BROOK TROUT SALVELINUS FONTINALIS DISTRIBUTION, GENETIC DIVERSITY, AND HABITAT USE IN AN ADIRONDACK RIVER SYSTEM, NEW YORK

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BROOK TROUT *SALVELINUS FONTINALIS* DISTRIBUTION, GENETIC DIVERSITY, AND HABITAT USE IN AN ADIRONDAK RIVER SYSTEM, NEW YORK

by

Carrianne E. Pershyn

A thesis
Submitted in partial fulfillment
of the requirements for the
Master of Science Degree
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College of Environmental Science and Forestry
Syracuse, New York
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Abstract


This study examined population dynamics, ecology, genetic diversity, and habitat use of wild Brook Trout in tributaries of the East Branch Ausable River, NY from headwaters to mouth. Brook Trout population abundance was estimated and fish community composition was documented along the longitudinal gradient of the East Branch Ausable River. Brook Trout were found throughout this watershed, and multivariate analysis demonstrates that habitat variables influence community assemblage. In addition to elevation, gradients of forest cover, temperature, and percent impervious surfaces explained variation of fish distribution in this watershed. Population genetic analyses demonstrated that natural reproduction of wild and hatchery fish is occurring in the headwaters. Brook Trout in the headwaters of the Ausable River are an admixed population of wild and domestic-Temiscamie fish, and results show lasting effects of fish stocking on the genetic diversity and population status of this system.

Key Words: Brook Trout, Population genetics, Adirondack ecology, coldwater fisheries, habitat preferences.

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Chapter I: Brook Trout Distribution and Fish Community Composition in Upper Ausable Lake and the Tributaries of the East Branch Ausable River, Adirondacks, NY

Abstract: This study examined population dynamics and habitat use of wild Brook Trout in tributaries of the East Branch of the Ausable River, NY, from the protected headwaters to Ausable Forks. Brook Trout abundance and fish community diversity analyses were completed for near-river reaches of 21 tributaries and a lake that forms the headwaters of the East Branch Ausable River. Brook Trout were found to occupy study reaches in 13 tributaries throughout the entire gradient of the East Branch. Physical and chemical habitat variables were measured at all study sites, and these were compared to landscape variables to evaluate which habitat or local landscape variables may limit habitat suitability and Brook Trout occupancy within the East Branch Ausable system. Overall fish community diversity and species richness increased along the longitudinal gradient, and results suggest that elevation, maximum temperature, percentage of impervious surfaces, and percent forest cover best described the variability across study sites. This study helps document the current distribution and status of Brook Trout and other fish species in the Ausable River watershed, can be used to discern whether the lower tributary reaches provide important habitat for young salmonids, and will provide valuable information to future studies of Brook Trout movement in the river and tributaries.

Introduction

In the Northern Forest region that encompasses much of the northeastern United States and eastern Canadian provinces, Brook Trout *Salvelinus fontinalis* are one of two iconic native stream-dwelling salmonids, and much like the aquatic invertebrates they feed on, are an ecological indicator species of functional, coldwater streams, ponds, and rivers. Despite the large proportion of public land and large tracts of privately held land in the Northeast, Brook Trout face major human-induced threats, including habitat fragmentation, increasing summer water temperatures, and competition from non-native and introduced species, including Brown Trout *Salmo trutta* (EBTJV 2011, Carlson et al. 2016). Brook Trout have been identified by New York State Department of Conservation (NYS DEC) as a Species of Greatest Conservation Need (NYS DEC 2015). This means they are faced with a series of threats, are in decline, and require conservation action to ensure stable populations and to prevent them from becoming endangered. Brook Trout are native to all 18 watersheds of New York State, and their presence is an indicator
of excellent water quality and ecological integrity (Carlson et al. 2016). While Brook Trout occur in high abundance in intact, well protected watersheds, their range has contracted in all New York watersheds due to habitat fragmentation, riparian buffer and forest loss leading to water temperature increases, and past introductions of non-native species (Hudy et al. 2008, Carlson et al. 2016). Habitats that provide optimal physical requirements necessary for Brook Trout growth and natural reproduction are small and fragmented in much of the state; limited intact populations remain across their native range. These intact habitats are characterized by streams with high amounts of forest cover, cool water temperatures, proximity to lands with little nutrient or pollutant runoff, and those having undamaged riparian zones that minimize erosion. In much of the historic range of Brook Trout, these conditions are often only met in headwaters of river systems and streams within smaller forest blocks; these are often fragmented by road crossings and other barriers, including just above or below areas of sub-optimal habitat (Hitt et al. 2016). In New York State’s Adirondack Park, however, Brook Trout are found throughout watersheds, from headwaters to river mouths. The Ausable River in the northeastern part of the Adirondack Park is world-renowned for its trout fisheries, long stretches of scenic and wild landscapes, and excellent hatches of aquatic insects; past management has provided a long history of economically positive recreation opportunities to the region.

