
	<i>Channa melasoma</i>	1	-	10

Note. 'n' is the number of site sampled in each year. "--" indicates absence of species in respective sampling.

Appendix 5.2

Table A5.2. Fish occurrence (+) at each sampling site for the year 2008. Species are arranged alphabetically by family.

Family	Species	Site													
		North-west					South				East				
		Tasoh	Bayu	Chepir	Hijau	Kenas	Tengkek	Bendul	Ledang	Berlumut	Berkelah	Jin	Peres	Belatan	
Cyprinidae	<i>Crossocheilus oblongus</i>					+	+			+	+				30.77
	<i>Cyclocheilichthys apogon</i>											+		+	15.38
	<i>Devario regina</i>	+	+	+	+	+									38.46
	<i>Garra cambodgiensis</i>		+	+	+								+	+	38.46
	<i>Hampala macrolepidota</i>		+							+					15.38
	<i>Labiobarbus fasciatus</i>									+					7.69
	<i>Labiobarbus leptocheilus</i>										+	+			15.38
	<i>Lobocheilos rhabdoura</i>		+		+	+	+				+				38.46
	<i>Luciosoma setigerum</i>									+	+				15.38
	<i>Mystacoleucus marginatus</i>		+	+		+	+			+	+	+	+		61.54
	<i>Neolissochilus soroides</i>				+	+	+	+			+				46.15
	<i>Osteochilus scapularis</i>						+			+					15.38
	<i>Osteochilus vittatus</i>						+			+	+	+		+	38.46
	<i>Osteochilus waandersi</i>						+			+	+	+		+	38.46
	<i>Parachela oxygastroides</i>											+			7.69
	<i>Poropuntius smedleyi</i>								+	+		+	+		38.46
	<i>Puntius banksi</i>							+		+	+	+			30.77
	<i>Puntius binotatus</i>		+	+	+		+						+	+	46.15
	<i>Puntius lateristiga</i>		+	+						+	+	+	+		46.15
	<i>Rasbora argyrotaenia</i>											+			7.69
<i>Rasbora elegans</i>							+	+	+		+			30.77	
<i>Rasbora notura</i>												+		7.69	
<i>Rasbora paucisqualis</i>											+	+		15.38	
<i>Rasbora paviana</i>		+											+	15.38	

Table A5.2. Continue.

Family	Species	Site													
		North-west					South				East				
		Tasoh	Bayu	Chepir	Hijau	Kenas	Tengkek	Bendul	Ledang	Berlumut	Berkelah	Jin	Peres	Belatan	
Balitoridae	<i>Barbucca diabolica</i>													+	7.69
	<i>Homaloptera leonardi</i>		+			+									15.38
	<i>Homaloptera nebulosa</i>		+				+						+		23.08
	<i>Homaloptera parclitella</i>				+	+				+	+		+	+	46.15
	<i>Homaloptera smithii</i>			+		+				+	+	+		+	46.15
	<i>Homaloptera tweediei</i>				+	+						+		+	30.77
	<i>Homaloptera zollingeri</i>				+	+	+	+		+	+		+		53.85
Cobitidae	<i>Acantopsis dialuzona</i>										+			+	15.38
	<i>Lepidocephalichthys hasseltii</i>													+	7.69
	<i>Pangio filinaris</i>										+				7.69
Nemacheilidae	<i>Nemacheilus masyae</i>						+				+		+		23.08
	<i>Nemacheilus selangoricus</i>													+	7.69
Bagridae	<i>Batasio fluviatilis</i>	+	+	+	+										38.46
	<i>Hemibagrus gracilis</i>										+				7.69
	<i>Hemibagrus nemurus</i>		+		+	+				+	+	+	+	+	61.54
	<i>Leiocassis poecilopterus</i>										+	+	+	+	30.77
	<i>Mystus castaneus</i>										+				7.69
	<i>Pseudomystus stenomous</i>										+				7.69
Siluridae	<i>Ompok siluroides</i>	+	+												15.38
	<i>Silurichthys hassaltii</i>	+							+		+			+	30.77
	<i>Silurichthys schneideri</i>		+	+	+										23.08
Sisoridae	<i>Glyptothorax major</i>		+	+	+	+	+	+		+	+	+	+	+	76.92
	<i>Glyptothorax siamensis</i>		+	+	+	+	+	+			+	+			61.54
Amblycipitidae	<i>Amblyceps foratum</i>		+	+	+	+					+	+			46.15
Clariidae	<i>Clarias leiacanthus</i>	+									+				15.38

Table A5.2. Continue.

