

USING MACROINVERTEBRATE COMMUNITIES TO ASCERTAIN THE EFFECTS OF LAND USE IN TWO NORTHEAST GEORGIA STREAMS

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REFERENCE: *Proceedings of the 2007 Georgia Water Resources Conference*, held March 27–29, 2007, at the University of Georgia.

Abstract. The Soque River is listed under the Clean Water Act as an impaired waterway, yet there have been no finalized studies to date characterizing the impact of such impairments on the biological communities within the Soque. This study compared aquatic macroinvertebrate communities between Camp Creek (CC), an “impaired” tributary within the Soque River watershed, and the Middle Fork of the Broad River (MFBR), a “reference” stream in national forest lands. We hypothesized that CC would exhibit an altered community composition consistent with a disturbed watershed as compared to MFBR, which is not developed. Three replicate samples, including aquatic macroinvertebrates, substrate, and standard water chemistry parameters, were collected at each site using the EPA’s Rapid Bioassessment Protocol. Results showed that CC contained significantly more silt and clay and lower dissolved oxygen than MFBR. With respect to macroinvertebrates, CC contained significantly greater numbers of tolerant families and significantly fewer intolerant families. This supported the hypothesis that CC would exhibit community characteristics associated with disturbance. Additionally, we compared our methodology to conventional screening methods in the same ecoregion. The comparison of the two methods suggests that our methodology provides equivalent information regarding stream condition without the need to key to genus or species taxonomic levels and simultaneously allows for quantitative statistical analysis of the data.

INTRODUCTION

The Soque River and its watershed are located entirely within Habersham County in Northeast Georgia. This river and its tributaries supply the drinking water for many rural municipalities in the County and provide an important recreational resource. The Soque itself is a tributary of the Upper Chattahoochee River, and, as such, contributes significantly to the quantity of water in Lake Lanier, the primary water source for much of Metro-Atlanta. Meanwhile, Habersham County, like many counties in Northeast Georgia, continues to grow, placing additional demands on the Soque River. Yet, despite the importance of the Soque to Habersham County and locales

downstream, this river and its watershed have yet to be scientifically studied. Consequently, very little is known about the impacts of growth and the subsequent land use changes on this valuable resource.

Over the last 10 years, surveys of the Soque River have indicated that portions of the river and/or its tributaries contain excessive sediment and fecal coliform contamination. As a result, the Georgia Environmental Protection Division (GAEPD) placed the Soque on the §303(d) list for impaired waters (GAEPD, 2006). This action ultimately led to the formation of the Soque River Watershed Partnership and the securing of a Clean Water Act (CWA) §319(h) grant from USEPA to study the watershed and formulate a comprehensive watershed protection plan.

As part of this ongoing characterization project, we evaluated the ability to use aquatic benthic macroinvertebrate communities as indicators of land use impacts in Camp Creek, a tributary to the Soque. We chose macroinvertebrates because they are good indicators of localized conditions within a stream, and they integrate both short- and long-term environmental variations in streams through the nature of their complex life cycles that range from several months to several years (Southerland and Stribling, 1995). We hypothesized that Camp Creek, located in a very developed part of the Soque watershed, would be characterized by tolerant macroinvertebrate families as compared to our reference stream, the Middle Fork of the Broad River, which is located in National Forest lands.

METHODS

Sampling Sites

Both streams in this study, the Middle Fork of the Broad River (MFBR) and Camp Creek (CC), are third order streams located in the Southern Inner Piedmont subcoregion (Figure 1). The drainage areas for both sites were similar (18,631,510 m² for MFBR; 14,434,482 m² for CC), as was the gradient for the sampled catchments (290 m for MFBR; 200 m for CC). According to satellite imagery compiled by the US Forest Service, the MFBR watershed is approximately 86% forested with 6% of land area designated urbanized or for transportation.

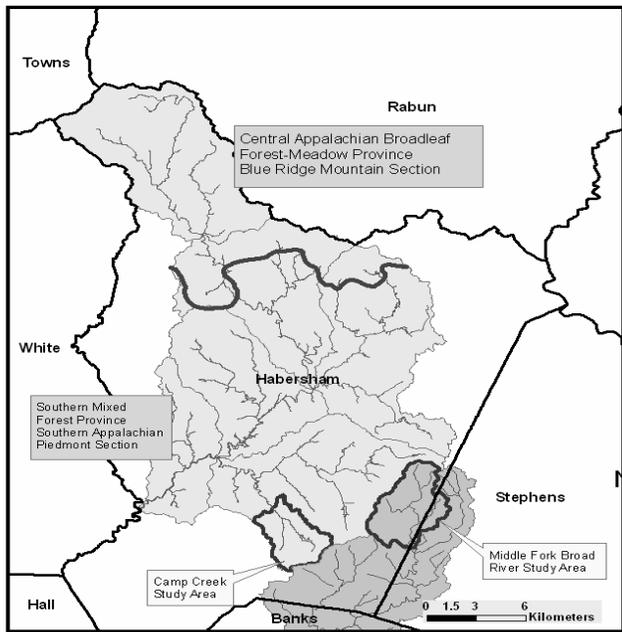


Figure 1: Sampling sites in the Camp Creek and Middle Fork of the Broad River watersheds.

