

## LONGITUDINAL STUDY OF WARM SPRING (PENNSYLVANIA)

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### ABSTRACT

The purpose of this study was to determine if macroinvertebrate-family dominance shifts along the length of a circumneutral springbrook emanating from Warm Spring (Huntingdon, Pennsylvania). Three samples of macroinvertebrates were taken at each of four sites located at ~150 m intervals. Width, depth, temperature, pH, substrate composition, amount and type of aquatic vegetation, and surrounding physical characteristics were recorded at each site. Significant differences in macroinvertebrate dominance were observed among sites and related to various longitudinal environmental changes.

*Keywords: Biomonitoring, longitudinal progression, macroinvertebrate diversity, River Continuum Theory, Warm Spring.*

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### INTRODUCTION

Biomonitoring is becoming increasingly important because of increasing human impact on the environment. Biomonitoring uses biological indicators, such as macroinvertebrate diversity and composition, to estimate ecosystem health. However, the comparability of such indicators depends on how broadly an ecosystem is defined. This problem of scale is especially important for biomonitoring done in streams, which vary environmentally along their lengths.

According to the River Continuum Concept, a river, from headwaters to ocean, can be thought of as a single ecosystem with a continuum of biotic and abiotic factors, instead of several successive ecosystems (Vannote *et al.*, 1980; Minshall *et al.* 1983). The River Continuum Concept predicts that various functional (feeding) guilds of macroinvertebrates should vary in species richness and relative abundance along the length of a river, due to changes in food type and availability, amount of sunlight, water depth and velocity, and streamside vegetation, bank type and erosion. In general, shredders dominate in headwaters and in shaded regions, scrapers are most abundant in intermediate sized sections of rivers, and collectors increase in diversity with downstream distance, whereas predators are evenly distributed along the length of river (Vannote *et al.*, 1980; Hawkins and Sedell, 1981).

Therefore, we tested the hypothesis that, along the length of a springbrook from headwaters to mouth, there should be a shift in macroinvertebrate diversity and family dominance accompanying parallel changes in environmental conditions. We employed longitudinal progression analysis, which is the process of sampling both biotic and abiotic factors along the length of a relatively narrow moving body of water (e.g., stream or springbrook). Identifying such longitudinal changes is important, as it would show that stream location must be controlled when using biomonitoring to compare the health of different streams.

## FIELD SITE

Warm Spring is located adjacent to Cold Spring Road in Huntingdon, Pennsylvania. This springbrook is approximately 600 m long and flows into Standing Stone Creek. Surrounding vegetation includes mosses, sedges, skunk cabbage, shrubs, and various evergreen and deciduous trees. The pH of the spring is ~7.0, ranging from 6.8 to 7.2. Water temperature is relatively constant at the headwaters and fluctuates increasingly with distance downstream. In addition, with progression downstream, water depth increased, width narrowed, and flow rate decreased. Pictures of the 12 sample sites are available on request.

## METHODS AND MATERIALS

A D-frame kick-net was used to collect macroinvertebrate samples, which were transported in Ziploc bags, and stored in a cold room until analysis. A week before sampling, pH was measured, using Markson field pH meters. At this time, Brannon max-min thermometers were also put in place at each sampling site and read at the time of sampling (except for the thermometer at site D, which because of a mishap was read a week after sampling). Depth, width, and flow measurements were made the week after sampling. Water-flow rate was estimated using an orange bobber and a meter stick. It rained a few days before these measurements were made, but environmental conditions appeared to remain constant.

We divided the springbrook into four 150-m sections, A, B, C, and D - beginning at the mouth with A, and concluding at the headwaters with D. Beginning our sampling at the mouth minimized disturbance at successive sampling sites. Springbrook length was estimated using Elaine Kneller's pace (~1.5 m per stride).

The amount of time spent sampling at each site was adjusted to substrate type (i.e. sand, silt, gravel, and vegetation) using PASS (Pennsylvania Assessment Scoring System). At each site, three samples were taken across the width of the spring. We sampled in this manner in order to identify potential variation in horizontal, as well as vertical, spring conditions and macroinvertebrate diversity.

Macroinvertebrates were extracted from associated sediment by sieving and dilution. Based on alive or preserved specimens, families were identified by sight or with the help of identification keys.

