CRC Freshwater Ecology Project A240

Quantifying flow habitat biota relationships in riverine ecosystems.

Ecological response to manipulations of the hydrology in slackwater and flow patches on the Broken River

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Year 1 Synthesis Report

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Abstract:

River systems are diverse complex systems consisting of an array of patches that are largely formed through spatially and temporally variable geomorphic and hydrological processes. Flow is perhaps the overriding force in the structure and function of these patches. In this study we altered the nature of two major patch types in a lowland river (main channel flowing and slackwater) by directing flow into slackwater environments thereby creating a flowing patch and by directing flow away from an edge environment thereby creating a slackwater patch. We measured a range of biotic and abiotic variables in order to study the effects of altering flow characteristics within patches.

Our results indicated that created flow and slackwater patches were equivalent to the natural habitats with respect to both their biotic and abiotic characteristics. Although there was no difference in the abiotic character and primary productivity of the flowing and slackwater patches, distinct biotic communities existed in these patch types. Microinvertebrate, fish and shrimp abundance was greatest in the slackwater habitats, whereas macroinvertebrate abundance was greatest in the flowing patch. Thus, the hydraulic nature of a patch determined the biotic communities of the patch.

These distinct biotic communities may lead to a distinct food web structure in the two patch types and we present a conceptual model of a riverine flow-mediated food web. In addition, our results support the dynamic hierarchical patch model of organisation in river systems. Together, these models provide a valuable means of investigating patterns and process within a river system and highlight the need to maintain or reinstate the natural flow regime to ensure the spatial and temporal variability of patches for riverine health.

Introduction

Riverine systems are complex and consist of a mosaic of patches that are discontinuous at both the broad longitudinal and lateral dimension and the local small scale patch (Thorp et al. in press). Patches are increasingly being viewed as nested within a hierarchical system, which vary both spatially and temporally. Little is understood about patch structure and their importance to lowland river function. However, the patch mosaic is likely to be important for various ecological processes such as nutrient cycling, refuge, predator avoidance, recruitment and biodiversity. Therefore, the spatial and temporal formation and connectivity of patches may be fundamental to maintaining the integrity of riverine systems (Power and Dietrich 2002; Thorp et al. in press).

Patches may be defined by almost any combination of habitat variables, however the overriding force defining patch character is flow (Power and Dietrich 2002; Thorp et al. in press). The temporal character of riverine hydraulics and hydrology influences the availability of patches, their character, metabolic functioning and the linkages and exchange of biota both within and between patches. Previous work has identified two discrete patch types within the main channel in lowland rivers; slackwater and main channel flowing (King in press; Richardson et al. 2004).

Slackwater patches within rivers are often small shallow areas of still water formed by sand bars, woody debris and bank morphology. These patches are thought to be highly productive and several studies have indicated that slack-water habitats are important rearing habitats for many species of fish and shrimp (Humphries et al. 1999; Humphries et al. 2002; King 2002; Schiemer et al. 2002; Richardson et al. 2004). Similar habitats play the same role in other river systems (Brown and Coon 1994; Copp 1997; Baras and Nindaba 1999; Ponton et al. 2000). Slackwaters provide protection from fast currents, have an abundant biofilm and contain high densities of zooplankton and microbenthos prey for the young stages of fish and shrimp (Pace et al. 1992; Rundle and Hildrew 1992; Thorp et al. 1994; Robertson, 1995; Basu and Pick 1996; Humphries et al. 1999; King, 2002).

By contrast, main channel flowing patches provide a different habitat for riverine biota (Brunke et al. 2001). Flowing waters impart many demands and challenges on biota that may either enhance or limit their populations (Hart and Finelli 1999). It is, therefore, not surprising that flowing waters generally contain distinct biotic communities (Sheldon and Walker 1998; Nelson and Lieberman 2002). For example, planktonic primary producers, planktonic microfauna and larval and juvenile stages of fish and shrimp may be unable to maintain populations in a flowing environment (Baranyi et al. 2002; Richardson et al. 2004).

Distinct biotic communities related to flow suggest that food web structure is likely to be different between patches and, indeed, flow has been shown to be a major determinant of food web structure (Power and Dietrich 2002). Community structure and food webs associated with different lowland river floodplain habitats are rarely the focus of research, however some studies have indicated that different communities do exist between highly connected (at times) adjacent patches (Sheldon and Walker 1998). Most studies of food webs in lotic environments have been carried out in small scale experiments, generally associated with small streams (Woodward and Hildrew 2002).

If we wish to maintain the integrity of a river system it is important to understand spatial and temporal variability of the patch mosaic and the subsequent impacts on food webs and river functioning (Power and Dietrich 2002). In an attempt to address this important knowledge gap we undertook a comprehensive study of abiotic and biotic characteristics of two major patch types in a lowland river in south-eastern Australia. In this paper we describe the physico-chemical, productivity and biotic communities of natural and created flowing and slackwater patches and discuss the potential for alterative pathways for energy transfer within each of these patches.

Site Description

The Broken River, a mid-slope tributary of the Goulburn River (Figure 1), has a mean annual discharge of 200,000 ML and approximately 10% is diverted for off-stream use. The impoundments, Lakes Nillahcootie (built 1967) and Mokoan (built 1971), are the primary regulating bodies and flows are release during summer and autumn. The lower reaches of the Broken River consist mostly of long, meandering runs, comprising alternating shallow (<1 m) and deep (1-3 m) areas with still to moderate velocities (0-0.5 ms^{-1}). Instream structure comprises snags derived from riparian river redgums and aquatic macrophytes, dominated by common reed (*Phragmites australis*).

Experimental Design and Methods

Slackwater experiments were conducted in the Broken River above Casey Weir between November 2003 and March 2004. This section of the Broken River was chosen to maximize the pool of potential species which could be affected by the alterations to the slackwater habitats (approximately 10 species of fish) and minimised changes in river height during the experiment due to irrigation releases. Two sampling reaches were accessed through private properties "Morago" and "Mokoan Park" (approx. 5 to 8 km north of Benalla).

Sand bag walls were built in the two reaches during the first week of November to:

1. divert flow into seven slackwater habitats, creating a deeper, faster current environment ('created flows') (Figure 2a);
2. divert flow away from seven edge habitats, creating a shallow, zero current environment, to simulate a slackwater ('created slackwater') (Figure 2b);

Five of each treatment were selected from the seven after an assessment of the success of the manipulations. In addition, five natural slackwaters and five natural flowing areas were selected as controls (20 sampling units in total). Sampling took place every 4 weeks starting in mid December 2003 and finishing in early March 2004 (four trips).

