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Susquehanna River Heathland Coalition for Environmental Studies (SRHCES)

INTRODUCTION
H.W. “SKIP” WIEDER

FORWARD
A. LACHHAB AND C. A. IUDICA

SKIP WIEDER... THE ‘YES’ MAN
MARK LAWRENCE AND RENEE CAREY

MIDDLE CREEK WATER ASSESSMENT USING WATER QUALITY INDEX (WQI)
AHMED LACHHAB, MATTHEW BEREN, BRIAN ZUIDERVLIET

BIOMASS ACUMULATION OF METHYLMERCURY IN NEOVISON VISON (SCHREBER, 1777)
POPULATIONS OF THE SUSQUEHANNA RIVER VALLEY
MATTHEW R. BROWN AND CARLOS A. IUDICA

FACTORS INFLUENCING WALLEYE (SANDER VITREUS) YEAR CLASS STRENGTH IN THE UPPER SUSQUEHANNA RIVER
ROBERT T. WNUK

NATIVE AMERICANS IN THE SUSQUEHANNA RIVER VALLEY: AN ARCHAEOLOGICAL SUMMARY
DAVID J. MINDERHOUT

WATER QUALITY ASSESSMENT OF THE LOWER WEST BRANCH – SUSQUEHANNA RIVER:
FOCUS ON SEWAGE TREATMENT†
MELVIN C. ZIMMERMAN, LYNETTE DOOLEY

ASSESSMENT OF PASSIVE AND ACTIVE MACROINVERTEBRATE COLLECTION METHODS IN ADJACENT REACHES ON THE UPPER MAIN STEM OF THE SUSQUEHANNA RIVER
KATHERINE GUILD, ANDREW ANTHONY, MICHAEL BILGER, AND JACK HOLT

BIOASSESSMENT OF BENTHIC MACROINVERTEBRATES OF THE MIDDLE PENNS CREEK,
PENNSYLVANIA WATERSHED
JOHN PANAS, JONATHAN NILES, SAM SILKNETTER, MICHAEL BILGER

MUSSEL POPULATION AND DISTRIBUTION ON BUFFALO CREEK, AN AMERICAN EEL STOCKED TRIBUTARY TO THE WEST BRANCH SUSQUEHANNA RIVER
SEAN P. REESE, MICHAEL HUFFNER, JARED FEINDT

VARIABILITY IN MACROINVERTEBRATE COMMUNITIES OF THE SUSQUEHANNA RIVER IN CENTRAL PENNSYLVANIA

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CONTENTS
THE SUSQUEHANNA RIVER HEARTLAND COALITION FOR ENVIRONMENTAL STUDIES (SRHCES)

The Susquehanna River Heartland Coalition for Environmental Studies (SRHCES) is a unique partnership of six colleges and universities located along the Susquehanna River and provides a forum for research and education related to the River and its Watershed. Faculty and students from these institutions also collaborate with both public and private agencies and organizations to address related environmental and sustainability issues. This research and education also serves to increase public awareness of the value of this vital natural resource.

For over ten years, scientists from the SRHCES (Bloomsburg University, Bucknell University, King’s College, Lock Haven University, Lycoming College and Susquehanna University) have met monthly to discuss individual research projects, opportunities for collaborative projects, and to set future research priorities. Partnerships have also included other institutions of higher education. Over these ten years, more than 600 summer student internships have been sponsored by SRHCES and more than $2 million in summer projects funded. Much of this summer activity is then highlighted as part of the annual Susquehanna River Symposium held each fall at Bucknell University.

In 2013 the SRHCES joined the Conservation Catalyst Network, an international network formed to explore the unique role of colleges, universities and research institutions as catalysts for biodiversity conservation across large and complex landscapes. Membership has included opportunities for SRHCES collaboration and learning on both a national and international scale.

Opportunities now exist for the SRHCES and its new relationship with The Chesapeake Conservancy to expand its role and engage other partners for research and education within the Watershed. Through the work of the Conservancy, with significant involvement by the SRHCES, the Department of the Interior in 2011 designated the Susquehanna River as an extension of the Captain John Smith Chesapeake National Historic Trail. This national recognition has resulted in the launching of “Envision the Susquehanna,” an initiative that will engage even greater numbers of faculty and students, both within and outside the Watershed, in developing solutions for conserving the Susquehanna Watershed and its valuable resources.

By H.W. “Skip” Wieder
FORWARD

A. LACHHAB AND C. A. IUDICA

The decision to host the annual meeting of the Pennsylvania Academy of Science dates back to an encounter with Robert Coxe, the president of the Pennsylvania Academy of Science (PAS), during the annual meeting of 2012. We proposed Susquehanna University (SU) as the host for the 90th annual anniversary meeting for many reasons: Susquehanna faculty members and their students have been attending PAS for many years by large numbers and the geographical location of SU with the large number of universities and colleges located in its vicinity. Furthermore, many of those institutions are members of the Susquehanna River Heartland Coalition for Environmental Studies (SRHCES), which allows for a possible concurrent symposium on the upper main stem of the Susquehanna River and its tributaries, as well.

We both attended several follow-up board meetings after which Susquehanna University was approved to host the 2014 event. Without really knowing what it takes to host a regional meeting, we immediately accepted the challenge. The real excitement started as we began to prepare for this unique event. This meeting was a little challenging because it is quite different from the previous ones as it encompasses three main tasks namely the annual meeting, the symposium and the special issue for the Journal of the Pennsylvania Academy of Science (JPAS).

After SU showed support, we immediately started organizing and planning for the meeting. Subsequently, we shared our enthusiasm with Skip Wieder, the organizer of SRHCES and brought to his attention the idea of a symposium concurrent with the PAS annual meeting. He immediately embraced the idea of a symposium where affiliates of SRHCES could participate and present the latest Susquehanna River research and watershed-related issues. While we were organizing the meeting and the symposium, it became more and more obvious the crucial role Skip has played and continues to play in the efforts of SRHCES, not only in its everyday operation but also through his ability to connect with people and generate a unique synergy that motivates river and watershed scholarship, education, and action. Thus, we dedicate this special edition of JPAS to him.
Skip Wieder...The ‘Yes’ Man

Skip Wieder is a ‘yes man.’ That’s not to say he’ll easily acquiesce to any proposed idea or action, but rather, he is the man who—whether it’s fundraising, research, volunteering or advocacy, especially for widely accepted regional environmental and community goals—he can provide, or procure, or make plans for, the necessary ‘yes’ to make it happen. Maybe it was his hundreds of outings on streams, to fly fish, where Skip saw that our sense of place, the purity of water, and the conservation of the environment—all need to be ‘brought up issues,’ not just streamside, but in the offices, universities, hospitals, and in the public discourse. He already knew that education and action had to go hand-in-hand, whether it was a freshmen student taking their first water sample, or a local CEO making sure that a regional initiative was funded, whether it was a local doc wondering about common ailments or a mother concerned about the clear waters in which her child splashes. He understands the complex framework of physicians, researchers, parents, professors and students, corporation and charity, and theory and research/field experience, in which we can thrive to advance our work.

We dedicate this special edition of the Journal of the Pennsylvania Academy of Science to H.W. Wieder, the convener of the Susquehanna River Heartland Coalition for Environmental Studies and a friend of the Pennsylvania Academy of Sciences. This fly fisherman turned his love of peace and water, to political pushing, amplifying the giving voice to, and doubling the work of conservationists, hydrologists, Ecologists, and many others who love, and want to preserve our natural place. All the while, raising up young people, students, and interns, making sure activism has next chapter. Skip has both a BS and MBA from Bucknell University, has achieved the rank of Captain in the US Army, been a Senior Consultant and Senior Vice President at Geisinger Health System and a Vice President for Development and later a Treasure for Susquehanna University. He retired from those positions in 2008, after 24-years and is credited with leading the fundraising of more than $125 million dollars, to fund, furnish, and staff, facilities and programs now garnering global attention. Those results include the convening of the SRHCES and its dynamic research, educational and advocacy initiatives. In addition to all of the research and community partners in the coalition, Susquehanna University, Bucknell University, and Washington and Jefferson College can all join us in thanking Skip for his development efforts. WVIA, the local and regional United Ways and Degenstein Foundation have also enjoyed Skip’s leadership, insight and forward thinking. You’ll find Skip’s name on the boards and advisory councils of other champions our state and local water, land and air.

We thank his wife Linda, and daughters Lori and Lisa for loaning us the Skip they know as ‘husband’ and father. They call him family, and we’re proud to call him friend. (Lori or Lisa) says she has seen it first hand as she watched her father draw together several smaller United Way agencies, into a broader, more regional campaign. She says that larger group then met, and exceeded local expectations, “This is a good example of where dad saw the power of bring people together to work on common interests.” Economics PA recently honored Skip with the Adam Smith Leadership Award, and they said he is, “An extraordinary friend of infectious and unlimited enthusiasm who leads by example, inspires by his ‘can do’ attitude and always sees the glass as half full.” In a way, Skip’s has given us his…allowance. He gives individuals and entities with wealth a venue to allow their gifts and interests a place and personnel to carry out their vision. His work can allow scientists, professors, organizers, advocacy leaders and lay people a chance to gather, discuss, and turn their passions—into action; into monitored, peer reviewed and ‘deadline set’ urgency actions which are already benefiting our Susquehanna Valley. He allows our Valley’s interest in environmental conservation to focus on action, to see results and promote future betterment. Skip is a ‘yes man.’ He doesn’t always say it, but he knows who will. It’s no surprise, this dedication takes place as a surprise to Skip—he’s more focused on our success than he ever has been on his own accolades. Skip is a doer, a man of his word and a man who inspires. We thank him for that.

Rivers run through our history and folklore, and link us as a people. They nourish and refresh us and provide a home for dazzling varieties of fish and wildlife and trees and plants of every sort. We are a nation rich in rivers.

— (Charles Kuralt, On the Road With Charles Kuralt)

Written by: Mark Lawrence, Program Director, Newsradio 1070 WKOK
Reneé Carey, Program Director, North-central Pennsylvania Conservancy
MIDDLE CREEK WATER ASSESSMENT USING WATER QUALITY INDEX (WQI)†

AHMED LACHHAB¹, MATTHEW BEREN, BRIAN ZUIDERVLIET

Earth and Environmental Science Department, Susquehanna University, Selinsgrove, PA, 17870

ABSTRACT

Water quality Index (WQI) provides a single value to express overall quality of water which is calculated based on a number of measurable parameters. WQI was calculated based on 10 parameters that were determined during the period between June and July of 2012 and July of 2013 in an effort to assess the water quality of Middle Creek (MC) (Snyder, CO. PA). The Middle Creek (MC) is a 2nd order tributary stream flowing into Penn's Creek before joining the Susquehanna River. In this study, eleven sites were selected along MC between the head waters and its confluence with Penn's Creek. Physical properties were measured in the field, and grab-samples were tested for P, NO₂⁻, NO₃⁻, NH₃, biochemical oxygen demand (BOD), chemical oxygen demand (COD) and total suspended solids (TSS). The Composite WQI for all sites along MC was calculated to be 89.71, indicating that MC is in good condition regarding water quality and is capable of buffering nutrient and chemical runoff. Results have shown that certain parameters, such as temperature (T°), COD or BOD, can be used as proxies for predicting the WQI. Due to good correlation with WQI values, T°, COD or BOD can be used to assess water quality within a short period of time. In this study, T° and COD were found to give the best forecasting parameters, followed by BOD. The relationships found between WQI and these three parameters, allow for a simple test to provide an adequate assessment of the water quality of a given stream system. [ J PA Acad Sci 88(1): 4-12, 2014 ]

INTRODUCTION

The Middle Creek (MC) is located in Snyder County, Pennsylvania and is bordered by a large farmland region. Snyder County is comprised of 332 square miles and has a population of 39,702 (Figure 1). The headwater of this small stream starts as two separate branches, which merge and flow into Penn's Creek and eventually into Susquehanna River. It is recognized that high levels of pollution in the Susquehanna River and the Chesapeake Bay are caused by runoff from smaller upstream tributaries. Because it is difficult to tackle the cleanup of the water in The Susquehanna River and Chesapeake Bay, there is a need to address these issues at their sources. Runoff into Middle Creek comes mainly from agricultural non-point sources, such as animal facilities, grazing, pesticide spraying, plowing, planting, irrigation, fertilizing, and harvesting. The presence of non-point sources of pollution makes cleanup very challenging even towards the headwaters. In Snyder County, farmlands have been proven to be the cause of non-point source of pollution infiltrating into the MC via land runoff and improper drainage (Edwards and Seay 1987). In this study, a Water Quality Index along Middle Creek extension was calculated based on water quality analyses of all chemical and physical properties.

Water quality Index (WQI) is measured based on a number of parameters, which provides a single value that is used to express the overall quality of water. Each parameter is important in determining the Water Quality Index (WQI) of Middle Creek and its overall impact. While this is true, certain parameters tend to influence the water quality more significantly than others. A heavily weighted parameter with a small standard deviation will not have as drastic of an effect on the WQI as a lower weighted parameter with a high standard deviation. The WQI is a mathematical equation that combines many water parameters into a single number to represent the water quality of a body of water. The use of WQI is a simple practice, which allows adequate classification of water quality. The determination of WQI requires a normalization step in which each parameter is arranged on a scale from 1-100; 1 being the worst quality and 100 being the best. Lastly, a weighting factor is applied in accordance to the importance of each parameter as an indicator of water quality (Nives, 1999; Pesce and Wunderlin, 2000; Jonnalagadda and Mhere, 2001). Due to the fact that there are hundreds of individual parameters involved in water quality assessment which are generally not always represented within the WQI equation, WQI may not be the most precise technique if the individual parameters are not well selected. If these parameters are well selected;
WQI can be a good indicator of water quality. In this study, the parameters used to determine the WQI of MC and the corresponding values for each parameter and their weight are listed in Table 1. Among all the parameters measured in this study, temperature ($T^\circ$), chemical oxygen demand (COD) and biochemical oxygen demand (BOD) were found to exhibit strong correlation in regards to WQI. Based on data collected during this study, a correlation was established between WQI and these three parameters, allowing for one to estimate water quality in a straightforward method.

**METHODS**

This study focuses on the analysis of water quality using Water Quality Index (WQI) at 11 sites along MC. The 11 sites were labeled as A, B, C, D, E, F, G, H, I, Walker Lake (WL) and Faylor Lake (FL). The selection of these sites was made to collect a dataset capable of fully representing MC. One site was selected upstream from both WL and FL, namely the site H and site I, respectively; and one site was selected on each branch downstream from the lakes, namely the site F and site G, respectively. Five additional sites were selected between the merging point of the two branches of MC and Penn’s Creek near Susquehanna River (A, B, C, D, and E) (Figure 1). Samples were collected between June and July of 2012 and July of 2013. All sites were sampled ten times over this time period.

Physical properties including $T^\circ$, pH, electrical conductivity ($K_E$) and dissolved oxygen (DO) were measured in the field using a YSI 556 MPS multi-probe meter. Three sets of samples were collected and tested to determine nutrients and ion levels, as well as COD, BOD$_5$ and total suspended solids (TSS). Two nutrients were measured using a DR2800 spectrophotometer; nitrite (NO$_2^-$) and ammonia (NH$_3$). Two anions were measured using Dionex ICS-2000; nitrate (NO$_3^-$) and phosphorus (P).

Samples were placed into an incubator for five days at $20^\circ$C to measure the BOD$_5$ of each site. Each site was sampled and preserved by acidification to pH ≤ 2 using concentrated H$_2$SO$_4$ (Rice et al. 2012) for the measurement of their COD concentrations. The TSS was calculated based on an additional 250 mL sample filtered through a weighted standard glass-fiber, heated at 103-105 °C for one hour.

With all of the measured parameter concentrations, the WQI for Middle Creek was determined using the following equation:

\[
WQI = \frac{\left(\sum_i P_i \cdot C_i\right)}{\left(\sum_i P_i\right)}
\]

$P_i$ represents the relative weight of each parameter and $C_i$ is the normalized value of each parameter given in Table 1. WQI allows one to classify a given water system into several quality levels. A weighting factor is applied depending on the importance of each parameter as an indicator of water quality (Nives, 1999; Pesce and Wunderlin, 2000; Jonnalagadda and Mhere, 2001). The final value that is obtained from the equation is a value from 0-100. There are five water quality classifications ranking from poor water quality to excellent water quality (Table 2).
**RESULTS & DISCUSSION**

Physico-chemical parameters of the Middle Creek water quality are shown in Tables 3, 4 and 5. In this study, the Middle Creek was divided in three segments. These segments were selected to address the existing differences due to the impact of two water impoundments located along the two head water branches of Middle Creek. Segment one represents the downstream main branch starting from Site A near the confluence with Penn’s Creek to site E near the merging point of the two head water branches. Table 3 characterizes the main branch represented by 5 sampling sites (A, B, C, D and E). Table 4 corresponds to Walker Lake extension along the North Branch of the Middle Creek and is represented by 3 sites (H, WL and I). Table 5 characterizes Faylor lake extension represented by 3 sites (G, FL and F).

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**Table 1.** Values for $P_i$ and $C_i$ pertain to the parameters used to determine WQI of MC (J. Vicente et al., 2009). $K_E$ (mS/cm); TSS (mg/l); $P$ (mg/l); COD (mg/l); $BOD_5$ (mg/l); DO (mg/l); $T°$ (°C); $NO_2^-$ (mg/l); $NO_3^-$ (mg/l); Amm (mg/l) and pH.

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<th>7.0 - 8.5</th>
<th>7.0 - 9.0</th>
<th>6.5 - 7.0</th>
<th>6.0 - 9.5</th>
<th>5.0 - 10</th>
<th>4.0 - 11</th>
<th>3.0 - 12</th>
<th>2.0 - 13</th>
<th>1.0 - 14</th>
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<td>$&lt;8.0$</td>
<td>$&lt;10.0$</td>
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<tr>
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<td>$32/0$</td>
<td>$36/-2$</td>
<td>$40/-4$</td>
<td>$45/-6$</td>
<td>$&gt;45/ &lt; -6$</td>
</tr>
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</table>

**Table 2.** Scale from 0-100 representing the quality of water in accordance to WQI.

<table>
<thead>
<tr>
<th>WQI Quality Scale</th>
<th>Water Quality Index</th>
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<tbody>
<tr>
<td>91-100</td>
<td>Excellent water quality</td>
</tr>
<tr>
<td>71-90</td>
<td>Good water quality</td>
</tr>
<tr>
<td>51-70</td>
<td>Average water quality</td>
</tr>
<tr>
<td>26-50</td>
<td>Fair water quality</td>
</tr>
<tr>
<td>0-25</td>
<td>Poor water quality</td>
</tr>
</tbody>
</table>

---

Sites A through E (Figure 1)

Table 3 displays the average values (Avg), standard deviation (STD), minimum values (Min) and maximum values (Max) for sites A through E. The pH values remained between 7.66 and 8.92 and decreased slightly downstream. $K_E$ shows a gradual increase downstream probably due to runoff from farmland along MC. TSS values ranged from 0 to 31 mg/l. Sites D and C had the highest overall concentrations of TSS. The concentration of $NO_2^-$ was insignificant and no true pattern was visible in concentration. The concentration of $NO_3^-$ increased downstream with the exception of site A. The range of $NO_3^-$ concentrations was found to be between .529 and 10.205 mg/l. NH$_3$ concentrations were found to be very low in MC. The standard deviation of NH$_3$ was the second lowest for all parameters indicating a constant level of NH$_3$ throughout. The lack of $NO_2^-$ and NH$_3$ is most likely due to the short lived life of the two due to their rapid conversion to $NO_3^-$ from bacteria (BASIN, 2012). Phosphorus concentrations were very low with a slight increase downstream. The standard deviation of phosphorus by plants and its tendency to cling to soil particles (BASIN, 2012), as well as continuous base flow discharge diluting the stream water. COD had its highest concentration at site C with 21 mg/l and fell to 0 mg/l at site A. Increases in COD can be attributed to an increase in chemical pollutants from farmland runoff. BOD decreased from site E to site B, and then encountered a slight increase at site A. The maximum value was 2.7 mg/l at site E. Unpolluted streams tend to have a BOD of 5 mg/l or less making this stream very clean in respect to the amount of oxygen used by aerobic bacteria during decomposition. DO levels were quite high at all sites.
but were the highest at sites D and E. Sites D and E are both downstream from the lakes and are fairly close to the lakes. The increase of DO concentration in these two sites is due to the fast flow condition downstream from the dam and the turbulent system caused by the multiple riffles areas. The highest T° was at site D while the lowest T° was at site C. The T° fluctuation is most likely related to baseflow contribution, spring water and relative distance from the two lake extensions. Overall, the WQI for sites A through E was determined to be 90.95 ranking the quality of this water as good.

Table 3. Summary of Avg, STD, Max and Min of MC main extension (A, B, C, D, E). K_E (mS/cm); TSS (mg/l); P (mg/l); COD (mg/l); BOD_5 (mg/l); DO (mg/l); T° (°C); NO_2^- (mg/l); NO_3^- (mg/l); Amm (mg/l) and pH.

<table>
<thead>
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<th>NO_2^-</th>
<th>Amm</th>
<th>COD</th>
<th>BOD_5</th>
<th>T°</th>
<th>K_E</th>
<th>DO</th>
<th>pH</th>
<th>NO_3^-</th>
<th>P</th>
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Walker Lake Extension (H, WL, I)

The minimum pH value was 7.62, while the maximum pH

Figure 2. WQI values of MC averaged over ten sampling days taken between June July of 2012 and 2013, and the overall WQI of MC.
Figure 3. Relationship between BOD5 and WQI along all three extensions (Main, Walker and Faylor).

Figure 4. Relationship between COD and WQI along all three extensions (Main, Walker and Faylor).

Table 4. Summary of Avg, STD, Max and Min of WL Extension (H, WL, J). KE (mS/cm); TSS (mg/l); P (mg/l); COD (mg/l); BOD5 (mg/l); DO (mg/l); T° (°C); NO2⁻ (mg/l); NO3⁻ (mg/l); Amm (mg/l) and pH.

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<th>KE</th>
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The pH was higher at WL than at the other two sites. Site H had a higher pH than site I most likely because site H is downstream from WL. The highest $K_E$ was found at site I, dropped by approximately half at WL and increased at site H to a similar concentration as in site I. The increase in $K_E$ in both sites H and I is caused by groundwater influx to the stream. Site H is usually colder than any other site and the existence of several wetlands not far from this site is strong evidence of existing base flow discharge to MC. WL’s low reading of $K_E$ is most probably caused by the impoundment characteristics of the lake. The lack of turbulence does not allow for sediment to be stirred and causes much of the ions and nutrients to be settled at the bottom of the lake. TSS data set yielded a range from 0 to 65.2 mg/l. Site I had the highest concentration of NO$_2^-$ while WL had the lowest concentration. The concentration of NO$_3^-$ was the highest at site I and the lowest at WL. NH$_3$ concentrations were very similar at all three sites but proved to be the highest at site H and the lowest at site WL. There was no apparent trend between concentrations of NO$_2^-$, NO$_3^-$ and NH$_3$ at these three sites. Total phosphorus concentration was found at low concentration in WL extension. This is most likely due to the large amount of plant life that inhabits the lake and the settling of the nutrients due to a lack of turbulence. COD had its highest concentration at WL with a value of 35.2 mg/l. Sites H and I had maximum values of 21.1 mg/l and 15.1 mg/l respectively. WL’s elevated level of COD is most likely caused by the large amounts of organic matter that is present. The oxidation of this organic matter requires

**Table 5.** Summary of Avg, STD, Max and Min of FL Extension (G, FL, F). $K_E$ (µS/cm); TSS (mg/l); P (mg/l); COD (mg/l); BOD$_5$ (mg/l); DO (mg/l); T° (°C); NO$_2^-$ (mg/l); NO$_3^-$ (mg/l); Amm (mg/l) and pH.

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large amounts of oxygen. BOD was the lowest at site H and increases at WL before it returns to a similar concentration at site I. Organic matter decaying at the bottom of WL is presumably the cause for the increased BOD concentrations due to its breakdown from aerobic bacteria. As aerobic bacteria decompose this organic matter, they require oxygen to proceed with this process (BASIN, 2012). DO levels were high at these three sites. Site I had a concentration of 9.15 mg/l, WL had a concentration of 11.81 mg/l and site H had a concentration of 9.03 mg/l. WL’s high level of DO is believed to be caused from the release of oxygen during photosynthesis from the large amount of plants that inhabit the lake. WL had the highest T° of almost 8 °C. The lack of high discharge flow into WL and the direct insolation allow for excessive heating. Overall, the WQI for the WL extension was determined to be 87.89 classifying the water quality as good. Walker Lake extension has a lower WQI than sites A through E. WL is the main reason for this decrease. The highest WQI of WL was 88.08 and the lowest was 81.54. These scores bring down the overall WQI of Walker Lake extension. The results showed that pH, T°, COD and BOD₅ are the main parameters that diminish WL’s WQI.

Faylor Lake Extension (G, FL, F)

The pH values were in the range of 7.76 and 9.99. There were greater pH values at FL than at sites G and F. Site F had a higher pH than site G most likely due to its location downstream from FL. Kₑ was high in site G and low in FL. TSS values ranged from 1.6 mg/l at site F, to 60.4 mg/l at site G. NO₃⁻ concentrations were very low at all three sites. Site F had the highest concentration with a value of 0.023 mg/l. The low concentration of NO₂⁻ is most likely caused by the rapid conversion to NO₃⁻ by bacteria. NO₃⁻ had the highest concentrations at site G, while FL and site F had lower concentrations compared to site G. NH₃ concentrations at all three sites were very low. Site F had the highest concentration followed by FL. NH₃ is rapidly converted to either NO₃⁻ or nitrogen gas depending on the concentration of DO in the water. Since all three sites have high concentrations of DO, the NH₃ is most likely being converted into NO₃⁻ which would explain the high concentrations of NO₃⁻. Low concentrations of phosphorous were found within the FL extension. COD was relatively low at each site. Site G had the lowest concentration with 0 mg/l and FL and site F had similar concentrations of 13.32 and 13.46 mg/l, respectively. BOD was the highest at FL with a concentration of 3.18 mg/l and the lowest at site G with a concentration of 1.23 mg/l. Unpolluted streams should have a BOD of 5 mg/l or less, making this a healthy stream in regard to BOD. DO was very high at all three sites. FL had the highest DO concentration of 12.05 mg/l, while site F had the lowest concentration of 8.52 mg/l. FL had the highest T° of 28.05 °C. Site G had the lowest T° of 22.9 °C. The high T° level in FL is most likely caused by the lack of flowing water and the shallow depth of the lake. Site F experiences increased T°s due to its proximity to FL. Overall, the WQI for the FL extension was determined to be 89.44 making this water a good water quality. FL extension has a lower WQI than the main branch of MC but a slightly higher WQI than Walker Lake extension. The best WQI that Faylor Lake had was 91.92 and the lowest was 86.92. These low scores for FL bring down the overall WQI of the Faylor Lake extension. pH, To and COD are the main parameters that diminish Faylor Lake’s WQI.

WQI Analyses

WQI values varied from site to site due to the concentration and weight of each parameter tested. The overall WQI value for each day was determined to be in the range of good water to excellent water (Figure 2).

Data was collected during the month of June and July in 2012 and 2013 to allow for an in-depth WQI analysis. This large data set allowed for trends to be identified and analyzed. The WQI remained fairly consistent over the two testing periods suggesting that Middle Creek’s environment has remained for the most part unchanged. This consistency was important in determining which parameters were the driving forces of the WQI. The five most heavily weighted parameters used to calculate the WQI are TSS, DO, COD, BOD and NH₃. TSS and DO are the most heavily weighted by a factor of 4, while COD, BOD and NH₃ are weighted by a factor of 3 (Table 1). These heavily weighted parameters did not prove to influence the WQI as significantly as their relative weight would suggest. DO levels were above the maximum WQI range of 7.5 mg/l for each site, causing DO to be a constant within the WQI and thus not useful for water quality analysis. Even though DO may carry a higher weight in the WQI equation; it does not express itself in the final value as strongly as other, less weighted parameters. Due to the lack of variation and minute concentrations of NH₃, this parameter yielded inconclusive results. When analyzed using the WQI, concentrations of NH₃ corresponded to the maximum value of 100. Even though this parameter carries a weight of 3, it can be ignored due to the lack of variation between values.