## RESULTS

Tables 1-4 list the number of individuals collected per macroinvertebrate family in each of three samples at each sample site from mouth (A) to headwaters (D). Each table also includes the family richness, Simpson's diversity index, and family equitability for each sample site. Family richness and diversity was highest near the headwaters and next highest at site B. Family equitability varied erratically along the length of the springbrook. Amphipods were the most common macroinvertebrate at all collecting sites. Amphipods and Trichoptera were evenly distributed among all sites, whereas bivalves were most common in the silty and muddy downstream sites, and triclad flatworms, chironomid larvae, and hydropsychid caddis larvae were most abundant in the headwaters, where the substrate was coarser (including gravel and cobbles) (see also Tables 6-12). The greatest number of families of Trichoptera occurred at intermediate site B.

*Table 1. Number of individuals found per macroinvertebrate family in each of three samples collected at Sample Site A. The mean relative abundance ( $P_i$ ) of each family, and the species richness, Simpson's diversity index, and species equitability index at this site are also shown.*

Warm Spring- 4th quarter	A1	A2	A3	Total		Pi	Pi <sup>2</sup>
Amphipoda Gammaridae	17	91	195	303		0.7870	0.6194
Annelida Oligochaeta	4	0	6	10		0.0260	0.0007
Bivalvia Corbiculidae	2	3	19	24		0.0623	0.0039

Diptera Chironomidae	1	3	5	9		0.0234	0.0005
Diptera Chironomidae (pupae)	1	1	0	2		0.0052	0.00003
Diptera Tipulidae	0	3	3	6		0.0052	0.00003
Ephemeroptera Ephemeridae	7	4	6	17		0.0442	0.0019
Megaloptera Sialidae	1	0	2	3		0.0078	0.0001
Odonata Aeshnidae	1	1	0	2		0.0052	0.00003
Odonata Corydulegastridae	1	0	0	1		0.0026	0.00001
Trichoptera Hydropsychidae	2	1	0	3		0.0078	0.0001
Trichoptera Rhyacophilidae	4	1	0	5		0.0130	0.0002
Total organisms	37	108	236	385		0.9896	0.6268
FAMILY RICHNESS						S =	12
SIMPSON'S DIVERSITY						D =	1.595
EQUITABILITY						E =	0.133

Table 2. Number of individuals found per macroinvertebrate family in each of three samples collected at Sample Site B. The mean relative abundance ( $P_i$ ) of each family, and the species richness, Simpson's diversity index, and species equitability index at this site are also shown.

Warm Spring- 3rd quarter	B1	B2	B3	Total		Pi	Pi <sup>2</sup>
Amphipoda Gammaridae	55	26	50	131		0.6453	0.4164
Annelida Oligochaeta	4	2	21	27		0.1330	0.0177
Bivalvia Corbiculidae	4	7	2	13		0.0640	0.0041
Diptera Chironomidae	1	2	3	6		0.0296	0.0009
Ephemeroptera Ephemeridae	1	0	0	1		0.0049	0.00002
Megaloptera Sialidae	2	0	0	2		0.0099	0.0001
Odonata Corydulegastridae	0	4	0	4		0.0197	0.0004
Turbellaria Tricladida	3	0	0	3		0.0148	0.0002
Trichoptera Hydropsychidae	2	1	0	3		0.0148	0.0002
Trichoptera Limnephilidae	0	3	1	4		0.0197	0.0004
Trichoptera Phryganeidae	3	1	1	5		0.0246	0.0006
Trichoptera Rhyacophilidae	0	4	0	4		0.0197	0.0004
Total organisms	75	50	78	203		1.0000	0.4414
FAMILY RICHNESS						S =	12
SIMPSON'S DIVERSITY						D =	2.2654
EQUITABILITY						E =	0.1888

Table 3. Number of individuals found per macroinvertebrate family in each of three samples collected at Sample Site C. The mean relative abundance ( $P_i$ ) of each family, and the species richness, Simpson's diversity index, and species equitability index at this site are also shown.

Warm Spring- 2nd quarter	C1	C2	C3	Total		Pi	Pi <sup>2</sup>
Amphipoda Gammaridae	161	87	2	250		0.7184	0.5161
Annelida Oligochaeta	0	12	5	17		0.0489	0.0024
Bivalvia Corbiculidae	0	5	1	6		0.0172	0.0003