Climate change is likely to play a role in amplifying existing threats to Brook Trout and may lead to additional pressures such as increased water temperature and variable flow regime, with lower flows in summer and high flows at uncommon times during the growing season (Wenger et al. 2011, Bassar et al. 2016, Lynch et al. 2016). Wild Brook Trout populations may persist in areas that have some resistance to climate change, and New York State’s Adirondack Park is considered one of the strongholds of the northeastern US according to the Eastern Brook
Trout Joint Venture (EBTJV), (EBTJV 2005, Hudy et al. 2008). An EBTJV model of Brook Trout occupancy under severe future climate warming reveals the Ausable River watershed as a climate refuge, particularly small tributaries to the East Branch, (Interactive Catchment Explorer 2017, http://ice.ecosheds.org/ebtv/). The East Branch watershed as a whole has the third highest probability of Brook Trout occupancy under the most extreme climate warming scenarios (up to 6°C). Further analysis of these data indicates that the Ausable Lakes and Johns Brook subwatersheds have the highest probably of occupancy within the entire native range of Brook Trout (Interactive Catchment Explorer 2017, http://ice.ecosheds.org/ebtv/). Given recent projections of faster warming trends in the northeastern United States, (Karmalkar & Bradley 2017), gaining an understanding of the current trout population dynamics in New York State is critical for conservation planning for the coming decades.

**Critical habitat requirements for Brook Trout**

Like other species of North American trout, Brook Trout prefer cooler temperate and boreal habitats, and are found most commonly in streams, but also inhabit ponds and lakes throughout their native and introduced ranges (EBTJV 2005). They exhibit individual physical growth requirements and habitat preferences that are important to quantify in order to predict which habitats provide adequate conditions for Brook Trout to meet life cycle needs.

Brook Trout use multiple tributaries in their lifetime, and it has been documented that they use variable habitats throughout their life cycle (Kanno et al. 2014). Populations of Brook Trout are known to depend on tributaries with adequate spawning habitats for recruitment, and higher reproductive success has been shown for trout that move from lakes and ponds into tributaries to spawn (Warren et al. 2012). Huntsman and Petty (2014) also show that Brook Trout use proportionately more small streams for spawning, even if they inhabit larger streams for
much of the year. Curry et al. (1997) found that Brook Trout young-of-year (YOY) spawned in lakes will swim to small tributaries for summer, with most YOY arriving by midsummer. Some juveniles overwinter and spend the following summer in the tributaries. Habitat that may increase survival can be found in the tributaries; therefore, it is important to identify small streams as habitat for YOY Brook Trout. This also has implications for the conservation and improvement of lake populations (Curry et al. 1997). In Adirondack streams, juvenile Brook Trout prefer shallow, fast moving water; whereas adults prefer deeper pool habitats (Ecret & Mihuc 2013). In other places, salmonids are known to use a combination of habitats, including cool tributaries and warmer main stem rivers, with annual patterns dependent on temperature. This has been documented for western salmon and trout (Hartman & Brown 1987; Bramblett et al. 2002), and for Brook Trout (Petty et al. 2012; Huntsman & Petty 2014; Kanno et al. 2014; Hitt et al. 2016). Cool, groundwater-fed habitat areas provided at tributary confluences and sites immediately downstream in main stem rivers provide critical habitat and thermal refuge for Brook Trout (Baird & Krueger 2013; Kiffney et al. 2006; Petty et al. 2012; Al-Chokhachy et al. 2013).

In addition to the availability of heterogeneous physical habitat and flow patterns, thermal regimes within streams contributes to determining whether a habitat is suitable for Brook Trout. Water temperature plays a significant role in affecting Brook Trout biomass (Kratzer & Warren 2013). Brook Trout have distinctive requirements and have an optimal thermal range for growth between 10 and 16 °C, with an upper lethal limit of 23.5°C (MacCrimmon & Campbell 1969). Temperatures that fall above or below these limits will result in stress to the fish and its biological processes, including consumption, metabolism, and reproduction. Prolonged exposure
to suboptimal thermal habitat can result in altered feeding and reproductive behavior, including reduced redd construction or failure to spawn all together (Robinson et al. 2010).

Several studies have predicted how habitats will change for Brook Trout over time. It has been proposed that Brook Trout will likely be able to tolerate low summer flows (dewatering) in groundwater fed systems if temperatures remain the same, but that warming under surface flow conditions will be a major source of Brook Trout habitat loss (Nuhfer et al. 2017). Water bodies with groundwater inputs will stay cold during low flows; where there is little groundwater input, temperatures will warm exponentially (Nuhfer et al. 2017). Further, models that have incorporated Brook Trout temperature requirements and summer thermal regimes have been used to predict Brook Trout habitat and presence/absence under future climate scenarios (Picard et al. 2003, Hudy et al. 2008, ICE ECOSHEDS 2017). These models suggest Brook Trout occupancy will be highest in streams that remain thermally stable and conclude that management could be informed by these landscape scale models, but that reach scale investigations will reveal more about occupancy and habitat suitability (Picard et al. 2003). A study from the western US that assessed thermal controls of Yellowstone Cutthroat Trout *Oncorhynchus clarkii* and introduced Brook Trout suggested that as the native trout are marginalized to smaller habitats or as their ranges are constricted, they will be subject to narrower thermal and flow regimes, and that temperature changes will favor range expansion of non-native Brook Trout in this system (Al-Chokhachy et al. 2013). It is, therefore, possible to speculate that as Brook Trout are constricted to narrower habitats in their native range, populations of nonnative Brown Trout and Rainbow Trout *Oncorhynchus mykiss* may represent a significant threat to Brook Trout. Warming temperatures may lead to range expansion of Rainbow Trout and Brown Trout, due to their higher temperature tolerances than Brook Trout, and cause additional competitive
exclusion through competition with Brook Trout for habitat, food, and breeding sites (Kanno et al. 2014, Huntsman & Petty 2014).