Physico-chemical and Nutrient Data

Physico-chemical and nutrient data were collected from each of the 20 sampling units. Temperature, dissolved oxygen, turbidity, conductivity and pH were measured *in situ* using a Water Quality Checker (Horiba). Water samples were collected and frozen in the field, 200ml for total nitrogen, total phosphorus and 500 ml for chlorophyll-*a* and total suspended solids (TSS). Prior to freezing, 30 ml sub samples were filtered in the field (0.45 and 0.22 µm) for filterable reactive phosphorus, nitrate/nitrite, ammonium, dissolved organic carbon. Samples were analysed using standard protocols in the MDFRC analytical chemistry laboratory. Current speed was measured *in situ* Flow was measured *in situ* using an electromagnetic flow meter (Marsh M^{c}Birney Flow Mate 2000). Additional habitat descriptions in each sampling unit were noted including depth, area, fringing vegetation sediment type and percent cover of aquatic macrophytes.

Open Water Production

YSI Oxygen loggers were deployed on frames for 20 hours in four of each treatment and four of each control unit (16 sampling units). Oxygen loggers in slackwaters included a small submersible pump with a diffuser attached to ensure water circulation over the probe. Nine "Odyssey' Light loggers were deployed as close as possible to the probes to measure incident radiation.

Snag Biofilm Production

One hundred snag (instream woody debris) segments (diameter, 30-50 mm; length 300 mm) were collected from the sampling reaches. Each snag was numbered and surface area recorded. Five snags were attached by electrical cable ties to a 60 cm long Dexion "L" cross member (Figure 3). This cross member was bolted to one end of a 10 cm x 10 cm x 50 cm masonry block, then placed in the stream in November 2003 with the snags parallel to the stream flow.

Snag production chambers were constructed from 50 cm lengths of 40 mm diameter Perspex tube. Each tube was capped with rubber pan cones. A small submersible pump was installed to reticulate water through each tube. A rubber bung sealed one end of the tube and an YSI dissolved oxygen probe fitted with a bung sealed the other end. Sixteen of these were attached horizontally to two floating rafts so that they are completely submerged.

One seasoned snag segment was collected from each of the deployed platform samplers in 4 replicates of each treatment and control sampling units (16 sampling units). Each snag was carefully placed in a tube and the tubes purged of all air. Dissolved oxygen was be logged over a 20-hour period. At the end of the period, the snag surface area was recorded. A biofilm sample collected from the snag by scraping a 30 mm long segment of the snag. This was then frozen for enzyme and chlorophyll-*a* analysis.

Microfauna

Benthic microfauna samples were collected using a 12 volt Congo submersible inline pump with a pumping capacity of capacity 25 litres minute^{-1}. The pump inlet was held within 2 cm of the benthos and moved across the benthos until a 10 L sample (including sediment and associated detritus) was collected. The samples were then concentrated and preserved in 70% ethanol. In the laboratory, the samples were sub-sampled and counted in a Sedgewick-Rafter counting chamber and identified using a dark-field microscope. All microfauna were identified to the taxonomic level of Family or Genus following keys in Shiel (1995), with the exception of ostracods which were only identified to Class. All counts were converted to animals per litre prior to statistical analysis.

Macroinvertebrates

Macroinvertebrates were sampled using the snag segments as described in the snag biofilm production section above. On each sampling occasion, three snags were chosen randomly from each platform sampler. The snags were collected by holding a 500 μm mesh, "A" frame net over the selected snag and cutting the cable tie allowing the snag to fall into the net. The snag was then emptied into a plastic bucket and scrubbed down to remove all the animals. The animals were preserved in 70% ethanol, sorted and identified to lowest taxonomic level possible using the keys listed in Hawking (2000). The un-sampled snags remaining on the platform were scrubbed clean of biofilm and animals. The sampled snags were reattached to the platform which was then redeployment for subsequent sampling. Macroinvertebrate counts were converted to animal m^{-2} and taxonomic diversity determined. No macroinvertebrate data was available from the March sampling.

Fish and Shrimp

Fish and shrimp were collected using light traps (Humphries et al 2002) and a 'sweep net electrofisher' (SNE) (King and Crook 2002), covering an area of approximately 2 m^2. The samples were preserved in 95% ethanol and returned to the lab. Fish were identified to species using Serafini and Humphries (2004), measured and classed as adult juvenile or to one of four larval growth stages. Adult and juvenile shrimp were identified using keys modified from Williams (1980). Larval shrimp were identified to species using Fielder (1970); Benzie (1982) and Walsh (1993).

Data analysis

A single factor analysis of variance (ANOVA) was used to assess differences among treatments using the individual sampling units within each treatment as replicates using the statistical package Systat (Version 10, SPSS inc., Chicago, IL, USA). Multivariate analysis including non-metric multidimensional scaling (NMDS), Analysis of Similarity (ANOSIM), Simper and Bioenv, was used to analyse the individual components of the data and to analyse the total data set for underlying patterns using Primer v5 statistical package (Clarke and Warwick 2001).

Results

Multi-variate analysis

The physico-chemical, nutrient, production, respiration and habitat variables were summarised using PCA (Figure 4). PC 1 and PC 2 explained 17% and 13.7% of the variation in the data, respectively. There was a high degree of variability in the location of the flowing and slackwater habitats within the PCA plot. However, there was a slight separation of patch type along PC 2, with slackwaters generally having the lowest values along this axis. Total nitrogen concentration and sediment chlorophyll *a* were positively weighted on PC 2 and open water Chlorophyll *a*, community respiration, nett production, temperature and silt abundance were negatively weighted. There was a strong seasonal pattern within the data, with months separating out along PC 1, the January samples having the more positive values along this axis (not shown in Figure 4). NH_3, NO_x, conductivity and gross primary production were positively weighted and dissolved oxygen levels negatively weighted on PC 1.

The biotic community structure was assessed using MDS and analysis of similarity (Anosim). The created and natural slackwaters were significantly different from the created and natural flowing habitats (Figure. 5, Table 1). The created slackwaters were not significantly different from the natural slackwaters and the created flows were not significantly different from the natural flows. Specific taxa from each of the major groups (microfauna, macroinvertebrates shrimp and fish) characterized the flowing and slackwater patches and contributed substantially to the difference between these environments (Table 2.).