Decapoda Cambaridae	0	3	0	3	0.0086	0.0001
Diptera Chironomidae	3	2	1	6	0.0172	0.0003
Diptera Ptychopteridae	0	1	0	1	0.0029	0.00001
Gastropoda Physidae	14	0	2	16	0.0460	0.0021
Gastropoda Planorbidae	0	0	7	7	0.0201	0.0004
Lepidoptera Pyralidae	6	0	0	6	0.0172	0.0003
Megaloptera Sialidae	0	3	0	3	0.0086	0.0001
Odonata Calopterygidae	3	0	1	4	0.0115	0.0001
Odonata Corydulegastridae	2	4	1	7	0.0201	0.0004
Turbellaria Tricladida	7	3	0	10	0.0287	0.0008
Trichoptera Hydropsychidae	4	0	0	4	0.0115	0.0001
Trichoptera Limnephilidae	1	1	1	3	0.0086	0.0001
Trichoptera Phryganeidae	0	3	2	5	0.0144	0.0002
<b>Total organisms</b>	<b>201</b>	<b>124</b>	<b>23</b>	<b>348</b>	<b>1.0000</b>	<b>0.5238</b>
<b>FAMILY RICHNESS</b>					<b>S =</b>	<b>16</b>
<b>SIMPSON'S DIVERSITY</b>					<b>D =</b>	<b>1.9091</b>
<b>EQUITABILITY</b>					<b>E =</b>	<b>0.1193</b>

Table 4. Number of individuals found per macroinvertebrate family in each of three samples collected at Sample Site D. The mean relative abundance ( $P_i$ ) of each family, and the species richness, Simpson's diversity index, and species equitability index at this site are also shown.

Warm Spring- 1st quarter	D1	D2	D3	Total	Pi	Pi <sup>2</sup>
Amphipoda Gammaridae	147	152	114	413	0.5760	0.3318
Annelida Hirudinea	0	1	0	1	0.0014	0.000002
Annelida Oligochaeta	7	6	5	18	0.0251	0.0006
Coleoptera Elmidae	2	0	0	2	0.0028	0.000008
Decapoda Cambaridae	0	0	1	1	0.0014	0.000002
Diptera Chironomidae	50	1	4	55	0.0767	0.0059
Diptera Tipulidae	1	0	0	1	0.0014	0.000002
Gastropoda Physidae	1	0	0	1	0.0014	0.000002
Megaloptera Corydalidae (pupa/adult)	1	0	0	1	0.0014	0.000002
Megaloptera Sialidae	0	0	1	1	0.0014	0.000002
Odonata Calopterygidae	0	0	2	2	0.0028	0.000008
Odonata Cordulegastridae	0	0	1	1	0.0014	0.000002
Turbellaria Tricladida	114	12	18	144	0.2008	0.0403
Trichoptera Hydropsychidae	23	34	11	68	0.0948	0.0090
Trichoptera Limnephilidae	0	6	0	6	0.0084	0.0001
Trichoptera Rhyacophilidae	2	0	0	2	0.0028	0.000008
<b>Total organisms</b>	<b>348</b>	<b>212</b>	<b>157</b>	<b>717</b>	<b>1.0000</b>	<b>0.3877</b>
<b>FAMILY RICHNESS</b>					<b>S =</b>	<b>16</b>
<b>SIMPSON'S DIVERSITY</b>					<b>D =</b>	<b>2.5790</b>
<b>EQUITABILITY</b>					<b>E =</b>	<b>0.1612</b>

Table 5. Total number of individuals found per macroinvertebrate family at each of four sample sites located along the springbrook of Warm Spring. Italicized families showed significant differences in abundance among samples sites.

Totals	A	B	C	D	Total
<i>Amphipoda Gammaridae</i>	303	131	250	413	1097
Annelida Hirudinae	0	0	0	1	1
Annelida Oligochaeta	10	27	17	18	72
<i>Bivalvia Corbiculidae</i>	24	13	6	0	43
Coleoptera Elmidae	0	0	0	2	2
Decapoda Cambaridae	0	0	3	1	4
<i>Diptera Chironomidae</i>	11	6	6	55	78
Diptera Ptychopteridae	0	0	1	0	1
Diptera Tipulidae	6	0	0	1	7
Ephemeroptera Ephemeridae	17	1	0	0	18
Gastropoda Physidae	0	0	16	1	17
Gastropoda Planorbidae	0	0	7	0	7
Lepidoptera Pyralidae	0	0	6	0	6
Megaloptera Corydalidae (pupa/adult)	0	0	0	1	1
Megaloptera Sialidae	3	2	3	1	9
Odonata Aeshnidae	2	0	0	0	2
Odonata Calopterygidae	0	0	4	2	6
Odonata Corydulegastridae	1	4	7	1	13
<i>Turbellaria Tricladida</i>	0	3	10	144	157
<i>Trichoptera Hydropsychidae</i>	3	3	4	68	78
Trichoptera Limmophilidae	0	4	3	6	13
Trichoptera Phryganeidae	0	5	5	0	10
Trichoptera Rhyacophilidae	5	4	0	2	11
Total organisms	385	203	348	717	1653

A total of 23 families was found at all four sample sites (Table 5). Many families were not found at all four sample sites. For example, leeches (Hirudinae), elmid beetles, and corydalid larvae were only found in the headwaters. In contrast, aeshnid dragonfly larvae were only found at the mouth of the springbrook.