**Understanding fish community assemblage response to environmental gradients**

Several studies show common patterns of how fish assemblages change from headwaters to mouth in a river or in tributaries that flow into a river along a longitudinal gradient (Sheldon 1968, Horwitz 1978, Schlosser 1982, Fausch et al. 1984). Species richness and community diversity are expected to increase with stream size (Fausch et al. 1984), and stream size generally increases in lower watershed reaches. Habitat complexity and nutrient inputs found in large order streams offer greater diversity in lower stream reaches (Horwitz 1978, Fausch et al. 1984).

In addition to using indicators of diversity and evenness to describe salmonid distribution and fish assemblages across a longitudinal gradient, it is important to consider what other local habitat and landscape variables may influence species assemblage, such as drainage area, elevation, percent forest cover or development, as well as measures of water quality such as pH, dissolved oxygen, and water temperature. The importance of such variables in explaining the distribution of stream fish community assemblages has been well studied and modeled over time (Rich et al. 2003, Smith & Kraft 2005, Stanfield et al. 2006, Shultz et al. 2012, Walrath et al. 2016). Selected studies have shown elevation, temperature, absence of nonnative salmonids, and percentage of impervious surfaces as limiting factors to salmonid distribution (Rich et al. 2003, Stanfield et al. 2006), where other studies have shown the significance of watershed variables such as stream link and drainage area as being most important (Smith & Kraft 2005).

Brook Trout distribution and fish community diversity in Upper Ausable Lake and East Branch tributaries is documented. Fish distribution data are compared to physical and chemical habitat data to determine which measured variables relate to Brook Trout occupancy of near-
river tributary habitats within the East Branch Ausable system. Specific hypotheses for the project include:

a) The population of Brook Trout in Upper Ausable Lake is self-sustaining, consisting mostly of wild fish.

b) Brook Trout abundance has a linear relationship with stream order and temperature.

c) Given similar water quality across the study area, temperature and canopy cover will be limiting factors for fish community composition.

d) Among land use patterns in the Ausable watershed, patterns of development limit Brook Trout populations, followed closely by % forest cover.

e) Changes in fish diversity and community assemblage along a longitudinal gradient will be influenced by habitat variables including stream order and elevation.

f) In this watershed, Brook Trout abundance is greater in streams on protected (public or private) lands and less on Private residential lands.

Results from this study can be used to discern whether the lower tributary reaches provide important habitat for Brook Trout. This will provide valuable information to any future studies of Brook Trout movement in the river and tributaries and can inform future tributary habitat improvement projects and prioritize projects to improve aquatic organism passage.
Methods

Site description

The 132,000-ha Ausable River watershed in New York State’s Adirondack Park comprises two branches (East Branch and West Branch) that drain in a northerly direction from the interior of the Eastern High Peaks Wilderness, join in the town of Au Sable Forks to become the Main Stem and flow to Lake Champlain (Figure 1). The headwaters of both branches of the Ausable are well protected; the West Branch headwaters are located in a state wilderness area, and the East Branch headwaters are situated within the Adirondack Mountain Reserve (AMR). The AMR is a 2,832-ha private reserve with extensive public access created in 1887 to protect scenic lands and mountains of the Adirondacks from lumbering and environmental degradation. The streams and lakes that form the East Branch headwaters contain nearly pristine habitat that has remained intact and the fish community composition of Upper Ausable Lake is entirely native.

After leaving the AMR, the East Branch, classified by New York State as a recreational river, flows for 45 kilometers to the confluence with the West Branch Ausable River. Approximately 50 tributary streams flow into the East Branch, all with varying degrees of land
use, from protected wild forest or private lands, to commercially logged and private residential lands. There is a distinctive elevation gradient on the East Branch from the headwaters to the confluence with the West Branch in Au Sable Forks, with the headwaters at Upper Ausable Lake at 600 meters, dropping to 200 meters at Au Sable Forks. There are extensive public fishing rights on this segment of the river, and an extensive stocking history of Brook Trout, Brown Trout, and Rainbow Trout. The 1929 surveys completed by the New York State Conservation Department showed the Marcy Field Dam in Keene as a dividing line for Brook Trout habitat in the East Branch, with no Brown Trout being found in the river above this point (Greeley 1930).

![Figure 2. Longitudinal profile of East Branch Ausable River from Upper Ausable Lake to Ausable Forks](image)

Fish surveys conducted on the Adirondack Mountain Reserve (AMR) in 2014-2016 documented that Upper Ausable Lake has wild populations of Brook Trout, Lake Trout *Salvelinus namaycush*, and Round Whitefish *Prosopium cylindraceum*; the recreational fishery has been enhanced with stocked Brook Trout since the 1970s (Field 2009, Josephson et al. 2014, 2015). Starting in 2010, all stocked fish were marked with fin clips to denote the year that they were stocked. Angling on the AMR is restricted to Ausable Club members only who were instructed to fill out creel surveys and report any fish with hatchery-derived fin clips. From 2010
to 2016, only a few stocked fish were reported each year in fisheries assessments and creel surveys (Josephson et al. 2014, 2015, *creel survey data, unpublished*).