Bioenv was used to match environmental data with biotic patterns within the treatment habitats. Silt % abundance, flow and temperature were the best combination of threevariables that matched the biotic patterns (R = 0.528). The best individual variables were flow (R = 0.437), silt percent abundance (R = 0.355), *Persicaria* percent abundance (R = 0.226) and temperature (R = 0.186).

Water Quality

The nutrient status and physico-chemical status of the different habitat types were generally similar. Current velocity was the only significant difference between habitat types ($F = 32.846$, $P < 0.001$, Table 3). Current velocity was essentially zero in the slackwater habitats, with natural flow and created flow 0.22 and 0.21 ms^{-1}, respectively. Depth was greatest in the natural flows and least in the created slackwaters (0.4 m and 0.3 m, respectively). Turbidity was greatest in the created slackwaters; however, turbidity was also most variable in this habitat type.

Snag chlorophyll-*a* concentration (Figure 6) ranged from 0.3 to 2.9 µg cm^{-1} and was significantly different among treatments ($F = 3.393$, $P < 0.05$). Tukey test revealed that the natural flows had significantly higher chlorophyll-*a* content than the natural slackwaters ($P < 0.05$). However, there was no significant difference among the treatment habitats. Sediment chlorophyll-*a* ranged from 0.5 to 9.5 μg cm^{-1} and was not significantly different among treatments (Figure 6). Open water chlorophyll-*a*, particulate organic carbon (POC, Figure 7) and sediment carbon (Figure 6) ranged from to 2.0 to 40 µg L^{-1}, 0.005 to 0.011 g C L^{-1} and 5.0 to 107.3 g C m^{-2}, respectively and were not significantly different among treatments.

Production and respiration

Open water nett production was negative in all patch types, indicating a nett consumption of carbon, i.e heterotrophic, in all habitats. Neither gross primary production, community respiration or nett primary production were significantly different among any treatment (Figure ?) and ranged from -0.3 to 14.5, -43.0 to 2.3 and -28.3 and 2.0 mg $Cm^{-2}d^{-1}$, respectively.

Benthic Microinvertebrates and Snag Macroinvertebrates

Macroinvertebrate density ranged from 24 to 784 animals m^{-2} (Figure 8) and was significantly different among treatments ($F = 6.347$, $P < 0.01$). Tukey test revealed that the natural flow had significantly higher density of macroinvertebrates than the natural and created slackwaters ($P < 0.05$).

Microinvertebrate density ranged from 1 to 434 animals L^{-1} and was significantly different among treatments ($F = 10.377$, $P < 0.001$). Tukey test revealed that there was no difference between the same flow types but all comparisons between different flow types were significantly different with density significantly greater in the slackwater habitats (Figure 8).

Fish and Shrimp

The fish community was dominated by rainbow fish, mosquito fish and carp gudgeons and catch data was variable (Figure 8). Total fish numbers caught ranged from 0 to 89 per sample. Total fish abundance was low in the flowing habitats throughout and was significantly different between treatments ($F = 15.607$, $P < 0.001$). There was no significant difference in abundance among the same flow type but there was a significant difference between the different flow types ($P < 0.05$).

There was no significant difference in abundance of *Macrobrachium australiense* between treatments, abundance ranged from 0 to 7 animals per sample (Figure 8). However, there was a significant difference in the abundance of *Paratya australiensis* and *Caridina mccullochi* ($F = 13.460$, $P < 0.001$ and $F = 14.188$, $P < 0.001$, respectively). Their abundance per sample ranged from 0 to 73 and 0 to 63 respectively. Tukey test revealed that there was significantly more of both species in the slackwater habitats than in the flowing habitats ($P < 0.05$) with the exception of *P. australiensis* in the created slackwater and natural flowing habitats.

Discussion

The created and natural habitats of each flow type (slackwater and flowing) were not significantly different for any of the abiotic or biotic components investigated during this study. Therefore, creating slackwaters by directing flow away from an edge habitat and creating a flowing patch by directing flow through a slackwater habitat successfully simulated the natural habitats. For this reason the majority of this discussion will focus on the differences among the two flow patch types (flowing and slackwater).

There was no significant difference in the physico-chemical and environmental variables associated with the flowing and slackwater patches with the exception of current velocity and snag chlorophyll *a* concentration (both higher in the flowing patches). Production and respiration were similar between the two flow types as was nutrient status, benthic carbon abundance, physico-chemical parameters and open water and benthic chlorophyll *a*. Flow appeared to be the main force dictating the significant differences in biotic communities among the different flow types. The biotic communities in the created habitats resembled those of the natural habitats, both in terms of community structure and abundance. Flow and flow mediated habitat variables such as temperature and silt abundance were most strongly correlated with the biotic community structure. This relationship has been reported by others and flow is increasingly being seen as the over-riding force structuring the biotic communities in riverine systems through its impact on habitat and resource acquisition (Poff and Ward 1989; Lytle and Poff 2004).

Microinvertebrate, fish and shrimp densities were greater in the slackwater habitats, a finding consistent with Humphries et al. (1999), Richardson et al. (2004) and Baranyi et al. (2002). Higher microfauna densities in slackwaters may not be surprising as they require slow flowing areas to enable populations to build up due to their inability to maintain their position in a flowing environment (Sommer et al. 2004). Conversely, fish and shrimp (particularly larval and juvenile stages) may be actively selecting slackwater habitats, either as refuge from flow or in response to the increase in the microfaunal food resource, and supports the hypothesis that slackwaters are important nursery sites for fish and shrimp (Humphries et al. 1999; King, 2002; Richardson et al. 2004).

In contrast to the microfauna, fish and shrimp, snag macroinvertebrate density was highest in the flowing patches. This relationship between flow and macroinvertebrate density has been reported in several previous studies. For example, instream snag communities have been shown to have greater diversity, density and production than for any other stream habitats (Benke et al. 1984; O'Connor 1991; Johnson et al. 2003) and is generally attributed to increased flow providing additional food and habitat resources.