BOD vs. WQI

BOD’s data set had a large standard deviation between sites. This deviation causes the BOD to be a moderately accurate predictor in regards to the WQI. Along the main extension of MC, BOD was not an accurate predictor of the WQI (Figure 3). The addition of spring water to MC as well as the presence of few waste water treatment facilities
along MC causes inconsistencies in BOD concentrations and its relation to WQI. As BOD increases, the WQI should decreases. Figure 3 shows a horizontal line's trend which falsely indicate that an increase in BOD is not causing any increase in WQI. The relationship between WQI and BOD is not as apparent in this section of MC as it is in the other two extensions.

Along the Walker Lake extension, BOD has been found to be an accurate predictor of the WQI. The negative trend line indicates any decrease in WQI is caused by an increase in BOD concentration. Trend lines were created for each site to verify that this relationship remained constant throughout this extension. Along this extension, data points closely fit the trend line providing a more accurate approximation of the water quality classification. BOD’s relationship with the WQI is best displayed within the Walker Lake extension, most likely due to its proximity to the headwater and lack of infiltration from external water sources, such as springs and runoff streams.

The FL extension follows a similar trend of WL extension. Site F and FL show very similar negative trends due to their proximity to one another, while site G shows a positive trend line and a large deviation of data (Figure 3). This positive trend found at site G eliminates some confidence in the BOD parameter as a predictor of the WQI. COD may be used with more confidence to predict the WQI in this site.

COD vs. WQI

COD was the only heavily weighted parameter that was capable of accurately predicting the quality of water using the WQI along the Middle Creek. All eleven sites displayed negative trends correlating the COD and the WQI. As COD concentrations increased, the WQI values decreased (Figure 4). Figure 4 shows the trend of the relationship between WQI and COD along the main section of MC. Trend lines were created for each site to verify that this relationship remained constant throughout the main section. Due to the large number of parameters involved in the WQI, this trend may not be as extreme at certain sites as the WQI and COD concentrations would indicate. Site C for instance has a small negative slope in respect to other sites located along the main section of MC. This is mainly due to the single outlying data point located at approximately 22 mg/l. The same trend can be found along the Walker Lake and Faylor Lake extensions.

Along the Walker Lake extension, data points closely fit the trend line providing a more accurate approximation of the water quality classification. COD versus WQI relationship is best expressed within the Walker Lake extension due to its proximity to the headwater and lack of input from external water sources, such as runoff from streams.

Faylor Lake extension follows a similar trend as seen in Walker Lake extension. Site F and FL show very similar trends due to their proximity to one another, while site G located near the headwater showed a large array of data. The same trends were found at Faylor Lake extension and Walker Lake extension due to their similar locations in the watershed both in the headwaters. Given the results in the above figures, a single COD test is capable of approximating the water quality classification. Although COD is weighted much heavier in the WQI, the T° parameter can more accurately predict the WQI along various locations of MC.

$T°$ vs. $WQI$

T°s varied significantly along the main section of MC. Although there is a large variation in the T° data, all of the sites display a negative trend indicating as T° increases the WQI values decrease (Figure 5). Many of the sites in the main extension of MC encounter environmental changes due to waste treatment facilities, agricultural runoff and natural spring infiltration. This variation in environments causes a large degree of change of the T° parameter. The deviation in trend line slopes can also be attributed to other parameters influencing the WQI as well. The overall trend line profile of the WQI and T° relationship in figure 5 allows T° to be considered a reasonable predictor of the WQI classification. Similar trends can be found along both WL and Faylor Lake extensions (Figure 5). Along the Walker Lake extension, T° has been determined to be a moderately accurate indicator of WQI. Sites I and WL exhibit very comparable environments this can be seen by their very similar negative trend lines in figure 5. These trend lines provide confidence in the ability to use T° as a predictor of WQI values. Site H has a positive trend line most likely caused by the presence of a spring. This positive trend line reduces the confidence of the T° parameter as an accurate predictor of the WQI. Although, T° can still be a very valuable forecasting parameter if the testing site’s local water source is known. The Faylor Lake extension is very similar to the Walker Lake extension and provides comparable trends. Along the Faylor Lake extension all sites possess a similarly sloped negative trend (Figure 5). These similar slopes suggest that these three sites have comparable environments. These trend lines offer confidence in the ability to use T° to predict the values of WQI along the Faylor Lake extension. Given the results in the above figures, a single T° reading can give an approximation of the water quality classification along MC. Although T° is weighted much lower than COD and BOD in the WQI equation, it proves that it is capable of accurately predicting the WQI along various locations in MC.

The ability to be able to use one or two parameters to predict the quality of water in a given system has numerous benefits. The use of a forecasting parameter such as T°, COD or BOD, allows one to assess water quality in a short period of time. In this study, it was determined that T° and COD are the best forecasting parameters, followed by BOD. The relationships
found between WQI and Temperature, COD and BOD, allow a simple test to provide a good estimate of the water quality of a given water system. This can help reduce the cost of the methodology generally used in water quality studies and potentially decrease the number of persons conducting the water quality of a given stream. Although, it is not evident whether similar relationships between $T°$, COD and BOD, and WQI, can be found in other water ways, the wide spread use of WQI would provide sufficient data to determine the accuracy of the WQI along MC.

**AKNOWLEDGEMENTS**

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**LITERATURE CITED**


BIOACCUMULATION OF METHYLMERCURY IN NEOVISON VISON (SCHREBER, 1777) POPULATIONS OF THE SUSQUEHANNA RIVER VALLEY†

MATTHEW R. BROWN AND CARLOS A. IUDICA

Department of Biology, Susquehanna University, Selinsgrove, PA 17870

ABSTRACT

Being the longest non-navigable river on the eastern coast of the United States, the Susquehanna River and the surrounding areas support a vast number of plants, animals, and other organisms, creating a vast and complex food web within a large and biodiverse ecosystem. One of the most prominent and essential organisms within this food web is the American mink (Neovison vison). In recent years, studies have been conducted to determine the level of biomagnification of methylmercury in terrestrial organisms that reside at higher trophic levels. This particular study has found that American mink populations residing in the Susquehanna River Valley of Pennsylvania are reliable indicators of bioaccumulation of methylmercury due to their role as piscivorous carnivores residing at a high trophic level of the terrestrial food web. Analysis of methylmercury concentrations of 166 hair samples from collected mink specimens yielded 111 samples with concentrations in excess of the toxicity threshold of 1 mg kg\(^{-1}\) body weight. Furthermore, our data suggest that although mercury contamination is a global concern, geographical location of mercury producers, such as coal-burning power plants, and the relationship to the location of mink populations may be a large factor in bioaccumulation of mercury. In particular, samples taken from mink specimens within habitats in the northeastern region of Pennsylvania contained higher concentrations of methylmercury as well as a larger quantity of samples containing concentrations higher than the toxicity threshold than in samples from other regions of the state.

INTRODUCTION

Bioaccumulation of Mercury

Global cycle of mercury.--Elemental mercury (Hg\(^0\)), the only metal that exists as a liquid at room temperature, also exists as a gas with little tendency to dissolve in water (Onat 1974). In comparison to the air above, natural waters are supersaturated in Hg\(^0\), which in turn results in volatilization and ultimately a flux of Hg\(^0\) from water into the atmosphere (Fitzgerald et al. 1994). At uncontaminated sites, Hg occurs at concentrations of 1-20 parts per trillion; concentrations of Hg\(^0\) are higher near the air-water interface (Morel et al. 1998). Of the total mercury in the atmosphere, 95% is in the elemental state and is slowly oxidized by ozone in the solid-liquid interface of fog and cloud droplets to the mercuric state, Hg(II).

Mercury returns to the Earth’s surface by wet precipitation of Hg(II) with 60% being deposited to land and 40% to water (Morel et al. 1998). These percentages reflect the proximity of sources of Hg since water precipitation is three times less on land than on the oceans. However, since Hg\(^0\) reoxidizes fairly slowly to the mercuric state, Hg\(^0\) can remain in the atmosphere up to one year (Morel et al. 1998). From this data, it is clear that while anthropogenic point sources, such as metal and pulp production industries, coal-burning power plants, and waste handling and treatment facilities, are the principal emitters of mercury, the issue of mercury contamination is a global concern (Lindquist 1991; Morel et al. 1998).

Microbial uptake of mercury, methylation and bioaccumulation.--Before Hg(II) is methylated by sulfate-reducing bacteria and enters the aquatic food chain, it is transported at high concentrations into mer-carrying bacteria via specialized MerT transport proteins (Morel et al. 1998). At low concentrations, Hg(II) diffuses through the lipid membrane of lipid-soluble mercury complexes. This diffusion results in the covalent chemical bonding in the dichloro mercuric complex, HgCl\(_2\). This complex is the key chemical species in determining cellular uptake of mercury in oxic waters (Morel et al. 1998).

After this uptake, sulfate-reducing bacteria begin the process of methylation, which usually results from photochemical processes or catalyzation, by transferring an alkyl anion group to Hg(II), ultimately converting it to methylmercury (Morel et al. 1998). While Hg\(^0\), Hg(II), and methylmercury (MeHg) are all effectively accumulated in these planktonic bacteria, only concentrations of MeHg...
increase at higher trophic levels, or biomagnifies. Due to the lipid solubility of CH$_3$HgCl, MeHg is bioaccumulated in grazer animals and retained in muscle and fatty tissues. Bioaccumulation of MeHg primarily results from the ingestion of MeHg-containing food. When examining the number of trophic levels within an ecosystem, it has been observed that the presence of certain planktivores within an ecosystem correlates to the concentrations of mercury in top predators of the ecosystem (Cabana and Rasmussen 1994).

Environmental Methylmercury and Organisms

Methylmercury in fish and environmental concerns.—The bioaccumulation of MeHg in freshwater fish is well-documented and, in comparison to other organisms, has been researched extensively (Fujiki et al. 1977; Phillips and Buhler 1978; Bloom 1992; USEPA 1997a). It has been shown that large, long-lived piscivorous species, such as walleye (Sander vitreus), northern pike (Esox lucius), and lake trout (Salvelinus namaycush), are at a greater risk for dietary MeHg exposure and bioaccumulate much larger concentrations of methylmercury in comparison to herbivorous species (Scheuhammer et al. 2007). In particular, studies conducted by Peterson et al. (2007) found that in addition to all large fish sampled exceeding the wet weight detection limit of 0.0024 µg g$^{-1}$, the mean concentration in piscivorous fish (0.260 µg g$^{-1}$) was nearly three times that of nonpiscivores (0.090 µg g$^{-1}$). The current human consumption criterion in fish fillet set forth by the United States Environmental Protection Agency (USEPA) is 0.3 µg Hg g$^{-1}$. Using the regression model established by Peterson et al. (2007) to predict fillet concentrations from whole body concentrations, fish with whole body concentrations exceeding 0.185 µg Hg g$^{-1}$ had fillet concentrations that exceeded 0.3 µg Hg g$^{-1}$ and therefore exceeded the criterion set forth by the USEPA (Peterson et al. 2007).

These and other findings in fish containing concentrations exceeding acceptable levels for consumption have generated a large concern for a wide variety of reasons. Tissue concentrations of 6-20 mg Hg kg$^{-1}$ (wet weight in muscle) have been documented to impair fish behavior, gonadal development, production of sex hormones and overall reproductive success, as well as increase vulnerability and ultimately cause death (Friedmann et al. 1996; Wiener and Spry 1996). In addition to the effects on populations of fish, higher concentrations of MeHg directly impact human populations who rely upon fish consumption (USEPA 1997a). MeHg binds to proteins and free amino-acids that are components of muscle tissues and are not removed by any cooking or cleaning processes that do not destroy these tissues (Mergler et al. 2007). In recent studies, 5-10% of women of childbearing age in the United States were found with blood levels exceeding 5 µg Hg L$^{-1}$ (Schober et al. 2003); out of these women, those that are pregnant actively transfer MeHg to the fetus across the placenta via neutral amino acid carriers during gestation (Kajiwara et al. 1996). It is evident that the bioaccumulation and biomagnification of MeHg in fish has a detrimental impact on humans that rely upon fish as an integral part of their diet; in particular, embryonic development is severely affected.

Methylmercury in aquatic and terrestrial food webs.—The organisms that are at greatest risk for elevated MeHg exposure, bioaccumulation, and toxicology are long-lived, piscivorous species or other top consumers feeding in aquatic food chains. Beyond piscivorous fish, these species include aquatic mammals such as mink (Neovison vison) and otter (Lontra canadensis) as well as piscivorous birds such as common loons (Gavia immer), bald eagles (Haliaeetus leucocephalus), and osprey (Pandion haliaetus) in addition to some seabirds, such as albatrosses, shearwaters, herring gulls, and petrels (Heinz 1996; Thompson 1996). Both mink and otter are mammalian species that have been impacted the greatest by bioaccumulation and biomagnification of MeHg; studies have shown that diets containing more than 1 mg Hg kg$^{-1}$ wet weight caused neurological effects such as lethargy, ataxia, limb paralysis, tremors, convulsions, and ultimately death (Wiener et al. 2003). The lowest observable effects in mink occur at tissue concentrations of 1.1 mg Hg kg$^{-1}$ wet weight (USEPA 1997b). In birds, concentrations of 15 mg Hg kg$^{-1}$ wet weight or higher in a variety of tissues are associated with overt signs of MeHg intoxication and death. Concentrations in eggs of more than 1 mg Hg kg$^{-1}$ wet weight are associated with impaired hatchability and embryonic mortality (Wiener et al. 2003).

While species in aquatic food chains are at the highest risk of mercury exposure, research conducted by the Biodiversity Research Institute recently has found increased MeHg concentrations in species within terrestrial food webs (Evers et al. 2012). It has been concluded that Hg enters terrestrial ecosystems through the form of precipitation, which collects on soil and leaf litter; this litter is the primary site of Hg methylation by bacteria in terrestrial ecosystems. Various invertebrates consume leaf litter contaminated with Hg, which in turn are consumed by spiders, thus adding one to two trophic levels. Birds of the deep forest, such as the wood thrush (Hylocichla mustelina), as well other birds, including the rusty blackbird (Euphagus carolinus) and saltmarsh sparrow (Ammodramus caudacutus), consume spiders, insects, and other invertebrates. Recently, high concentrations of MeHg have been observed in these bird species resulting in lower reproductive success and ultimately unexpected population crashes (National Wildlife Federation 2006; Evers et al. 2012). These data and observations corroborate the findings of Cristol et al. (2008), who concluded that birds which consumed predatory invertebrates increased the opportunity for the biomagnification of Hg.

The impact of MeHg bioaccumulation in populations of Neovison vison residing in the Susquehanna River Valley is of particular concern due to the presence of multiple coal-
burning power plants in the area. When Hg-containing coal and oil is mined from the Earth’s crust and burned during various industrial processes, Hg is released into the atmosphere by industrial smokestacks and eventually returns to Earth where it is converted to MeHg by bacteria. Coal-fired power plants are the largest contributor to Hg contamination, accounting for over 40 percent of Hg emissions in the United States (National Wildlife Federation 2006). This information is especially pertinent to studying the effect and bioaccumulation of MeHg in mink populations of the Susquehanna River Valley due to the proximity of coal-burning power plants to the habitat of mink populations in Pennsylvania. In addition to other large coal-burning power plants in Pennsylvania, the GenOn Energy Shawville Station in Clearfield County is of particular concern for this study. Located on the banks of the Susquehanna River, the station is ranked twelfth in annual total mercury emissions in the nation and first in the state of Pennsylvania (Madsen and Randall 2011).

The Susquehanna River is the longest river on American east coast, and supports a vast diversity of organisms. Inferences on the impact of MeHg bioaccumulation on other key species within the aquatic and terrestrial food webs of the Susquehanna River can be made after analyzing and understanding the impact on local mink populations. Once relationships are drawn between tissue Hg concentrations, influencing factors, such as geographical location, age, and sex, and the short and long term effects on food webs, the detrimental impacts of MeHg bioaccumulation and biomagnification on the organisms of the Susquehanna River valley can be fully understood.

The purpose of this study was to investigate MeHg concentrations in populations of the American mink (*Neovison vison*) residing in various areas of the Susquehanna River watershed within Pennsylvania. The American mink is an integral component of both aquatic food web of the Susquehanna River and the terrestrial food web of the area surrounding the watershed, placing it at a higher trophic level. Its diet and placement within the food web, along with the relatively short average lifespan of 1-3 years, regardless of sex (Reid and Helgen 2008), makes the American mink a prime candidate for MeHg bioaccumulation.

**MATERIALS AND METHODS**

**Preparation and Identification**

Full body samples of *Neovison vison*, trapped in the Pennsylvania counties of Susquehanna, Wyoming, Juniata, Perry, Northumberland, Schuylkill, Dauphin, Lebanon, and Lancaster (Fig. 1) (with respective central coordinates 41.8113° N, 75.7755° W; 41.5375° N, 75.9609° W; 40.5563° N, 77.3430° W; 40.4226° N, 77.1840° W; 40.8632° N, 76.6873° W; 40.7172° N, 76.209° W; 40.3498° N, 76.455° W; 40.0677° N, 76.2812° W), were skinned, placed in large plastic bags and stored in freezers by various local trappers. Mink carcasses were then picked up and transported to freezers located at Susquehanna University. Prior to dissection, carcasses were removed from the freezer and allowed to thaw for at least eight hours; placing bagged samples in a warm water bath was found to be an effective method for thawing when time was limited.

Each carcass was assigned a number based upon the number of catalogued organisms processed before it. One gallon-sized ziploc bag and four 1 mL eppendorf tubes were labeled with this number; in addition to the number, the tubes were labeled with a letter corresponding to the sample to be placed inside, with “H” standing for “hair”, “L” for “liver”, “K” for “kidney”, and “M” for “muscle.”

The sex of each animal also was determined prior to dissection; this was done by examining its overall size as well as the presence or absence of a baculum. Since sexual dimorphism is prevalent in populations of the American mink (Thom et al. 2004), those that were larger in size and possessed a baculum were confirmed as males. Age of each individual was determined by examining the presence of certain teeth as well as the degree of wear and rounding of teeth. Age was defined using three categories: juvenile (J), adult (A), and senile adult (SA); juveniles were <1 year of age and defined by having all teeth present and little to no wear or rounding, adults were 1-3 years of age and defined by having some teeth missing, rounded molars, and an observable amount of wear on all teeth, and senile adults were > 3 years of age and defined by having multiple teeth missing, and teeth that were chipped, broken, and/or rounded and worn significantly.

Figure 1. Counties where specimens were captured by trappers.
Dissection Procedure and Processing of Samples

Already skinned carcasses had some intact skin (and hairs) patches around hands, feet, and muzzle. From those patches, hair samples were collected by cutting tissue under the hair follicles and using a pair of scissors to cut a sample measuring approximately one centimeter in both length and width to extract muscles. An incision was made by pinching the muscles located at the center of the gut, using the scissors to make the initial cut, and drawing the scissors up to the inferior sternum. Tissue samples were taken from the liver, kidney, and muscle located on the left thigh, all measuring approximately one centimeter in length, width, and height, and placed in their properly labeled 1 mL eppendorf tubes using forceps; all tubes were placed together in a labeled sandwich-sized ziploc bag and placed in the freezer for storage. All tools and instruments were cleaned and sanitized using bleach and soap between samples and at the end of the day.

All collected samples were analyzed using a DMA-80 direct mercury analyzer (Milestone Inc., Shelton, CT). Data collected from each sample after analysis included the mass of the sample, sample Hg concentration (in micrograms of Hg per kilogram of sample), height of the peak, and the amount of Hg (in nanograms).

All samples were analyzed based upon the MeHg concentration found within the sample, expressed in milligrams of MeHg per kilogram of body weight (mg MeHg kg⁻¹). In addition, samples were sorted based upon the geographical location of the samples from which the specimens were taken, as well as the sex and age of the specimens. Analysis of hair samples by geographic region was accomplished by dividing the areas where samples were collected into three distinct regions. Geographic Region 1, also referred to as the northern region, consisted of Susquehanna and Wyoming Counties. Geographic Region 2, also referred to as the central region, consisted of Northumberland, Schuylkill, Juniata, and Perry Counties. Geographic Region 3, also referred to as the southern region, consisted of Dauphin, Lebanon, and Lancaster Counties. Analysis of the influence of sex was completed by identifying each specimen as either male or female, and the relationship between age and MeHg concentration was examined by classifying each specimen as juvenile (less than 1 year old), adult (1 to 3 years old), or older adult (more than 3 years old).

RESULTS

General Analysis of MeHg Concentrations within Samples

In total, 166 hair samples were processed and analyzed. These samples were used as the primary source for MeHg bioaccumulation analysis in mink specimens. Overall, 111 of those samples (approximately 67%) contained MeHg concentrations greater than the threshold of 1 mg Hg kg⁻¹.

In addition, thirty-four mink samples were analyzed for MeHg concentrations in hair, muscle, liver, and kidney samples. Examination of these results indicates a positive correlation between MeHg concentration in hair and concentrations within the organs (muscle, liver, and kidney). Despite some outliers, higher concentrations within hair follicles corresponded with higher concentrations within organs. In addition, the average MeHg concentration within muscle and organs shared a similar, positive correlation with the MeHg concentrations in hair.

Analysis of Muscle, Liver, and Kidney Samples

In addition to the analysis of 166 hair samples, MeHg concentrations in muscle, liver, and kidney samples from the 34 specimens fully processed for MeHg were examined and compared with the concentrations from corresponding hair samples. In general, higher MeHg concentrations in hair samples corresponded with higher MeHg concentrations in organ (muscle, liver, and kidney) samples. However, an exact correlation between MeHg concentrations in hair samples and MeHg concentrations in the organ samples was not observed; the concentrations found in the organ samples, while decreasing with decreasing concentrations in hair samples, were variable (Fig. 2, 3a, and 3b).

In addition, MeHg concentrations in muscle, liver and kidney samples from the same specimen were found to correspond with one another. If higher concentrations were observed in one type of sample, higher concentrations were also observed in the other two types of sample (Fig. 2). Upon further observation, it was also discovered that MeHg levels
typically were the highest in kidney samples. Furthermore, MeHg concentrations found in kidney followed the most linear path and had the greatest amount of correlation with corresponding hair samples (Fig. 4). However, the $R^2$ value of 0.5081 indicates that these average concentrations do not follow a linear path.

**Figure 3A.** Comparison of MeHg concentrations in hair samples and average MeHg concentrations in corresponding muscle, liver, and kidney samples. As seen above, decreasing concentrations in hair samples correspond with decreasing concentrations in the average concentrations in corresponding organ (muscle, kidney, and liver) samples. However, the $R^2$ value of 0.5081 indicates that these average concentrations do not follow a linear path.

**Figure 3B.** Comparison of MeHg concentrations in hair samples and average MeHg concentrations in corresponding muscle, liver, and kidney samples with the omission of outliers. While collecting and analyzing MeHg concentration data, four specimens and the concentrations from the respective samples were identified as outliers: SU 551, SU 571, SU 572, and SU 593. When these samples are omitted from analysis, an $R^2$ value of 0.7411 can be observed, indicating a stronger linear relationship between MeHg concentration in hair samples and corresponding average MeHg concentration in organ samples.

**Correlation between MeHg Concentrations in Hair Samples and Geographic Regions**

A total of 166 hair samples were analyzed, including 71 hair samples from animals captured in Geographic Region 1, 63 samples from animals captured in Geographic Region 2, and 32 samples from animals captured in Geographic Region 3. Of the 71 samples from Region 1 (northern region), 61 samples, or approximately 86% of samples were found to contain MeHg concentrations in excess of the threshold of 1 mg kg$^{-1}$. In comparison, 33 out of 63 samples, or 51% of samples, from Region 2 (central region) were found with MeHg concentrations in excess of the threshold, and 17 out of 32 samples, or 53% of samples, from Region 3 (southern region) were found with MeHg concentrations over the threshold.

**Figure 4.** Comparison of MeHg concentrations in hair samples and MeHg concentrations in corresponding kidney samples. The $R^2$ value of 0.5468 indicates a weak linear relationship based upon the data collected. However, this $R^2$ value is the highest observed in the concentrations of the samples taken from the three selected organs (muscle, liver, kidney). In addition, if the concentrations collected from outlier samples SU 551, SU 571, SU 593, and SU 572 are excluded from the scatterplot, the $R^2$ value increases to 0.7377.

**Correlation between MeHg Concentrations in Hair Samples and Sex**

Out of the 166 hair samples collected, 102 samples were from males, and 64 samples were from females. During analysis, 69 of the samples from males, or 68% of samples, were found with MeHg concentrations in excess of 1 mg kg$^{-1}$. In addition, 43 of the 64 hair samples taken from females, or 67% of samples, were found with MeHg concentrations in excess of 1 mg kg$^{-1}$. This analysis suggests that, although a total of 112 specimens from both sexes were found with concentrations in excess of the MeHg threshold, there is no observable difference between bioaccumulation of MeHg in males and bioaccumulation in females.

**Correlation between MeHg Concentrations in Hair Samples and Age**

Out of 52 hair samples analyzed for correlation between MeHg concentrations and age, 12 samples were classified as juvenile (less than 1 year in age), while 31 samples were classified as adult and 9 samples as older adult. During analysis, 10 out of 12 juveniles (83%), 25 out of 31 (78%), and 8 out of 9 (89%), were found with MeHg concentrations in excess of 1 mg kg$^{-1}$. Further analysis of the impact of age on bioaccumulation of MeHg should be conducted with a larger sample size with samples being evenly distributed among
**DISCUSSION**

Results from the analysis of MeHg concentrations within the samples from mink specimens clearly indicate that *Neovison vison* can bioaccumulate toxic levels of MeHg. When analyzing hair samples, over two-thirds of hair samples from mink specimens contained levels of MeHg above the toxicity threshold. Therefore, data suggest that American mink populations in the Susquehanna River Valley bioaccumulate MeHg at high concentrations. It is clear that the role of American mink as a piscivorous carnivore and its position at a high trophic level within the terrestrial food web of the Susquehanna River Valley are contributing factors to the magnitude of MeHg bioaccumulation.

Results of MeHg analysis of all tissues indicated a concentration order of hair > kidneys > liver > muscle. In addition, a relationship between concentration found in hair and concentrations found in kidney, liver, and muscle samples could be observed; higher concentrations in hair samples corresponded with higher concentrations in organs and muscle tissue. These results are logical and expected when considering the known metabolic pathway of MeHg in mammals. When exposed to a toxicant, such as MeHg, mammals attempt to excrete the toxicant, resulting in bioaccumulation in hair follicles and epidermal cells. However, toxicants still bioaccumulate within organs with excretory functions, especially the liver and kidneys. Since methyl compounds are highly soluble in water, the bioaccumulation of MeHg at high concentrations within the liver and kidneys would be expected.

When discussing the impact of geographic location on mink populations, the large percentage of hair samples from Geographic Region 1 found with MeHg concentrations in excess of the toxicity threshold indicates the magnitude of MeHg bioaccumulation within minks is influenced by geographic location. Our results are directly influenced both by the presence of the GenOn Energy Shawville Station on the western branch of the Susquehanna River as well as the prevailing wind patterns of Pennsylvania. Shawville Station produces more than 315 kg (700 lbs) of Hg emissions per year, and with the prevailing winds coming to Clearfield County from the west and blowing to the northeast. It can be expected that large amounts of MeHg would be deposited in the northeastern counties of Pennsylvania, such as Susquehanna and Wyoming Counties. Although other coal-burning power plants are present in southwestern counties of Pennsylvania, it can be inferred that these plants do not have as large an impact due to smaller amounts of Hg emissions when compared to the GenOn Energy Shawville Station.

**CONCLUSION**

American mink populations residing in the Susquehanna River Valley are proficient bioaccumulators of MeHg. Our data also suggests that Hg contamination is an important factor in the bioaccumulation of MeHg in terrestrial organisms. Further research should be conducted on the influence of the GenOn Energy Shawville Station and other coal-burning power plants on the MeHg concentrations of other terrestrial organisms at higher trophic levels, as well as aquatic species of the Susquehanna River residing in the northeastern regions of Pennsylvania. Correlations between concentrations found in hair samples and those found in the liver and kidneys should also be investigated further by increasing sample size and collecting more organ samples.