**Field Data Collection**

*Stream surveys*: Depletion population surveys were conducted in 2015 and 2016 using Smith-Root backpack electrofisher units. Four tributaries on the AMR property were sampled in 2015 with two-pass depletion sampling, and 17 additional East Branch tributaries (downstream of AMR property) were sampled in 2016 with three-pass depletion sampling (Figure 3). All sampling took place at late summer low flows using one backpack electrofisher and one to two netters, and used block nets at both ends of the reach to ensure a closed sample population. On all 21 tributaries, study reaches were established in the first 50-100 m from the confluence with Upper Ausable Lake or the East Branch Ausable River. For each pass, all fish captured were identified to species, total length (TL, mm) was measured, and all salmonids were weighed (mg).

*Lake surveys*: Previous gill net surveys on Upper Ausable Lake from 2010 to 2015 targeted Lake Trout (Josephson et al. 2015), but also caught Brook Trout and Lake Whitefish. These surveys showed very low abundances of stocked Brook Trout (based on hatchery assigned fin clips), and recommendations based on this subsequently led to a halt in stocking of Brook Trout in spring 2015. In May and October of 2016, a survey of the fish community assemblage and a mark-recapture study of Brook Trout in Upper Ausable Lake were conducted using modified Oneida-style hoop trap nets with ½” mesh, a 75m leader, and 3.6m wings. Water temperatures were low enough to allow for 48-hour net sets (D. Josephson, *pers. comm.*). Five trap nets were deployed at five separate locations and the 48-hour net sets were replicated four times during May 11-19, 2016. Nets were deployed at the same five locations and 48-hour net sets were conducted three
times from October 10-16, 2016. Nets were set at 1 to 2 meter depth, and locations included areas near the outflow of Otis, Crystal, and Cedar Brooks, as well as near two potential spawning sites in the lake. At each net retrieval, all fish were identified to species, counted, all salmonids measured (TL, mm) and weighed (g), and all Brook Trout given a caudal fin clip (for temporary marking purposes) or noted as recaptures before release. All field research was completed with IACUC approval from the State University of New York College of Environmental Science and Forestry (IACUC protocol # 150801).

*Habitat Assessment:* Habitat surveys of stream width, depth, velocity, substrate, in-stream boulders, woody debris, pool class, % canopy cover, and forest type were recorded at 5-10 meter transects at all study reaches. In addition, water quality data were measured with YSI multi-parameter probes at each stream, including water temperature (°C), dissolved oxygen (mg/L and % saturation), pH, and specific conductivity (µS/cm). Elevation and Strahler stream order were obtained using GAIA GPS software; the USGS STREAMSTATS application (https://streamstats.usgs.gov/ss/) was used to delineate each tributary basin and then calculate drainage area, percent of elevation over 1200 feet, Mean June and July precipitation, maximum June temperature (°F), and percent forest cover. STREAMSTATS also calculated the percentage of impervious surfaces and percentage of developed (urban) land using National Land Cover Database (NLCD) 2011 for each study tributary basin. Average values for all tributaries are presented in Appendix B.
Figure 3. Study streams along the East Branch Ausable River, Black dots denote study reach locations.
Data Analysis

Fish Community Analysis

Brook Trout population abundance estimates were calculated for AMR tributaries using the Zippin method for two-pass removal electrofishing (Zippin 1956, Seber 1982; eq. 8.19 in Hayes et al. 2007). For better precision in population abundance estimates for sample reaches, three-pass depletion sampling was conducted in 2016 for all remaining tributaries. A general maximum-likelihood estimate was chosen as described by equations 8.24 through 8.27 in Hayes et al. (2007). With this approach, catchability ($\hat{q}$) is estimated directly; cumulative catch and estimated cumulative proportion of the population that catchability represents are used to calculate $\hat{N}$ (Gould and Pollock 1997; Hayes et al. 2007). Trout abundance per stream reach, estimated catchability, and associated 95% confidence intervals were generated. Trout density, expressed as number of fish per square meter, was calculated as the abundance estimate for the reach divided by the area of stream surveyed.

For Brook Trout captured in trap net surveys in Upper Ausable Lake, the Schnabel method of population estimation was used (Schnabel 1938; Seber 1982; Hayes et al 2007). Estimated population and variance (Seber 1982) were calculated using formulas 8.6 and 8.7 from Hayes et al. (2007), and since there were fewer than 50 recaptures, a table developed by Chapman (1948; reproduced in Seber 1982 and Hayes et al. 2007) was used to calculate 95% confidence intervals.