Slackwater and flowing patches each supported a unique biotic community that would appear to be determined by the hydraulic conditions within each patch type. This finding is consistent with those of Sheldon and Walker (1998) and Thorp et al. (in press). Primary production was similar between the two patch types and so did not appear to be a major factor determining species composition or food web structure, a finding consistent with Power and Dietrich (2003) and Brunke et al. (2001). Unique biotic communities in separate riverine habitats has been reported in previous studies (Sheldon and Walker, 1998). Sheldon and Walker (1998) found that three mesohabitat types in the lower Murray (channel, backwater and billabong) each contained unique macroinvertebrate communities and they suggested that flow was the major factor determining community structure. Thorp et al. (in press) also considered flow the major force structuring species distributions in rivers by largely determining the habitat template. In addition, Power and Dietrich (2003) and Dugger et al. (2002) have suggested that the maintenance of biodiversity and food web integrity is more likely to occur through the maintenance of a natural flow regime, which includes, seasonal floods and low flows, scouring and the maintenance of connectivity among habitats.

The establishment and maintenance of a temporally and spatially variable patch mosaic, with unique biotic communities, clearly indicate the potential for alternate food web structure and complexity to develop between two connected adjacent patches. In our study, slackwater habitats in the Broken River appear to support a more complex food web structure than in the flowing habitats and have the potential for more intense biotic interactions to occur (Thorp and Casper 2003). For example, the primary consumers within slackwaters were diverse and included; microinvertebrates, macroinvertebrates

and shrimp, thus providing multiple links between primary production and the higher level consumers such as macroinvertebrates, fish and birds. Furthermore, the slackwater food webs are potentially more planktonically based than flowing habitats. Slackwaters supported a higher abundance of microinvertebrates and a greater abundance of fish and shrimp larval stages, which require productive algal and zooplankton communities (Humphries et al. 1999; Schiemer et al. 2002). Slackwaters also have another level of predation provided by the planktonic predatory macroinvertebrates such as Hemiptera and Coleoptera, which can feed on a diverse range of prey from microinvertebrate to fish larvae (pers. comm. J. Hawking, MDFRC, September 2004).

Within the flowing patch, a more direct pathway to the highest trophic levels potentially exists. Zooplankton are largely absent from these habitats as are the small fish, shrimp and their larvae and the planktonic macroinvertebrate predators. The primary consumers in the flowing patches are predominantly macroinvertebrates, which provide a direct link to either fish or to fish via the freshwater prawn *Macrobrachium australiense*. The flowing, main channel is occupied by larger fish species such as Murray cod, which also have larger larval stages that are able to consume larger prey such as chironomid larvae (pers. comm. P. Humphries, MDFRC, September 2004). Our findings suggest that the food web structure of the flowing patches is a more direct pathway to the higher trophic levels and generally governed by stochastic events (Thorp and Casper 2003). In contrast, slackwater patch food web structure is more planktonically based and more complex and potentially determined by closer biotic interactions, as suggested by (Thorp and Casper 2003). An outline of this conceptual model is shown in Figure 9.

Patch availability and food web complexity will vary spatially and temporally due to flow variability, specific life-history strategies of the biota, and seasonal variations in the inputs of organic matter (Herwig et al. 2004; Robinson et al. 2002). Utilization of slackwaters by fish and their larvae is expected to be most intense over the spring-summer period as biological activity increases and slackwater utilisation reaches a maximum by species requiring these habitats as rearing habitats for young (Humphries et al. 1999, Richardson et al. 2004). While our study has only provided a snap shot of the potential food web structure of the patches, our data suggests a significant effect of flow

on food web complexity and community structure.

The hydraulic nature of patches appears to determine the biotic patterns observed and would appear to fit within the hydrogeomorphic patch and functional process zone model described by Thorp et al. (in press). Thorp et al. (in press) provide a model which portrays a river network as a mosaic of hydrogeomorphic patches rather than continuous gradient of physical and biological conditions. Within these hydrogeomorphic patches, unique functional zones develop due to the provision of unique resources and habitats Thorp et al. (in press). Our results appear to fit within this hierarchical patch dynamics model and would appear to be a valuable means of investigating patterns and processes in the riverine landscape. An understanding of the spatial and temporal variability of patch development and function and the role in food web dynamics is essential for both the ecological understanding of river systems and for the appropriate management to ensure the integrity of the river ecosystem is maintained.

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Table 1. ANOSIM results of biotic community structure analysis.

Comparison	R	Sig. level %
CF vs CS	0.465	0.4
CF vs NF	0.036	30.6
CF vs NS	0.769	0.1
CS vs NF	0.285	2.7
CS vs NS	0.031	31.3
NF vs NS	0.664	0.2
Global	0.389	0.1

Table 2. Simper analysis indicating taxa contributing most to the difference between patch types and taxa characterizing each of the patch types.

Flow vs Slackwater	Flow	Slackwater
Caridina (S)	Chironominae	Chironominae
Paratya (S)	*Ecnomus*	*Paratya*
Macrothrix (S)	Orthocladinae	Tanypodinae
Carp gudgeon (S)	Tanypodinae	Ostracoda
Shrimp larvae (S)	Baetidae	*Macrothrix*
Neothrix (S)	Caenidae	*Ecnomus*
Illyocryptus (S)	Oligochaeta	*Illyocryptus*
Ecnomus (F)		

Table 3. Mean and S.E. (n = 4) of abiotic variables.

Treatment	Mean se	NH3 µgN/L	NOX µgN/L	TN µgN/L	FRP µgP/L	TP µgP/L	DOC µgC/L	Av.Depth (cm)	Flow m/s	pH	Cond $mScm^{-1}$	NTU	DO mg/L	Temp
CF	x	12.4	29.5	604.0	20.5	77.5	5246.0	37.5	0.21	6.8	0.1	19.7	5.6	20.4
	se	4.9	9.4	15.4	0.9	2.4	390.3	2.5	0.02	0.2	0.0	5.2	1.2	0.9
CS	x	14.2	25.1	588.3	20.1	76.9	5441.3	29.9	0.01	6.8	0.1	29.2	5.7	21.2
	se	5.9	8.3	18.2	2.7	4.2	341.8	1.2	0.01	0.2	0.0	9.2	1.2	0.6
NF	x	13.6	28.1	602.3	20.5	76.3	5060.0	40.4	0.22	6.8	0.1	22.0	5.7	21.1
	se	6.2	8.5	8.7	1.0	2.1	262.7	3.3	0.01	0.2	0.0	4.7	1.2	0.5
NS	x	14.7	27.8	586.7	18.3	68.4	5808.0	36.8	0.01	7.0	0.1	21.5	5.6	21.2
	se	6.9	9.7	14.3	1.2	8.5	662.5	2.4	0.01	0.2	0.0	6.1	1.1	0.6