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**LITERATURE CITED**


FACTORS INFLUENCING WALLEYE (SANDER VITREUS) YEAR CLASS STRENGTH IN THE UPPER SUSQUEHANNA RIVER†

ROBERT T. WNUK1

Pennsylvania Fish and Boat Commission, Sweet Valley, Pennsylvania 18656-0088

ABSTRACT

Age-0 Walleye were monitored in the upper Susquehanna River from 1995 through 2010. I used these data to examine factors that influenced year class strength and to construct a predictive model. Mean river flow in May demonstrated the strongest relationship with year class strength ($r^2 = 0.57$). A model consisting of May flow, June flow, and July air temperature explained 86.7% of the variation in the data from 1995 through 2006. This model successfully predicted Walleye year class strength for data from 2007 through 2010 (mean prediction error = 13.1/hr).

INTRODUCTION

Walleye (Sander vitreus) are an important sportfish in the United States, accounting for 39.1 million angling days outside of the Great Lakes in 2006 (U.S. Department of the Interior 2007). Walleye fisheries are maintained through stocking, natural reproduction, or a combination of both. For completely self-sustaining fisheries, knowledge of factors that influence year class strength is critical to management success. Year class strength can impact population abundance, age structure, growth rate, and ultimately, the number of large fish available to anglers (Allen and Hightower 2010).

Research has demonstrated the importance of numerous factors to Walleye year class strength in lentic systems. Significant biotic factors have included spawning stock size (Madenjian et al. 1996; Hansen et al. 1998; Beard et al. 2003), cannibalism (Hansen et al. 1998), predation and competition (Hansen et al. 1998; Beard et al. 2003; Quist et al. 2003; Hoxmeier et al. 2006), prey availability (Ritchie and Colby 1988; Madenjian et al. 1996; Hoxmeier et al. 2006), and exotic species invasion (Mercado-Silva et al. 2007). Significant abiotic factors have included water level fluctuations (Kallemeyn 1987; Willis and Stephen 1987; Quist et al. 2003), surface area (Nate et al. 2000), water current (Yingmang et al. 2009), and temperature (Kallemeyn 1987; Madenjian et al. 1996; Hansen et al. 1998; Schupp 2002; Quist et al. 2003; Hoxmeier et al. 2006).

In contrast, studies of factors influencing Walleye year class strength in lotic systems have been scarce. Pitlo (2002) found strong correlations between the rate of spring warming and the number of age-0 Walleye collected during the fall on an impounded reach of the Mississippi River. Chalupnicki et al. (2010) found that Walleye egg density in Deacon Brook, New York, depended on physical habitat. Several researchers related spring discharge in tributary rivers to Walleye recruitment in downstream lakes (Swain 1974; Johnston et al. 1995; Paul 2013). None of these studies, however, examined Walleye year class strength past the larval stage in a free-flowing area of a large river.

The Pennsylvania Fish and Boat Commission (PFBC) monitored the abundance of age-0 Walleye in the upper Susquehanna River annually from 1995 through 2010. These data provided valuable insights into fluctuations in the adult Walleye population. I examined these data to determine the variables influencing Walleye year class strength and to create a predictive model.

METHODS

The upper Susquehanna River in Pennsylvania extends 294 km from the Pennsylvania/New York border downstream to the confluence with the West Branch Susquehanna River. This portion of the river is free-flowing and averages 250 m wide. Major sport fisheries exist for Walleye and Smallmouth Bass (Micropterus dolomieu). Neither species is native to the river but both have been naturalized for many years. The last Walleye stocking in the upper Susquehanna River occurred in 1967 (Daniels 1983).

We used night electrofishing to collect Walleye from the upper Susquehanna River. All electrofishing took place along the shoreline in October or November when water temperatures ranged from 10 to 20 °C (Borkholder and
The pulsed DC electrofisher consisted of a 5.5 m flat-bottomed aluminum boat with four copper droppers per side. Electricity was produced with a 5000 watt generator and operating output was in the range of 4-6 amps. We captured as many Walleye as possible and measured them to the nearest 25 mm length group. Age-0 fish were generally easy to separate from older fish by length-frequency distributions, but we occasionally took scale samples on questionable individuals to verify their ages.

We sampled at four fixed sites (Figure 1): Wysox, Tunkhannock, Union, and Bloomsburg. Most sites were sampled annually but river flows occasionally prevented sampling at some sites. Sample sites ranged from 1.9 to 2.3 km long. Electrofishing time at each site was one hour. The single hour was broken into three runs of 20 minutes each. Catch per hour (CPH) for a given site was the mean of the three 20 minute runs. Mean CPH for a given year was the overall mean from all sites.

Age-0 CPH data were not normally distributed (Shapiro-Wilk test, W = 0.858, p = 0.018) so the data were log transformed. The transformation successfully normalized the data (Shapiro-Wilk test, W = 0.912, P = 0.127). All statistical analyses were performed with R Version 2.14.2 (R Development Core Team 2012). Alpha was set at 0.05.

To detect a significant stock-recruitment relationship, I used the Ricker model (Ricker 1975) because I expected significant predation on juveniles by older fish. The linear form of the Ricker equation was:

$$\log_e \left( \frac{R}{S} \right) = a - bS + \varepsilon$$

where R was the CPH of recruits in year t+1, S was the CPH of the spawning stock in year t, a and b were model parameters, and ε indicated that the errors were expected to follow a normal distribution. For spawning stock, I used age-3 and older, age-4 and older, and age-5 and older fish. Differentiation of these age groups was by length-frequency distribution based on previous age and growth studies (PFBC unpublished data).

I used Pearson correlations (Zar 1984) to identify variables that had a significant influence on Walleye year class strength. The biotic variables I examined were CPH of age-1 and older Smallmouth Bass, CPH of age-1 and older Walleye, CPH of esocids [Northern Pike (Esox lucius) and Muskellunge (Esox masquinongy) combined], and CPH of age-0 Walleye in the previous year. Smallmouth Bass CPH data were from annual summer monitoring conducted from 1995 through 2001 and again from 2005 through 2010 (PFBC unpublished data). We collected age-1 and older Walleye and esocids at the same time that we collected age-0 Walleye.

The abiotic variables I examined were water flow and air temperature. I obtained flow data for the months of March through September, 1995 through 2010, from the US Geological Survey gauging station at Wilkes-Barre, Pennsylvania (http://waterdata.usgs.gov/pa/nwis/uv?01536500, accessed February 2011). The gauging station was located in the middle of the study reach. I calculated mean flow for each month and then expressed those values as percent departures from the long-term monthly means. Percent departures from long-term means were needed when trying to apply the model from the upper Susquehanna River to the lower Susquehanna River.

Water temperature data for the upper Susquehanna River were not available so I used air temperature as a surrogate. I obtained air temperature data for the months of March through September, 1995 through 2010, from the National Weather Service observation station at the Wilkes-Barre/Scranton International Airport (http://www.erh.noaa.gov/bgm/climate/avp.shtml, accessed February 2011). The only exception was March 1995 because these data were missing from the database. The weather station, located 5.6 km east of the river, is approximately in the middle of the study reach. I substituted mean monthly air temperature for the mean monthly river temperature values. Hoxmeier et al. (2006) used a similar technique and were able to demonstrate a strong (p < 0.0001) correlation between cooling degree days and mean summer water temperatures.

The variables I chose for entry to the model were those that demonstrated significant correlations to age-0 Walleye CPH. To minimize multicollinearity, however, I eliminated one of each set of variables that were significantly correlated to each other. Next I split the age-0 CPH data into training (1995 through 2006) and testing (2007 through 2010) data sets. The training data set was used to build the model and the testing data set was used to validate it. I constructed the model with multiple regression (Zar 1984) using forward selection based on the Akaike Information Criterion (Haddon 2001). Eigenvalue analysis was used to test for multicollinearity in the candidate models.

Finally, I tested for significant differences in the length of age-0 Walleye between good and poor recruitment years.
with a two sample Kolmogorov-Smirnov test. I defined good years as those where CPH exceeded the 75th percentile and poor years as those where CPH fell below the 25th percentile. The good years were 1995, 1999, 2005, and 2010. The poor years were 1998, 2000, 2002, 2003, 2006, and 2009. The purpose of this testing was to determine if warmer summer temperatures promoted faster growth and therefore higher survival.

**RESULTS**

Annual mean CPH of age-0 Walleye ranged from 0.50/hour in 2000 to 201.50/hour in 1999 (overall mean = 70.4; Table 1). Age-0 CPH generally followed the same trend at all sites in a given year (Figure 2), indicating that the factors which influenced year class strength were functioned across all sampling sites.

The fitted Ricker curve for age-3 and older Walleye was \( \log_e(R/S) = 3.2626 - 0.3073S \). The intercept was significant \( (p = 0.012) \) but the slope was not \( (p = 0.420) \). Further, the overall model failed to explain a significant amount of variation in year class strength \( (F = 0.695; df = 1, 13; p = 0.420; \text{adjusted } r^2 = -0.022) \). The same was true for age-4 and older \( (F = 0.261; df = 1, 13; p = 0.618; \text{adjusted } r^2 = -0.056) \) and age-5 and older \( (F = 2.852; df = 1, 13; p = 0.115; \text{adjusted } r^2 = 0.117) \) Walleye.

Correlation analysis found six variables that significantly influenced Walleye year class strength (Table 2). Among the biotic variables, year class strength was significantly correlated with CPH of age-1 and older Walleye \( (p = 0.006) \) in the current year and with CPH of age-0 Walleye in the previous year \( (p = 0.004) \). Both correlations were negative.

There were four significant correlations among the abiotic variables. These were flow in May \( (p = 0.001) \) and

---

**Table 1. Mean catch per hour of age-0 Walleye in the upper Susquehanna River from 1995 through 2010. NS = Not Sampled.**

<table>
<thead>
<tr>
<th>Year</th>
<th>Wysox</th>
<th>Tunkhannock</th>
<th>Union</th>
<th>Bloomsburg</th>
<th>Annual Mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>1995</td>
<td>155.13</td>
<td>204.71</td>
<td>NS</td>
<td>NS</td>
<td>179.92</td>
</tr>
<tr>
<td>1996</td>
<td>15.00</td>
<td>13.00</td>
<td>NS</td>
<td>NS</td>
<td>14.00</td>
</tr>
<tr>
<td>1997</td>
<td>30.00</td>
<td>91.00</td>
<td>NS</td>
<td>NS</td>
<td>60.50</td>
</tr>
<tr>
<td>1998</td>
<td>4.00</td>
<td>8.00</td>
<td>NS</td>
<td>6.00</td>
<td>6.00</td>
</tr>
<tr>
<td>1999</td>
<td>104.00</td>
<td>212.00</td>
<td>327.00</td>
<td>163.00</td>
<td>201.50</td>
</tr>
<tr>
<td>2000</td>
<td>0.00</td>
<td>0.00</td>
<td>1.98</td>
<td>0.00</td>
<td>0.50</td>
</tr>
<tr>
<td>2001</td>
<td>3.96</td>
<td>75.00</td>
<td>178.64</td>
<td>7.77</td>
<td>66.34</td>
</tr>
<tr>
<td>2002</td>
<td>1.02</td>
<td>0.00</td>
<td>12.62</td>
<td>0.00</td>
<td>3.41</td>
</tr>
<tr>
<td>2003</td>
<td>28.43</td>
<td>21.57</td>
<td>9.80</td>
<td>15.69</td>
<td>18.87</td>
</tr>
<tr>
<td>2004</td>
<td>17.00</td>
<td>33.66</td>
<td>69.31</td>
<td>36.00</td>
<td>38.99</td>
</tr>
<tr>
<td>2005</td>
<td>193.07</td>
<td>103.00</td>
<td>94.12</td>
<td>NS</td>
<td>130.06</td>
</tr>
<tr>
<td>2006</td>
<td>4.90</td>
<td>14.00</td>
<td>12.87</td>
<td>10.48</td>
<td>10.56</td>
</tr>
<tr>
<td>2007</td>
<td>63.00</td>
<td>98.00</td>
<td>174.00</td>
<td>39.00</td>
<td>93.50</td>
</tr>
<tr>
<td>2008</td>
<td>52.00</td>
<td>133.67</td>
<td>111.00</td>
<td>NS</td>
<td>98.89</td>
</tr>
<tr>
<td>2009</td>
<td>7.07</td>
<td>11.04</td>
<td>39.96</td>
<td>25.49</td>
<td>20.89</td>
</tr>
<tr>
<td>2010</td>
<td>149.45</td>
<td>106.86</td>
<td>331.96</td>
<td>139.60</td>
<td>181.97</td>
</tr>
</tbody>
</table>

Grand Mean: 70.37
Table 2. Simple correlations between natural log transformed catch per hour values of age-0 Walleye to biotic and abiotic variables. Bold type indicates a statistically significant (p < 0.05) result.

<table>
<thead>
<tr>
<th>Variable</th>
<th>t</th>
<th>df</th>
<th>p</th>
<th>r</th>
<th>r²</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age-1+ Smallmouth Bass</td>
<td>-0.729</td>
<td>11</td>
<td>0.481</td>
<td>-0.215</td>
<td>0.046</td>
</tr>
<tr>
<td>Age-1+ Walleye</td>
<td>-3.228</td>
<td>14</td>
<td>0.006</td>
<td>-0.653</td>
<td>0.426</td>
</tr>
<tr>
<td>Esocids</td>
<td>-0.072</td>
<td>14</td>
<td>0.944</td>
<td>-0.019</td>
<td>0.000</td>
</tr>
<tr>
<td>Age-0 Walleye (previous year)</td>
<td>-3.506</td>
<td>13</td>
<td>0.004</td>
<td>-0.697</td>
<td>0.486</td>
</tr>
<tr>
<td>March flow</td>
<td>-0.010</td>
<td>14</td>
<td>0.922</td>
<td>-0.027</td>
<td>0.001</td>
</tr>
<tr>
<td>April flow</td>
<td>-0.699</td>
<td>14</td>
<td>0.496</td>
<td>-0.184</td>
<td>0.034</td>
</tr>
<tr>
<td>May flow</td>
<td>-4.310</td>
<td>14</td>
<td>0.001</td>
<td>-0.755</td>
<td>0.570</td>
</tr>
<tr>
<td>June flow</td>
<td>-2.710</td>
<td>14</td>
<td>0.017</td>
<td>-0.586</td>
<td>0.343</td>
</tr>
<tr>
<td>July flow</td>
<td>-1.879</td>
<td>14</td>
<td>0.081</td>
<td>-0.449</td>
<td>0.202</td>
</tr>
<tr>
<td>August flow</td>
<td>-0.809</td>
<td>14</td>
<td>0.432</td>
<td>-0.211</td>
<td>0.044</td>
</tr>
<tr>
<td>September flow</td>
<td>-0.199</td>
<td>14</td>
<td>0.845</td>
<td>-0.053</td>
<td>0.003</td>
</tr>
<tr>
<td>October flow</td>
<td>-0.327</td>
<td>14</td>
<td>0.748</td>
<td>-0.087</td>
<td>0.008</td>
</tr>
<tr>
<td>March air temperature</td>
<td>-1.992</td>
<td>13</td>
<td>0.068</td>
<td>-0.484</td>
<td>0.234</td>
</tr>
<tr>
<td>April air temperature</td>
<td>0.070</td>
<td>14</td>
<td>0.945</td>
<td>0.019</td>
<td>0.000</td>
</tr>
<tr>
<td>May air temperature</td>
<td>-0.086</td>
<td>14</td>
<td>0.933</td>
<td>-0.023</td>
<td>0.001</td>
</tr>
<tr>
<td>June air temperature</td>
<td>2.255</td>
<td>14</td>
<td>0.041</td>
<td>0.516</td>
<td>0.266</td>
</tr>
<tr>
<td>July air temperature</td>
<td>2.280</td>
<td>14</td>
<td>0.039</td>
<td>0.520</td>
<td>0.270</td>
</tr>
<tr>
<td>August air temperature</td>
<td>1.129</td>
<td>14</td>
<td>0.278</td>
<td>0.289</td>
<td>0.084</td>
</tr>
<tr>
<td>September air temperature</td>
<td>1.657</td>
<td>14</td>
<td>0.120</td>
<td>0.405</td>
<td>0.164</td>
</tr>
</tbody>
</table>

Table 3. Correlation matrix for variables that were significantly correlated to age-0 Walleye catch per hour. Bold type indicates a significant correlation.

<table>
<thead>
<tr>
<th>Variable 1</th>
<th>Variable 2</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age-1+ Walleye</td>
<td>Age-0 Walleye (prev. year)</td>
<td>0.060</td>
</tr>
<tr>
<td>Age-1+ Walleye</td>
<td>May flow</td>
<td>0.001</td>
</tr>
<tr>
<td>Age-1+ Walleye</td>
<td>June flow</td>
<td>0.281</td>
</tr>
<tr>
<td>Age-1+ Walleye</td>
<td>June air temperature</td>
<td>0.715</td>
</tr>
<tr>
<td>Age-1+ Walleye</td>
<td>July air temperature</td>
<td>0.555</td>
</tr>
<tr>
<td>Age-0 Walleye (prev. year)</td>
<td>May flow</td>
<td>0.000</td>
</tr>
<tr>
<td>Age-0 Walleye (prev. year)</td>
<td>June flow</td>
<td>0.919</td>
</tr>
<tr>
<td>Age-0 Walleye (prev. year)</td>
<td>June air temperature</td>
<td>0.919</td>
</tr>
<tr>
<td>Age-0 Walleye (prev. year)</td>
<td>July air temperature</td>
<td>0.120</td>
</tr>
<tr>
<td>May flow</td>
<td>June flow</td>
<td>0.166</td>
</tr>
<tr>
<td>May flow</td>
<td>June air temperature</td>
<td>0.212</td>
</tr>
<tr>
<td>May flow</td>
<td>July air temperature</td>
<td>0.088</td>
</tr>
<tr>
<td>June flow</td>
<td>June air temperature</td>
<td>0.067</td>
</tr>
<tr>
<td>June flow</td>
<td>July air temperature</td>
<td>0.959</td>
</tr>
</tbody>
</table>

| June air temperature                 | July air temperature                 | 0.027|
June (\(p = 0.017\)) and air temperature in June (\(p = 0.041\)) and July (\(p = 0.039\)). Flow correlations were negative while temperature correlations were positive. The strongest significant correlation was May flow (\(r^2 = 0.570\)) and the weakest significant correlation was June air temperature (\(r^2 = 0.266\)). There was no significant correlation between year class strength and flow during sampling in October (\(p = 0.748\)).

Some of the significant variables were correlated to each other. May flow was significantly correlated with CPH of age-1+ Walleye from the current year (\(p = 0.001\)) and with CPH of age-0 Walleye from the previous year (\(p < 0.001\); Table 3). June air temperature was significantly correlated with July air temperature (\(p = 0.027\)). I removed CPH of age-1+ Walleye, CPH of age-0 Walleye, and June air temperature from consideration in the model. These three variables explained less of the variation in age-0 CPH than their correlates.

The initial variable in the multiple regression model was May flow. This model was significant (\(F = 12.57, p = 0.005, \text{adjusted } r^2 = 0.513\); Table 4). Each of the remaining variables (June flow, the interaction between May and June flow, and July air temperature) improved the model fit (adjusted \(r^2 = 0.733, 0.839, \text{and } 0.917\), respectively). The addition of July air temperature, however, caused significant multicollinearity (condition number = 349.85). Grand mean centering this variable removed the problem (condition number = 5.832). The final model was \(\log_e(\text{age-0 CPH}) = -4.9708 + -0.893 \times (\text{May flow}) + -0.957 \times (\text{June flow}) + -1.023 \times (\text{May flow: June flow}) + 0.403 \times (\text{grand mean centered July air temperature}).\) This model was significant (\(F = 19.38, p = 0.001\)) and explained 86.7% of the variation in the training data set. Autocorrelation was insignificant (Durbin-Watson test, \(p = 0.349\)) and the model residuals approximated a normal distribution (Shapiro-Wilk test, \(W = 0.900, p = 0.159\)).

Predicted CPH values from the model based on the training data set (1995 – 2006) closely matched actual CPH values from the test data set (2007 – 2010). Average prediction error for the four test years was 15.7% (Table 5). In all cases the actual CPH values fell within the 95% confidence limits of the predicted values. However, the confidence intervals were wide enough, especially when the model predicted large year

<table>
<thead>
<tr>
<th>Year</th>
<th>Actual Catch Per Hour</th>
<th>Predicted Catch Per Hour</th>
<th>Percent Error</th>
<th>Lower 95% Confidence Limit</th>
<th>Upper 95% Confidence Limit</th>
</tr>
</thead>
<tbody>
<tr>
<td>2007</td>
<td>93.50</td>
<td>71.12</td>
<td>-23.93%</td>
<td>34.54</td>
<td>146.45</td>
</tr>
<tr>
<td>2008</td>
<td>98.89</td>
<td>109.02</td>
<td>10.25%</td>
<td>57.26</td>
<td>207.56</td>
</tr>
<tr>
<td>2009</td>
<td>20.89</td>
<td>25.06</td>
<td>19.96%</td>
<td>10.05</td>
<td>62.45</td>
</tr>
<tr>
<td>2010</td>
<td>181.97</td>
<td>197.56</td>
<td>8.57%</td>
<td>81.72</td>
<td>477.64</td>
</tr>
</tbody>
</table>

Average Prediction Error: 15.7%
classes, that they had little practical value (Figure 3).

Mean length of age-0 Walleye was 179.4 mm for strong year classes and 178.4 mm for weak year classes. The length-frequency distributions of age-0 Walleye were not significantly different between strong and weak years (two-sample Kolmogorov-Smirnov test, D = 0.25, p = 0.964).

DISCUSSION

Walleye year class strength in the upper Susquehanna River was highly variable. Mean CPH values ranged from 0.50 to 201.50/hour. Comparatively, year class strength was also variable in the upper Mississippi River, which had a maximum CPH value of 107.10/hour (Pitlo 2002). Year class strength in the upper Susquehanna River was generally greater than in the upper Mississippi River, but comparable data for other rivers were not available.

Walleye populations in lakes have typically exhibited stock-recruitment relationships (Madenjian et al. 1996; Hansen et al. 1998; Beard et al. 2003). However, no such relationship was evident for the upper Susquehanna River. It was possible that the relationship did not exist. Environmental variables may have influenced year class strength independent of spawning stock size (Van Den Avyle and Hayward 1999). Alternatively, it was possible that the relationship existed but could not be detected. In a review of marine flatfish data, Iles (1994) assumed that a stock-recruitment relationship existed but failed to detect it in 14 out of 20 species.

Data from the upper Susquehanna River data may not have been suitable to detect a stock-recruitment relationship. Indexing adults during the early spring would have given more accurate estimates of spawning stock size than sampling during the fall, and sampling larvae would have given more accurate measurements of the stock-recruitment relationship than sampling juveniles. Additionally, Maceina and Pereira (2007) recommended using at least 20 years of data to model stock-recruitment relationships but this study only used 16 years.

Environmental variables strongly influenced Walleye year class strength in the upper Susquehanna River. May flow alone accounted for 57.0% of the variation and a model consisting solely of abiotic variables accounted for 86.7% of the variation. Biotic variables also influenced year class strength but did not contribute to the multiple regression model.

The relationship between flow and year class strength for the upper Susquehanna River was negative. Others have demonstrated relationships between flow in rivers and Walleye year class strength. Some relationships were negative (Mion et al. 1998; Anderson et al. 2006) while others were positive (Swain 1974; Johnston et al. 1995; Paul 2013), but all were based on larval drift and survival. The larval drift stage in the upper Susquehanna River generally occurs in April and there was no relationship between April flow and year class strength.

June and July air temperatures exhibited positive relationships with year class strength in the upper Susquehanna River. Positive relationships between temperature and Walleye year class strength have also been shown in lakes (Kallemein 1987; Madenjian et al. 1996; Quist et al. 2003; Hoxmeier et al. 2006) and in the upper Mississippi River (Pitlo 2002). In many of these studies, however, temperature influenced year class strength during the early spring when fish were spawning, eggs were incubating, and/or larvae were hatching. In the upper Susquehanna River temperature influenced year class strength in late spring and summer when the fish were juveniles.

I hypothesized that warmer air temperatures in June and July promoted faster growth and therefore higher survival. Such was not the case, however, as mean length of age-0 Walleyes in the upper Susquehanna River was the same for poor and good year classes. It was possible that density dependent effects (Sass et al. 2004) masked the influence of temperature on juvenile growth. Nevertheless, the specific mechanism through which temperature operated on year class strength was unknown.

The multiple regression model based on the 1995 - 2006 data successfully predicted age-0 CPH for 2007 - 2010. Average prediction error was 15.7%, which was acceptable for management purposes. Although successful for the upper Susquehanna River, the model may be specific to that river. For example, I used the model to predict Walleye year class strength in the lower Susquehanna River, but predictions for that reach were always much higher than actual values. One reason the model failed was because air temperatures for the lower river were higher than those for the upper river. The relationship between July air temperature and Walleye year
class strength was positive for the upper Susquehanna but negative at the higher temperatures of the lower Susquehanna. This suggests that the true relationship between July air temperature and walleye year class strength was quadratic, with high survival occurring at moderate temperatures and low survival occurring at higher and lower extremes.

In summary, this study provided one of the first examinations of Walleye year class strength in a free flowing river. Various biotic and abiotic factors influenced year class strength, but more research is needed to identify and refine model variables. A model based solely on abiotic factors successfully predicted year class strength for the upper Susquehanna River but may be specific to that reach.

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LITERATURE CITED


NATIVE AMERICANS IN THE SUSQUEHANNA RIVER VALLEY:
AN ARCHAEOLOGICAL SUMMARY†

DAVID J. MINDERHOUT1

Bloomsburg University, Bloomsburg, PA 17815

ABSTRACT

Native Americans have lived in the Susquehanna River Valley for at least 10,000 years. Archaeological research along the banks of the river have discovered a rich prehistory stretching from the Paleoindian era through the Archaic and Woodland periods up to and through early contact with Europeans. This paper summarizes the major environmental changes that affected the cultural evolution of Native Americans over this long time span and the technological innovations that occurred. Because the same areas in which Native Americans made their camps or villages have also been desirable areas for subsequent European settlement and industrial development, the archaeological record is incomplete and a number of questions remain unanswered and require additional research. Among them are the origins of various archaeological cultures; the size of native populations at in various time periods; and why agriculture/horticulture was so late in developing along the river. A brief discussion of Native American migrations and relocation in the Contact Period is included. Attention is also given to the emergence of organizations over the last two decades in the river basin which claim native descent.

INTRODUCTION

Archaeological and historical research have confirmed that Native Americans lived in the Susquehanna River Valley for at least 10,000 years. Evidence of Native American activity and technology can be found in abundance along both the North and West Branches of the river - as well as the main branch of the river that subsequently flows into the Chesapeake Bay. Investigative research by professional and amateur archaeologists has occurred in the region since the 1920's, and artifact collectors have recovered projectile points, pottery sherds and other detritus of everyday existence for long before that. Indeed, every rise and subsequent receding of the river reveals the existence of more artifacts for enthusiastic collectors, and each spring often finds those collectors scanning newly plowed fields along the river for whatever they can find; the author has seen private collections numbering in the thousands of items. Nonetheless, despite the abundance of artifacts and the many centuries of native habitation, many questions remain about native life along the river, and the archaeological record remains incomplete (Carr and Adovasio 2002; Raber and Cowin 2003; Minderhout 2013).

There are three important reasons for this lack of a complete record. The first, and most significant, is that the areas in which Native Americans made their camps or villages have also been desirable locations for colonial-era and modern farms, construction, and industrial development. In their overview of the North Branch of the river for the U.S. Army Corps of Engineers in 1988, Geidel et al.(1988) noted that “Early researchers (Wren 1914; Schrabisch 1926) reported a large number of sites in the Wyoming Valley area. Some of these sites were already severely disturbed when they were reported. Many of these have been obliterated by subsequent development of the valley.” (Geidel, et al. 1988). Indeed, much of the contemporary archaeological research along the river occurs as a part of required environmental impact reports conducted before modern construction occurs. Even if an archaeological site is deemed significant enough to warrant careful excavation before construction begins, the time constraints under which the archaeologists work mean that the site will be destroyed before a thorough investigation is completed.