Community diversity indices were calculated for lake and tributary data including species richness, Shannon-Weiner index of diversity ($H'$), and Shannon’s evenness ($J'$) (Kwak &
Peterson 2007, Gotelli 2008). Shannon-Weiner Index, which accounts for the total number of species and their abundances, was calculated for each site as follows (Kwak & Peterson 2007):

\[ H' = - \sum_{i=1}^{s} (p_i)(\log_e p_i) \]

Where \( s \) = number of species, and \( p_i \) = proportion of the population represented by the \( i \)th species. Evenness is a measure of similarity between relative species abundance per site, and this was calculated for the Shannon-Weiner index as \( J' \) (Kwak & Peterson 2007):

\[ J' = \frac{H'}{H'_{\text{max}}} = \frac{H'}{\log_e s} \]

Multivariate Community Assemblage Analysis

Multivariate statistical methods were used to determine the response of fish assemblages at sites to environmental variables using XLSTAT and Package VEGAN in R (Oksanen et al. 2018). Density of fish species (#/m\(^2\)) at all tributary sites were \( \log(x + 1) \) transformed to give less weight to dominant species (Lepš & Šmilauer 2003, Smith & Kraft 2005), and then were compared to each other using a Correspondence Analysis (CA). Rainbow Trout were present at less than three study sites (<10% of total sites), so were removed from the analysis to prevent any influence from rare species. Next, a Principal Components Analysis (PCA) was run for all habitat and landscape variables; six local and six landscape environmental variables were reduced to 3 local and 4 landscape variables based on collinearity observed in PCA. Next, Canonical Correspondence Analysis (CCA) was run again on species assemblages and the reduced set of environmental variables. Backward selection of variables was then used to find a set of significant environmental variables that explain most of the variation and three additional
variables were removed because they did not explain variation among sites with any statistical significance. This process balances a possible overfitting of the model and chooses those variables with the most explanatory power. Permutation tests were used to assess the significance of each variable. The final CCA from these iterations was used for interpretation of all species assemblage-habitat associations.

Results

Fish Sampling

Fish were collected at all 21 tributary sites using electrofishing surveys. In 2015, 201 fish were captured from AMR tributaries in backpack electrofishing surveys, and 1,035 fish were captured in 2016 East Branch tributary surveys. On all 21 tributaries, study reaches were located in the first 50-100 m from the confluence with Upper Ausable Lake or the East Branch Ausable River. Brook Trout were abundant in the four AMR tributaries, and present in 10 of 17 study streams outside of AMR property (Table 1). Of the 12 species captured in tributary electrofishing surveys, Blacknose Dace *Rhinichthys atratulus* and Longnose Dace *Rhinichthys cataractae* were the most abundant (23% relative abundance each), and Blacknose Dace were the most prevalent species, caught at 81% of study sites (Table 1, Appendix A).
Table 1. Fish species documented in the East Branch Ausable River tributaries and relative abundance and prevalence (%) at 21 East Branch Ausable River tributaries, New York.

<table>
<thead>
<tr>
<th>Common name</th>
<th>Latin name</th>
<th>Relative abundance (%)</th>
<th>Prevalence (%)</th>
<th>Species Code</th>
</tr>
</thead>
<tbody>
<tr>
<td>Brook Trout</td>
<td>Salvelinus fontinalis</td>
<td>9.6%</td>
<td>61.9%</td>
<td>ST</td>
</tr>
<tr>
<td>Brown Trout</td>
<td>Salmo trutta</td>
<td>1.7%</td>
<td>28.6%</td>
<td>BT</td>
</tr>
<tr>
<td>Rainbow Trout*</td>
<td>Oncorhynchus mykiss</td>
<td>1.6%</td>
<td>9.5%</td>
<td>RT</td>
</tr>
<tr>
<td>White Sucker</td>
<td>Catostomus commersonii</td>
<td>1.9%</td>
<td>23.8%</td>
<td>WS</td>
</tr>
<tr>
<td>Slimy Sculpin</td>
<td>Cottus cognatus</td>
<td>16.8%</td>
<td>81.0%</td>
<td>SS</td>
</tr>
<tr>
<td>Blacknose Dace</td>
<td>Rhinichthys atratulus</td>
<td>23.0%</td>
<td>81.0%</td>
<td>BND</td>
</tr>
<tr>
<td>Longnose Dace</td>
<td>Rhinichthys cataractae</td>
<td>22.8%</td>
<td>81.0%</td>
<td>LND</td>
</tr>
<tr>
<td>N. Redbelly Dace</td>
<td>Chrosomus eos</td>
<td>1.0%</td>
<td>23.8%</td>
<td>NRD</td>
</tr>
<tr>
<td>Tessellated Darter</td>
<td>Etheostoma olmstedi</td>
<td>3.3%</td>
<td>42.9%</td>
<td>TSD</td>
</tr>
<tr>
<td>Fantail Darter</td>
<td>Etheostoma flabellare</td>
<td>1.1%</td>
<td>19.0%</td>
<td>FTD</td>
</tr>
<tr>
<td>Creek Chub</td>
<td>Semotilus atromaculatus</td>
<td>9.1%</td>
<td>66.7%</td>
<td>CC</td>
</tr>
<tr>
<td>Common Shiner</td>
<td>Luxilus cornutus</td>
<td>8.1%</td>
<td>33.3%</td>
<td>CSH</td>
</tr>
<tr>
<td>TOTAL</td>
<td></td>
<td></td>
<td>n=1235</td>
<td></td>
</tr>
</tbody>
</table>