Contrastingly, CC is approximately 38% forested with 37% of land area designated urbanized or for transportation (NARSAL, 2001).

Field Sampling

Three consecutive 100 m stretches (replicates) were sampled along each stream ($n=3$). For MFBR, this began at 34.52921° N and 83.43593° W and ended at 35.453097° N and 83.43807° W. For CC, sampling began at 34.55272° N and 83.53045° W and ended at 34.55098° N and 83.52938° W. All sampling was conducted in late August 2005 and according to the EPA Rapid Bioassessment Protocol for each replicate at each site (Barbour et al., 1999; GAEPD, 1999), Macroinvertebrate samples were collected using D-frame nets, and water chemistry parameters were collected with a YSI 6920 Multiprobe Sonde (YSI, Yellow Springs, Ohio). Substrate data were collected using a modified Webblemen Pebble Count per Harrelson, Rawlins, and Potyondy (1994). Biological samples were labeled and preserved in the field with ethanol.

Sample Processing

Preserved samples were returned to the laboratory for subsampling per the methods described by Caton (1991). Macroinvertebrates were identified to the family level using Merritt and Cummin's *Introduction to Aquatic Insects of North America* (1996) and Brigham, Brigham, and Gnilka's *Aquatic Insects and Oligochaetes of North and South Carolina* (1982). The specific taxa and number of

individuals found in each sample were recorded. Classified individuals were placed in glass vials containing ethanol preservative.

Statistical Analysis

For most comparisons, the mean simple abundance values for each site (MFBR or CC) were utilized at either the order or family taxonomic level. The composite EPT taxa variable was calculated for each replicate as the total number of individuals present in the insect orders Ephemeroptera, Plecoptera, and Trichoptera, and a mean for each site was computed. The Hilsenhoff Biotic Index (HBI; Hilsenhoff, 1987) was calculated for each replicate using family tolerance values per Gibson et al. (1996). For this index, values range from 0 to 10, with higher values indicating the presence of tolerant taxa (relative impairment). Similarly, the Hughes/Williams index was calculated per Hughes (2005) and Williams (2004). For this index, a lower score is indicative of impairment. For both indices, mean values were compared between sites.

All statistical analyses were conducted with Stat View 5.0.1 (SAS, Cary, NC). One replicate for the MFBR had to be excluded from the analysis because it did not meet the a priori criterion of containing at least 160 macroinvertebrates. Equality of variance and normality were evaluated for all variables prior to analysis. Parametric variables were then analyzed using two-tailed, unpaired t-tests. Nonparametric variables, including comparisons of index values, were analyzed using Mann-Whitney U analyses. In either instance, $\alpha = 0.05$.

RESULTS

With respect to physical-chemical parameters, CC had significantly greater specific conductance (CC $0.06 \pm 0.003 \mu\text{S}$; MFBR $0.032 \pm 0.0 \mu\text{S}$; $p=0.0014$) and lower dissolved oxygen (CC $8.01 \pm 0.13 \text{ mg/L}$; MFBR $8.82 \pm 0.134 \text{ mg/L}$; $p=0.0067$). Furthermore, substrate analysis indicated a significant increase in percent silt and clay in CC (CC 20.7 ± 2.3 ; MFBR 3.5 ± 3.5 ; $p=0.0066$).

With respect to macroinvertebrates, there were no differences in the number of individuals sampled, or in the number of orders and families present at each site (Table 1). The two sites did differ, however, in which orders and families were present. At the order level, CC samples contained significantly more dipterans (true flies), while MFBR samples contained significantly more plecopterans (stoneflies), coleopterans (beetles), megalopterans (dobsonflies), and ephemeropterans (mayflies) (Table 1). At the family level, samples from CC contained significantly more dipterans from the family Chironomidae, while samples from MFBR contained significantly more ephemeropterans from the family Ephemerillidae, plecopterans from the families Perlidae, Capniidae, and Peltoperlidae, and tricopterans (caddisflies) from the family Hydropsychidae

(Table 2). Comparison of the total number of Ephemeropteran, Plecopteran, and Tricopteran (EPT) individuals at each site further revealed that samples from MFBR contained significantly more EPT individuals than CC (Table 1).