Family	Species	Site													
		North-west					South				East				
		Tasoh	Bayu	Chepir	Hijau	Kenas	Tengkek	Bendul	Ledang	Berlumut	Berkelah	Jin	Peres	Belatan	
Belonidae	<i>Xenentodon cancilloides</i>					+						+			15.38
Hemiramphidae	<i>Hemiramphodon pogonognathus</i>	+												+	15.38
Syngnathidae	<i>Doryichthys martensii</i>											+	+	+	23.08
Synbranchidae	<i>Monopterus albus</i>		+	+	+	+								+	38.46
Mastecembelidae	<i>Macrogathus maculatus</i>		+	+	+		+	+					+	+	53.85
	<i>Mastacembelus favus</i>		+	+	+						+	+	+	+	53.85
	<i>Mastacembelus unicolor</i>												+		7.69
Nandidae	<i>Nandus nebulosus</i>													+	7.69
Pristolepididae	<i>Pristolepis grootii</i>											+			7.69
	<i>Pristolepis fasciatus</i>													+	7.69
Gobiidae	<i>Schismatogobius</i> sp. cf. <i>marmoratus</i>												+		7.69
Osphronemidae	<i>Betta pugnax</i>	+	+				+				+			+	38.46
Channidae	<i>Channa gachua</i>	+	+											+	23.08
	<i>Channa lucius</i>									+			+		15.38
	Alpha diversity	11	21	16	16	19	13	5	2	17	26	24	22	27	

Appendix 5.3

Table A5.3. Fish occurrence (+) at each sampling site for the year 2009. Species are arranged alphabetically by family.

Family	Species	Site											
		North-west			South				East				
		Bayu	Chepir	Hijau	Tengkek	Bendul	Ledang	Berlunut	Berkelah	Peres	Belatan		
Cyprinidae	<i>Crossocheilus oblongus</i>				+	+		+	+			40.00	
	<i>Cyclocheilichthys apogon</i>								+		+	20.00	
	<i>Devario regina</i>	+	+	+								30.00	
	<i>Garra cambodgiensis</i>	+	+	+						+	+	50.00	
	<i>Hampala macrolepidota</i>	+		+				+		+		40.00	
	<i>Labiobarbus fasciatus</i>							+	+			20.00	
	<i>Labiobarbus leptocheilus</i>			+							+	20.00	
	<i>Lobocheilos rhabdoura</i>		+	+	+				+			40.00	
	<i>Luciosoma setigerum</i>								+			10.00	
	<i>Mystacoleucus marginatus</i>	+	+					+	+	+		50.00	
	<i>Neolissochilus soroides</i>	+	+	+	+	+			+			60.00	
	<i>Osteochilus vittatus</i>								+		+	20.00	
	<i>Osteochilus waandersi</i>						+	+	+		+	40.00	
	<i>Poropuntius smedleyi</i>					+	+		+	+		40.00	
	<i>Puntius banksi</i>	+			+	+		+	+			50.00	
	<i>Puntius binotatus</i>	+	+								+	30.00	
	<i>Puntius lateristriga</i>	+					+	+	+	+		50.00	
	<i>Raiamas guttatus</i>								+			10.00	
	<i>Rasbora bankanensis</i>							+				10.00	
	<i>Rasbora dusonensis</i>								+			10.00	
	<i>Rasbora elegans</i>				+			+				20.00	
	<i>Rasbora notura</i>									+		10.00	
	<i>Rasbora paucisqualis</i>								+			10.00	
<i>Rasbora paviana</i>										+	10.00		
<i>Tor tambra</i>									+		10.00		

Table A5.3. Continue.

Family	Species	Site											
		North-west			South				East				
		Bayu	Chepir	Hijau	Tengkek	Bendul	Ledang	Berlumut	Berkelah	Peres	Belatan		
Balitoridae	<i>Homaloptera nebulosa</i>	+	+	+						+		40.00	
	<i>Homaloptera ogilviei</i>									+		10.00	
	<i>Homaloptera parclitella</i>				+	+	+		+	+		50.00	
	<i>Homaloptera smithi</i>								+			10.00	
	<i>Homaloptera zollingeri</i>	+	+	+	+				+	+		60.00	
Cobitidae	<i>Acantopsis dialuzona</i>							+		+	+	30.00	
	<i>Lepidocephalichthys hasselti</i>										+	10.00	
	<i>Pangio piperata</i>									+		10.00	
Nemacheilidae	<i>Nemacheilus masyae</i>								+	+	+	30.00	
	<i>Nemacheilus selangoricus</i>				+					+	+	30.00	
Bagridae	<i>Batasio fluviatilis</i>	+	+	+							+	40.00	
	<i>Hemibagrus nemurus</i>	+	+	+						+	+	50.00	
	<i>Leiocassis poecilopterus</i>									+		10.00	
	<i>Mystus castaneus</i>								+		+	20.00	
	<i>Pseudomystus fumosus</i>								+			10.00	
	<i>Pseudomystus leiacanthus</i>									+	+	20.00	
Siluridae	<i>Pseudomysus stenomus</i>										+	10.00	
	<i>Kryptopterus bicirrhis</i>										+	10.00	
	<i>Ompok siluroides</i>	+									+	20.00	
	<i>Silurichthys hasselti</i>								+			10.00	
	<i>Siluruchthys schneideri</i>	+	+	+							+	40.00	
Akysidae	<i>Akysis hendriksoni</i>										+	10.00	
Sisoridae	<i>Glyptothorax major</i>	+	+	+	+	+			+	+	+	80.00	
	<i>Glyptothorax siamensis</i>	+	+	+	+	+				+		60.00	
Amblycipitidae	<i>Amblyceps foratum</i>	+	+	+						+		40.00	