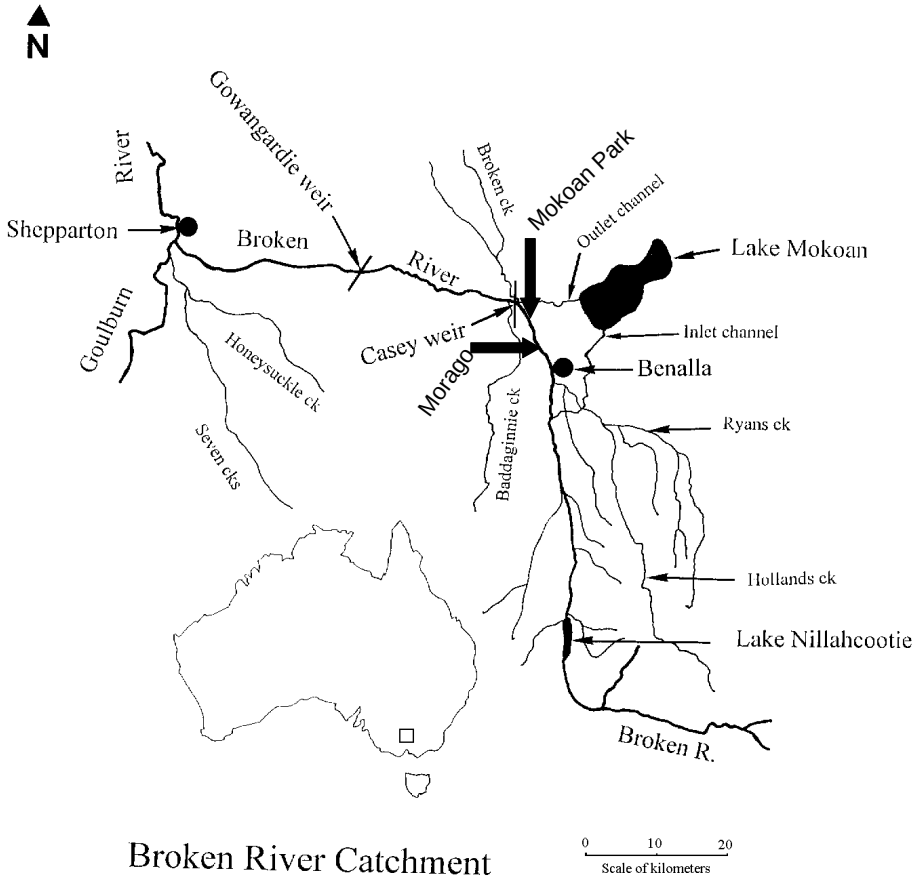

Figure 1. Broken River Catchment indicating sampling sites, Mokoan Park and Morago.

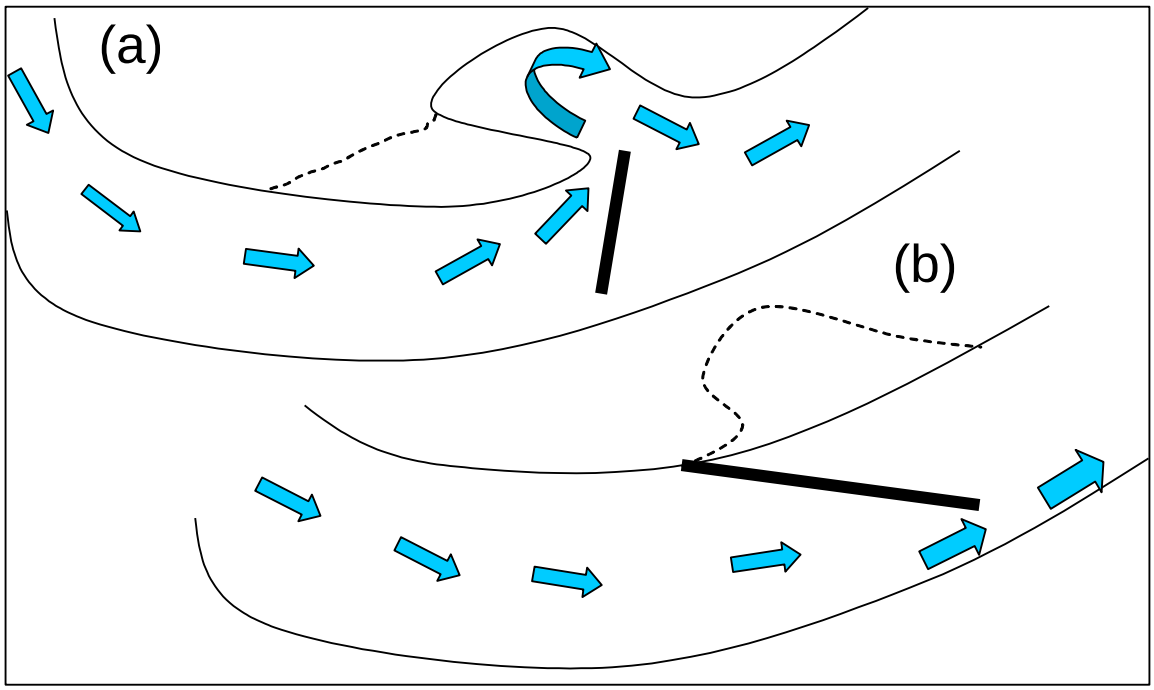

Figure 2: Diagrammatic representation of (a) ‘created flow’ habitat and (b) ‘created slackwater” habitat using sandbag walls.

Figure 3. Platform sampler for snag segments.