A second reason has to do with the nature of native life itself. For most of the time Native Americans have lived along the Susquehanna River, they have been socially organized into small, nomadic bands. These bands seldom maintained a camp long enough for a wide variety of evidence to be recovered in an archaeological excavation. Highly desirable locations have been used and reused as encampments in many places along the river for centuries, but few occupations left behind much other than a few stone tools and the remains of hearths. Foraging bands have few material possessions - basically only the essential tools for their survival. Even after agriculture was introduced into the river valley around 3000

†Accepted for publication March 1, 2014.
†Corresponding Author: Professor Emeritus of Anthropology, 63 Guys Lane, Bloomsburg, PA 17815, (570)594-5344
years ago, native communities remained small and were often abandoned periodically as the soil in an area became less fertile and wild game and plant foods became overutilized, a process of perhaps fifteen years in contact-era villages. Except for stone tools - and the flakes and fragments left behind in their manufacture - and broken pottery after its introduction - there is little in the material culture of native cultures to be preserved and recovered by an archaeologist centuries later. Much of what existed must be inferred. For example, for centuries, native cultures made dwellings out of branches set into the soil and bent into hemispherical or loaf shapes; these frameworks were subsequently covered with a bark sheathing to create a shelter. In Pennsylvania’s acid soils, these building materials quickly decompose, but the process of decomposition discolors the soil in which a branch was set - called a post mold by archaeologists. Thus, the size and shape of a dwelling can be inferred by the position of post molds in a carefully excavated site. But, as can be seen, these remains are nothing like Egyptian or Mayan ruins which were the product of huge, permanent communities building in stone.

The final reason - and the one less often spoken of - has to do with the presence or absence of a professional archaeologist in a given area. Over the last 100 years, there have been relatively few archaeologists resident in Pennsylvania to conduct the necessary research; a literature review of Pennsylvania prehistoric archaeology reveals the same names repeated over the decades again and again. Often this has to do with the presence of a supporting institution, such as a university or the Pennsylvania State Museum in Harrisburg, in a given area. As a result, certain counties along the river are well known in the archaeological record. These include Dauphin and Lancaster Counties, where archaeologists from the State Museum or Franklin & Marshall University could be found, or Lycoming County, where the archaeologist James Bressler, in conjunction with the Lycoming County Historical Society, worked for many years. Other counties along the river, such as Columbia and Montour Counties are underrepresented in the archaeological record, not because there was nothing there to be found, but more often because there was no resident archaeologist to take a professional interest. As an example, in the previous reference by Geidel et al. (1988) it is noted, for instance, that almost no archaeology had been conducted on the North Branch of the river or its tributaries.

As a result, there are many unanswered or unresolved questions about prehistoric Native American communities in the Susquehanna River Valley. It is clear, however, that in the 10,000 years of the archaeological record, native cultures were not uniform and unchanging. The major changes that have been recorded are conventionally divided into three eras by archaeologists, the Paleoindian (16,000 to 10,000 years Before Present [BP]) Archaic (10,000 to 3000 BP) and the Woodland (3000 BP to European contact in the early 17th century). All of these eras are represented along the river - and often in the same site.

**THE PALEOINDIAN ERA**

The oldest archaeological site in Pennsylvania, and indeed one of the oldest, reliably dated archaeological sites in the Americas, is the Meadowcroft Rock Shelter, located in the southwest corner of the state. This site, excavated by James Adovasio and his associates, beginning in 1973, reveals centuries of repeated habitation with clearly stratified occupation layers. The earliest of these was radiocarbon dated by Adovasio to 16,000 years BP; other sources, such as Neusius and Gross (2007), choose to average the earliest dates found at the Shelter to arrive at a date of 14,500 years BP. For many years, this site was a source of controversy among archaeologists largely because Adovasio’s dates did not conform to the standard theories of the peopling of the Americas at that time. Discoveries made in Clovis and Folsom, New Mexico in the 1920’s revealed a foraging culture that existed in the Americas 11,500 BP, a date that corresponded with what geologists then believed about the opening of the land bridge across the Bering Strait between Siberia and Alaska 12,000 years ago. A series of archaeological discoveries across the Americas over the next few decades, which revealed a similar stone tool technology all dating to between 10,000 and 11,500 years, created an insistence that no Native Americans could have been in the Western hemisphere before 11,500 years ago. These people came to be called Paleoindians. Adovasio’s careful research at Meadowcroft, as well as the collaboration of his radiocarbon dates and the subsequent discovery of other older sites in places such as Chile and Virginia, eventually led most archaeologists to accept an earlier connection between the Old and New Worlds.

However, in the Susquehanna River Valley, the oldest known Paleoindian site is the Shoop Site, located in Dauphin County, about 16 miles from the river. Originally discovered in the 1920’s by George Gordon, and subsequently partially surveyed and excavated by John Witthoft of the State Museum, this site sits on a hilltop. Typical Paleoindian stone tools, including projectile points and scrapers, are scattered throughout the site. A more recent excavation of the site by the State Museum in 2009 dated the site to 11,000 years B.P. In Pennsylvania, this time period, and the archaeological sites associated with it, falls during the last period of glaciation or Ice Age. This “Ice Age” was not as often imagined, in that the entire state was not covered in ice. Rather a line of glaciers stretched across the state from the Delaware Water Gap in the east to just north of Williamsport in the central region to New Castle in the west. A border region of arctic tundra perhaps 40 kilometers wide bordered the ice, but the rest of the state was ice-free. Much of the ice-free area was covered with a Canadian-like sparse boreal forest, but evidence shows that the river valleys were bordered with
deciduous forests, making them a suitable foraging area for Paleoindians. (The Susquehanna River existed in its approximate same location at this time, though the river was longer, in that the Chesapeake Bay had not yet formed. The river, therefore, flowed directly to the Atlantic Ocean.)

Paleoindians left very few artifacts behind, and so it is hard to say with precision what their lives might have been like. It is conventional to assume that they lived much like Inuit hunter-gathers of the Arctic tundra in Alaska and northern Canada in the first half of the 20th century. Other foragers studied by anthropologists in the early 20th century lived fairly similar existences. Thus, Paleoindians are thought to have lived in small, extended family groups. They were probably nomadic, moving from camp to camp as resources allowed. If they were like more modern foragers, there would have been a complementary gender division of labor in which men hunted the larger game animals, such as deer or caribou, and women gathered wild plant foods and smaller sources of animal protein, such as birds or rabbits. The Susquehanna River undoubtedly provided a rich abundance of fish, eels, freshwater shellfish and edible aquatic plants then as it would throughout the prehistoric period.

The stone tool most often associated with Paleoindian culture is the Clovis point, a long tapered laurel-leaf shaped point, made to fit on the tip of a spear. A Clovis point often has an impression along the length of its base, called a flute, which made it easier to secure it to a wooden spear. In the Southwest and Mexico, Paleoindian hunting sites have been excavated with Clovis points imbedded in or near the remains of large mammals, such as mammoths or the extinct giant bison. Megafauna, such as mammoths, certainly existed in the Northeast 10,000 years ago, but by date no human tools have been found in association with their remains. Instead, the few food remains found at Paleoindian sites in the Northeast include charred fish bones and the bones of deer, caribou and moose, as well as a few remains of edible plants. While the long, beautifully-made Clovis points dominate descriptions of Paleoindian stone tools, the most commonly found Paleoindian tool is a stone scraper, used perhaps to deflesh hides or shape or debark wood. Scrapers are the most abundant tool found at the Shoop Site.

Perhaps the most intriguing aspect of a Paleoindian tool assemblage in Pennsylvania is the stone from which it is made. Not every rock or stone is suitable for making a tool, and “stone age” cultures are often very selective about their raw materials, trading or sometimes traveling great distances to find suitable stone. This is particularly striking in the case of Pennsylvania Paleoindian sites, where tools have been found made of rocks from as far as 800 kilometers away from the site. One particularly desirable stone appears to have been what is called Onondaga chert, a flint found in New York State. Onondaga chert tools have been found at the Shoop Site. The presence of stone from distant locations suggests either that Paleoindians covered great distances in search of highly desirable raw materials, or that they engaged in trade with neighboring groups. Neither suggestion can be confirmed from the current evidence, and some archaeologists have argued for more prosaic explanations - such as stone being displaced by glacial action or washing downstream in a river.

The Shoop Site, situated as it is on a hilltop, is interpreted as a place where a Paleoindian encampment could keep watch over the surrounding valleys for the movement of large game; other such Paleoindian sites are found throughout the state. But Paleoindians tools are also found in sites along the Susquehanna River itself, especially at the bottom of multi-layered, stratified sites.

THE ARCHAIC ERA

By 10,000 years ago, the climate in the Susquehanna River Valley, as well as in the rest of Pennsylvania was becoming warmer and more like contemporary conditions. Initially a dense coniferous forest covered the area, but by 9000 B.P. a more diverse, deciduous forest dominated by oaks, chestnuts, hickories and other trees dominated both the Valley and the state. This deciduous forest could support a wide variety of animal life, and thus greater populations of humans. Some archaeologists suggest that the population of Pennsylvania increased five-fold during this period. If that was so, then the territories over which individual bands of foragers roamed probably became smaller than in the Paleoindian Era, and the utilization of resources within each territory became more intense. One indication of this is the decreased use of exotic stone from distant sources. If Paleoindians collected their own stone, they must have traveled a hundred miles or more in the course of an annual cycle; this also suggests that their numbers were few. If they were like 20th century foragers, they probably had only limited contact with other bands, with months or even years going by without making contact with people other than their own extended families. (See Lee and Devore 1966; Dahlberg 1981 for discussions of 20th century foragers and their economies.) In the Archaic Era, people made more use of locally available stone, even though the environment was warmer and probably less difficult.

Technology changed as well. No longer were flintknappers turning out long Clovis spear points; shorter projectile points with notched bases become the signature tool of the Archaic Era. These points were still attached to spears, but it is inferred that Archaic hunters had added the spear thrower or atlatl to their weaponry. A spear thrower is a notched wooden stick, perhaps 12 to 18 inches in length. The butt of the spear is placed against the notch, and the hunter then hurls the spear by grasping the handle of the spear thrower. This increases the axis of and the force behind the throw, allowing the hunter to hurl a spear farther and faster than by the force of the arm alone. Spear throwers were made of wood, and none has survived to the modern era from the
Archaic, but stone spear thrower weights are often found in Archaic sites. A spear thrower weight, often called a banner stone, is a flat rock that has been chipped to produce a notch that sits over the handle of the thrower behind the spear; the extra weight adds force to the throw. These efficient weapon innovations are seen in hunting cultures world-wide at about this same time. Archaic peoples along the Susquehanna are also notching flat stones in this time period to serve as net sinker weights, suggesting the use of fiber nets for fishing. An important part of Native American subsistence along the river would have been the anadromous fish, such as shad, that migrated up the Susquehanna from the Atlantic (see Becker 2006) in such enormous quantities to spawn that an 18th century Moravian missionary would record Native Americans on the North Branch of the river catching two thousand shad in a single morning; the fish were smoked or dried for later use. Nets would have been a very useful tool in this circumstance. (Hamilton 1957).

Other technological changes seen during the Archaic Era are the greater frequency of pounding and grinding tools, suggesting that nuts, berries and seeds were becoming a more important part of native diets. Greater regional variety in tool kits also becomes apparent. While projectile points with notched bases continued to be the characteristic Archaic spear point, local differences in manufacture and stone type grow. (See Fogelman 1988).

By the end of the Archaic Era, pottery is seen for the first time in the Susquehanna River Valley. The idea of storage or cooking vessels was probably not new to Native Americans in the region. Baskets and skin vessels were undoubtedly in use long before the appearance of ceramics, but because of the non-durable materials from which they are made, they do not survive in the archaeological record. But even after contact with Europeans, and in some cases into the 19th century, Europeans would record Native Americans heating water for cooking in skin or birch bark containers. (To do this, rocks are heated in an open fire and then transported to a container of water by wooden carrying tongs; eventually the water is raised to a temperature that will cook food.) The idea of vessels was not new to the Susquehanna region, but the idea of ceramic pottery was. It is believed that pottery was introduced into the region from the Southeast, where it was in use much longer. This inference is supported by the fact that the earliest pots were shaped like steatite (or soapstone) containers, which are found in Late Archaic sites, and which had also originated in the Southeast; because soapstone is not found natively in Pennsylvania, it, too, must have been a trade item. (See Neusius and Gross 2007) When steatite is first removed from the ground, it is relatively soft and can be carved; it also has the soapy surface texture that gives it its common name. The soapstone vessels found in the Southeast and in Late Archaic sites are shallow, flat-bottomed vessels with low walls and sometimes lugged handles; they may have been used for cooking or as a ceremonial vessel, since they are not common. The first pottery to appear in the Late Archaic in the Susquehanna region mimics these shallow steatite vessels. Soon, however, the shallow bowls would become replaced in Native American life by the more characteristic tall vessel with a thin tapered wall, a raised rim and surface decorations from cords, net impressions or surface incising. Once pottery is introduced into the river area, broken pottery sherds become a common part of camp or village detritus.

In general, most archaeologists seem to agree that the Archaic was a period of increasingly more benign environments/climate, population growth, reduced territories in which to move around, and increased regional variation in technology. In the early Woodland Era, however, it appears that Susquehanna populations began to decline.

THE WOODLAND ERA

By 3000 years ago, the climate in the Susquehanna River Valley was very much like what it is today, and Native Americans living in the river valley began to exhibit technological innovations and social patterns very much like what the first Europeans to arrive in the Valley encountered in the early 17th century. As noted in the last section, pottery was well established in native culture. in the late Archaic, and the Woodland Era would eventually see the bow and arrow and agriculture added to the Archaic technological array. By the end of the Era, just before European contact, Woodland peoples would be living in large, stockaded villages dependent on the cultivation of what the Iroquois call the Three Sisters: maize or corn, squash and beans.

However, at the beginning of the Woodland Era there is an apparent decline in population along the river that has long puzzled archaeologists. Douglas MacDonald suggested in 2003 that populations (based on the number of living sites discovered) declined between 65 and 80% 3000 years ago, not only in the Susquehanna River Valley, but throughout the Middle Atlantic geographical region. Given the abundance and relatively temperate nature of the Early Woodland environment, what could account for this decline? Some have suggested a massive migration out of the Mid-Atlantic to the south, though there is no evidence in the southern areas of a sudden population increase. Jay Custer argued in 2000 that the existence of fewer sites overall was a result of greater concentration of people in fewer and fewer communities - communities that were larger and more permanent. Again, no evidence has been seen to support this connection, i.e., while it is true that Woodland settlements did eventually become larger and more permanent, especially after the introduction of agriculture, there is no evidence of this in the Early Woodland Era.

Raber (2008) has suggested a seemingly more prosaic explanation that is tied to questions raised at the beginning of this essay - that what appears to be an overall population decline is actually a result of the lack of comprehensive
archaeological survey and excavation process. As he notes (2008,16), “...to infer depopulation, we must assume that there exists a reliable, unbiased sample of archaeological sites for all periods and that there is a direct and unambiguous relationship between the number of sites and prehistoric populations.” But because of the problems noted earlier, “…site recovery has been spotty and unsystematic...few areas have been subject to systematic professional survey and few sites have been adequately tested and evaluated.” This applies, according to Raber, to both the Susquehanna River Valley and Pennsylvania generally. Raber also suggests that Early Woodland sites are difficult to recognize for two reasons. First, the sites are deeply buried along the river and the streams and other waterways that flow into it, making Early Woodland sites and artifacts difficult to find. Second, the differences between projectile points and other technological remains from the Late Archaic and Early Woodland are small and hard to quantify. Early Woodland peoples were still living as foraging bands in camp sites that were briefly inhabited; the larger, agriculture-based, more permanent settlements of the Middle and Late Woodland had yet to appear. Thus, not only is the archaeological record incomplete for the Early Woodland time period, but also the stone technology in use could easily be mistaken for an Archaic assemblage.

**THE INTRODUCTION OF AGRICULTURE/HORTICULTURE**

Native people in the Susquehanna River Valley had been collecting and consuming wild plant foods for centuries before evidence of deliberate cultivation occurs. While the hunting of large game animals tends to capture the imagination of observers of foraging cultures, anthropologists know from studies of more modern foragers that day-to-day consumption is often dependent on plant foods and small animals and fish. This is one reason anthropologists have replaced the older label, “hunting-and-gathering,” for these band-level societies with the more descriptively accurate term, “foraging.” (see Lee and DeVore 1968). In the archaeological record, the remains of large animals tend to be preserved longer and better than delicate fish bones and seeds or pollen from collected plants, though as archaeological discovery techniques have improved over the years, much more evidence of this type has been recovered, even from Paleoindian sites, such as the 10,000 year-old Shawnee-Minisink site in the Delaware River Valley, near the Delaware River Gap. As noted earlier, in the Archaic Era, as deciduous forests replaced coniferous ones, the remains of tree nuts and the tools to process them become much more common in archaeological sites. In the Early Woodland Era, the remains of plants such as goosefoot (Chenopodium sp.) which are known to have been collected and even apparently cultivated from sites in the Midwest and New York State appear in sites in Pennsylvania. There is also evidence from the contact period that Native Americans deliberately transplanted nut tree seedlings, wild strawberries and other berry-producing wild plants to make them more readily available to native communities (see Minderhout and Franz 2009). Actions like these would not appear in the archaeological record.

The domestication and cultivation of maize, beans and squash was established in Mexico by 6000 years ago, and gradually spread north and east into the rest of North America (see Neusius and Gross [2007] for a discussion of this process). The archaeological record to date suggests that the three crops did not arrive as a package in the river valley, but instead appear at different times - squash by 4900 BP, maize by 1000 BP, and beans at 650 BP. (Minderhout 2013). The earliest dates for the cultivation of maize and beans in the Susquehanna River region are significantly later than those for other parts of the state; maize, for example, is found at the Meadowcroft Rock Shelter by 2300 BP. In fact, it appears from the archaeological record that Three Sisters cultivation was well underway in all the areas surrounding the Susquehanna River Valley, including the Delaware, Ohio-Allegheny and the Potomac River drainages. There is no obvious reason for the late start for cultivation in the Susquehanna region. It was certainly true that the rich natural environment of the region produced substantial quantities of animal and plant protein. As already noted, the annual river cycle of shad and other anadromous fish combined with the deer, bear, other wildlife and wild plants, provided a regular source of food,(3) which could have undermined the motivation to cultivate crops - but the same could be said of the other river valleys. Becker (2010) has already provided archaeological evidence and period literature documentation to show that this had happened with the Lenape in the 17th century in southeastern Pennsylvania, i.e., that the Lenape in that region did not practice agriculture even at this late date because of the abundance of wild foods in the lower Delaware River. Regardless, the late onset of agriculture in the Susquehanna region remains a question to be answered.

The form of agriculture that did eventually become established in the Susquehanna River Valley is called horticulture or extensive agriculture by anthropologists. Horticulture is still practiced today, primarily in the tropics, where it often takes the form of swidden or slash-and-burn agriculture. In the Susquehanna region, Native Americans in the Woodland and early contact periods would clear an area for planting near their settlements by first removing the small trees, shrubs and underbrush. Larger trees had to be removed more gradually, since stone ax heads cannot easily cut a full-growth tree like an oak. Rather, large trees were killed either by girdling - removing a strip of bark around the circumference of the trunk - or by setting a fire at the base of the tree. Once the trees had died, and their leaves had fallen, a crop could be planted in and around the remaining trunks. These were not continuous fields, as seen in modern
farms which use the land much more intensively than a horticulturalist. Rather, dirt and plant debris were piled into mounds or hills, and the seeds of maize, beans and squash were planted in them together. The three crops germinate at about the same time and grow together in a complementary fashion, with the vining beans using the corn stalks as support, and the squash vines growing across the ground to serve as a ground cover. Hills were spaced three to six feet apart from one another, but modern research estimates that as many calories per acre were generated in these fields as in modern intensive farming (see Mt. Pleasant 2006). However, since the fields were not fertilized (other than by composted leaves and stalks), these fields would become less productive over time. This would coincide with reductions in game animals as a result of continuous hunting. Thus, native communities would be required to move periodically to a more productive environment; 18th century contact era communities, such as the Mohawks of New York State, moved on average about every ten to twelve years. (Englebrecht 2003).

**MIDDLE/LATE WOODLAND CULTURES**

With the emergence of agriculture and pottery, native communities in the Susquehanna River Valley became larger and more permanent than the transient hunting camps of earlier periods. These larger communities translate into larger and more diverse archaeological sites and thus take on an identity in the archaeological record unlike those of earlier foragers. Thus, in the Woodland Period, two archaeological cultures figure prominently in the prehistory of the river valley. They are the Clemson Island Culture (1100 to 800 BP) and the Shenks Ferry Culture (800 to 500 BP). Both are named for the geographical location where they were first detected, not for their particular ethnicity, though archaeologists have certainly speculated on what contact-era cultures to which they might have been linked. Clemson Island is named for a large island in the Susquehanna River north of Harrisburg, Pennsylvania. Archaeologists were drawn to the site because of a large burial mound which was first excavated in 1929. Numerous archaeological surveys of the island and of Woodland sites on both the main and west branches of the river have shown that the Clemson Island people were a widely distributed and successful agricultural society. Both large permanent settlements and smaller camps are found in this time period, all linked by the distinctive conical pottery produced by Clemson Island people and their pattern of burials.

Clemson Island communities are of three types: larger spatially organized villages, smaller hamlets, and small camp sites. The differences between villages and hamlets are essentially those of size and organization. Villages show signs of planning, with homes placed in the center of the community and activity and storage areas surrounding the homes on the periphery. In particular, activities such as butchering game animals and smoking fish seem to have been kept away from homes. The homes themselves are oval or elongated with rounded corners. It is hard to not be reminded of contact-era Iroquois longhouses by them; Clemson Island pottery is also very similar to later Owasco and Iroquois ceramic traditions. At the Ramm’s Site, one house structure is roughly 31 meters long by 10 meters wide (95 feet by 35 feet), a very sizable structure which again reminds modern scholars of Iroquois longhouses. Iroquois longhouses housed several extended families linked matrilineally, or through the mother’s lineage, and some were over 32 meters or 100 feet in length.

Excavations of Clemson Island sites turn up evidence of the cultivation of maize, squash and beans, Chenopodium and wild barley, as well as the seeds of many wild plants, including blackberries and tree nuts. There is also abundant evidence of fishing and hunting. The small camp sites are thought to be hunting camps. By this point in the Woodland Period, the bow and arrow was widely in use, as evidenced by the small, triangular stone arrowheads that are typical of Middle and Late Woodland cultures. These projectile points were made of both imported stone, such as rhyolite, and local cherts or flints.

What led to the excavation of the first Clemson Island site was the obvious presence of a large burial mound, and mounds are found with many of the larger villages. All of these mounds had been disturbed prior to archaeological investigation; many had been plowed over by modern farmers or topsoil had been removed to farmers’ fields. The excavated mounds reveal both male and female skeletons, as well as both adults and children. A wide variety of burial styles were utilized from single, disarticulated skeletons to semi-flexed complete skeletons to isolated skulls and long bones. Even after having been plowed over or disturbed in other ways, the mounds were quite large, being 7.6 to 9.1 meters at the base (25 to 30 feet) and 1.8 meters or six feet high. They were not produced in a single episode, but were added to over time. Many pottery fragments are mixed in with the soil from which the mound was constructed, which suggests that it might have been taken from landfills. Since Native Americans did not have draft animals or wheeled vehicles, the mounds must have been built up by hand, basket-full by basket-full. These were not general community cemeteries, but burials for the few. In three mounds excavated on Clemson Island, each mound contained the remains of approximately thirty individuals, a small number compared to the total number of people who must have lived in these large settlements. The small number of burials plus the effort involved in the creation of the mounds suggests some form of social ranking in Clemson Island communities.

The presence of burial mounds reminds archaeologists of the two earlier large mound building cultures of Ohio, the Adena (2800 to 1900 BP) and Hopewell (1900 to 1500 BP) cultures. These two large, agricultural cultures with their elaborate earthworks spread their influence through
other areas in the Mid-West and the Middle Atlantic, as mounds appear in Western Pennsylvania, Kentucky, and West Virginia, but until the Clemson Island culture, these distinctive features did not penetrate the Susquehanna River Valley - and are not found again after the disappearance of the Clemson Island culture around 800 BP. What is known is that late in the Clemson Island period, native people seem to have abandoned islands and moved to the river’s floodplains for their villages. As will be discussed later, it is suspected that in time the Clemson Island people left the Susquehanna River region and migrated north. (see Stewart [1990, 2003] for further discussions of Clemson Island Culture.)

The Clemson Island Culture was succeeded by - and perhaps driven out by - the Shenks Ferry Culture. The Shenks Ferry culture is named for a site in Lancaster County originally excavated by Donald Cadzow in 1931-32. The site is on a tributary of the Susquehanna River known as Grubb Creek; the Shenks family had owned a ferry service on the river in the 19th century, and the area had become named for them. While the original site is in Lancaster County, Shenks Ferry sites are found all along the main and west branches of the river; much of the work on the Shenks Ferry Culture has been conducted in Lycoming County by James Bressler and his associates (see Bressler and Rockey 1997, Bressler and Rainey 2003). Unlike the Clemson Island people, for most of their history, Shenks Ferry people lived in small villages or hamlets. Like other Middle and Late Woodland cultures in Pennsylvania, theirs was a mixed economy of horticulture, fishing, hunting and gathering wild plants. They lived in small, bark covered round homes, of the type that would subsequently be called wigwams by anthropologists, and produced a variety of cord-marked or incised pottery vessels as well as an extensive stone tool technology, including triangular arrow points, scrapers, and axes.

Then around 500 BP, Shenks Ferry villages began to change. Communities grew fewer in number as people came together in larger, denser settlements. These larger villages were fortified, with upright log stockades surrounding them. Individual homes also became larger and oval-shaped, like Iroquois longhouses. At the Ault site, described by Bressler and Rockey (1997), a stockade made up of poles from the surrounding forest ringed the entire village, as indicated by post molds. The archaeologists could detect the remains of a mound of dirt piled both inside and outside of the base of the stockade, and a water-filled moat five feet wide and up to twelve feet deep ringed the stockade. In the outside berm of dirt, stakes had been stuck pointing outward. Two openings have been detected in the stockade, and the archaeologists believe that a watch tower was set next to the larger of the two. The effort involved in cutting that many trees with stone axes and digging that large of a moat would have been intensive, and it is hard not to assume that the Shenks Ferry people needed to defend themselves against some aggressor, often assumed to be the Susquehannocks who were moving into the Susquehanna Valley at about this time. There is no evidence, however, of conflict at the Ault Site, and Bressler and Rockey (1997) estimate that the palisade poles would have lasted no longer than six years in the moist, acid soil in which they were set. It appears that the site was abandoned, a phenomenon that is repeated all along the Susquehanna River’s west and main branches at about this time.

Archaeologists are interested in what the relationship was between the earlier Clemson Island culture and the Shenks Ferry people. Earlier in the 20th century it was assumed that the Shenks Ferry people were directly derived from the Clemson Island people, and that the Shenks Ferry Culture had developed in situ. This was an easy assumption to make, as Bressler and Rainey assert that every Shenks Ferry community on the West Branch was built on a Clemson Island village site (2003). Excavations of Shenks Ferry sites on the West Branch reveal a variety of Clemson Island and Shenks Ferry artifacts, usually separated in different strata, but also intermixed as a result of river flooding, field preparations, and the Shenks Ferry custom of digging storage pits for their agriculture produce and garbage.

However, more recently, similarities have been noted between pottery traditions along the Potomac River in Maryland and Shenks Ferry pottery on the Susquehanna. Pottery serves as a useful tool in archaeological interpretations of the cultures that possess it. Each culture tends to make its pottery in a distinctive fashion, in shape, clay composition, exterior design and even the kind of temper added to the clay to give it strength in the firing process, and these traditions are transmitted through the generations with few changes. Thus, Shenks Ferry pottery is rounder than Clemson Island pottery and generally is decorated over the entire surface of the pot, unlike Clemson Island pots which are often unmarked, except for a row of dots pushed into the clay around the raised rims. Shenks Ferry pottery is generally incised with parallel lines of cut designs over the entire surface. These differences, plus the knowledge that the Clemson Island people abandoned their large island communities at about the same time as Shenks Ferry cultures begin to appear along the Susquehanna leaves many to believe that the Shenks Ferry people were invaders from Maryland who displaced the Clemson Island people.

Bressler and Rainey (2003) note that on the West Branch a distinctive kind of pottery emerges after the presumed contact between the Clemson Island and Shenks Ferry people that seems to merge features of both pottery styles. This is called the Stewart style of Shenks Ferry ceramics; it is not seen in the main branch Shenks Ferry sites, but it does appear in archaeological sites in central and northwestern Pennsylvania (Myers 2013). Bressler interprets this to mean that there was some peaceful interaction among Clemson Island and Shenks Ferry people on the West Branch. He also suggests that eventually the Clemson Island people moved out of Pennsylvania into southwestern New York and became the Seneca people of the contact era. (Bressler and Rockey 1997). This theory fits with the controversial theory of Snow...
(1994) that the Iroquois/Haudensosaunee cultures of New York State, and their antecedent, the Owasco archaeological culture, originated in the Susquehanna River Valley.