Table A5.3. Continue.

Family	Species	Site										
		North-west			South				East			
		Bayu	Chepir	Hijau	Tengkek	Bendul	Ledang	Berlumut	Berkelah	Peres	Belatan	
Clariidae	<i>Clarias leiacanthus</i>				+							10.00
	<i>Clarias meladerma</i>										+	10.00
Belonidae	<i>Xenentodon canciloides</i>									+		10.00
Hemiramphidae	<i>Hemirhamphodon pogonognathus</i>								+		+	20.00
Synbranchidae	<i>Monopterus albus</i>	+	+	+					+		+	50.00
Mastecembelidae	<i>Macrognathus maculatus</i>	+		+	+	+				+	+	60.00
	<i>Mastacembelus favus</i>	+	+	+					+	+		50.00
	<i>Mastacembelus unicolor</i>									+		10.00
Nandidae	<i>Nandus nebulosa</i>										+	10.00
Gobiidae	<i>Schismatogobius</i> sp. cf. <i>marmoratus</i>									+		10.00
Osphronemidae	<i>Betta pugnax</i>							+				10.00
Channidae	<i>Channa gachua</i>	+				+					+	30.00
	<i>Channa lucius</i>							+				10.00
	<i>Channa melasoma</i>								+			10.00
Alpha diversity		21	16	18	12	9	4	11	27	26	27	

Appendix 6.1

Table A6.1 Fish species of the small streams in Peninsular Malaysia classified as common (category A) based on Rabinowitz classification.

Species	No. of region	No. of stream	Abundance
<i>Acantopsis dialuzona</i>	3	17	178
<i>Amblyceps foratum</i>	2	26	311
<i>Batasio fluviatilis</i>	2	12	214
<i>Crossocheilus oblongus</i>	3	17	928
<i>Cyclocheilichthys apogon</i>	2	13	118
<i>Garra cambodgiensis</i>	2	19	353
<i>Glyptothorax major</i>	3	36	768
<i>Glyptothorax siamensis</i>	3	12	203
<i>Hampala macrolepidota</i>	3	25	126
<i>Hemibagrus nemurus</i>	3	29	144
<i>Hemirhamphodon pogonognathus</i>	2	11	122
<i>Homaloptera nebulosa</i>	3	16	278
<i>Homaloptera parclitella</i>	3	18	147
<i>Homaloptera smithi</i>	3	14	127
<i>Homaloptera tweediei</i>	2	9	110
<i>Homaloptera zollingeri</i>	3	20	303
<i>Labiobarbus fasciatus</i>	2	4	109
<i>Labiobarbus leptocheilus</i>	2	10	104
<i>Lobocheilos rhabdura</i>	3	10	160
<i>Macrognaathus maculatus</i>	3	24	191
<i>Mastacembelus favus</i>	3	22	125
<i>Mystacoleucus marginatus</i>	3	31	866
<i>Nemacheilus masyae</i>	2	14	129
<i>Nemacheilus selangoricus</i>	3	16	117
<i>Neolissocheilus soroides</i>	3	27	578
<i>Osteochilus vittatus</i>	3	23	424
<i>Osteochilus waandersii</i>	3	17	623
<i>Poropuntius smedleyi</i>	3	27	1984
<i>Puntius banksi</i>	3	22	584
<i>Puntius binotatus</i>	2	21	552
<i>Puntius lateristiga</i>	3	23	346
<i>Rasbora elegans</i>	2	9	177
<i>Rasbora paucisquamis</i>	2	7	175
<i>Rasbora paviana</i>	2	18	567

Table A6.2. Fish species of the small streams in Peninsular Malaysia classified as rare (category B) based on Rabinowitz classification.