* Not included in final CCA analysis

Within the tributaries, as few as one, and as many as eleven species were captured per stream (mean species richness = 8.83, SD = 5.39). Three species of juvenile salmonids were captured across the watershed. Brook Trout was the only salmonid caught in AMR tributaries, sympatric with Slimy Sculpin *Cottus cognatus*, three species of dace, Blacknose Dace, Longnose Dace, and Northern Redbelly Dace *Chrosomus eos*, Creek Chub *Semotilus atromaculatus*, and Tessellated Darter *Etheostoma olmstedii*. Species richness increased from upstream to downstream reaches and four additional species were captured in downstream tributaries (Common Shiner *Luxilus cornutus*, White Sucker *Catostomus commersonii*, Brown Trout, and Rainbow Trout *Oncorhynchus mykiss*); species distributions across East Branch study sites are presented in Appendix A. Brook Trout occurred at 13 of 21 tributaries. Brown Trout were captured at six sites outside of AMR property; they were the only salmonid at Gulf and Cascade Brooks, and were found in sympatry with Brook Trout at Mossy Cascade, Phelps 2, and Lewis Brooks. All three salmonids were sympatric at the farthest downstream site, Rocky Branch. Brook Trout and Rainbow Trout were sympatric only at Walton Brook.
Trap net surveys on Upper Ausable Lake captured 16,608 fish. Thirteen fish species were captured, all native to New York State except for a single Rainbow Trout, which likely swam up the Carry River from Lower Ausable Lake (Table 2). In May 2016, 67 Brook Trout were captured with three recaptures, and 21 Brook Trout were captured in October 2016 (one recapture). Catch per unit effort was 16.75 Brook Trout per 48-hr net set for May 2016, and 7 Brook Trout per 48-hr net set in October 2016. The recapture rate of marked Brook Trout for both sampling events was 4.5%, and the estimate of the total population of Brook Trout in the lake using the Schnabel method for May catch data is 673 individuals, with a 95% confidence interval of 69 to 1151 fish (Table 2). None of the Brook Trout captured in trap net surveys had an existing hatchery fin clip, suggesting these are wild fish.

Table 2. Total trap net catch by species, Upper Ausable Lake, 2016

<table>
<thead>
<tr>
<th>Common name</th>
<th>May</th>
<th>October</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Brook Trout</td>
<td>67 (recaptured=3)</td>
<td>21</td>
<td>88</td>
</tr>
<tr>
<td>Round Whitefish</td>
<td>1</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>Common Shiner</td>
<td>5,674</td>
<td>1,602</td>
<td>7,276</td>
</tr>
<tr>
<td>White Sucker</td>
<td>2,724</td>
<td>439</td>
<td>3,163</td>
</tr>
<tr>
<td>Lake Chub</td>
<td>1,934</td>
<td>2</td>
<td>1,936</td>
</tr>
<tr>
<td>Brown Bullhead</td>
<td>720</td>
<td>1,543</td>
<td>2,263</td>
</tr>
<tr>
<td>Longnose Dace</td>
<td>553</td>
<td>0</td>
<td>553</td>
</tr>
<tr>
<td>Pumpkinseed</td>
<td>101</td>
<td>1,081</td>
<td>1,182</td>
</tr>
<tr>
<td>Creek Chub</td>
<td>22</td>
<td>70</td>
<td>92</td>
</tr>
<tr>
<td>Slimy Sculpin</td>
<td>17</td>
<td>0</td>
<td>17</td>
</tr>
<tr>
<td>Blacknose Dace</td>
<td>12</td>
<td>6</td>
<td>18</td>
</tr>
<tr>
<td>N. Redbelly Dace</td>
<td>7</td>
<td>0</td>
<td>7</td>
</tr>
<tr>
<td>Rainbow Trout</td>
<td>0</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td><strong>Grand Total</strong></td>
<td><strong>11,832</strong></td>
<td><strong>4,766</strong></td>
<td><strong>16,598</strong></td>
</tr>
</tbody>
</table>

**Schnabel Pop. Estimate**  
673 Brook Trout  (69 to 1151, 95% CI)

Brook Trout abundance and density estimates (#/m²) within study stream reaches were calculated for eight of the study reaches (Table 3). Due to insufficient catch data (i.e., if catch did not decline with consecutive passes, catchability is <0.1), five tributaries were omitted from the analysis. Sufficient data were collected to estimate population abundances for Brown Trout at Rocky Branch and Rainbow Trout at Walton Brook (Table 3).
Table 3. Trout population estimates for 2-pass and 3-pass depletion surveys on tributaries of the East Branch Ausable River. Associated 95% confidence intervals for maximum likelihood estimates of 3-pass survey sites are presented in parentheses.

<table>
<thead>
<tr>
<th>Site</th>
<th>Method</th>
<th>Area, (m²)</th>
<th>Brook Trout Abundance</th>
<th>Density (#/m²)</th>
<th>Rainbow Trout Abundance</th>
<th>D (#/m²)</th>
<th>Brown Trout Abundance</th>
<th>D (#/m²)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cedar</td>
<td>Zippin</td>
<td>195</td>
<td>12.8</td>
<td>0.07</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Crystal1</td>
<td>Zippin</td>
<td>169.8</td>
<td>16</td>
<td>0.09</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Sawtooth</td>
<td>Zippin</td>
<td>219.6</td>
<td>9.67</td>
<td>0.04</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Deer</td>
<td>Max-likelihood</td>
<td>65</td>
<td>15 (48, -18)</td>
<td>0.23</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Flume</td>
<td>Max-likelihood</td>
<td>247.5</td>
<td>1 (1366, -1364)</td>
<td>0.00</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Walton</td>
<td>Max-likelihood</td>
<td>255.5</td>
<td>9 (26, -7)</td>
<td>0.04</td>
<td>17 (29,5)</td>
<td>0.07</td>
<td></td>
<td>0</td>
</tr>
<tr>
<td>Phelps2</td>
<td>Max-likelihood</td>
<td>290</td>
<td>25 (28, 22)</td>
<td>0.09</td>
<td>0</td>
<td>q too low</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rocky</td>
<td>Max-likelihood</td>
<td>418</td>
<td>q too low</td>
<td>n/a</td>
<td>q too low</td>
<td>6 (7, 5)</td>
<td>0.01</td>
<td></td>
</tr>
</tbody>
</table>