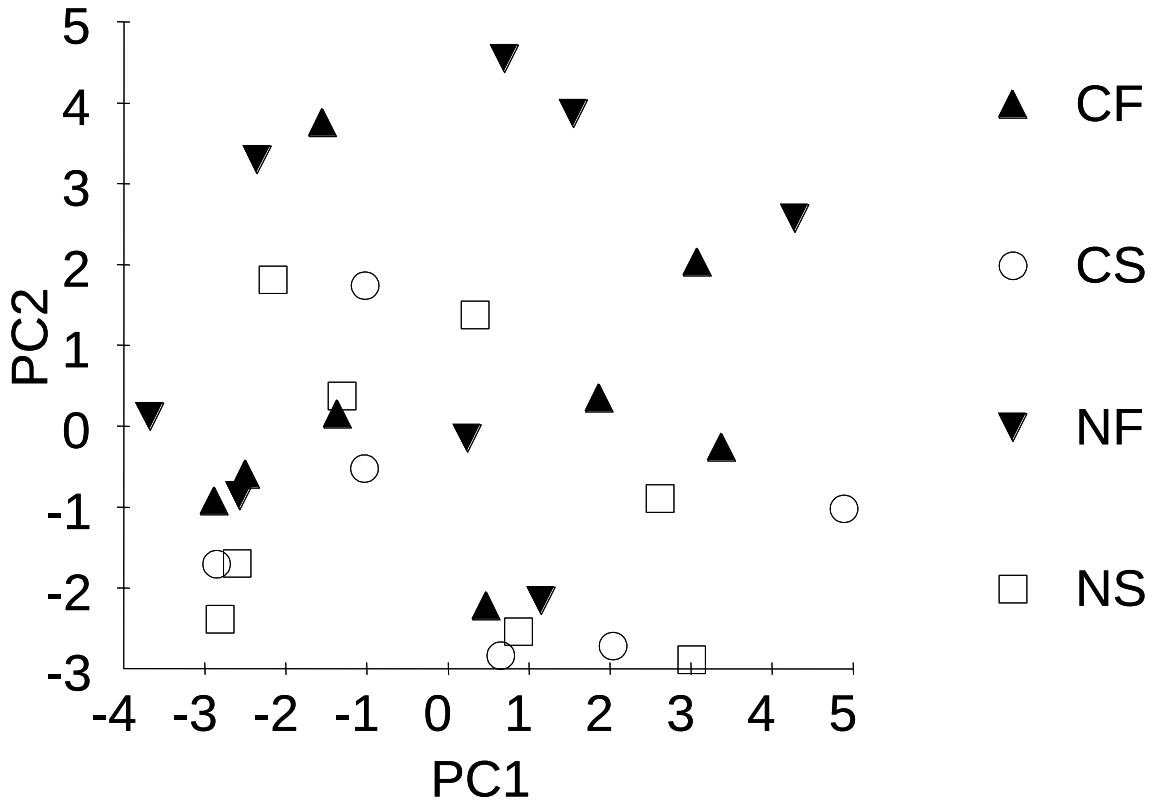

Figure 4. PCA of the physico-chemical, nutrient, production, respiration and habitat variables.

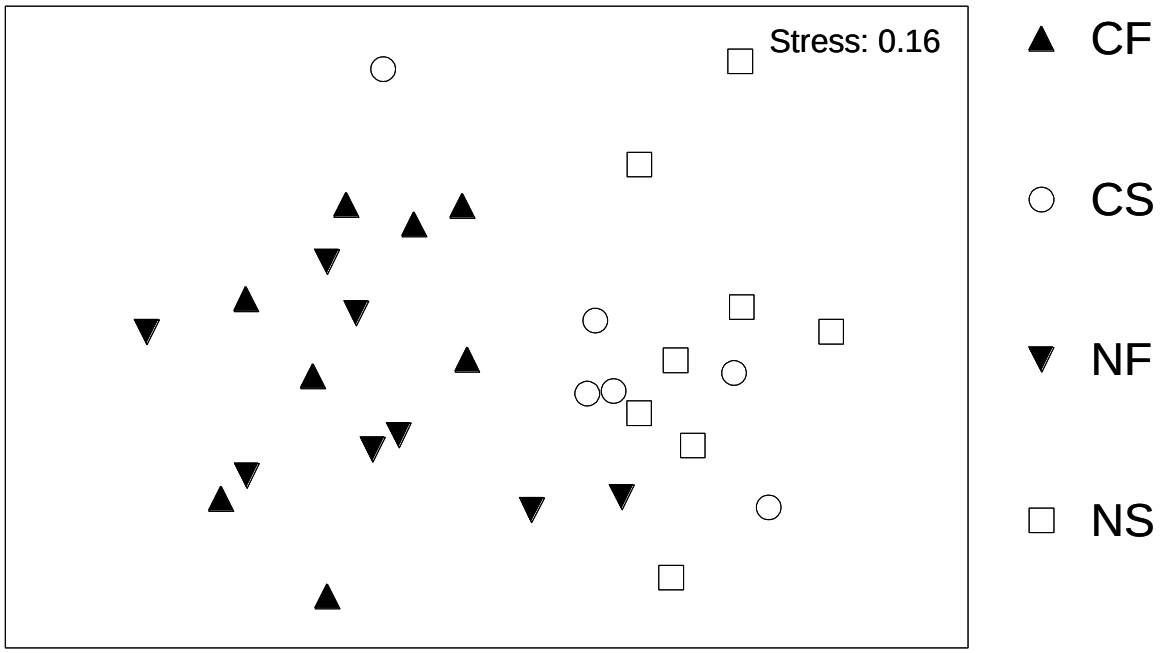

Figure 5. MDS ordination of biotic community structure.