Using the HBI index, CC exhibited a significantly higher index score as compared to MFBR (CC 5.5; MFBR 3.9; $p=0.0160$). Alternatively, using the Hughes/Williams Index, CC showed a significantly lower index value as compared to MFBR (CC 24.0; MFBR 57.0; $p=0.0124$).

DISCUSSION

The two study sites are within the Southern Inner Piedmont subcoregion and of comparable stream order, gradient, and drainage area. Consequently, their macroinvertebrate communities should be similar (USDA Forest Service, 1993). However, our results clearly demonstrate that these two streams are not biologically comparable. We postulate that the differences are directly attributable to differences in land use between the two watersheds.

Several lines of evidence support this conclusion. Firstly, the physical and chemical parameters strongly suggest an impact of development along CC in terms of increased sedimentation (siltation) and lowered dissolved oxygen levels (e.g., loss of riffles, etc.). The satellite imagery data further support these findings in that the CC watershed lacks significant forest cover, a characteristic that is widely known to increase the risk of sedimentation in streams.

Secondly, these conditions of increased sedimentation and lowered dissolved oxygen levels tend to favor more tolerant taxa, such as the dipterans (Barbour et al., 1995; DeShon, 1995). This was clearly observed in the number of dipterans, especially chironomids, present in CC as compared to MFBR.

Thirdly, the two sites did not differ in the overall number of orders or families present (overall richness), but they most certainly did differ in terms of the number of individuals present in these orders and families (abundance). Moreover, the differences observed were only present in families known to be good indicators of water quality (Barbour et al., 1999). Without exception, CC samples contained more individuals from tolerant families, such as the chironomids, while MFBR samples contained significantly more individuals from the intolerant EPT families.

Lastly, the two biotic indices used also indicated that CC was impaired as compared to MFBR. All of this data strongly points to an impact of land use on the macroinvertebrate communities of Camp Creek.

Interestingly, our methodology for evaluating these two streams is somewhat unusual. We used replicate sampling locations and keyed organisms to the family level. Conventional screening methods used today typi-

Table 1. Macroinvertebrate Results – Orders

Measured Variable	Mean	SD	p-value
<i>Total Individuals in Sample</i>			
CC	235.7	4.9	0.0833
MFBR	209.5	7.8	
<i>Total Orders Present</i>			
CC	6.7	0.6	0.2394
MFBR	7.5	0.7	
<i>Total Families Present</i>			
CC	14.0	3.5	0.1040
MFBR	20.5	2.1	
<i>Total Diptera</i>			
CC	209.7	15.2	0.0247
MFBR	97.5	45.9	
<i>Total Ephemeroptera</i>			
CC	4.7	1.3	0.0361
MFBR	22.5	9.2	
<i>Total Plecoptera</i>			
CC	2.0	2.6	0.0178
MFBR	42.0	15.6	
<i>Total Megaloptera</i>			
CC	0.0	0.0	0.0068
MFBR	2.5	0.7	
<i>Total Coleoptera</i>			
CC	3.7	0.6	0.0052
MFBR	10.0	1.4	
<i>EPT Composite Total</i>			
CC	16.0	5.3	0.0458
MFBR	94.5	44.5	

cally sample only one location on each stream (no replication) but do require that organisms be keyed to the genus or species level. The data are then used to calculate one or more biotic indices which are used to semi-quantitatively compare sites. However, because there is no replication, statistical analysis is virtually impossible.

In this study, our sampling regime was more labor intensive than conventional methods (we took replicate samples), but the time required to key out the macroinvertebrates was greatly reduced, likely more than compensating for the time required to collect the samples. Importantly, our methodology provided equivalent information regarding stream condition without the need to key-

Table 2. Macroinvertebrate Results – Families

Measured Variable	Mean	SD	p-value
<i>Total Chironomidae</i>			
CC	165.7	7.1	0.0068
MFBR	69.0	25.5	
<i>Total Ephemerillidae</i>			
CC	1.0	1.0	0.0017
MFBR	9.0	0.0	
<i>Total Perlidae</i>			
CC	0.7	0.6	0.0311
MFBR	16.5	7.8	
<i>Total Capniidae</i>			
CC	1.3	2.3	0.0151
MFBR	22.0	7.1	
<i>Total Peltoperlidae</i>			
CC	0.0	0.0	0.0068
MFBR	2.5	0.7	
<i>Total Hydropsychidae</i>			
CC	9.0	1.7	0.0123
MFBR	16.0	0.0	

nus or species taxonomic levels and simultaneously allowed for quantitative statistical analysis of the data. This suggests that our more analytically robust methods may be a suitable alternative to the screening methods used today, while providing the added benefit of statistically supported conclusions.

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