Total macroinvertebrate abundance varied significantly among sampling sites, the lowest numbers occurring at site B, and the highest numbers at the headwaters (site D) (Table 6). We also tested for inter-site differences in abundance for six families for which sufficient samples sizes were available (Tables 7-12). Five families, the Gammaridae, Chironomidae, Corbiculidae, Hydropsychidae, and Tricladida, showed significant inter-site differences in abundance, whereas one, the oligochaete worms, did not. All of these results must be interpreted cautiously because they lump counts from only three samples per site.

Table 6. Inter-site comparison of total numbers of macroinvertebrates.

A	B	C	D	Total	
385	203	348	717	1653	(Observed count)
413	413	413	414	1653	(Expected count)

$$\text{Chi-Sq} = 0.491 + 35.795 + 2.776 + 40.588 + 0.491 + 35.795 + 2.776 + 40.588 = 159.300$$

$df = 3; P < 0.001.$

*Table 7. Inter-site comparison of gammarid amphipod abundance.*

A	B	C	D	Total
303	131	250	413	1097 (Observed count)
274	274	274	275	1097 (Expected count)

$$\text{Chi-Sq} = 0.729 + 25.246 + 0.550 + 13.840 + 0.729 + 25.246 + 0.550 + 13.840 = 80.728$$

$$df = 3; P < 0.001$$

*Table 8. Inter-site comparison of oligochaete abundance.*

A	B	C	D	Total
10	27	17	18	72 (Observed count)
18	18	18	18	72 (Expected count)

$$\text{Chi-Sq} = 1.143 + 0.900 + 0.014 + 0.000 + 1.143 + 0.900 + 0.014 + 0.000 = 4.114$$

$$df = 3; P = 0.249$$

*Table 9. Inter-site comparison of corbiculid bivalve abundance.*

A	B	C	D	Total
24	13	6	0	43 (Observed count)
11	11	11	10	43 (Expected count)

$$\text{Chi-Sq} = 2.414 + 0.083 + 0.735 + 5.000 + 2.414 + 0.083 + 0.735 + 5.000 = 16.466$$

$$df = 3; P = 0.001$$

*Table 10. Inter-site comparison of chironomid abundance.*

A	B	C	D	Total
11	6	6	55	78 (Observed count)
20	19	19	20	78 (Expected count)

$$\text{Chi-Sq} = 1.306 + 3.380 + 3.380 + 8.167 + 1.306 + 3.380 + 3.380 + 8.167 = 32.466$$

$$df = 3; P = 0.000$$

*Table 11. Inter-site comparison of triclad flatworm abundance.*

A	B	C	D	Total
0	3	10	144	157 (Observed count)
39	39	39	40	157 (Expected count)

$$\text{Chi-Sq} = 19.500 + 15.429 + 8.582 + 29.391 + 19.500 + 15.429 + 8.582 + 29.391 = 145.803$$

$$df = 3; P < 0.001.$$

Table 12. Inter-site comparison of hydropsychid abundance.

A	B	C	D	Total
3	3	4	68	78 (Observed count)
19	19	20	20	78 (Expected count)

$Chi-Sq = 5.818 + 5.818 + 5.333 + 13.091 + 5.818 + 5.818 + 5.333 + 13.091 = 60.121$   
 $df = 3; P < 0.001.$

Table 13 shows the relative abundance of macroinvertebrates in each of four feeding guilds for each of the four sampling sites. These data are expressed as percentages in Fig. 1.

Table 12. Inter-site comparison of the relative abundance of macroinvertebrates in four functional (feeding) guilds.