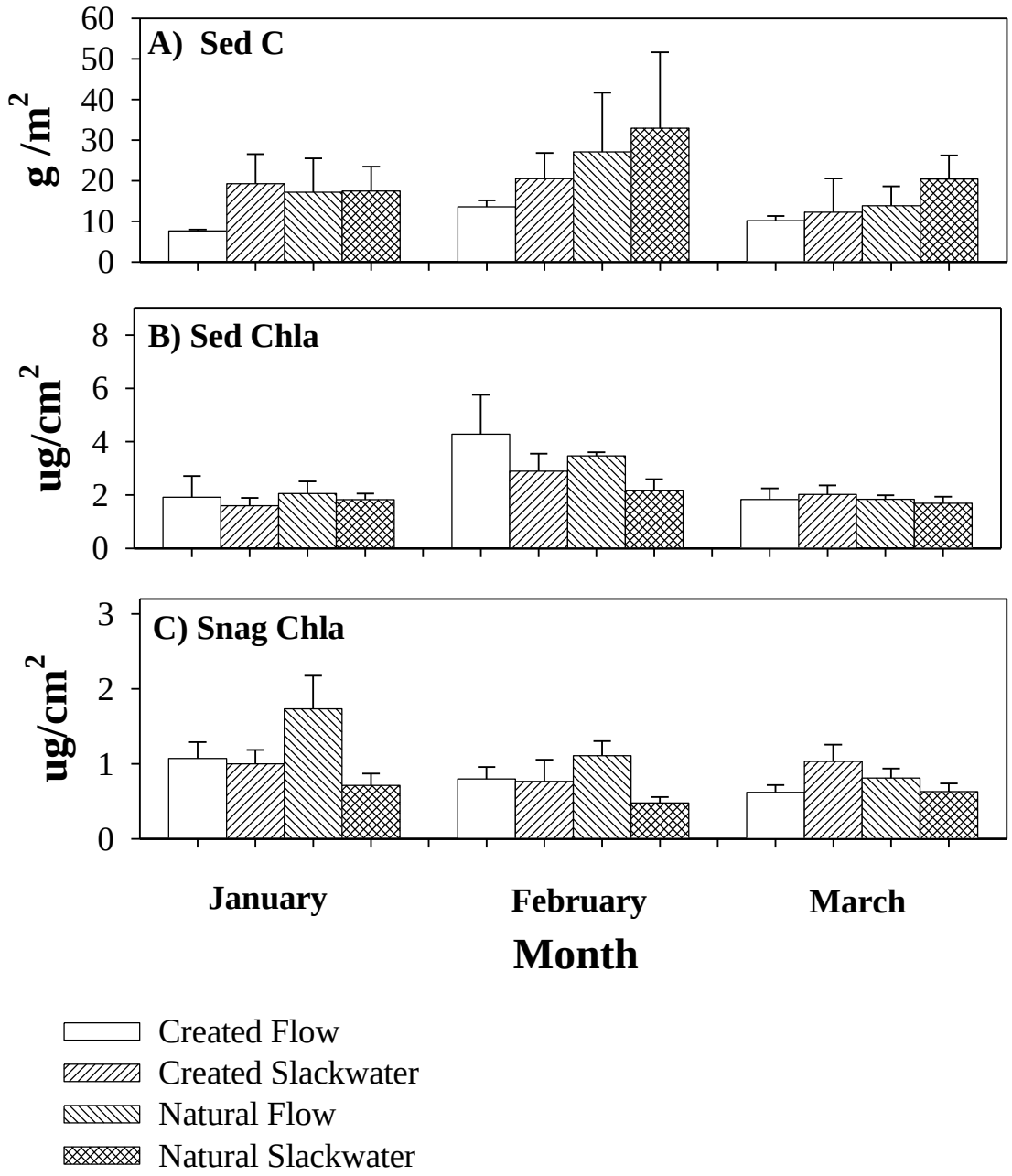

Figure 6. Sediment carbon content and sediment and snag chlorophyll *a* content.

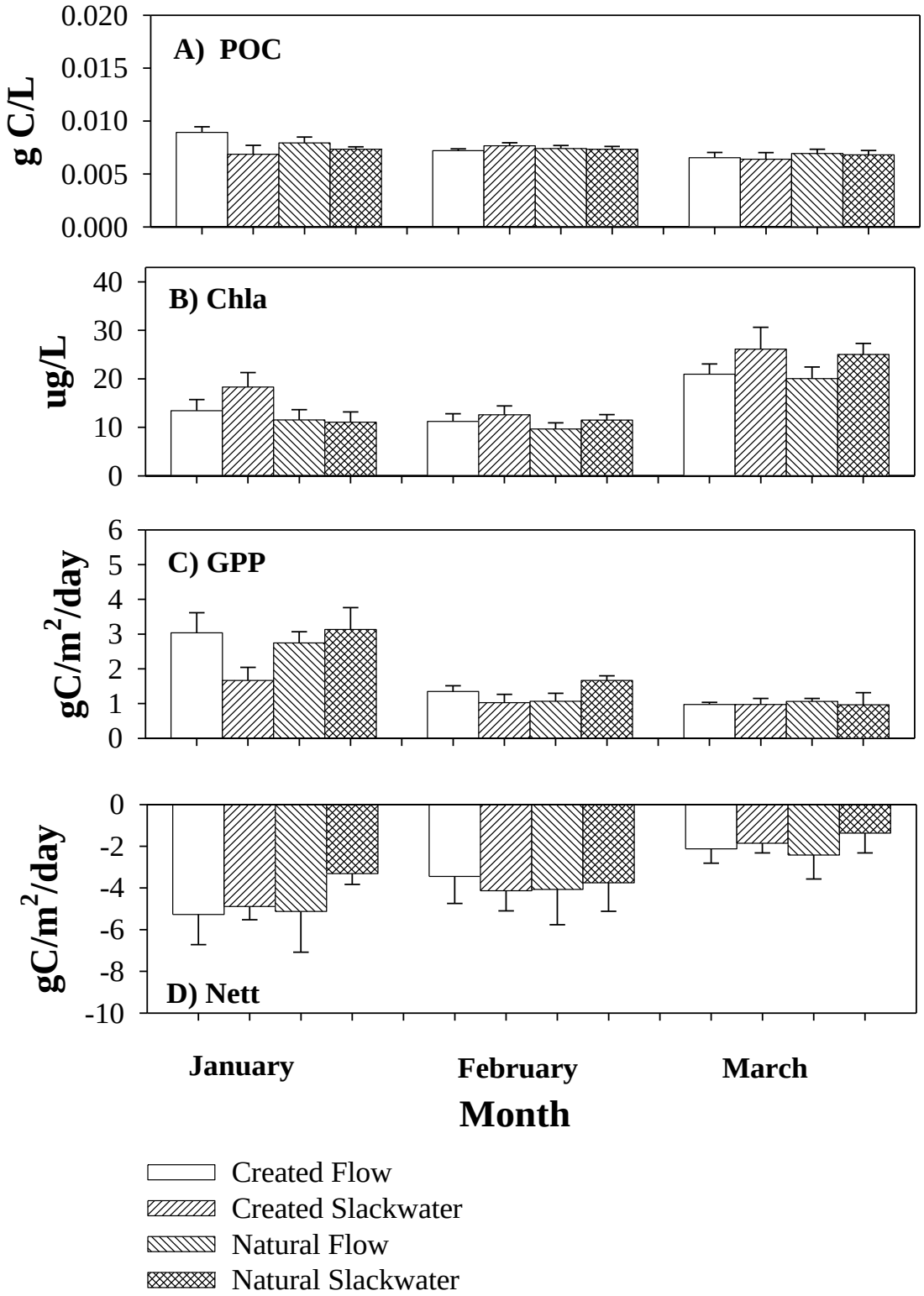

Figure 7. Particulate organic carbon (POC), chlorophyll a (Chla), gross primary production (GPP) and Nett primary production (NPP) for open water.