*Distribution and Community Diversity*

Mean Shannon species diversity index values from all tributary survey sites is 1.29, with a range from 0 to 1.95. Here, values near zero are representative of low diversity, and values of one and above represent sites with high diversity (Table 4). Brook Trout relative abundance in samples decreased with longitudinal stream position, with the exception of Phelps 2 (67%). Diversity was highest at the farthest downstream tributary, Rocky Branch (1.95), and while there is a general trend of increasing diversity along the longitudinal gradient of the East Branch, a few streams had high diversity and evenness values in the upper reaches (Mossy Cascade, Flume, and Phelps 1; Table 4).
Table 4. Study streams, brook trout presence, and measures of community diversity on 21 Ausable tributaries. Streams are listed in order from headwaters (upstream) to Au Sable Forks (downstream).

<table>
<thead>
<tr>
<th>Sample Year</th>
<th>Stream Name</th>
<th>Strahler Stream Order</th>
<th>Elevation (m)</th>
<th>Brook Trout Presence</th>
<th>Brook Trout Relative Abundance (%)</th>
<th>Species Richness</th>
<th>S-W Index of Diversity* (H')</th>
<th>Evenness (J')</th>
</tr>
</thead>
<tbody>
<tr>
<td>2015</td>
<td>Cedar</td>
<td>1</td>
<td>621</td>
<td>Present</td>
<td>100%</td>
<td>1</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td>2015</td>
<td>Crystal 1</td>
<td>1</td>
<td>618</td>
<td>Present</td>
<td>16.5%</td>
<td>6</td>
<td>1.19</td>
<td>0.48</td>
</tr>
<tr>
<td>2015</td>
<td>Otis 1</td>
<td>1</td>
<td>616</td>
<td>Present</td>
<td>47.6%</td>
<td>3</td>
<td>1.00</td>
<td>0.40</td>
</tr>
<tr>
<td>2015</td>
<td>Sawtooth</td>
<td>1</td>
<td>614</td>
<td>Present</td>
<td>52.8%</td>
<td>3</td>
<td>0.95</td>
<td>0.38</td>
</tr>
<tr>
<td>2016</td>
<td>Crystal 2</td>
<td>1</td>
<td>342</td>
<td>Present</td>
<td>30%</td>
<td>4</td>
<td>1.17</td>
<td>0.47</td>
</tr>
<tr>
<td>2016</td>
<td>Deer</td>
<td>1</td>
<td>343</td>
<td>Present</td>
<td>50%</td>
<td>4</td>
<td>1.09</td>
<td>0.44</td>
</tr>
<tr>
<td>2016</td>
<td>Mossy</td>
<td>1</td>
<td>327</td>
<td>Present</td>
<td>2.5%</td>
<td>8</td>
<td>1.68</td>
<td>0.68</td>
</tr>
<tr>
<td>2016</td>
<td>Flume</td>
<td>1</td>
<td>317</td>
<td>Present</td>
<td>1.6%</td>
<td>6</td>
<td>1.44</td>
<td>0.58</td>
</tr>
<tr>
<td>2016</td>
<td>Johns</td>
<td>3</td>
<td>310</td>
<td>Absent</td>
<td>0%</td>
<td>5</td>
<td>1.34</td>
<td>0.54</td>
</tr>
<tr>
<td>2016</td>
<td>Phelps 1</td>
<td>2</td>
<td>308</td>
<td>Present</td>
<td>5.3%</td>
<td>6</td>
<td>1.38</td>
<td>0.56</td>
</tr>
<tr>
<td>2016</td>
<td>Porter</td>
<td>1</td>
<td>301</td>
<td>Absent</td>
<td>0%</td>
<td>6</td>
<td>1.24</td>
<td>0.50</td>
</tr>
<tr>
<td>2016</td>
<td>Walton</td>
<td>2</td>
<td>278</td>
<td>Present</td>
<td>19.1%</td>
<td>3</td>
<td>1.04</td>
<td>0.42</td>
</tr>
<tr>
<td>2016</td>
<td>Dart</td>
<td>2</td>
<td>250</td>
<td>Absent</td>
<td>0%</td>
<td>7</td>
<td>1.63</td>
<td>0.66</td>
</tr>
<tr>
<td>2016</td>
<td>Gulf</td>
<td>2</td>
<td>252</td>
<td>Absent</td>
<td>0%</td>
<td>5</td>
<td>1.37</td>
<td>0.55</td>
</tr>
<tr>
<td>2016</td>
<td>Cascade</td>
<td>2</td>
<td>251</td>
<td>Absent</td>
<td>0%</td>
<td>7</td>
<td>1.37</td>
<td>0.55</td>
</tr>
<tr>
<td>2016</td>
<td>Clifford</td>
<td>3</td>
<td>242</td>
<td>Absent</td>
<td>0%</td>
<td>8</td>
<td>1.83</td>
<td>0.74</td>
</tr>
<tr>
<td>2016</td>
<td>Styles</td>
<td>2</td>
<td>234</td>
<td>Absent</td>
<td>0%</td>
<td>6</td>
<td>1.38</td>
<td>0.56</td>
</tr>
<tr>
<td>2016</td>
<td>Phelps 2</td>
<td>1</td>
<td>233</td>
<td>Present</td>
<td>66.7%</td>
<td>5</td>
<td>1.02</td>
<td>0.41</td>
</tr>
<tr>
<td>2016</td>
<td>Lewis</td>
<td>2</td>
<td>209</td>
<td>Present</td>
<td>2.1%</td>
<td>8</td>
<td>1.68</td>
<td>0.68</td>
</tr>
<tr>
<td>2016</td>
<td>Otis 2</td>
<td>2</td>
<td>196</td>
<td>Absent</td>
<td>0%</td>
<td>4</td>
<td>1.29</td>
<td>0.52</td>
</tr>
<tr>
<td>2016</td>
<td>Rocky</td>
<td>3</td>
<td>188</td>
<td>Present</td>
<td>0.5%</td>
<td>11</td>
<td>1.95</td>
<td>0.78</td>
</tr>
</tbody>
</table>