**THE SUSQUEHANNOCKS**

Approximately 500 years ago, the people called the Susquehannocks began to move from the Spanish Hill region near Sayre, Pennsylvania down the North Branch of the Susquehanna River, eventually creating several large towns in Lancaster County, the most important of which was probably Washington Boro. Very little is known about the Susquehannocks, especially compared to the Lenape/Delaware people of southeastern Pennsylvania, New Jersey and northern Delaware from the same post-contact time period. They first appear in the annals of Captain John Smith, who met a party of them in his travels up the Chesapeake Bay from Jamestown in 1608. Smith had reached the falls of the Susquehanna River, where the river flows into the Bay, but could go no farther north because the falls blocked his passage. While staying among the Tockwogh people at this intersection, a contingent of people whom the Tockwogs called Sasquesahanocks, visited to engage in trade, and Smith famously described them as fiercely-garbed, giant warriors. (see Wallace 1981) from a town presumed to be Washington Boro on the river to the north. Ironically, the river took its name from Smith’s record of this visit, though no one knows for sure what they called themselves. A 19th century scholar named John S. Clark collected everything he could find from 17th and 18th century sources about these Native Americans (in Murray 2008), but he could only determine that “Susquehannock” was of Iroquoian origin. French colonial figures called them Andaste or Gandastogues (which later is Anglicized as Conestogas), and the Dutch called them Black Minquas after the Lenape term for these people. To put it simply, no one seems to have cared much for these people. “Minqua” in Lenape means “treacherous,” and “Gandastogue” translates as “people of the blackened ridge pole,” a presumed reference to the villages they had burned. Most 17th century sources describe them as “warlike,” and it is widely presumed that the last of these people was executed in Lancaster by the vigilante group called the Paxton Boys in 1763 in retaliation for Native American atrocities during the French & Indian War (1755-1763). The explanation accepted by most for their exodus from the Spanish Hill region is that they were driven out by the Five Nations’ Iroquois in retaliation for previous conflicts, and subsequently their numbers were considerably reduced by smallpox (first recorded among them in 1661) and wars with both the Senecas and Maryland colonists. (see Wallace 1981; Tooker 1984). As in the oft-quoted expression, that “History is written by the victors,” there is little good ethnographic information on the Susquehannocks.

There is considerable archaeological data, however, especially as reported and/or recorded by Kent in Susquehanna’s Indians (1984). The archaeological data confirms that Susquehannock sites appear on the North Branch of the river in the early 1500’s, such as the Blackman and Kennedy sites (see Smith 1970; McCracken 1984, 1989) and in better known and larger sites, such as Washington Boro in Lancaster County, which was settled around 1550. The Lancaster County sites, in particular, feature large stockaded communities which housed in some cases thousands of people. Kent’s excavations at Washington Boro led to the conclusion that the stockade there surrounded an area of approximately 250,000 square feet and may have housed 1700 to 2000 people. (1984, 338). What can be gleaned from these sites is that the Susquehannocks were most likely typical Late Woodland people with a stone technology and a mixed economy of hunting, fishing and horticulture. Like the Iroquois, to whom they are assumed to be directly related, in that contact-era accounts describe Susquehannocks living comfortably in Iroquois villages (Englebrecht 2003), they lived in longhouses and were a matrilineal culture. They buried their dead outside the palisade walls, and hundreds of burials have been found, often by developers putting in modern housing developments in areas in Lancaster County where the Susquehannocks lived in the 17th century. These burials have a wide variety of grave goods associated with them, especially goods of European manufacture, items of metal and glass, such as beads, metal pots and pieces of armor. The assortment of European-made goods associated with Susquehannock sites from the 17th century brings to mind Jennings’ 1968 argument that what compelled the Susquehannock migration was not war with the Iroquois, but a desire to relocate closer to sources of trade with Europeans.

While it is widely assumed that the Susquehannocks wiped out the Shensky people, there is no direct evidence for this - no scorched villages, or scenes of destruction found in other parts of the world where such conflict took place in the past. All that is known for certain is that the Shensky people lived along the river, but that after 1500 AD, they were gone. Burials have been uncovered of both Shensky and Susquehannock people, and the two cultures are associated with different body types, with Shensky people being larger boned, more robust and taller (an interesting finding given Smith’s descriptions of the Susquehannocks as giants, a finding not supported by the forensic evidence, see Becker [1991]). Bressler, however, believes that pottery taken from some Susquehannock sites in Lancaster County show some Shensky characteristics, which led him to theorize that some Shensky women were assimilated into Susquehannock culture post-contact, probably as captives; pottery was a woman’s skill among Susquehanna’s Native Americans. (Bressler and Rockey 1997).
NATIVE AMERICANS IN THE SUSQUEHANNA RIVER VALLEY
17TH CENTURY POST CONTACT

After Europeans began to settle in the Middle Atlantic colonies, Native Americans were forced to relocate to areas where they had not lived previously. Thus, the 17th and 18th centuries become periods of successive migrations in and out of the Susquehanna River Valley. Two key events led to a mixing of native peoples in the valley. The first was the ceding of the Pennsylvania colony from the British crown to William Penn in 1681. Before coming to “Penn’s Woods” in 1682, Penn wrote a letter to be read by his agents to Native Americans in his new colony in which he expressed a desire to live in brotherhood and peace with the native people, a resolve he reinforced upon arrival in contacts with representatives of the Lenape and a series of land purchases in which he legally obtained land for European colonists. This brief period, stretching from Penn’s arrival in 1682 to his death in England in 1718, made Pennsylvania a relative sanctuary for Native Americans from all over the thirteen colonies. Thus, groups such as the Tuscaroras, Nanticookes, Conoy, Saponi and others migrated into Pennsylvania to escape the pressures of colonization and conflict elsewhere. While, some, like the Tuscaroras, chose to only briefly settle in Pennsylvania, many chose to live permanently in the new colony, many in the Susquehanna River valley, as the river provided a relatively easy means of transportation. Thus, too, a Shawnee town was established on the North Branch of the river by 1702.

The second significant event was the decision of the Pennsylvania colonial legislature to cede responsibility over Native Americans in the colony to the Iroquois in 1731. The creation of the League of the Iroquois in earlier centuries, which brought together as allies the original five nations of the Iroquois - Mohawks, Oneidas, Onondagas, Cayugas and Senecas - had strengthened the Iroquois into a powerful force that could deal effectively with traditional enemies, such as the Hurons, and perhaps the Susquehannocks. The introduction of the fur trade into the Northeast also strengthened the position of the Iroquois, as they quickly took advantage of the willingness of Europeans to trade items such as guns and powder to the Iroquois in exchange for beaver and other pelts. The combination of these elements made the Iroquois a political power with which colonial governments, at least initially, had to deal diplomatically. By the late 17th century, the Iroquois were routinely venturing into Pennsylvania colony in search of beaver pelts and European trade goods. In order to deal with the “Indian problem,” the Pennsylvania legislature gave the Iroquois a kind of suzerainty in Pennsylvania’s Indian affairs. This was revoked in the Second Treaty of Fort Stanwick in 1784.

To play out their new role appropriately, the League chose an Oneida named Shikellamy to represent them at Shamokin (now Sunbury) at the confluence of the North and West Branches of the river and to resolve conflicts between Pennsylvania’s natives and the colonial government, (as described in Merrell 1999). Shikellamy assumes this role in 1742. One example of the Iroquois role in Pennsylvania’s native affairs is the Iroquois order to the Lenape of southeastern Pennsylvania to relocate to the Wyoming Valley on the North Branch of the river in 1742. Thus, this series of events inserts both the Iroquois and Native Americans from other parts of Pennsylvania (and other Middle Atlantic colonies) into Susquehanna Valley life.

The French and Indian War (1755 to 1763) and the subsequent Pontiac’s Rebellion in 1763 profoundly changed Pennsylvanians’ relations with Native Americans. In retaliation for their involvement in Pontiac’s Rebellion, Lenape/Delawares are forced to withdraw into Ohio. All across Pennsylvania, native people, including the many who had intermarried with Europeans, began to hide their identities, especially in the wake of the Scalp Act, enacted by the Pennsylvania colonial legislature during the war. The Scalp Act promised to pay cash for native scalps, without consideration for whether or not the scalp was taken from a participant in the conflict. As one of my informants, a Seneca descendant from York County, has said “Well, the war ends, and the treaty of 1784 comes along. Okay, we’re supposed to move to Ohio. Well, these people in Pennsylvania, I think they just hunkered down. Their homes were here. They had been here generation after generation by that time. They had nice farms and stuff. So they just hunkered down and didn’t leave. Then once the word comes out that, hey, you’re supposed to move to Ohio, they said, ‘No, I’m not. I’m settled in here. This is where my family is, my extended family.’ And they didn’t go. They hunkered down, kept their mouths shut - ‘I’m not Indian - I’m not going to tell them.’ It becomes underground.”

Another informant, a Lenape descendant, put it this way: “But a good amount of people stayed behind and assimilated and grew up in the back woods and grew up in the back area along the rivers and streams - stayed behind...It’s not that odd of a deal. There’s still places you can go up there and never be seen again. And that’s what a lot of our people did, you know. But as I was growing up, my grandmother would say to me ‘Don’t forget you’re an Indian. That’s who you are. You’re Lenape.’ So I grew up that way.”

A NATIVE AMERICAN RESURGENCE IN THE SUSQUEHANNA RIVER VALLEY

In the second half of the 20th century, a nationwide resurgence of interest in and concern for Native Americans resulted in people of mixed heritage, like those living in Pennsylvania, asserting their claims to Native American identity. The Red Power movement in the late 60’s and early 70’s combined with greater advocacy for Native American rights and welfare and a more positive view of Native
Americans as environmentally friendly and spiritually holistic, led many to throw off their fears and embrace a native heritage. (see, for instance, Clifton 1989; Nagel 1998). This has been particularly true for people living east of the Mississippi, where there has been a growing effort to obtain state and/or federal recognition and a growth in tribal associations, powwows, sweat baths and vision quests, and other native themed events. While this has been more difficult in Pennsylvania than in other states - Pennsylvania remains the only one of the 48 contiguous states to have neither reservation land nor official recognition for any group claiming native heritage - the numbers of people claiming native identity continues to grow here as well. In the 2010 U.S. Census, 81,092 Pennsylvanians claimed native status, a 54% increase over the 2000 Census. Fifty-eight percent of those responding claimed mixed or combined heritage - native and other. This number is consistent with reports from other states in the Northeast; nationwide 55% of the 5,220,579 persons reporting native heritage reported a mixed background. According to Weslager (2003), the first European/Lenape baby was born in 1638, and Europeans and natives in Pennsylvania colony intermarried for decades.

In 1980, a Lenape descendant, Carla Messinger, created the Lenni Lenape Historical Society in 1980, followed by the opening of the Lenni Lenape Museum in Allentown in 1982. By the 1980’s several Native American organizations were functioning in Pennsylvania, including the Eastern Delaware Nations on the North Branch of the Susquehanna River. In 2008, the University of Pennsylvania opened its Penn Center for Native American Studies, the first university-level Native American study center in the state; this was followed by an exhibit, “Fulfilling a Prophecy: The Past and Present of the Lenape in Pennsylvania,” at the university’s Museum of Anthropology and Archaeology. The exhibit was transferred to the Lenape Nation of Pennsylvania which opened a museum and visitor center in Easton in 2010. In 2009, Bucknell University on the West Branch of the river sponsored a two day symposium on Native Americans in the Susquehanna River Valley. This historic first was followed by another at Bucknell in 2010 - the first official meeting between representatives of the Lenape Nation of Pennsylvania and the League of the Iroquois from New York State. In general, there is a general momentum growing for people claiming native descent in Pennsylvania, and a new chapter being written about Native American life in the Susquehanna River Valley.

ACKNOWLEDGEMENTS

As always, I wish to acknowledge my former student, Andrea T. Frantz, M.A., R.N., whose interest in Native Americans in contemporary Pennsylvania, drew me to this research and who became my co-researcher and frequent co-author. This work would not have been possible without her assistance.

NOTES

1. The dates given for the Paleoindian, Archaic and Woodland eras are combinations of dates given in a variety of sources, including Fogelman (1988); Adovasio and Carr (2002); Stewart (2003); and Neusius and Gross (2007). Dates for the onset of each of these periods vary from source to source. “Paleoindian” is also spelled as PaleoIndian and Paleo-Indian in other sources.

2. For decades, the Clovis-first theory dominated archaeologists’ thinking about the peopling of the New World, to the extent that any suggestion that earlier migrations might have occurred was dismissed out of hand. The careful research and use of dating techniques by Adovasio at Meadowcroft and by Tom Dillehay at the Monte Verde site in Chile (with dates of 12,700 to 12,300 B.P. for the upper-most layers of this stratified site - see Dillehay 2000) convinced most, but not all, archaeologists that a pre-Clovis migration must have occurred.

3. In addition to the abundance of food stuffs already mentioned, Heverly in his 1926 history of Bradford County, Pennsylvania writes that the Susquehanna floodplain was “covered with a forest of white pine, black walnut, butternut, poplar and elm and the slopes and ridges with hemlock, yellow pine, oak, chestnut, ash, cedar, basswood, cucumber, pepper-ridge, ironwood and other species. Deer roamed the hills and valleys, which were infested with bears, wolves, panthers and wildcats. The region abounded in turkeys and various wildfowl. A recent book by Greenberg (2014) notes that passenger pigeons existed in such great numbers in the Northeast and Midwest that a flock took days to pass overhead. John James Audubon estimated one flock he witnessed to contain over two million birds. Nesting birds were so numerous that branches broke under the weight of the nests, and squabs could be harvested from the ground in the hundreds. Kent (1984) adds that “The fertile limestone and alluvial soils, the seemingly unique weather patterns, and the longer growing season make this basin one of the today’s richest agricultural areas in the northeastern United States. And so it must have been for the agriculturally based Shenks Ferry and later the Susquehannock Indians.”

4. Bressler and Rockey (1997) also note that maize requires a 160 day growing season and exposure to full sun to mature and set the edible seeds. Thus, the effort of clearing a field had to include removing the large trees not only from the field itself, but also for a distance surrounding each field so that sun could reach the developing plants.
LITERATURE CITED


WATER QUALITY ASSESSMENT OF THE LOWER WEST BRANCH – SUSQUEHANNA RIVER: FOCUS ON SEWAGE TREATMENT†

MELVIN C. ZIMMERMAN1, LYNETTE DOOLEY

Biology Program, Clean Water Institute, Lycoming College, Williamsport PA 17701.

ABSTRACT

The object of this study was to describe and determine the water quality of the Lower West Branch of the Susquehanna River between Lock Haven and Sunbury. Sites were selected in relation to location of sewage treatment plants along this stretch of river. Water chemistry data (pH, alkalinity, nitrate nitrogen, nitrite nitrogen, dissolved oxygen, temperature, conductivity, orthophosphorus, total phosphorus, total dissolved solids, and turbidity) are presented from 2005 to 2013. Macroinvertebrate kick samples were collected from sample sites in the summer of 2013. These data were subjected to the EPA Rapid Bioassessment Protocol II (RBA-Family Level), Hillenhoff Biotic Index and Shannon-Wiener Diversity Index in an attempt to describe water quality. All nine of the sewage treatment plants in this section of the river have made improvements to address discharge and combined sewer overflows (CSO’s) concerns in the last decade. The overall quality of the water appears to have improved as a number of Chesapeake Bay Initiatives on sewage treatment plants has taken place. Noticeable success of the new standards for sewage treatment plants that have been or are currently being upgraded will need continued monitoring to demonstrate overall water quality improvements. [ J PA Acad Sci 88(1): 40-46, 2014 ]

INTRODUCTION

The West Branch Susquehanna River sub basin drains an area of approximately 6,982 square miles from Carrolltown to Northumberland, Pennsylvania (LeFevre 2003). Three different ecoregions are found in this area; Northern Appalachian Plateau, North Central Appalachians and Central Appalachian Ridges and Valleys (Omernik 987). A State of the Heartland report in 2005 (West Branch Task Force) summarized DEP’s 305(b) list of impaired waters of the West Branch and showed 57.6% (1,153 miles) were impaired by AMD, 24% (480 miles) by agriculture, but less than 4 miles (0.2%) from point sources which includes sewage treatment plants. Over the last decade much attention has been given to the upgrade of the municipal sewage treatment plants in the lower West Branch Susquehanna because of their combined overflow problems. The lower West Branch corridor (77 miles in the Central Appalachian ridge and valley) encompasses 161.8 square miles and winds through four counties (Clinton, Lycoming, Union and Northumberland) between Lick Run near Lock Haven and the confluence with the North Branch Susquehanna at Sunbury. The corridor (see Figure 1) contains all or part of 44 municipalities and nine sewage treatment plants (see Table 1). Fifty two percent of the entire West Branch watershed (3,647 square miles) drains into the lower section and includes 105 tributary streams (Shenk, 2011; NPC, 2005).

Figure 1. Map and sampling locations of Study Area.

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1Corresponding Author: 700 College Place, Box 152, Williamsport, PA 17701, 570-321-4185, zimmer@lycoming.edu
Background on Sewage Treatment plants along the lower West Branch

A majority of the sewage treatment plants in the lower West Branch corridor were built during the 1950's. Currently there are nine permitted wastewater treatment plants located in the lower West Branch Susquehanna River (Susquehanna River Basin Commission, SRBC). Due to the Chesapeake Bay Initiative, there are many upgrades either in progress or have been recently finished. These upgrades use Nutrient Reduction Technology (NRT) and Biological Nutrient Removal (BNR) to reduce nitrogen, phosphorous

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Table 1. Lower West Branch Susquehanna Wastewater Treatment Plants.
and/or sediment discharges. In addition, most municipalities are developing strategies to reduce the stormwater runoff (Combined Sewage Overflow-CSO). When projects are completed in 2014, the number of current plants will be reduced from nine to eight (Regan, 2013).

Lock Haven Municipal Authority (LMHA) is an activated sludge plant with an average treated flow of 2.2 million gallons daily influent flow and permitted a maximum treatable flow of 7 million gallons daily (MGD). In 2010, a $26 million dollar upgrade involved building an overall new plant to lower the amount of total phosphorous and total nitrogen to satisfy their new permit.

Tiadaghhton Valley Municipal Authority (TVMA), the previous trickling filter secondary sewage treatment plant was in Jersey Shore PA. The Jersey Shore plant is being phased out in 2013-2014 and the new Tiadaghhton Valley Municipal Authority was formed with the building of a new $20 million wastewater facility in Nippenose Township. The new plant will serve three municipalities and is projected to discharge 19,178 pounds of nitrogen (down from 53,000 pounds in 2011) and 2,057 pounds of phosphorous (down from 7,000 pounds in 2011).

Williamsport Sanitary Authority (WSA) is in the process of completing a $125 million combined project to upgrade both the central plant and the west plant. The improvements are to meet nutrient reductions and to handle storm water flows. Both plants received updated activated sludge biological nutrient removal (BNR) improvements as well as additional storage capacity during wet weather to reduce combined sewer overflows.

Both plants’ combined nitrogen discharge in 2010-11 was 602,251 pounds. The cumulative totals for 2013 were 189,443 pounds with a cap of 230,970 pounds. The plants’ combined phosphorous discharge for 2010-11 was 54,017 pounds which improved to 28,755 pounds in 2013 with a limit of 30,002.

Lycoming County Water/Sewer Authority (LCWS) is located in Montoursville, PA and consists of a Sequencing Batch Reactor. In 2012, a $10 million upgrade was completed on the plant. Average nitrogen concentrations since 2012 were 2.7 ppm, which is far under the 16.6 ppm in 2009 and better than the 7.1 ppm in 2010. The target concentration is 6 ppm. Average phosphorous concentrations in 2009 and 2010 were 1.59 ppm and 0.65 ppm, respectively. In 2013 the average concentration was 0.45 ppm, under the 0.8 ppm target goal.

Proposed West Branch Regional Wastewater Treatment Plant

Rather than go through a host of expensive upgrade projects with the current Muncy and Montgomery treatment plants, which are in the flood zone, a new plant is in development with plans for completion in 2014.

Currently the West Branch Regional Authority (WBRA) located in Muncy is a trickling filter plant with primary clarifiers, aerobic sludge digestion, and chlorine disinfection. The plant has an average flow of 0.7 MGD and is permitted to 1.4 MGD maximum capacity.

The Montgomery Township Municipal Sewer Authority (MTMS) is a conventional activated sludge flow-through plant with primary clarifiers, aerobic operating at 0.6 MGD on average waste flow and is permitted to 0.85 million gallons per day (MGD) maximum capacity. The combined discharges for both treatment plants for water year 2011-12 for nitrogen was 115,000 pounds a year, and phosphorous was 5,700 pounds. The cap limits, combined for both plants, for nitrogen is 41,000 pounds a year and 5,500 pounds of phosphorous. The new plant’s activated sludge BNR technology is designed to meet these goals.

Milton Regional Sewer Authority (MRSW) currently MRSW treats the boroughs of Milton, West Chillisquaque Township, East Chillisquaque Township, Turbot Township, Borough of Watersontown and Delaware Township. The plant is an activated sludge secondary treatment plant with primary clarification, aerated activated sludge tanks, aerobic digestion, dissolved air flotation, secondary clarification, and chlorine disinfection. Current average daily flow is 1.6 MGD with a maximum permitted flow of 3.42 MGD. However, after new 2014 upgrades are completed they will be permitted to 4.25 MGD maximum flow daily. The largest portion of the new upgrade will be the addition of two 7.5 million gallon anaerobic reactors. The methane gas which is generated by this process will be used to power generators, in the plant as well as produce additional electricity for Pennsylvania Power and Light. The waste heat from these generators will be used to dry their cake sludge to make a product which they hope to sell.

Kelly Township Municipal Authority (KTMA); located in Lewisburg is an extended air activated sludge treatment process. There have not been any major upgrades in recent years. KTMA used to treat an average of 2.8 to 3.2 million gallons a day (MGD). Currently KTMA treats an average of 1.2 MGD even though their permit allows treatment for 3.75 MGD. The sewage treatment plant in Sunbury, discharges into the North Branch Susquehanna and is located near the confluence with the West Branch.

The purpose of this project was to add to the ongoing data set on water chemistry and macroinvertebrates of the lower West Branch Susquehanna River being developed by the six college/universities of the Susquehanna River Heartland Coalition for Environmental Study (SRHCES). Summarized here is a partial analysis of data collected by the Lycoming College Clean Water Institute (CWI) since 2005.
MATERIALS AND METHODS

Eleven study sites (see Figure 1) between Lock Haven and Sunbury were sampled monthly during the summer months (May – October) from 2005 through 2013. Grab samples were collected for water analysis from the right, center and left banks and analyzed for DO (dissolved oxygen ppm) and temperature (YSI model 55). Grab samples of water were collected and transported back to the laboratory on ice. In the lab pH (Oakton model 510) and alkalinity (ppm CaCO$_3$; titration following Standard Methods, 2005) were completed. Conductivity (µs/cm) and TDS (ppm) were analyzed with a Oakton Model 410 series probe. Concentrations (ppm) of nitrate nitrogen, nitrite nitrogen, ortho-phosphorous and total phosphorous were analyzed following the EPA approved methods for the HACH DR 5000. Macroinvertebrates were collected following the PADEP protocols using a D frame kick net (500 micron), (PADEP 2003, 2009). A random 300 count macroinvertebrate sample from each location was identified to family and processed using Hilsenhoff (1987, 1988) and the Rapid Bioassessment Protocol II of Plafkin (et al. 1989).

RESULTS AND DISCUSSION

Table 2 summarizes the mean values for water chemical parameters for the Lower West Branch Susquehanna River sample sites 2005-2013. These values are useful as a baseline description for the area, while realizing that there can be significant site and year differences. Some of this variability is shown for alkalinity (Figure 2), nitrate nitrogen (Figure 3), and total phosphorous (Figure 4). The values shown in these figures are concentrations and not adjusted for flow. During each summer of one study a significant difference in (α = 0.05, Rank Sum Test) alkalinity from spring to fall occurred from upstream (Lock Haven to downstream Sunbury). No significant difference was observed in nitrogen or phosphorous. Similar values and trends are documented in SRBC reports (LeFevre 2003, Shenk 2010, Steffy and Clark 2011, McDonigal 2011). Flow adjusted concentrations to calculate load will be applied in future monitoring at these sites. McGonigal (2011) reports the loads for total nitrogen and total phosphorous in Lewisburg, Pennsylvania (between Milton and Chillisquaque) for 2010.

Table 2. Mean ± SD Summer Water Chemistry for the Lower West Branch Susquehanna River 2005-2013.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Mean ± SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>DO ppm</td>
<td>7.6 ± 1.3</td>
</tr>
<tr>
<td>pH</td>
<td>6.2 ± 0.9</td>
</tr>
<tr>
<td>Alkalinity (ppm CaCO$_3$)</td>
<td>3.1 ± 9.8</td>
</tr>
<tr>
<td>Conductivity (µs/cm)</td>
<td>246 ± 101</td>
</tr>
<tr>
<td>TDS (ppm)</td>
<td>128 ± 62</td>
</tr>
<tr>
<td>Nitrate Nitrogen ppm</td>
<td>0.91 ± 0.16</td>
</tr>
<tr>
<td>Nitrite Nitrogen ppm</td>
<td>0.09 ± 0.04</td>
</tr>
<tr>
<td>Ortho Phosphorous ppm</td>
<td>0.011 ± 0.01</td>
</tr>
<tr>
<td>Total Phosphorous ppm</td>
<td>0.75 ± 0.29</td>
</tr>
</tbody>
</table>

Figure 2. Alkalinity (ppm CaCO$_3$) of the Lower West Branch Susquehanna River 2005-2013.

Figure 3. Nitrate Nitrogen (ppm) of the Lower West Branch Susquehanna River 2005-2013.

Figure 4. Total Phosphorous (ppm) of the Lower West Branch Susquehanna River 2005-2013.
He observed concentrations of 0.82 ppm N and 0.04 ppm P and calculated loads based on flow of 15,893 (x1000) and 858 (x1000) pounds.

Figures 5, 6 and 7 indicate changes in alkalinity, nitrate nitrogen and total phosphorous from upstream (Lock Haven) to downstream (Sunbury) for the month of June 2005 and 2013. A significant increase in downstream alkalinity ($\alpha = 0.05$; Rank sum test) concentrations is shown but no significant trend occurs for nitrogen or phosphorous. The differences seen between the two years at each site may be due to flow differences between a wet (average flow >1000 m$^3$/sec 2005) and dry (average flow <1000 m$^3$/sec 2013) year. Previous SRBC reports by LeFevre (2003); Shenk (2010); Steffy and Clark (2011) and McGonigal (2011) all show significant increases in these parameters between the upper, mid, and lower sections of the West Branch Susquehanna. The upper and mid reaches of the West Branch (above Lock Haven) are still recovering from AMD impacts while the lower section appears more influenced by agriculture non-point sources and point sources such as sewage discharges.

Table 3 presents preliminary results on the water quality of the lower West Branch Susquehanna based on family level macroinvertebrate kick sample data above and below sewage treatment plants for summer 2013. These data suggest some minor changes below sewage treatment plant discharges but no clear conclusion can be made. Shenk (2011) describes the water quality lower West Branch of the Susquehanna as slightly impaired but a more detailed site survey of water quality based on macroinvertebrate data reported in Buda (2010) shows moderate impairment in river at Lock Haven and non-impaired below Lewisburg.

In conclusion, this report provides a snapshot of conditions along the Lower West Branch Susquehanna River. Although samples were taken above and below sewage treatment plants the contributions of non-point source inputs is not known. Further analysis of water chemistry trends will be enhanced by analysis of deployed SONDE data (such as collected by a SONDE maintained by Bucknell University Environmental Center in Milton, see link http://www.eg.bucknell.edu/sri/monitoring) as well as adjusting concentration data with flow to calculate changes in load for nitrogen and phosphorous. Identification of macroinvertebrates to species is ongoing as well as analysis of Rock basket and Hester-Dendy samplers placed in sections of the river since 2005. When completed these data will improve the interpretation of water quality of the Lower West Branch Susquehanna River.