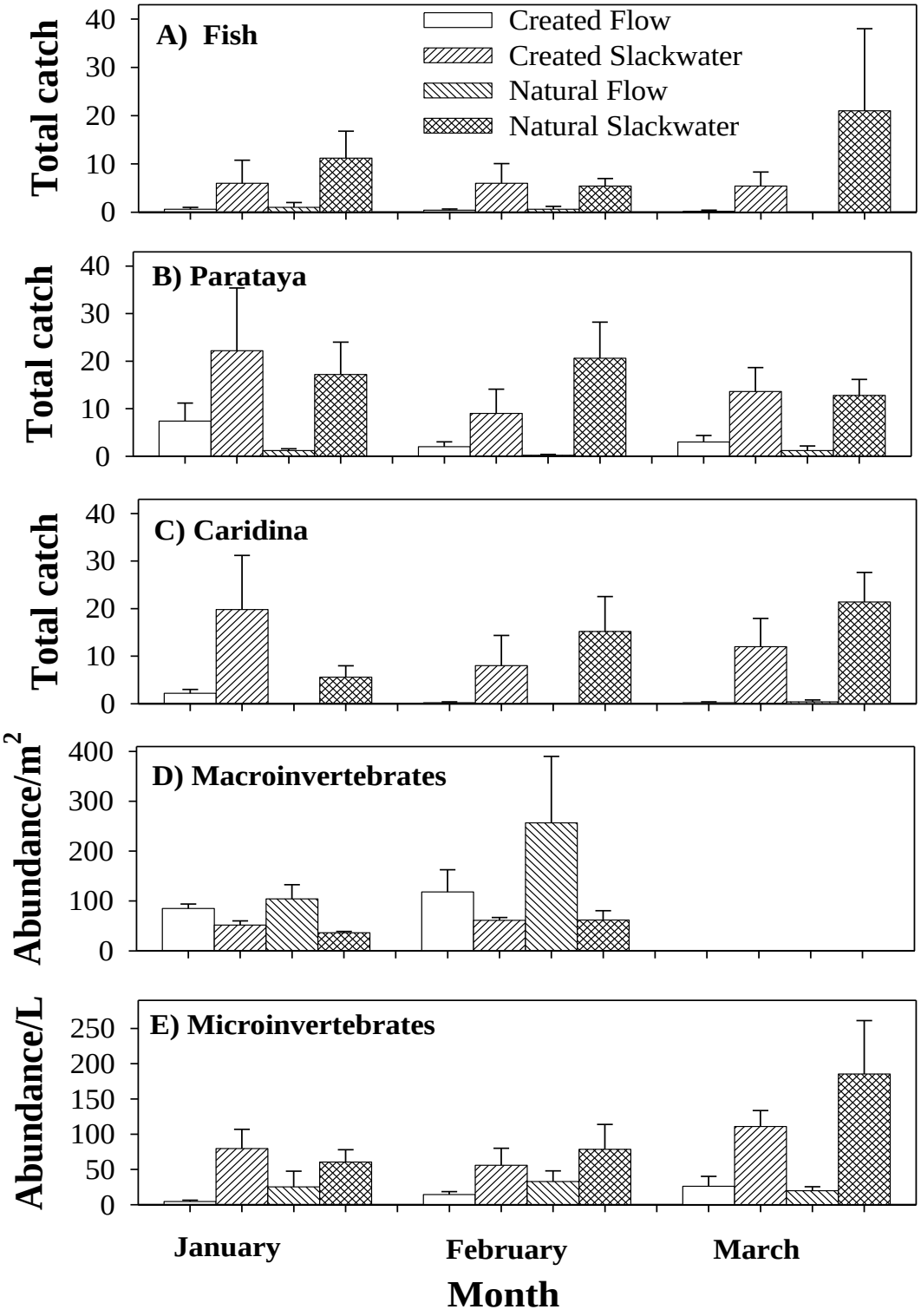

Figure 8. Fish, shrimp (*Parataya* and *Caridina*), macroinvertebrate and microinvertebrate data.

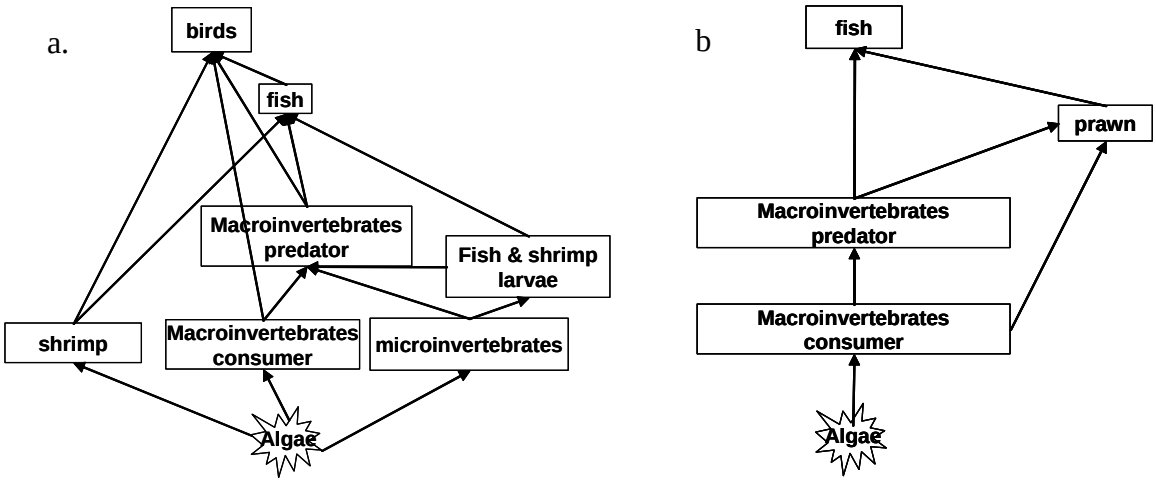

Figure 9. Proposed food web structure in a) slackwater patches and b) flowing patches.