	A	B	C	D
Predator	11	13	27	153
Shredder	309	140	264	420
Collector/Filterer	55	23	17	123
Scraper	10	27	40	19
Other	0	0	0	2

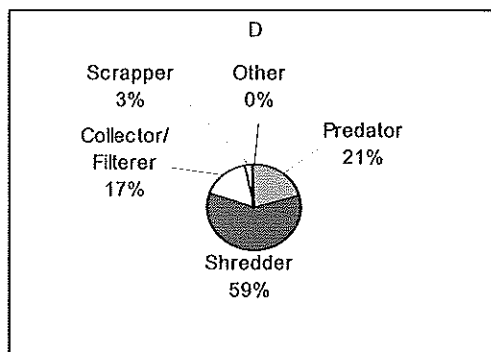
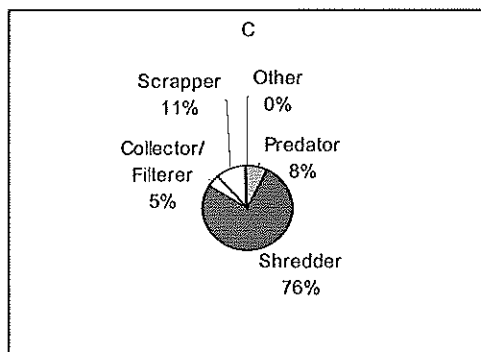
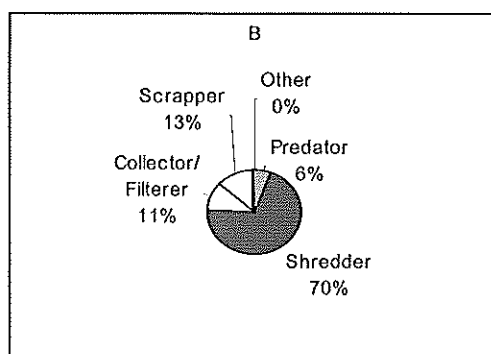
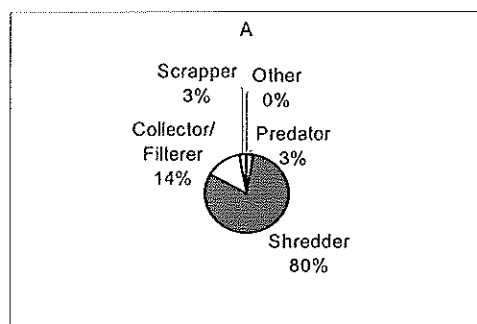


Figure 1. Pie charts showing the percentage of macroinvertebrate individuals in four functional feeding guilds at four sites along the springbrook of Warm Spring.

Shredders (mostly amphipods) were dominant (59-80%) at all sampling sites, but especially at the mouth of the springbrook (site A). The highest relative abundance of collectors (17%) and predators (21%) occurred at site C, which was muddy and well-vegetated.

An intersite comparison of the abiotic factors in Warm Spring (Table 13) revealed that the headwaters (D) site appeared to be most distinctive. The water depth and temperature range is lowest and the flow rate highest at site D. The pH is near neutral at all sites. Other abiotic factors, such as width, did not appear to vary systematically with downstream distance.

*Table 13. Inter-site comparison of various abiotic factors in Warm Spring.*

SITE	WIDTH (m)	DEPTH (m)	FLOW (m/s)	TEMP (°C)	pH
A	1.97	0.11	0.226	Min = 9 Max = 15	6.8
B	2.27	0.12	0.321	Min = 10 Max = 20	6.9
C	5.40	0.14	0.326	Min = 17 Max = 16	7.2
D	3.67	0.08	0.413	Min = 17 Max = 17	6.9

## DISCUSSION

A significant shift in family dominance occurred longitudinally in Warm Spring. Some of the changes in the relative abundance of specific families appeared to be related to longitudinal changes in substrate. Bivalves prefer silty substrates in which they can bury themselves and where they can find fine particulate organic matter to feed upon. Thus, it is not surprising that bivalves were most common at the mouth of the springbrook where it was relatively silty and muddy. In contrast, triclad flatworms prefer stony substrata, and thus are most common in the headwaters where gravel and cobbles are prevalent.

Family richness and diversity were highest in the headwaters and lowest at the mouth of the springbrook. Perhaps the reduced temperature fluctuations at the source of Warm Spring has favored the occurrence of more families of macroinvertebrates than at thermally more variable downstream sites. The thermal stability of the headwaters may also explain why total macroinvertebrate abundance was higher here than at downstream sites. Other factors that may be important in causing changes in macroinvertebrate diversity, composition and abundance along the length of Warm Spring are variation in width, flow rate and amounts of leaf litter and aquatic vegetation. For example, the highest family equitability and second highest family diversity were observed at site B, which had substantial amounts of leaf litter and other debris, major food sources for lotic macroinvertebrates.

This study suggests that longitudinal location should be taken into account when using macroinvertebrate diversity and composition in water-quality indicators in biomonitoring studies.

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