Species	No. of region	No. of stream	Abundance
<i>Betta pugnax</i>	3	16	84
<i>Channa gachua</i>	3	18	87
<i>Channa lucius</i>	3	10	29
<i>Channa striata</i>	3	7	10
<i>Clarias leiacanthus</i>	3	20	80
<i>Danio albolineatus</i>	2	6	38
<i>Doryichthys martensii</i>	2	10	41
<i>Hemibagrus gracilis</i>	2	6	32
<i>Homaloptera leonardi</i>	2	4	88
<i>Leiocassis poecilopterus</i>	2	15	61
<i>Luciosoma setigerum</i>	2	4	13
<i>Mastacembelus unicolor</i>	2	3	22
<i>Monopterus albus</i>	2	22	67
<i>Monotrete lieurus</i>	2	4	7
<i>Ompok siluroides</i>	2	9	32
<i>Osteochilus scapularis</i>	3	7	70
<i>Parachela oxygastroides</i>	2	3	19
<i>Pristolepis fasciatus</i>	2	9	32
<i>Pristolepis grootii</i>	2	7	17
<i>Pseudogobiopsis oligactis</i>	2	6	31
<i>Silurichthys hasseltii</i>	2	12	87
<i>Silurichthys schneideri</i>	2	13	87
<i>Tor tambra</i>	2	8	13
<i>Trichopodus trichopterus</i>	2	4	5
<i>Xenentodon canciloides</i>	2	15	32

Table A6.3. Fish species of the small streams in Peninsular Malaysia classified as rare (category C) based on Rabinowitz classification.

Species	No. of region	No. of stream	Abundance
<i>Rasbora caudimaculata</i>	2	2	26

Table A6.4. Fish species of the small streams in Peninsular Malaysia classified as rare (category D) based on Rabinowitz classification.

Species	No. of region	No. of stream	Abundance
<i>Rasbora bankanensis</i>	2	2	8

Table A6.5. Fish species of the small streams in Peninsular Malaysia classified as rare (category E) based on Rabinowitz classification.

Species	No. of region	No. of stream	Abundance
<i>Channa melasoma</i>	1	4	10
<i>Devario regina</i>	1	17	951
<i>Homaloptera ogilviei</i>	1	4	16
<i>Mystus castaneus</i>	1	6	14
<i>Nanobagrus fuscus</i>	1	4	18
<i>Neolissocheilus hendersoni</i>	1	2	57
<i>Rasbora argyrotaenia</i>	1	4	152
<i>Rasbora dusonensis</i>	1	4	30
<i>Rasbora notura</i>	1	13	390
<i>Schistura robertsi</i>	1	2	27

Table A6.6. Fish species of the small streams in Peninsular Malaysia classified as rare (category F) based on Rabinowitz classification.

Species	No. of region	No. of stream	Abundance
<i>Acanthopsoides molobrion</i>	1	2	9
<i>Achiroides leucorhynchus</i>	1	2	2
<i>Aplocheilus panchax</i>	1	2	5
<i>Lepidocephalichthys hasselti</i>	1	2	5
<i>Osphronemus gouramy</i>	1	2	2
<i>Pangio piperata</i>	1	2	2
<i>Pseudomystus leiacanthus</i>	1	3	5
<i>Pseudomystus stenomous</i>	1	2	7
<i>Raiamas guttatus</i>	1	4	4

Table A6.7. Fish species of the small streams in Peninsular Malaysia classified as rare (category G) based on Rabinowitz classification.

Species	No. of region	No. of stream	Abundance
<i>Acanthocobitis zonalternans</i>	1	1	12
<i>Barbucca diabolica</i>	1	1	2
<i>Mystacoleucus chilopterus</i>	1	1	10
<i>Nandus nebulosus</i>	1	1	2
<i>Oxygaster anomalura</i>	1	1	3
<i>Pangio semicineta</i>	1	1	2
<i>Puntius lineatus</i>	1	1	16
<i>Puntius partipentazona</i>	1	1	3
<i>Schismatogobius</i> sp. cf. <i>marmoratus</i>	1	1	3
<i>Syncrossus beauforti</i>	1	1	47
<i>Syncrossus hymenophysa</i>	1	1	4

Table A6.8. Fish species of the small streams in Peninsular Malaysia classified as rare (category H) based on Rabinowitz classification.

Species	No. of region	No. of stream	Abundance
<i>Acrochordonichthys rugosus</i>	1	1	1
<i>Acrochordonichthys septentrionalis</i>	1	1	1
<i>Akysis hendriksoni</i>	1	1	1
<i>Betta stigmosa</i>	1	1	1
<i>Clarias meladerma</i>	1	1	1
<i>Kryptopterus bicirrhis</i>	1	1	1
<i>Monotrete palembangensis</i>	1	1	1
<i>Oxyeleotris marmoratus</i>	1	1	1
<i>Pangio filinaris</i>	1	1	1
<i>Puntius orphoides</i>	1	1	1