ACKNOWLEDGEMENTS

This work has been supported by grants from the Degenstein Foundation. Funds were used to support summer interns. Over the years several undergraduate interns have been involved with the project. The main author would like to acknowledge the contributions of Lynette Dooley, Chelsea Brewer, Quentin Reinfond and Laura Walter.
Table 3. West Branch Macroinvertebrate Kick Sample Analysis, 2013.

<table>
<thead>
<tr>
<th>Site</th>
<th>Total Taxa</th>
<th>Shannon-Weiner Index-Species Diversity</th>
<th>Hillsenhoff Family Biotic Index</th>
<th>Hillsenhoff Water Quality</th>
<th>EPA Rapid Bioassessment Protocol II Biological Condition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Above Lock Haven Wastewater Treatment</td>
<td>19</td>
<td>2.98</td>
<td>3.43</td>
<td>Excellent</td>
<td>Non-Impaired</td>
</tr>
<tr>
<td>Below Lock Haven Wastewater Treatment</td>
<td>15</td>
<td>2.75</td>
<td>4.42</td>
<td>Very Good</td>
<td>Moderately Impaired</td>
</tr>
<tr>
<td>Above Tiadiaghton Valley Municipal Authority</td>
<td>13</td>
<td>2.47</td>
<td>4.33</td>
<td>Very Good</td>
<td>Moderately Impaired</td>
</tr>
<tr>
<td>Below Tiadiaghton Valley Municipal Authority</td>
<td>6</td>
<td>1.75</td>
<td>4.81</td>
<td>Good</td>
<td>Moderately Impaired</td>
</tr>
<tr>
<td>Above Williamsport Water/Sewer Authority</td>
<td>14</td>
<td>2.87</td>
<td>3.10</td>
<td>Excellent</td>
<td>Moderately Impaired</td>
</tr>
<tr>
<td>Below Williamsport Water/Sewer Authority</td>
<td>13</td>
<td>2.99</td>
<td>2.28</td>
<td>Excellent</td>
<td>Moderately Impaired</td>
</tr>
<tr>
<td>Above Williamsport Water/Sewer Authority Central</td>
<td>19</td>
<td>3.25</td>
<td>2.95</td>
<td>Excellent</td>
<td>Excellent</td>
</tr>
<tr>
<td>Below Williamsport Water/Sewer Authority Central</td>
<td>14</td>
<td>2.93</td>
<td>3.68</td>
<td>Very Good</td>
<td>Excellent</td>
</tr>
<tr>
<td>Above Lycoming County Sewer/Water Authority</td>
<td>19</td>
<td>3.49</td>
<td>3.22</td>
<td>Excellent</td>
<td>Non-Impaired</td>
</tr>
<tr>
<td>Below Lycoming County Sewer/Water Authority</td>
<td>16</td>
<td>3.04</td>
<td>3.45</td>
<td>Excellent</td>
<td>Moderately Impaired</td>
</tr>
<tr>
<td>Above West Branch Regional Authority (Muncy)</td>
<td>22</td>
<td>3.10</td>
<td>3.27</td>
<td>Excellent</td>
<td>Moderately Impaired</td>
</tr>
<tr>
<td>Below West Branch Regional Authority (Muncy)</td>
<td>21</td>
<td>3.04</td>
<td>2.88</td>
<td>Excellent</td>
<td>Moderately Impaired</td>
</tr>
<tr>
<td>Above Montgomery Township Municipal Sewer Authority</td>
<td>22</td>
<td>3.48</td>
<td>3.22</td>
<td>Excellent</td>
<td>Non-Impaired</td>
</tr>
<tr>
<td>Below Montgomery Township Municipal Sewer Authority</td>
<td>18</td>
<td>2.60</td>
<td>2.90</td>
<td>Excellent</td>
<td>Moderately Impaired</td>
</tr>
<tr>
<td>Above Milton Regional Sewer Authority</td>
<td>13</td>
<td>1.95</td>
<td>2.15</td>
<td>Excellent</td>
<td>Moderately Impaired</td>
</tr>
<tr>
<td>Below Milton Regional Sewer Authority</td>
<td>7</td>
<td>2.03</td>
<td>2.33</td>
<td>Excellent</td>
<td>Moderately Impaired</td>
</tr>
<tr>
<td>Above Kelly Township (Lewisburg) Municipal Sewer Authority</td>
<td>17</td>
<td>2.87</td>
<td>3.06</td>
<td>Excellent</td>
<td>Non-Impaired</td>
</tr>
<tr>
<td>Below Kelly Township (Lewisburg) Municipal Sewer Authority</td>
<td>11</td>
<td>2.48</td>
<td>3.36</td>
<td>Excellent</td>
<td>Non-Impaired</td>
</tr>
</tbody>
</table>
LITERATURE CITED


ASSESSMENT OF PASSIVE AND ACTIVE MACROINVERTEBRATE COLLECTION METHODS IN ADJACENT REACHES ON THE UPPER MAIN STEM OF THE SUSQUEHANNA RIVER†

KATHERINE GUILD, ANDREW ANTHONY, MICHAEL BILGER, AND JACK HOLT

Department of Biology, Susquehanna University, Selinsgrove, PA 17870

ABSTRACT

Macroinvertebrates are functional indicators of stream health based upon their sensitivity to pollution. Our study utilized different passive and active benthic macroinvertebrate collection methods (D-net, Surber sampler, rock baskets, and Hester-Dendy multiblade samplers) during the summer and fall of 2012 and 2013. Collections were taken on both sides of the west channel in the west channel of the upper main stem of the Susquehanna River near Shamokin Dam, PA. Sampling sites each included seven locations, one for passive sampling and six longitudinal locations for active sampling. Overall, we collected 50 taxa of macroinvertebrates identified to family-level, which allowed us to calculate pollution tolerance values and other comparative metrics. The Proportional Bray-Curtis Similarity Index analysis describes a very low to moderate overlap between benthic macroinvertebrate communities collected by active and passive methods (2% - 43%). Furthermore, other metrics including the Shannon Diversity and Hilsenhoff Biotic Indices reflected the variability in occurrence of pollution intolerant taxa according to method and location. The greatest variation occurred in percent EPT which showed a range of 0% to 56% in a single sample period using different methods. Passive sampling methods selectively collected colonizers and omitted other taxa (e.g. burrowers and mollusks) illustrating their bias in sampling. Overall, the metrics did not support the use of one technique over another. Rather, they supported the practice of using both passive and active collection methods in order to use macroinvertebrate community estimates to assess water quality in large rivers that have a wetted channel of cobble, silt, and sand like the upper main stem of the Susquehanna River. Based on our results we concluded that active samplers which target different habitats together with passive samplers which allow comparisons from one site to another would be the most appropriate methods to use in the upper main stem of the Susquehanna River.

INTRODUCTION

Biological community assemblages are important, not only in understanding the trophic dynamics of a system, but also in inferring the health of the system. Benthic macroinvertebrates are ubiquitous organisms in freshwater ecosystems, which collectively have a wide range of tolerances to pollution (Hilsenhoff 1987 and 1988) and, therefore, reflect organic pollution levels in a system. Many live in annual cycles and quickly react to shifts in chemical and physical parameters allowing them to be useful candidates for bioassessments (Voshell 2002). Macroinvertebrate families have been assigned pollution tolerance values allowing them to provide general insight into stream health based on their frequency and diversity (Hilsenhoff 1988).

Large riverine ecosystems are principally unobserved or neglected in part because of the magnitude of the environment, but also because variable flow causes habitat mosaics from one reach to the next with the movement of substrate material, epifauna, and mixing of the chemical composition of the water (Armitage 2006, Poff, et al. 2009, Poff and Zimmerman 2010). Thus, large nonwadeable streams are not just scaled up small wadeable streams, which are far easier to sample than large wadeable or nonwadeable rivers. Due to the sheer size and variation of a river from bank to bank and along its length between reaches, many more samples are essential for capturing the biological diversity of these habitats (Blocksom and Johnson 2011). Additionally, numerous techniques such as the D-frame net and Surber sampler are not generally implemented within high discharge systems. Therefore, river assessment programs sometimes neglect biological monitoring of riverine systems, apply wadeable methods to shallower areas in the river, or leave out assessment parameters that are too complicated to measure (Flotemersch et al. 2006).

Typically, field methods for the collection of benthic macroinvertebrates fall into two broad categories that we refer to as passive and active methods. Passive methods generally employ artificial substrates, which can be effective in large river systems and relatively inexpensive to make (Czerniawska-Kusza 2004). Such substrates have to be deployed and then retrieved after a colonization period. Active methods involve the direct capture of animals from a mosaic of substrates and can be accomplished during a
both types of methods vary in time investments and collection results (Lenat 1988). Passive methods, which can sample taxa that are normally excluded from other conventional sampling techniques, utilize artificial substrates that tend to collect those organisms that actively seek to colonize or randomly drift into the samplers during the short deployment period. However, due to the ease of using these methods and by standardizing habitat for further bioassessment, they are common in water quality analysis. Merritt et al. (1996) claim that such passive methods give an effective representation in a large river mosaic; however, Meier et al. (1979) suggest results can be skewed by the particular time of year that the passive sampler is left in the field, due to the emergence periods of different taxa. For example, Hester-Dendy Multiplate Samplers reach a peak in colonized taxa after a few weeks and then slowly decline in diversity (Meier et al. 1979). The downside to using artificial substrate samplers is the bias towards specific taxa (Peckarsky 1984) due to the composition and structure of the passive device. Furthermore, collections can be distorted due to tampering by those who use the river for recreation.

Active collection methods are fundamentally more cost effective because a single sampling trip is required to collect the invertebrates; whereas, passive methods require at least two trips for deployment and collection. In addition, active techniques require little training for performance. Both types of methods have shortcomings that can determine the composition of the collection and interpretation of data. In wadeable streams, collections by active sampling methods (i.e., Surber sampler) are subject to the uneven distribution of benthic macroinvertebrates (Peckarsky 1984). Thus, neither type of collection method evaluates certain substrates fully due to the loss of individuals during collection or the inability to gather particular individuals that are overlooked in the execution of the technique (Klemm et al. 1990, Flannagan and Rosenberg 1982, Rosenberg and Resh 1982, Peckarsky 1984).

Evaluations of aquatic environments rely upon accurate descriptions of benthic macroinvertebrate communities, usually by a set of metrics or indices, each of which describes different aspects of the environment. These indices are only effective if the samples are collected using proper technique (Peckarsky 1984); however, different methods may yield biased results thereby influencing the outcome of the analysis. Although these sampling methods are common in wadeable streams, comparative studies of results taken within the same reach of a river are rare (Johnson et al. 2006). This paper focuses on the analysis of active and passive methods used during four sample periods at established sample locations on the upper main stem of the Susquehanna River in summer and fall 2012 and 2013. By comparing the resulting macroinvertebrate collections taken by different methods and the standard metrics generated by those collections, we seek to determine the overall efficacy of active and passive sampling methods in accurately representing benthic macroinvertebrate communities within the river for water quality assessment.

**SITE DESCRIPTION**

Both sampling reaches were located in the upper main stem of the Susquehanna River seven kilometers south of the confluence of the North and West branches (Figure 1). Figure 1 illustrates the differences in turbidity, which signifies the poor lateral mixing as seen by the distinct horizontal stratification of the West Branch and North Branch waters. For example, during summer 2013, the average Secchi depth of the West and North Branch plumes was 0.98 m and 0.39 m, respectively. Other measures such as conductivity and alkalinity show similar horizontal stratification.

Two sites initially were placed across from each other in the west channel 200 meters above the Shady Nook boat ramp near Shamokin Dam, PA and were designated for the placement of the passive collection samplers. The active collection methods were employed at 100 m intervals in a 500 m reach beginning 50 meters above the passive method collection sites on either side of the river. Both sites lie below the Adam T. Bower inflatable dam between Shamokin Dam and...
and Sunbury, PA and a low head dam associated with the Sunbury Generation Powerplant. The West Branch plume reach (WBP; N 40° 49.533, W 76° 50.183) which is near the west shore and in the West Branch plume, also lies about a kilometer south of the powerplant. The North Branch plume reach (NBP; N 40° 49.533 W 76°50.028), which is located on the west side of Byers Island, is fed by North Branch water. The substrates of both reaches are similar, being dominated by a mosaic of cobble and sediment (Table 1). The WBP reach, however, has spotty beds of aquatic plants, mainly Vallisneria.

METHODS

Passive Methods

We deployed rock baskets (RB) and Hester-Dendy multiplate samplers (HD) four times in 2012 and 2013, in June and September each year (with the exception of summer of 2013 when we deployed in late May, see Table 1). In all deployments, the passive samplers were organized in a diamond shape with the RB samplers at the three upstream corners of the diamond and the HD samplers at the downstream corner. The approximate surface area of each passive sampler was 0.3 m² and 0.1 m² for RB and HD samplers, respectively. Both RB and HD samplers were elevated above the sediment by mounting them on cinderblocks and securing them with zip-ties. All deployments used RB samplers filled with number four limestone. Only in summer and fall 2013 did we use paired treatments of RB in which one basket was elevated on a cinderblock and the other was placed directly on the substrate. Three HD samplers were attached with zip ties to a cinderblock at the southernmost point of the diamond. This formation of passive samplers was deployed in the river where the bottom was deeper than one meter below the level of the continuously wetted shore at both WBP and NBP sites. In general, the passive samplers remained in the water for 6 weeks, but the exposure period was cut to 4.5 weeks in October 2012 due to the approach of Hurricane Sandy.

All passive samplers were removed from the river, in accordance with EPA guidelines (Johnson et al. 2006, Barbour et al. 1999). The HD samplers were collected in individually labeled Ziploc® bags for transportation. RB samplers were gently removed from the cinderblocks and slipped into sieve buckets, which faced upstream to catch any animals that might escape and to incorporate them into their respective sample collections. RB samples were carried back to the laboratory in labeled five gallon buckets, and each rock was hand-cleaned to remove any invertebrates that remained attached to the stones. Similarly, we hand-cleaned each plate from the HD. All collections (RB/HD) were placed in labeled half gallon jars filled with 95% ethanol.

Active Methods

We used a modification of the Large River Bioassessment Protocol (Johnson et al. 2006) in which we established a 500 meter reach on both sides of the west channel with six locations set every 100 meters. Over a period of four weeks, Surber sampler (SS) and D-frame net (DN; each 500 μm mesh) kick samples were taken. Neither active method employed in this study was ideal for work in large rivers. Both require relatively shallow water and high enough flow rate to capture the invertebrates in their respective nets. Indeed, SS methods are designed for flowing water less than 0.3 m deep. Despite the limitations, especially of the SS method, both active sampling methods were used at varying depths (0.20-1.0 m).

At any one active sample site (see Figure 1), 10 DN kicks were taken according to the relative importance of the different substrate types: cobble/river rock, sediment and aquatic vegetation. The substrate was assessed in a line perpendicular to the channel from the wetted edge to a depth of 1 m, and sampled proportionally to the substrate (Table 1). For example, if a particular sample location were determined to have approximately 50% cobble and stone, then 5 of the 10 DN kicks would be done in cobble/stone substrate from the wetted edge to 1 m. Together, all 10 kicks at each of the sample locations were combined as a composite sample. Similarly, composite SS samples were made by combining one shallow and one deep subsample. The organisms collected were placed in separate, labeled half gallon containers filled with 95% ethanol for preservation.

Table 1. The composite percentage of substrate types sampled at the West Branch plume reach (WBP) and the North Branch plume reach (NBP) for the active sampling during the course of the study. The percentages are mean values for the six subsample sites in the 500 m reach.

<table>
<thead>
<tr>
<th>SUBSTRATE</th>
<th>FALL 2012</th>
<th>SUMMER 2013</th>
<th>FALL 2013</th>
</tr>
</thead>
<tbody>
<tr>
<td>Stone</td>
<td>47%</td>
<td>81%</td>
<td>34%</td>
</tr>
<tr>
<td>Sediment</td>
<td>28%</td>
<td>11%</td>
<td>41%</td>
</tr>
<tr>
<td>Aquatic Plant</td>
<td>25%</td>
<td>8%</td>
<td>25%</td>
</tr>
</tbody>
</table>
Identification and Metrics

Following DEP protocol a high intensity illuminator was used to pick a minimum of 300 individuals, and all individuals were picked from samples with fewer than 300 organisms (Flotermersch et al. 2006). An Amscope 3.5x-90x dissection microscope, together with Voshell (2002), Merritt et al. (2008) and McMahon and Bogan (2001) were used to identify 50 invertebrate taxa to family level classification. All invertebrates collected were preserved and stored in 20 mL glass vials filled with 95% ethanol. Pollution tolerance values were assigned based on family ordination (Hilsenhoff 1988; Chalfant 2007, PADEP 2012).

For each of the sampling methods, values were calculated for the Hilsenhoff Biotic Index (HBI), the Shannon Diversity Index (SDI), percent Ephemeroptera, Plecoptera, and Trichoptera (%EPT) and the Proportional Bray-Curtis similarity Index (BCI) relative to site. These metrics were generated according to Chalfant (2007), Bloom (1981), Bray and Curtis (1957) and Mandaville (2002).

RESULTS

The results describe a high variability from sampling season to sampling season and method to method and can be seen in the metrics that were calculated from the collected samples (Figures 2-4). For example, at WBP during fall 2013, the HBI (Figure 2) values ranged from 3.42 to 6.78, which defined that part of the river as having excellent to poor water quality, respectively. Typically, the variation in HBI was less than that of the SDI (Figure 3; 1.15 to 2.24 SDI) and %EPT (Figure 4; 20% to 83%). In some cases, however, there was marginal difference between the metric scores. For example, RB and HD samplers collected at WBP in the fall 2012 were very close in HBI scores (4.88 and 5.07, respectively; Figure 2). This similarity was not observed for the %EPT from samples collected by the same two methods at WBP (2% RB and 8% HD sampler; Figure 4). The SDI (Figure 3) tended to be highest with the active versus passive sampling methods, especially from collections obtained by the DN (active) and RB (passive) methods (1.95 and 1.47, respectively). This variability can be observed in the taxa that were collected through different methods (Table 2). A common occurrence table was created to generate an overview of the collected taxa at the family level (Table 2). For example, the active sampling methods collected burrowing mayflies, such as Potamantidae and Ephemeridae, which were not collected by passive sampling methods. On the other hand, members of the Heptageniidae were observed in every type of sample (with the exception of one set, the RB sampers collected during the fall 2012). Taxa from two different years (fall 2012 and 2013) were averaged to generate a table to compare sample methods (Table 3). Overall the active methods collected more taxa than the passive. For example DN collected the highest
Table 2. The taxa occurrence table describes the observed taxa over the two year sampling period. This indicates the occurrence of taxa in collections taken by the two most common sampling methods D-net (DN, white columns) and limestone rock baskets (RB, gray columns). Taxa that have been observed with a frequency of <0.10 are denoted by +. Any taxa with a frequency >0.10 are denoted as ++. Taxa not observed in these sampling methods are listed as 0. EPT taxa are delineated: Ephemeroptera (red), Plecoptera (blue), and Trichoptera (brown).
number of taxa (49), while HD samplers collected the lowest (12).

Each sample following enumeration and identification was normalized by calculating proportional occurrence of each family. BCI community tables (Figures 5 and 6) support the mosaic of similar and dissimilar communities depending on method and site. The values do not differentiate between the types of macroinvertebrates that were shared or excluded between samples; instead, this metric compares two communities by the degree of overlap in frequency of each taxon. Figure 5 illustrates the percent similarity between communities in a matrix of 16x16. The communities sampled by active methods describe a smaller overlap (range 12% very low - 67% high) than passive sampling (3% very low - 85% very high; Figures 5). For example, active methods of sampling during the fall 2012 had a wide range of overlap between sampling methods and sites, which range from high (67%) to very low percent similarity (12%). The SS samplers had a very low overlap with most methods (2%-65%). The passive sampling methods used during the summer sampling periods (2012 and 2013) described a moderately strong pattern of overlap. Only HD samples collected in summer 2013 at the NBP show an overlap below 18% (Figure 6). Each method indicates a low to high overlap based on method and date. While there is moderately strong overlap in communities by the different methods used in the summer sampling periods, the strongest overlap of passive samplers are described in the NBP (60%-69% Figure 6).

The BCI also was used to explore similarities in community composition between rock baskets on cinderblocks and those in direct contact with the substrate during summer and fall 2013. The highest overlap between elevated and substrate baskets (33%-84%; Figure 7) was at WBP; conversely the NBP collections had the lowest overlap (27%-73%).

<table>
<thead>
<tr>
<th>D12S1</th>
<th>D12S2</th>
<th>D13S1</th>
<th>D13S2</th>
<th>S12S1</th>
<th>S12S2</th>
<th>S13S1</th>
<th>S13S2</th>
<th>LR13S1</th>
<th>LR13S2</th>
<th>LR12S1</th>
<th>LR12S2</th>
<th>HD12S1</th>
<th>HD12S2</th>
<th>HD13S1</th>
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<td>30%</td>
<td>58%</td>
<td>38%</td>
<td>24%</td>
<td>48%</td>
<td>7%</td>
<td>5%</td>
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</tbody>
</table>

Figure 5. Proportional Bray-Curtis Similarity Index matrix which compares communities of collected macroinvertebrate taxa to estimate similarity at sample sites during fall 2012 and fall 2013. Each site was coded to the method and year for example D12S1, the format is method/year/sampling period/location (D=D-Net, S=Surber sampler, RB= Limestone Rock basket, HD= Hester-Dendy multiplate Sampler). S1 indicates the WBP sampling reach, while S2 indicates NBP reach. The macroinvertebrate communities collected at given sites and by given methods are expressed as percent similarity or overlap. Orange is coded as very poor overlap. Yellow is poor overlap. Green is moderate overlap. Blue is high overlap and dark blue is very high overlap.

Figure 6. Proportional Bray-Curtis Similarity Index matrix compares communities of collected macroinvertebrate taxa to estimate similarity at sample sites during the summer 2012 and 2013. Each site is coded, for example RB12S1; the format explains the sampling method/year/sampling period/location (RB= Limestone Rock basket, HD= Hester-Dendy Multiplate Sampler). S1 indicates WBP sampling reach, while S2 indicates NBP reach. The macroinvertebrate communities collected at given sites and by given methods are expressed as percent similarity or overlap. Orange is coded as very poor overlap. Yellow is poor overlap. Green is moderate overlap. Blue is high overlap and dark blue is very high overlap.
Figure 7. Proportional Bray-Curtis Similarity Index matrix compares communities of collected macroinvertebrate taxa to estimate similarity at sample sites during the fall and summer 2013. Each site is coded, for example FE1; the format explains the sampling year/location in water column/sampling location 1 indicates samples were collected at West branch plume reach (WBP) and 2 indicate North Branch plume reach (NBP). The macroinvertebrate communities collected at given sites and by given methods are expressed as percent similarity or overlap. Orange is coded as very poor overlap. Yellow is poor overlap. Green is moderate overlap. Blue is high overlap and dark blue is very high overlap.

### DISCUSSION

The BCI comparisons suggest that passive and active methods do not produce the same macroinvertebrate community estimates (Figures 5 and 6). These differences could be due to actual differences in the communities or because of bias inherent in the sampling method. For example, passive samplers (e.g. rock baskets) tend to collect colonizers such as drifting larvae relative to residential larvae (Johnson et al 2006).

In an attempt to attract burrowers and sediment-dwelling taxa into a rock basket, we deployed one set on the sediment as duplicates to others that were elevated. The community sampled by the elevated RB samplers at WBP during fall 2013 had very high overlap with the substrate RB samplers (Figure 7), but the NBP elevated RB samplers had a moderate overlap (Figure 7). The relatively high overlap in taxa, whether elevated or not, suggests that possible drifting organisms or crawlers are very similar during summer and fall. Thus, the location of the RB deployment in the water column was less important.

Active methods (e.g. DN and SS samplers) collect organisms that live not only on or under rocks, but also those organisms that inhabit deeper substrates or fine sediments (e.g. Potamanthidae, Ephemideri or Oligochaeta). Thus, animals that are stationary (e.g. *Corbicula*) or burrowers (e.g. Ephemideri) are unlikely to colonize passive substrates that are deployed for relatively short times and are elevated above the sediment. This was borne out by our collections (see Table 3). Active methods collected many *Corbicula* and Ephemideri; whereas, the passive methods did not collected them at all. Indeed, both groups made up more than 10% of collections (fall 2012, summer 2013, and fall 2013) taken by active sampling.

Overall, the DN method was most effective in collecting a broad sample of benthic macroinvertebrate taxa. Table 3 illustrates that the DN technique collected samples that had 140% more taxa compared to the SS method during fall 2012 and 2013 (42 and 29 taxa, respectively). Of the passive sampling methods tested Table 3 shows that RB samplers are more effective at collecting macroinvertebrate taxa than HD (24 and 12 taxa, respectively). More importantly, the DN method collected all but two of the taxa represented during the fall sampling periods. The SS and RB methods each collected one unique family (Ceratopogonidae and Chloroperlidae, respectively). The HD method collected the fewest number and no unique taxa. Between the two passive methods, the RB samplers have a larger surface area and collect a high diversity of taxa, including sensitive EPT taxa (such as Perlidae).

Each one of the sampling methods has its own inherent set of biases or problems that will affect the metrics, causing variability. Different collection methods produce differences in community estimates of benthic invertebrates which create variability in HBI, SDI, percent EPT scores for each sample. For example, depending upon the collection method used, HBI scores for the benthic macroinvertebrate community during fall 2013 describes WBP water quality as ranging from poor to excellent (3.75-6.77), and the NBP water quality during the same period is good to excellent (3.56-4.85). However, during fall 2012 the HBI scores for both WBP and NBP are less variable (fair to good and good to excellent, respectively).

Samples collected by active methods had greater taxa richness (Table 2) and higher SDI scores (Figure 3) than samples collected by passive means. Percent EPT reflects variability very well in that the invertebrate community collections taken by active methods have higher relative numbers of EPT taxa than did the passive methods (Figure 4). For example, in fall 2012 the DN technique collected more EPT taxa, while samples collected by the SS and passive methods had below 10% EPT (Figure 4).

Meier et al. (1979) suggest that variations in populations of benthic macroinvertebrates in artificial substrates like HD samplers could be attributed to time of exposure of the sampler and the creation of niches due to the loss of individuals. This suggestion is supported by Czerniawska-Kusza (2004) who explore the use of passive artificial substrates in assessing lowland rivers in Poland. Though there is greater time investment in using passive samplers than the active sampling methods, both Czerniawska-Kusza (2004) and Meier et al. (1979) support the use of passive artificial substrates despite the inherent bias and variability because these methods of collection are relatively easy to perform and they are inexpensive.

Field samples, especially passive artificial substrates that must be deployed for a given period of time, can experience many types of problems (e.g. extreme weather, high water...
events, unexpected construction impacts, human tampering, etc). We experienced several complications during collection of samples over the two year period of our study. During fall 2012, the RB samplers were collected 1.5 weeks early due to Hurricane Sandy. This might have impacted the possible taxa observed and total numbers of individuals due to reduced potential colonization time. In summer 2013, the Susquehanna River experienced a moderate high water event during the collection period, which decreased the area for active subsampling. In addition, the water was higher during the collection of RB samplers making the execution of appropriate methods difficult and dangerous.

Ordinarily, methods are not analyzed for their efficacy to evaluate water quality based on metrics generated by collections of macroinvertebrate communities within the same reach. Furthermore, the efficacy of methods for large river assessments needs to be understood to evaluate the accuracy and potential biases from each method. Even with its inherent biases the RB sampler is a much easier and better choice than the HD to use as an artificial substrate. One advantage is the standardization of substrate used that allows the comparison of one part of the river to the next. Further assessments of artificial substrates are needed to understand ways to mitigate their inherent biases. While the SS method works well in small order streams and wadeable river systems, in deeper water it may lose its utility as a quantitative method. If measured by number of taxa collected, active methods are superior and provide a higher resolution estimate of the actual macroinvertebrate community at a location in the river. Still active samples are not without problems and do not allow easy comparisons from one location to another in the river. Thus, we recommend that assessments of the Susquehanna River in the middle Susquehanna Valley include both active (DN) and passive (RB) methods of sampling.

ACKNOWLEDGEMENTS

Table 3. A common taxa list was generated between the two sampling years. This indicates the occurrence of benthic macroinvertebrates collected by all sampling methods D-net (DN), Surber sampler (SS), limestone rock basket (RB), and Hester-Dendy Multiple sampler (HD). Taxa that have been observed with a frequency of <0.10 are denoted by +. Any taxa with a frequency >0.10 are denoted as ++. Taxa not observed in these sampling methods are listed as 0.

This project was supported by in part by Susquehanna University, the Susquehanna River Heartland Coalition for Environmental Studies, and the Degenstein Foundation.

We would like to acknowledge the assistance of many students who helped especially during the collection phases of this project: Marc Santiago, Ian Murray, Austin Iovoli, Rachel Norbuts, and Matthew Smith. Also, we are indebted to an anonymous author who offered thoughtful comments which helped to clarify our arguments.
LITERATURE CITED


BIOASSESSMENT OF BENTHIC MACROINVERTEBRATES OF THE MIDDLE PENNS CREEK, PENNSYLVANIA WATERSHED†

JOHN PANAS, JONATHAN NILES1, SAM SILKNETTER, MICHAEL BILGER

Department of Biology, Susquehanna University, Selinsgrove, PA 17870

ABSTRACT

During October and November 2011, an assessment of the benthic macroinvertebrate assemblage was conducted in the middle Penns Creek (PA) watershed. The survey consisted of 10 tributary sites within a 40km portion of the watershed. The goals were to establish baseline conditions for headwater streams in this section of the watershed, determine their current biotic health, and suggest possible designated use upgrades. All sample sites were low-order (1-3) streams typically of higher gradient. We calculated the Pennsylvania Benthic Macroinvertebrate Index of Biotic Integrity at each site based on the following biotic indices: Beck’s Index, Total Taxa Richness, EPT (Ephemeroptera + Plecoptera + Trichoptera) Taxa Richness (Pollution Tolerance Values 0-4), Shannon Diversity Index, Hilsenhoff Biotic Index, and Percent Sensitive Individuals (Pollution Tolerance Values 0-3). All study streams are currently designated by Pennsylvania Department of Environmental Protection (PA DEP) as Cold Water Fish (1), High Quality (6), or Exceptional Value (3) streams. We found six streams to be of highest biotic quality (IBI score >80). Benthic macroinvertebrate IBI scores for Little Poe Creek (93.2) exceeded the current designated use of High Quality by PA DEP, and should be considered for a re-designated increase to Exceptional Value. Panther Run (51.9) received the lowest benthic macroinvertebrate IBI score, possibly due to low total organisms which may suggest it could be experiencing ecological stressors. Our overall results indicate these Penns Creek streams to currently be of good biotic health, however long-term monitoring may be necessary to further assess anthropogenic impacts within the watershed.

INTRODUCTION

Headwater streams tend to be highly susceptible to environmental changes due to their small drainage area and size, making natural and anthropogenic impacts more intense than in larger systems (Wallace et al. 1996; Angradi 1999; Pond 2010). Both physicochemical properties and aquatic biota have been shown to be negatively altered from anthropogenic stressors (Woodcock and Huryn 2007). Benthic macroinvertebrate have been found to be excellent indicators of water quality due to their limited mobility, short life spans, and varying sensitivity to pollutants (Fore et al. 1996). By analyzing the diversity of taxa, an understanding of various environmental stressors can be determined which may be impacting watersheds (Rosenberg and Resh 1993; Barbour et al. 1999). Various biotic indices and calculations can be used to assess these impacts. In Pennsylvania, selected indices are integrated into a benthic macroinvertebrate Index of Biotic Integrity (PA DEP 2012). The benthic macroinvertebrate Index of Biotic Integrity (IBI) calculation is a widely used biologically based metric that allows aquatic scientists to determine the integrity of fluvial systems, and is an accepted determinant for the designated usage of that waterway (Goodnight 1973; Barbour et al. 1999; PA DEP 2012).

The Pennsylvania Department of Environmental Protection (PA DEP) is the chief governing agency of water quality in the state, and issues varying levels of stream protection based on calculation of a benthic macroinvertebrate IBI and other water quality standards (PA DEP 2012). PA DEP's highest protection is awarded under the classifications of Exceptional Value (EV), High Quality (HQ), and Cold Water Fish (CWF); these classifications provide varying levels of protection for waterways (PA Code 2009; PA DEP 2012). By definition, an EV stream has excellent water quality, resulting in the highest environmental protection. A HQ stream has slightly lower water quality, and will only be altered under social or economic justification. CWF designation allows for the protection of salmonids and other biota indigenous to cold water habitat (PA Code 2009; PA DEP 2012).

During October and November 2011, 10 headwater streams in the middle Penns Creek (PA) watershed were assessed to determine the biotic health of the middle Penns Creek drainage. The 40km area of study is of major ecological,
sociological, and economic importance, yet still remains largely undeveloped making its protection necessary for the future. The goals of the study were to catalogue headwater stream benthic macroinvertebrate communities, to determine a Pennsylvania benthic macroinvertebrate Index of Biotic Integrity for those streams and to evaluate study streams for possible change in designated use by PA DEP.

MATERIALS AND METHODS

Study sites

Penns Creek is located in central Pennsylvania with the headwaters originating in Centre County. The creek flows nearly due east through Mifflin, Union, and Snyder Counties emptying into the Susquehanna River just below Selinsgrove, PA. The middle Penns Creek drainage is comprised of a mosaic of residential areas, agricultural land, and forested mountain terrain. The area was once historically logged, and extensive agriculture continues throughout the watershed. Ten streams, all tributaries of middle Penns Creek were chosen within the watershed: Cherry Run, Elk Creek, Furnace Run, Laurel Run, Little Poe Creek, Panther Run, Pine Creek, Poe Creek, Swift Run, and Weikert Run (Figure 1). A 100m reach was established on each stream nearest the confluence with Penns Creek. Streams selected were located within the Approved Trout Water or Class A Wild Trout sections of Penns Creek (PA FBC 2013).

Benthic macroinvertebrate sampling

Benthic macroinvertebrates were collected from October 15 and November 22, 2011 following the procedures established by Barbour et al. (1999) and PA DEP (2012). Six kick composite benthic macroinvertebrates samples were taken from riffle habitat within the 100m reach using a 12 inch wide x 10 inch high 500-micron mesh D-frame net. Sampling areas were 1 m², and the substrate was disturbed for one minute to a depth of 10 cm. Composite samples were placed into a 500-micron sieve bucket, rinsed, and then transferred into a wide mouth jar and preserved in 95% ethanol (Barbour et al. 1999). Large sticks, rocks, and plant materials were rinsed with stream water, examined for organisms and then discarded. To prevent site-to-site contamination the net was thoroughly checked for attached benthic macroinvertebrates and vigorously rinsed prior to leaving the site.

Data analysis

To develop the benthic macroinvertebrate IBI, the following indices were calculated: Total Taxa Richness; Ephemeroptera, Plecoptera, and Trichoptera (EPT) Taxa Richness (Pollution Tolerance Values 0-4); Modified Beck’s Index; Hilsenhoff Biotic Index; Shannon Diversity Index; Total Percent Sensitive Individuals (Pollution Tolerance Values 0-3); and a benthic macroinvertebrate IBI utilizing the six combined metrics (Appendix 1). All indices were calculated using the most current PA DEP protocols and tolerance values (PA DEP 2012). The IBI scores for all streams in the study, except Elk Creek were calculated using the small-stream IBI standardization values (PA DEP 2012). Due to the watershed size (~ 50 m²) at the sampling location we used the large-stream IBI standardization values for Elk Creek (PA DEP 2012). The possible designated stream use was determined by the total calculated benthic macroinvertebrate IBI scores (HQ+EV: IBI ≥ 80); and CWF attaining use with an IBI ≥ 63 (PA DEP 2012). Data was then given to the appropriate county Conservation District who forwarded it PA DEP to determine final designated use.

RESULTS AND DISCUSSION

Results

Overall macroinvertebrate biodiversity in the study streams was of high biotic quality as six of the ten streams exceeded an overall IBI score of 80. Ten genera (Epeorus, Leuctra, Swelta, Tallaperla, Acroneuria, Pteronarcyis, Agapetus, Dolophilodes, Wormaldia, and Diplectrona) were
identified with a pollution tolerance value of 0; and all study sites had at least one of these genera present (Appendix 1). Two streams, Little Poe Creek and Weikert Run, had a benthic macroinvertebrate IBI Score ≥92, the minimum for classification to be considered as EV. Both received an exceptionally high calculated benthic macroinvertebrate IBI score (Table 1), exceeding their current designated usage of HQ by PA DEP. Little Poe Creek had present, nine of the ten genera with a pollution tolerance value of 0 (Appendix 1). Two streams currently designated HQ, Pine Creek and Swift Run, had an IBI score >90, which are close to the EV threshold set by PA DEP. Two tributaries, Cherry Run and Furnace Run, had a benthic macroinvertebrate IBI score ≥80, the minimum for designation as HQ by PA DEP. Elk Creek, Laurel Run and Poe Creek had a benthic macroinvertebrate IBI score >63 and <80; the necessary score for designation as CWF (Table 1). Panther Run received the lowest benthic macroinvertebrate IBI scores of our sample set with an IBI of 51.9.

Six streams (Cherry Run, Furnace Run, Little Poe Creek, Pine Creek, Swift Run, and Weikert Run) had adjusted standardized Total Taxa Richness of at least 75.0 (Table 1) with Cherry Run a maximum of 100.0. Six streams (Cherry Run, Furnace Run, Little Poe Creek, Pine Creek, Swift Run, and Weikert Run) had an adjusted standardized EPT Taxa Richness greater than 70.0 with Swift Run the maximum of 100.0. Nine streams (Cherry Run, Elk Creek, Furnace Run, Laurel Run, Little Poe Creek, Pine Creek, Poe Creek, Swift Run, and Weikert Run) had an adjusted standardized Beck’s Index metric score exceeding 50.0; both Little Poe Creek and Swift Run had a maximum value of 100.0 (Table 1). We found that seven streams (Furnace Run, Laurel Run, Little Poe Creek, Panther Run, Pine Creek, Poe Creek, and Weikert Run) had adjusted standardized Hilsenhoff Biotic Index scores exceeding 90.0 with Furnace Run and Weikert Run a maximum of 100.0. In regards to species diversity, six streams (Cherry Run, Furnace Run, Little Poe Creek, Pine Creek, Swift Run, and Weikert Run) had adjusted standardized Shannon Diversity Indexes greater than 90.0, with Pine Creek a maximum of 100.0. Finally, we found in regards to sensitive genera, that seven streams (Furnace Run, Laurel Run, Little Poe Creek, Pine Creek, Poe Creek, Swift Run, and Weikert Run) had adjusted standardized Percent Sensitive Individuals score greater than 70.0 (Table 1).

**Discussion**

We used six accepted metrics developed by PA DEP (Total Taxa Richness, Total EPT Taxa Richness (PTV 0-4), Modified Beck’s Index, Hilsenhoff Biotic Index, Shannon Diversity Index, and Percent Sensitive Individuals (PTV 0-3)) to determine the Pennsylvania benthic macroinvertebrate Index of Biotic Integrity for each stream. Our benthic macroinvertebrate IBI calculations showed that the majority of streams (9 of 10) should be under the designations of Cold Water Fishes, High Quality waters, or Exceptional Value waters.

Panther Run, did not meet the minimum for any of these classifications based on the Benthic Macroinvertebrate IBI scores, even though it is currently under designated use by PA DEP as HQ. Our Benthic Macroinvertebrate IBI score was much lower than the minimum necessary for HQ (Table 1). The sample had less than 160 organisms, and a low frequency of individuals and pollution sensitive genera. Location of this stream is in a remote section of the wilderness which is

<table>
<thead>
<tr>
<th>Stream Name</th>
<th>Total Taxa Richness</th>
<th>EPT Taxa Richness</th>
<th>Beck’s Index</th>
<th>Hilsenhoff Biotic Index</th>
<th>Shannon Diversity Index</th>
<th>Percent Sensitive Individuals</th>
<th>Benthic Macroinvertebrate IBI</th>
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</thead>
<tbody>
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<td>Cherry Run</td>
<td>100.0</td>
<td>78.9</td>
<td>65.8</td>
<td>88.3</td>
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<td>50.0</td>
<td>59.1</td>
<td>93.3</td>
<td>78.6</td>
<td>49.7</td>
<td>64.8</td>
</tr>
<tr>
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<td>89.5</td>
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<td>100.0</td>
<td>92.7</td>
<td>98.9</td>
<td>89.4</td>
</tr>
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<td>73.7</td>
<td>50.0</td>
<td>94.1</td>
<td>89.7</td>
<td>93.9</td>
<td>78.0</td>
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<td>96.0</td>
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<td>18.4</td>
<td>92.7</td>
<td>65.0</td>
<td>70.5</td>
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<td>81.6</td>
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<td>81.1</td>
<td>79.5</td>
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<td>100.0</td>
<td>88.0</td>
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<td>65.1</td>
<td>90.8</td>
</tr>
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<td>Weikert Run</td>
<td>78.8</td>
<td>89.5</td>
<td>92.1</td>
<td>100.0</td>
<td>92.4</td>
<td>100.0</td>
<td>93.6</td>
</tr>
</tbody>
</table>

Table 1. The adjusted standardized metric values for the ten study sites within the middle Penns Creek (PA) watershed, and their combination into a calculated benthic macroinvertebrate IBI for each site. The Elk Creek metrics were calculated with large-stream metric standardization values, all other streams were calculated with small-stream standardization values (PA DEP 2012).
very underdeveloped. Low scores may have been due to site selection, as the site closest the mouth was downstream of a gravel road crossing, possibly having a negative effect on a small location of the creek. According to PA DEP protocols if a sample results in fewer than 160 total organisms in the entire sample, the IBI and assessment procedures may not apply exactly and this could be an improper IBI assessment due to the low total number of organisms (PA DEP 2012).

The overall health of the other headwater streams appears well, as we were able to identify 10 genera in 9 families that had a pollution tolerance value of 0 (Appendix 1). Every stream contained at least one genus with a pollution value of 0, indicating that these streams have the potential to support healthy and diverse benthic macroinvertebrate communities. All genera with a pollution tolerance value of 0 were in the orders Ephemeroptera, Plecoptera, or Trichoptera which are deemed as excellent indicators towards overall stream health. We found both the frequency of genera and individuals had a strong correlation with the calculated benthic macroinvertebrate IBI score and our six metrics (Table 1, Appendix 1).

Our results support the current designated use of many Penns Creek tributaries by PA DEP, but also indicate that certain streams should be proposed for re-designation under a higher classification by PA DEP. Concern for the overall health of the system may be necessary; as some tributaries classified under a higher designated use by PA DEP, failed to meet the minimum scores based on our benthic macroinvertebrate IBI calculations (Table 1). This may be an indicator that these streams are influenced by anthropogenic ecological stressors or possibly other factors such as seasonality or collection method.

### Exceptional Value Waters:

The highest quality streams were Little Poe Creek and Weikert Run. These streams exceeded the minimum benthic macroinvertebrate IBI score of 92 for consideration as EV waters by PA DEP (Table 1). They were of exceptional biological quality, and contained many genera with a pollution tolerance value of 0 (Appendix 1). Other pollution sensitive taxa were also present, and all streams had high species diversity. The high numbers of pollution sensitive taxa and high species diversity were responsible for producing exceptional scores in our six metrics and the overall benthic macroinvertebrate IBI score.

Little Poe Creek and Weikert Run produced IBI scores that exceeded their current HQ designated usage (Table 2). Based on our benthic macroinvertebrate IBI calculations, we propose that they be considered for re-designation to EV. Our data shows that 85 individuals from 9 genera had a pollution tolerance value of 0, which is an excellent indicator of the overall biotic health. These streams also had a benthic macroinvertebrate IBI score exceeding 93, which is exceptionally high for low-order headwater streams (PA DEP 2012).

Pine Creek and Swift Run which are two streams currently designated HQ: had IBI’s >90 which are close to the EV threshold. Pine Creek has sections which are currently both HQ and EV. Our sample site was located in the designated HQ section (Downstream Boundary of Hook Natural Area to Stony Run) between designated EV sections. More benthic macroinvertebrate collection should be conducted on these two to determine if these streams could be considered EV waters.

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**Table 2.** Current designated stream use by Pennsylvania Department of Environmental Protection (PA DEP), our IBI calculated stream use and proposed action based on calculated benthic macroinvertebrate IBI. Designated stream usage by PA DEP is determined by the calculated benthic macroinvertebrate IBI scores (EV+ HQ: IBI ≥ 80; CWF: IBI ≥ 63). Exceptional Value (EV), High Quality (HQ), and Cold Water Fish (CWF) are the protections awarded by PA DEP.

<table>
<thead>
<tr>
<th>Stream Name</th>
<th>Current DEP Stream Use</th>
<th>Benthic Macroinvertebrate IBI</th>
<th>IBI Calculated DEP Stream Use</th>
<th>Proposed Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cherry Run</td>
<td>EV</td>
<td>81.8</td>
<td>HQ</td>
<td>Evaluate for impairment</td>
</tr>
<tr>
<td>Elk Creek</td>
<td>HQ-CWF</td>
<td>64.8</td>
<td>CWF</td>
<td>Evaluate for impairment</td>
</tr>
<tr>
<td>Furnace Run</td>
<td>CWF</td>
<td>89.4</td>
<td>HQ</td>
<td>Upgrade</td>
</tr>
<tr>
<td>Laurel Run</td>
<td>CWF</td>
<td>78.0</td>
<td>CWF/ possible HQ</td>
<td>Evaluate for upgrade</td>
</tr>
<tr>
<td>Little Poe Creek</td>
<td>HQ-CWF</td>
<td>93.2</td>
<td>Possible EV</td>
<td>Upgrade</td>
</tr>
<tr>
<td>Panther Run</td>
<td>HQ</td>
<td>51.9</td>
<td>Non-attaining</td>
<td>Evaluate for impairment</td>
</tr>
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<td>Pine Creek</td>
<td>HQ-CWF</td>
<td>90.8</td>
<td>HQ/ possible EV</td>
<td>Evaluate for upgrade</td>
</tr>
<tr>
<td>Poe Creek</td>
<td>HQ-CWF</td>
<td>70.6</td>
<td>CWF</td>
<td>Evaluate for impairment</td>
</tr>
<tr>
<td>Swift Run</td>
<td>HQ</td>
<td>90.8</td>
<td>HQ/ possible EV</td>
<td>Evaluate for upgrade</td>
</tr>
<tr>
<td>Weikert Run</td>
<td>HQ-CWF</td>
<td>93.6</td>
<td>Possible EV</td>
<td>Upgrade</td>
</tr>
</tbody>
</table>
High Quality Waters:

Pine Creek, Swift Run, Cherry Run and Furnace Run exceeded the minimum benthic macroinvertebrate IBI score (≥80) for designated use as a HQ water. Pine Creek, Swift Run, Furnace Run are currently under HQ classification, and Cherry Run is under EV. Cherry Run scores were lower than PA DEP classification, but this score was still an excellent indicator of high water quality. The lower than expected benthic macroinvertebrate IBI score (81.8) for Cherry Run may have been due to sampling location, seasonality or processing reasons resulting in an apparent decrease in IBI score. More benthic macroinvertebrate collection should be conducted to determine if the stream no longer meets the minimum requirement for EV waters and to identify possible reasons for decline.

Cold Water Fishes Designation:

Elk Creek contains a Class A Wild Trout population within the sampling location (PA FBC 2013); and therefore, it automatically receives a minimum designation of HQ-CWF. PA DEP also lists this area under the usage of EV. Despite these protections, our benthic macroinvertebrate IBI scores indicate that water quality of Elk Creek may be deteriorating, as scores were far from its designated classification by PA DEP. Our calculated benthic macroinvertebrate IBI score of 64.8, did not meet the EV designation by PA DEP, which is correlated with low scores in our other six metrics (Table 1). Concentrated sampling in upstream sections of Elk Creek may help identify potential sources of non-point or point source pollution that could be responsible for the decline in the benthic macroinvertebrate assemblage. Laurel Run and Poe Creek both had benthic macroinvertebrate IBI scores that were > 63 and < 80, designating their use as CWF. Our determined use for Laurel Run is the same as PA DEP, but with a score of 78.0, future sampling may be conducted to see if its classification should be higher than its current status. The benthic macroinvertebrate IBI score (70.6) for Poe Creek was lower than PA DEP's current classification of HQ-CWF. The Poe Creek sample had less than 160 total organisms and thus the IBI and assessment procedures may not apply and this could be an improper IBI assessment due to the low total number of organisms (PA DEP 2012). Further sampling of this stream may be necessary to determine if there has been a permanent decline in overall water quality.

ACKNOWLEDGEMENTS

This work was supported by the Degenstein Foundation and the Department of Biology at Susquehanna University. We thank B. Thorpe Halloran for his assistance with Figure 1.

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Appendix 1. Total BMI taxa list present across the 11 study sites in upper Penns Creek watershed sampled from Oct. 15-Nov. 22, 2011.
MUSSEL POPULATION AND DISTRIBUTION ON BUFFALO CREEK, AN AMERICAN EEL STOCKED TRIBUTARY TO THE WEST BRANCH SUSQUEHANNA RIVER†

SEAN P. REESE¹, MICHAEL HUFFNER², JARED FEINDT²

¹Susquehanna River Initiative, Bucknell University Environmental Center, Bucknell University, Lewisburg, PA
²Bucknell University Lewisburg, PA

ABSTRACT

In 2009 the United States Fish and Wildlife Service began stocking young American eel into Buffalo Creek, a small agriculturally impacted stream that feeds into the West Branch of the Susquehanna River. The freshwater mussel *Elliptio complanata* is known to have higher success rates completing its life cycle using American eel as the host fish for its glochidia (Lellis et al. 2013). The objective of this study was to determine if the American eel will affect mussel populations within their first 5 years of reintroduction into Buffalo Creek and hopes to be a baseline study for future research. A total of ten sites were randomly distributed throughout Buffalo Creek with each site consisting of four 5m x 5m quadrants. In the first year of the study (2012) most mussels found were large *E. complanata* adults indicating that they had been present before the eel reintroduction. In 2013 we recorded almost twice as many mussels as last year and four new species (*Strophitus undulates*, *Lampsilis cariosa*, *Alasmidonta marginata*, and *Villosa iris*).

INTRODUCTION

Freshwater mussels are one of the most endangered taxonomic groups in the United States and can filter suspended sediments and particles from the water column and doing so can reduce turbidity and improve water quality (Newell 2004). Although numerous studies of mussel populations have been done in various parts of the country, there has not been extensive research conducted on the mussels of the Susquehanna River. Strayer’s (1999) work on the upper river basin compared presence/absence data from 1955-1965 to his own mussel surveys at the same sites in 1996-1997. His results suggest that there was very little change in mussel communities during the 30 year time span between the two surveys (Strayer and Fetterman 1999). As there are few additional studies available regarding the abundance of mussel communities on the Susquehanna River, it is difficult to make strong conclusions about mussel growth and decline. In an effort to aid these studies and to supplement the data that are present, we conducted a survey in 2009 on the West Branch of the Susquehanna in Milton, Pennsylvania, downstream of Milton State Park and approximately 1.5 miles upstream of where Buffalo Creek enters the West Branch (Figure 1). During that survey 903 mussels were found with a density transformed CPUE of 0.77 mussels/m². Mussel densities by surveyed cell ranged from 0 (a pro-rated bank survey) to 2.37/m² (a mid-channel cell). Of the 903 mussels found, *Lampsilis cariosa* was the most dominant species averaging 0.59 mussels per m² with a maximum of 1.93 mussels per m² and *E. complanata* averaging 0.089 mussels per m², second most dense mussel. While *E. complanata* is the most widespread freshwater mussel species in the Atlantic drainage, the Susquehanna River watershed contains far fewer *E. complanata* than neighboring watersheds like the Delaware (USFWS and USGS 2010). Looking at size distribution by species, we believe *E. complanata* is suffering from a loss of recruitment. One major factor behind this lack of young *E. complanata* may be the loss of the American eel from the upper Susquehanna River basin due to damming.

*Anguilla rostrata*, or the American eel, comprised roughly twenty-five percent of the total fish biomass in many locations along the Susquehanna River before damming (Minkinnen and Park 2008). American eels are catadromous fish, living in freshwater for most of their lives until sexual maturity and migrating to salt water (Sargasso Sea) to reproduce. Young eels return to freshwater to start the cycle all over again. Although there have been sporadic stockings of eels in the Susquehanna River basin, the population of American eels has been very small upstream of Conowingo Dam since the 1970’s (SRAFRC 2010). In order to improve water quality and strengthen a weak population, juvenile American eels were reintroduced into Buffalo Creek and Pine Creek upstream of all major dams on the West Branch of the Susquehanna River through a joint effort of the U.S. Fish and Wildlife Service and the U. S. Geological Survey.

Freshwater mussels have a unique interaction with fish.
Many use fish as a host for their glochidia or in their larval stage to complete metamorphosis into their juvenile stage. Some mussel species are generalists and can use a variety of fish species as their host while some mussel species are functionally dependent on a specific host fish to complete their life cycles (Haag 2012). Mussels without the specific host fish interaction face complications with reproduction and a diminishing population and eventual extirpation or extinction. American eels are the primary host fish of larval (glochidia) E. complanata and improves the success rate of E. complanata completing their life cycle when using American eels as their host fish (Lellis et al. 2013).

**MATERIALS AND METHODS**

We chose ten sites to survey in Buffalo Creek in Union County, PA. Five sites were randomly chosen upstream of the eel reintroduction site between Lewisburg and Mazeppa, and five sites were selected at random locations downstream of the introduction site over an area of four river miles (Figure 2). Due to logistics we avoided the approximate 1.3 km stretch of stream that ran through the property of the Lewisburg Federal Penitentiary. At each site, water quality measurements, including pH, dissolved oxygen, and temperature, were taken using a YSI 600 XLM V2 multiparameter water quality sonde. Furthermore, habitat and embeddedness at each site were recorded by the survey team at the time of mussel collection. To standardize our search methods, four 5m x 5m quadrants were made at the center of the creek using a premade dive array which divided the stream into four sections (Figure 3). Using an effective sampling fraction greater than 0.05, we determined an effective search time of five minutes per quadrant (Smith et al. 2001). Each quadrant was surveyed using a random start and timed search. A total of twenty minutes over the entire 10m x 10m site provided a comprehensive mussel density. The species of each individual found was recorded, and each mussel was weighed, measured, and photographed before being returned to the habitat and quadrant in which it was found. A three tiered sieve series ranging from 0.5 inch to 500 micron mesh was used for all excavations. Each quadrant had an excavation preformed in a 1 m² area to a depth ≥ 10 cm or to hardpan to search for juvenile mussels. Excavated material was passed through the sieve series, and mussels retained on the different mesh sizes of the sieves were identified and recorded.

**RESULTS AND DISCUSSION**

From June 2009 through August 2012 approximately 88,000 glass eels were introduced into Buffalo Creek in Union County, PA. In July 2012 we began conducting yearly quantitative surveys for freshwater mussels. In 2012 we found 111 mussels with E. complanata being the only species found alive. In 2013 we found five species of mussels, Strophitus undulates, Lampsilis cariosa, Alasmidonta marginata,
Villosa iris and Elliptio complanata, which had the highest densities. Of the 198 mussels found in 2013 E. complanata were the most abundant comprising 95% of the mussels found while V. iris was the least abundant at 0.01% (Table 1). We found higher densities of mussels in 2013 and there were signs of increased recruitment in young E. complanata from 2012 to 2013 (Figure 4). In the summer of 2012 we found 9 E. complanata under 60 mm in length compared to 24 E. complanata under 60 mm in length in 2013 (Table 2). The cumulative CPUE for our entire 10 sites in 2013 was 58.8 mussels per hour. Our individual CPUE for each site ranged from 0 in downstream quadrants where substratum was heavily embedded to 204 mussels per hour in one of our upper sites. Higher densities of mussels continued to be more commonly found upstream in areas that had more favorable habitat consisting of mostly cobble/gravel substrate with lower degrees of embeddedness (Figure 5). Embeddedness refers to the extent to which rocks (gravel, cobble, and boulders) are surrounded by, covered or sunken into the silt, sand, or mud of the stream and can hinder a mussel’s ability to burrow. Water quality was recorded at each site with the average water temperature at 22.4 °C in 2013 while 2012 had an average water temperature of 25.6 °C.

**CONCLUSION**

We saw a correlation between embeddedness and number of mussels found suggesting the more impacted the substrate, the lower the population of mussels. The majority of mussels were observed upstream in more favorable, less embedded habitats. While there is not a way to easily and accurately quantify embeddedness, the lower sections of creek were clearly impacted creating unfavorable conditions for populations. Burrowing is a technique that mussels use to provide additional anchorage in streams and rivers to help prevent dislodgement and protection from predation. Some species use burrowing as an adaptation for drought survival and throughout the winter months (Haag 2012). The inability for mussels to burrow due to embeddedness can be a major factor for the absence of mussels in our lower sites.
We saw an increase in the total number of specimens and species in 2013 from 2012. Factors for the increase of young *E. complanata* in 2013 could be cooler water temperatures, lower seasonal flows and the presence of more American eel available as host fish. Although mussel distribution is directly correlated with the geographical distribution of its host fish, other factors such as habitat can limit distribution and dispersal. Future biennial studies will be structured to assess the impacts of water quality, habitat, and introduction of juvenile eels on mussel population recruitment in Buffalo Creek.

### LITERATURE CITED


### Table 2. Size class comparison 2012 to 2013 (note all live mussels found in 2012 were *E. complanata*).

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ABSTRACT

Aquatic habitats vary widely in physical, chemical, and biological factors that can directly influence macroinvertebrate communities. Large rivers are spatially heterogeneous ecosystems with habitats affected by proximity to river banks, channel morphology, tributary confluences and human activities. Yet, large rivers remain largely understudied and are generally sampled in easily accessible near-bank areas, leaving macroinvertebrate communities undocumented from deeper, faster mid-channel habitats. Our goals were to document variability in macroinvertebrate community structure in the Susquehanna River and its two main tributaries, to determine the importance of upstream vs. local conditions, and to assess differences in near-bank vs. mid-channel sampling areas. We collected benthic macroinvertebrate samples in summer 2011 from the West Branch, North Branch, and mainstem Susquehanna River using rock baskets to standardize substrate effects across sites. We documented higher abundances of many genera in mid-channel sampling locations compared to near-bank locations but found no significant differences in taxa richness. Many taxa showed particular distribution patterns among river sites, but little correlation between upstream sampling locations and sites directly downstream. Therefore, our results indicate macroinvertebrate communities are primarily driven by the interaction of local habitat conditions.

VARIABILITY IN MACROINVERTEBRATE COMMUNITIES OF THE SUSQUEHANNA RIVER IN CENTRAL PENNSYLVANIA†


Biology Department, Bucknell University, Lewisburg, PA 17837

INTRODUCTION

Aquatic habitats differ in physical, chemical, and biological factors including variations in depth, flow, water chemistry, substrate type, and availability of organic matter, and are colonized by an array of aquatic invertebrates. Due to habitat variations, benthic communities as a whole are adapted to utilize the specific resources available within a locale (Huryn and Wallace 1987). These resources are not uniformly distributed, and habitat heterogeneity creates high biodiversity within river systems. Habitat conditions within rivers vary with proximity to river banks, channel morphology, and tributary confluences. In addition, human activities can modify physical and chemical conditions in rivers across broad scales due to landscape level changes (Allan et al. 1997) or at fine scales due to point-source discharges. These variations in physical and environmental conditions act as ‘filters’ which may exclude species from being present at a certain locale (Poff 1997). Determining which ecological variables are responsible for controlling community composition is difficult, especially when considering many variables are inherently interrelated. For example, past and current flow patterns determine substrate composition (Leopold 1994), and the distribution of many benthic organisms can be influenced by flow and substratum characteristics (Gurtz and Wallace 1984). Biological interactions (including competition and predation) may also function to further regulate community structure. Therefore, the presence of certain species at a locale directly reflects that habitat’s characteristics and species interactions (Poff 1997).

River systems also possess dynamic upstream-downstream interactions as a result of hydrologic and biological linkages between habitats. Due to the dispersal abilities of aquatic invertebrates, representatives of species may only exist in a habitat temporarily, or may display strong colonization in a habitat, due to continuous immigration from adjacent or upstream areas to which they are better adapted. This ‘mass effect’ arises particularly from the downstream drift of invertebrates in search of better habitat but may also arise via dispersal of flying adults choosing oviposition sites (Townsend 1989). Community structure of benthic invertebrates in rivers is therefore a product of natural variation in habitat conditions, human impacts on these habitat factors, biological interactions within the community, and dispersal by drift or flight. Streams within the same drainage basin provide an excellent model for studying variations in macroinvertebrate community structure by providing a similar species pool for colonization.

Large rivers remain relatively unstudied in ecological research (Rempel et al. 2000), primarily due to the difficulty

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Corresponding Author: mmctamma@bucknell.edu, (570) 577-3975
in obtaining biological samples from deep, fast flowing water. Furthermore, when large river surveys are conducted, samples are generally taken from more easily accessible river margins, leaving mid-channel sites undocumented (Collier et al. 2013). It has been suggested that mid-channel habitats in large rivers are hostile habitats, where deep water and high water velocities increase energetic demands on benthic organisms (Church 1992). However, Collier et al. (2013) found higher abundances of Trichoptera and Diptera and increased taxa richness in mid-river sampling sites compared to near-bank sites. Important differences in community structure might not be observed if sampling is restricted to shallow near-shore habitats. In particular, biodiversity of a river might be underestimated if certain taxa are only present in less accessible mid-channel habitats but surveys focus on near-bank sites.

The Susquehanna River and its tributaries represent a unique research opportunity due to their large size yet relative accessibility for sampling. In addition, the Susquehanna River is very wide and therefore likely varies considerably between mid-channel and near-shore locations. Human communities along the Susquehanna River and in its watershed also create a patchy landscape influencing water quality through municipal discharges, power-plant operations, agriculture, and coal mining. The confluence of the major branches of the river provides a unique opportunity to explore variability within the river potentially caused by connections to upstream communities. Satellite imagery of the Susquehanna River indicates visible differences in turbidity between the West Branch and North Branch, and lateral non-mixing is evident within the mainstem, below the confluence, for many miles. The stratification of water types upon entering the Susquehanna River may be an important factor in regulating macroinvertebrate communities, creating variations in community structure on opposing sides of the river.

The objectives of this study were to measure benthic macroinvertebrate community structure in the Susquehanna River in order to assess the relative importance of longitudinal connections or local conditions in determining community structure and compare the influence of sampling locations (near bank vs. mid-channel) on community structure within a river reach.

**MATERIALS AND METHODS**

**Study sites**

The Susquehanna River in central Pennsylvania is fed by two main branches. The North Branch flows from Lake Otsego in Cooperstown, NY and runs through primarily agricultural areas, historically mined areas (coal, iron), and several large municipalities. The West Branch originates near Carrolltown, PA and flows through predominantly forested land with some history of coal mining and then through some agricultural land prior to its confluence with the North Branch at Northumberland and Sunbury, PA. Downstream from the confluence, the Susquehanna River flows southward to Havre de Grace, MD where it forms the northern end of Chesapeake Bay. The North Branch is slightly larger than the West Branch and contributes approximately 60% of the discharge of the Susquehanna River at Sunbury, PA (USGS 2012).

We sampled the West Branch near Milton, PA (MIL), approximately 10 miles upstream from the confluence, and the North Branch near Danville, PA (DAN), approximately 12 miles from the confluence. Both branches were sampled at three locations across the river, near the left and right banks (LB, RB) and in the mid channel (Mid). Sampling locations in the Susquehanna River mainstem (SHA) were collected 5 miles below the confluence of the branches, near Hummels Wharf, PA, in a section of the river bisected by Byers Island. We sampled in the western channel near the river bank (SHA1) and Byers Island (SHA2) and the eastern channel near Byers Island (SHA3) and the eastern river bank (SHA4). Further complicating site selection in the mainstem is the presence of an electrical power plant on the west side of the river that discharges warm water to the western channel approximately 1 mile upstream from SHA1. As a result, we added a site along the western river bank approximately 1 mile upstream from the power plant discharge (SHA5).

**Invertebrate collection**

Invertebrates were passively collected using rock baskets, cylindrical baskets (length= 30 cm, diameter= 18 cm) made of large wire mesh and filled with substrate. Cobble substrate was collected from an exposed gravel bar in a nearby stream and thoroughly cleaned and dried before filling baskets with similar sized rocks. Three rock baskets were deployed on 9-10 June 2011 at each sampling location, which resulted in 9 rock baskets at each upriver site (LB, RB, and Mid at MIL and DAN) and 15 at the downstream (SHA) sites. Each rock basket was secured to a cinder block and placed on the river bottom for a period of 6 weeks. Each basket was collected from the river intact on 20-21 July 2011 by carefully removing the basket from its cinder block and transferring it to a submerged bucket. Each bucket was covered for transport back to the lab. Invertebrates were removed from substrates by hand, preserved in 70% ethanol, and identified to genus when possible (Chironomidae and non-insects only to family level). Two species of *Maccaffertium* were noted and differentiated as *Maccaffertium* NB and WB (no bands and with bands, addressing obvious differences in ventral patterns). Rock baskets were chosen to standardize substrate across the sites and to simplify sampling, as conventional kick-net benthic samples can be difficult to obtain from large
rivers.

Water quality

Physicochemical water parameters (temperature, pH, dissolved oxygen, conductivity) were measured in situ using a calibrated sonde (YSI Model 6920, Yellow Springs Instruments, Yellow Springs, OH). Depth was measured at each locale with a meter stick, and velocity was measured at 0.6 of depth using a flow meter (Flo-Mate 2000, Marsh-McBirney Inc., Frederick, MD). One liter grab samples were collected to quantify total suspended solids (TSS) and seston chlorophyll a. Water from grab samples was filtered onto pre-weighed glass fiber filters (1.0 μm mesh). For TSS, filters were dried and re-weighed. For seston chlorophyll a, photosynthetic pigments were extracted by submerging filters in 90% ethanol overnight and analyzed on a spectrophotometer. Water samples for chemical analysis were filtered (0.7 μm mesh glass fiber filters) in the field and transported to the lab on ice. These samples were then used to determine concentrations of ammonium using the OPA method (Holmes et al. 1999) and soluble reactive phosphorus using the ascorbic acid method (APHA 1998).

Data analysis

Benthic macroinvertebrate community structure was compared among sites using density of organisms per rock basket, composition of different taxonomic groups, proportions of each functional feeding group, and multivariate ordination (nonmetric multidimensional scaling). Principal component analysis was used to compare physical and chemical conditions across the sites.

RESULTS

Water temperatures ranged from 22-28 °C across all sites, with higher amounts of variation at the SHA sites (Table 1). SHA1 had the highest temperature of 28 °C due to the upstream warm water discharge. The pH and DO were similar across all sites ranging from pH of 7.5-8.9 and DO of 8.2-10.3 mg/L. Average pH was slightly higher at DAN compared to MIL, which was reflected at respective downstream sites with SHA5 and SHA1 presenting a slightly lower pH than other SHA sites. TSS and Chl a analysis showed available food resources varied greatly between tributaries, and directly affected downstream sites. TSS at DAN ranged from 15.90-17.59 mg/L but was much lower at MIL (1.36-2.67 mg/L). TSS at downstream SHA sites obviously reflected respective upstream tributaries. SHA5 and SHA1, located on the west bank of the Susquehanna, had low concentrations of suspended solids (1.70 mg/L) while locales in the middle and east side of the river had higher TSS (10.90-11.70 mg/L), more similar to TSS at DAN. This upstream-downstream linkage was also evident in Chl a analysis where SHA5 and SHA1 locales contained much lower levels of suspended Chl a (2.15-7.05 μg/L), similar to MIL (7.52-7.63 μg/L). DAN contained markedly high concentrations of Chl a (27.60-41 μg/L), which was reflected at SHA2 SHA3 and SHA4 (33.67-39.07 μg/L). Phosphorus was low (<6 μg/L) at all sites and did not show any obvious spatial pattern. Ammonium ranged from 18.4 μg/L at DAN to 49.3 μg/L at SHA4 and was inconsistent among the study sites.

PCA ordination of habitat variables (Figure 1) showed dramatic similarity among sites from the West Branch (MIL) and sites along the western bank downstream of the confluence (SHA5, SHA1). Other SHA sites grouped closer to DAN sites, indicating that physical and chemical conditions were more similar among these sites than these sites were to MIL, SHA1 and SHA 5.

Invertebrate densities per rock basket were highest in the mid-channel DAN samples (averaging 2700 individuals per rock basket) and second highest (approx. 900 individuals per rock basket) at MIL mid-channel (Figure 2). At MIL and DAN, samples near the river banks had significantly lower invertebrate density than mid-channel samples (One-way ANOVA, p<0.05). Invertebrate densities at SHA sites were highest at SHA2 and lowest at SHA3 and SHA 4 on the eastern side of Byers Island.

Filterers were proportionally the most abundant functional feeding group (FFG) at MIL and DAN, comprising 35-55% of all individuals (Figure 3). Over 5,000 filtering individuals were collected in the DAN mid-channel samples, which was over 2x more individuals than any other group at any

Figure 1. PCA ordination of habitat variables from sites in the West Branch (MIL), North Branch (DAN), and mainstem (SHA) Susquehanna River.
Furthermore, hydropsychid caddisflies made up approximately 54% of all filtering invertebrates collected at MIL and 76% at DAN. Scrapers were the most dominant FFG at all SHA sites with the exception of SHA4 where collector gatherers were most common. Heptageniidae made up a large proportion of scrapers collected across our study sites (76% at MIL, 81% at DAN, 91% at SHA1, 90% at SHA 2, 94% at SHA 3, 82% at SHA 4, 94% at SHA5). The collector gatherers that dominated SHA4 were all Chironomidae. Predators and shredders were rare at all sites.

**Figure 2.** Invertebrate densities sites in the West Branch (MIL), North Branch (DAN), and mainstem (SHA) Susquehanna River. Bars show mean density (n=3) + 1 SE.

**Figure 3.** Functional feeding group (FFG) composition of invertebrate communities at sites in the West Branch (MIL), North Branch (DAN), and mainstem (SHA) Susquehanna River. Each bar represents the sum of 3 replicate samples. SH= Shredders, SC= Scrapers, PR= Predator, CG= Collector Gatherer, FL= Filterer.

**Figure 4.** Insect order composition at sites in the West Branch (MIL), North Branch (DAN), and mainstem (SHA) Susquehanna River.

**Table 1.** Physicochemical characteristics of sites in the West Branch (MIL), North Branch (DAN), and mainstem (SHA) Susquehanna River where rock baskets were deployed.

<table>
<thead>
<tr>
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<td>RB</td>
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highest proportion of individuals at DAN (46%), but were less dominant at MIL (21%) and SHA (10%). Diptera were 21% and 22% of benthic invertebrates at MIL and DAN, respectively, and were highly variable across SHA sites (4% at SHA1 to 53% at SHA4).

The majority of Ephemeroptera collected across all sites were Heptageniidae. Heptageniidae comprised 53% of all Ephemeroptera at MIL, with *Isonychia* contributing 22% and Baetidae 12%. Baetidae were equally distributed across the channel at MIL while Heptageniidae abundance was higher in near bank samples. DAN also contained a high abundance of Heptageniidae mayflies, contributing 38% of all Ephemeroptera, while Baetidae and *Isonychia* made up 21% and 18% of mayflies, respectively. Unlike the MIL site, Heptageniidae at DAN were only more abundant along one bank and equal in density at the other bank and mid channel site. However, Baetidae appeared to prefer near bank sites at DAN. The downstream SHA sites were all heavily dominated by Heptageniidae, comprising 75-90% of all Ephemeroptera with Baetidae and *Isonychia* making up 1-16% of all Ephemeroptera with Baetidae only contributing 1-16%.

*Isonychia* were most abundant at mid-channel sites at both DAN and MIL but were found in relatively low abundances at SHA sites.

Multivariate ordination of taxonomic information from the rock baskets showed consistent benthic invertebrate community structure among samples collected from MIL and DAN and variable community structure in SHA samples (Figure 5). In general, SHA1, SHA2, and SHA5 grouped together, and SHA3 and SHA4 grouped with LB and RB DAN samples. DAN mid-channel samples were more closely grouped with samples from MIL and SHA 1, SHA2 and SHA5. Densities of *Leucrocuta* and *Maccaffertium* NB (Heptageniidae) were strongly correlated with axis 1 (r=0.85, r=0.78) along with *Proclœon* and *Heptagenia* (r=0.47, r=0.47). Taxa negatively correlated with axis 1 included *Ferrisia* (Ancylidae) (r=−0.53) and *Stenacron* (Heptageniidae) (r=−0.43). Axis 2 correlated with densities *Maccaffertium* (r=0.49), *Leucrocuta* (r=0.40), and *Proclœon* (r=0.39). SHA5, SHA1 and SHA2 all contained particularly high densities of Heptageniidae, and all SHA samples contained large proportions of Ephemeroptera.

Particular genera of heptageniid mayflies were distributed differently among river sites and at different locations within a particular site (Figure 6). MIL was dominated by *Maccaffertium* WB (44%) and *Stenacron* (31%) with a total of 1317 Heptageniidae individuals collected. DAN was dominated by *Leucrocuta* (33%) and a different species of *Maccaffertium* NB (34%) with 1564 Heptageniidae individuals collected. SHA5 included high densities of *Maccaffertium* NB (37%) and *Leucrocuta* (34%) while SHA1 primarily consisted of *Leucrocuta* (50%). *Maccaffertium* WB, *Maccaffertium* NB and *Stenacron* occurred in much lower densities, making up 17%, 15% and 14% of Heptageniidae at SHA1, respectively. Heptageniidae at SHA2 were similarly dominated by *Leucrocuta* (42%) with *Maccaffertium* NB (29%) and *Heptagenia* (23%) comprising a large portion of...
the samples. *Heptagenia* were oddly abundant at this site. The lowest heptageniid abundances were recorded at SHA3 (274 individuals) and SHA4 (167 individuals). SHA3 was dominated by *Stenacron*, which made up approximately 50% of all Heptageniidae individuals, while *Leucrocuta* contributed 30%. SHA4 contained high proportions of *Leucrocuta* (56%) and *Maccaffertium* NB (32%). All Heptageniidae were recorded in higher densities in mid-channel locations of MIL and DAN. *Stenonema* was only collected in abundances greater than 2 individuals from the mid-channel samples at DAN (39 individuals collected).

Baetid mayflies also showed distinct patterns between rivers and among sites (Figure 7). *Baetis* and *Pseudocloeon* were the most abundant baetids at MIL (41% and 32% of total samples, respectively), while *Baetis* made up 83% at DAN. *Procloeon* accounted for 94% of total baetid mayflies at SHA1 and 89% at SHA5, but only 12% of baetids at SHA2 where *Pseudocloeon* dominated with 53%. SHA3 and SHA4 were both dominated by *Procloeon* (100% and 60% respectively). All baetids at MIL were more abundant at mid-channel sites. However, *Baetis, Plauditus* and *Pseudocloeon* at the DAN sites did not prefer mid-channel sites and were at least 2x greater in density on the right bank (4x greater for Pseudocloeon). Densities on the left bank were similar to those in the mid-channel. *Acentrella* was only present at SHA1 and SHA2 (3 individuals collected).

Overall Trichoptera taxa richness was low at all sites (12 taxa), and many taxa were rare and represented by few individuals. Hydropsychidae were more abundant than all other Trichoptera, comprising 93-100% of all caddisfly larvae collected at a given site (100% of all Trichoptera at SHA3 and SHA4). *Chimarra* (Philopotamidae) was collected from DAN at higher abundances than other sites (154 individuals, only 9 other Chimarra individuals collected). Hydropsychid density was highest in mid-channel samples at DAN and MIL. *Cheumatopsyche* was the dominant trichopteran taxa at MIL and made up 90% of all hydropsychids collected at a given site (100% of all Trichoptera at SHA3 and SHA4). *Chimarra* (Philopotamidae) was collected from DAN at higher abundances than other sites (154 individuals, only 9 other Chimarra individuals collected). Hydropsychid density was highest in mid-channel samples at DAN and MIL. *Cheumatopsyche* was the dominant trichopteran taxa at MIL and made up 90% of all hydropsychids collected (Figure 8). Conversely, *Cheumatopsyche, Hydropsyche* and *Macrostromum* demonstrated nearly equal abundances (approximately 33% each) at DAN. Very low abundances of all hydropsychids (and Trichoptera in general) were recorded in the mainstem. Cheumatopsyche were the most abundant hydropsychids present at SHA sites, which contained very few *Hydropsyche* and no other Macrostromum. SHA3 samples contained only 8 *Cheumatopsyche* and no other Trichoptera representatives.

Chironomidae were the most abundant dipters and were the only dipters present at all SHA sites. Chironomidae showed no distributional patterns at SHA sites, but were more abundant in mid-channel sites in both DAN and MIL. *Diptera* at MIL were 93% Chironomidae and 7% *Prosimulium* (Simulidae). The DAN site showed slightly more diversity with 76% of all Diptera consisting of Chironomidae, and 23% Simulidae (both *Prosimulium* and *Simulium* present in nearly equal proportions). *Hemerodromia* (Empididae) were also present in DAN.

**DISCUSSION**

A total of 57 taxa were collected across all study sites, with the highest richness appearing at the DAN site with 41 taxa. MIL sites contained 33 taxa while SHA sites ranged from 16 at SHA4 to 29 at SHA5. Richness was similar in mid-channel and near-bank sites, although mid-channel sites supported higher invertebrate densities. Density was highest at DAN and was most likely driven by high concentrations of suspended organic matter, especially algae. It is unclear why densities were so low at SHA sites, but all of the sampling locations we used in this reach of the river were near either river banks or Byers Island. Based on our observations from MIL and DAN, we suspect mid-channel locations at SHA would contain higher densities of macroinvertebrates than the sites we sampled.

Filterers proportionally dominated MIL and DAN sites, comprising 35-55% of all functional feeding groups. Both TSS and Chl a (seston) averages reached high concentrations at DAN (16.7 mg/L TSS and 36.7 µg/L Chl a), providing a plentiful energy source for filtering invertebrates (Vannote et al. 1980). However, MIL sites had relatively low concentrations (compared to DAN sites) of only 2 mg/L of TSS and 7.6 µg/L of Chl a and had proportionally fewer filterers than DAN.

Both TSS and Chl a showed similar concentrations in downstream sites as in their respective upstream tributaries (SHA2, SHA3 and SHA4 similar to DAN, and SHA5 and SHA1 similar to MIL), so we expected filterers to show similar abundances to their respective upstream branches. However, this was obviously not the case, as scrapers were more abundant at all downstream SHA sites (with the exception of SHA4). Because both filterers and scrapers require stable substrate, we hypothesize these groups might be competing for space. Heptageniid mayflies made up the vast majority of all scrapers collected, and might be superior competitors for space compared to filtering hydropsychids or could establish populations on introduced rock baskets more quickly and prevent subsequent colonization by caddisfly larvae.

Higher abundance of many taxa at MIL and DAN sites relative to SHA sites may simply be due to sampling techniques because both MIL and DAN sites contained a mid-channel sampling location. Filterers, collector gatherers and scrapers were all more abundant in mid-channel locations at MIL and DAN. Approximately 75% of all filtering taxa collected from the MIL and DAN sites were from mid-channel samples. This pattern also existed for scrapers and collector gatherers, where 50-60% of all individuals were collected from mid-channel sites. Georgian and Thorp (1992) found that hydropsychid larvae preferentially colonize higher velocity habitats in order to increase rates
of prey capture. Water velocities in mid-channel reaches at MIL and DAN were slightly higher compared to near bank sites. Although SHA sites contained sampling locations that were technically mid-channel (for the entire river), Byers Island created hydrology at “mid-channel” sites (SHA2 and SHA3) more similar to near bank conditions.

A variety of net-spinning caddisfly species generally occur within a drainage basin, but are distributed based on feeding preferences and water velocity (Hildrew and Edington 1979). Different species of net spinning caddisflies construct nets of varying mesh sizes in order to filter a particular size of food particles (Ferrier and Wissing 1979, Ross and Wallace 1983, Wallace and Malas 1976, Wallace 1975, Wallace and Sherberger 1974). Some species construct coarse mesh nets to selectively filter large particles where others, like Macrostemum, build fine mesh nets capable of capturing fine detritus (Wallace and Sherberger 1974). Our results clearly show distribution patterns of net spinning caddisflies, particularly in the Hydropsychidae. The distribution of the genus Macrostemum is restricted to the DAN site, where it occurs in equal abundance with Hydropsyche and Cheumatopsyche. Macrostemum was notably nearly or completely absent from all other study locations. Interestingly, Chimarra (Philopotamidae), which also constructs fine mesh nets (Williams and Hynes 1973), was collected at DAN in higher numbers than other caddisflies. The presence of these fine mesh net spinning caddisflies at the DAN site is likely attributed to availability of a preferred seston particle size, or a favorable change in competition dynamics with other taxa considering water velocities did not vary greatly between sites.

In July 2005, the Susquehanna River Basin Commission conducted surveys of benthic invertebrates in the Susquehanna River using rock basket transects at locations very close to the sites we used (Hoffman 2006). Certain aspects of this agency’s deployment prevent direct comparisons with our data. For example, the number of individuals per rock basket cannot be directly compared to because rock baskets were not of the same design or size. In addition, SRBC baskets placed near our SHA location were not located on either side of Byers Island, and only one was retrieved during their study, so we cannot compare results from this site. That being said, there are several useful comparisons between our studies that support general trends or suggest patterns that might vary over time.

Both studies indicate filterers are the dominant functional feeding group at both the West Branch and North Branch sites. One of the most common filter-feeding groups in both studies was the Hydropsychidae family of caddisflies, but distributions of genera from this family differed between the two studies. In our study, hydropsychid caddisflies were more abundant in mid-channel sites of the West Branch and North Branch. However, hydropsychids were equally abundant across the West Branch and more abundant near the banks in the North Branch samples from Hoffman (2006). Hydropsychidae genera at DAN in our study were equally distributed among Cheumatopsyche, Hydropsyche, and Macrostemum. Hoffman’s results indicated Macrostemum was more abundant than other genera at DAN. Both studies indicated Cheumatopsyche is more abundant than other hydropsychid genera in the West Branch.

Both studies indicated high abundance of Ephemeroptera nymphs in the West Branch, but our results showed the family Heptageniidae as the most abundant, not Isonychiidae as found in SRBC rock basket samples (Hoffman 2006). Mayflies were the also the most abundant order in SRBC samples from the North Branch (Hoffman 2006), but caddisflies were the most abundant order in our samples from DAN (North Branch). Furthermore, our results indicate greater diversity of Baetidae mayflies in the Susquehanna River. Hoffman only reports Baetis, Heterocloeon, Centroclit, and Acentrella, with the last two in low abundances. Our results indicate the additional presence of Pseudocloeon, Procloeon, and Plauditus, with no observed Centroclit, from these same sites. Clearly, there are many similarities that reveal consistent patterns in the Susquehanna River over time using the same sampling approach, but certain traits of the benthic community, especially composition at finer taxonomic resolutions, vary either spatially or temporally and cause differences between these two studies.

Physicochemical measurements between studies varied due to sampling dates. However, both studies indicated higher DO and pH in the North Branch compared to the West Branch. Results from Hoffman (2006) indicated water temperatures were higher in the North Branch compared to the West Branch, but our results showed the opposite. This could be due to relatively lower flows in the West Branch relative to the North Branch when we studied them in 2011. Measurements from Hoffman (2006) described similar amounts of TSS for the North Branch and West Branch, where our results indicate the North Branch carried a significantly higher TSS load than the West Branch.

It appears most communities were driven primarily by the interaction of local habitat conditions. Using identical substrates in the rock baskets should reduce taxonomic variability that would naturally exist between sites, which suggests benthic invertebrates across our study sites were likely affected by water quality and food resources. Linkages to upstream reaches were apparent with certain aspects of water quality, but community structure appeared to be determined primarily by site specific factors and secondarily by longitudinally connected variables. Furthermore, sampling near shore might be more convenient and easy, but benthic invertebrates were significantly more abundant and represented different proportions of many taxa in mid-channel samples.

Downstream sampling locations were not ideal for direct comparison to upstream sites. In the future, sampling locations in downstream reaches should be in similar channel
locations and should be selected to minimize potential impacts on individual sites. The warm water discharge from the Sunbury power plant affected SHA1 exclusively. Similarly, Shamokin Creek, a major tributary affected by coal mine drainage (Cravotta and Kirby 2004), affected SHA4 exclusively. These site-specific human impacts could lead to unique benthic macroinvertebrate assemblages and contribute to the idiosyncratic and inconsistent communities in the river at SHA. However, the extensive variability in benthic macroinvertebrate communities across a single transect provides support for expanding large river surveys to adequately assess biodiversity of the Susquehanna River and responses to human activities in a watershed.

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LITERATURE CITED