**Shannon-Weiner index of diversity, where values near 0 are representative of low diversity, and values of 1 and above represent sites with high diversity. This index takes species abundance and evenness into account within each sample.

Relative abundance (%) of all fish species surveyed in tributaries from the headwater reaches to Au Sable Forks show variable patterns from the headwaters downstream (Figure 4).

Brook Trout relative abundance declines from the headwater tributaries to the mid-reaches of the East Branch near Keene Valley, and is only present in high abundance again at streams that flow through a substantial amount of state land, including the Walton and Phelps 2 sites. Longnose Dace, Blacknose Dace, Slimy Sculpin, and Creek Chub were the next most abundant species overall. Fantail Darter *Etheostoma flabellare* and Northern Redbelly Dace are the more uncommon species that appear in several samples in the mid- and lower-reaches of the East Branch.
Summary of habitat characteristics

Tributary surveys provided a robust dataset on physical and chemical habitat offered within each study reach. Habitat surveys were completed July 6-8, 2015 at the four AMR tributaries, and the remainder of the tributaries were surveyed on September 9, 2016. On all 21 tributaries, habitat surveys were completed in the same study reaches as tributary surveys, (located in the first 50-100 m from the confluence with Upper Ausable Lake or the East Branch Ausable River). The tributaries were characterized by temperatures ranging from 10.9 to 14.9°C, pH ranging from 5.5 to 8.1, and dissolved oxygen ranging from 7.1 to 10.7 mg/L (77 to 99.1% saturation) (Appendix B). Canopy cover at stream reaches ranged from less than one percent to 80%, and mean stream
width was 4.1 meters, with a maximum mean width of 9.1 meters. Percent of subwatershed forest cover had a range of 93.5 to 100%, and the percentage of developed urban land was low overall, with a maximum of 6.1% based on STREAMSTATS. This development mostly occurs in the form of housing development and businesses in the towns of Keene, Keene Valley, and Jay. Likewise, the percentage of impervious area in each subwatershed, as determined from the NLCD 2011 impervious dataset, had a maximum value of 0.7%. Maximum June Temperature, as determined by STREAMSTATS was 21.8°C.

*Fish Community Assemblages*

The final CCA included ten fish species; Rainbow Trout were eliminated due to rarity (Table 1). Variable selection resulted in one local and three landscape level habitat variables (Table 5). Variables included in the final CCA are elevation, % forest cover, % impervious surfaces, and June max temperature (Table 5); these were stronger gradients than the other variables. The first two axes of the CCA represent 58.2% and 23.1% of the variation of species density at sites, respectively. All four variables weight heavily on the first axis. CCA axis 1 is representative of variation in June maximum temperature (JUNMAXT), % impervious surfaces (LC11IMP), and % forest cover (FOREST), and elevation (ELEV) (Figure 5). Note that percent forest represents the total forested area within the tributary drainage basin and was more important for explaining fish assemblage than reach-scale canopy cover estimates. Study sites appearing to the right side of axis 1 are warmer and more developed (more impervious surfaces within sub-watersheds), where sites on the left are cooler and more forested. Likewise, study reaches at the highest elevations are placed above axis 2 in the upper left quadrant and those with more forest cover are beneath axis 2 in the lower left quadrant (Figure 5). The appearance of species on this CCA is relative to their preferences within these habitat variables. For example,
Brook Trout are present at high elevations. Brook Trout are also present when forest cover is very high. And Brook Trout are present at sites with lower June max temperatures. They were present at one site without these conditions met, at Rocky Branch which is a warmer stream with less forest cover. In contrast, Brown Trout clearly fall on the other end of the forest cover spectrum and are present in sites with warmer temperatures and less cover in the Ausable watershed. Any species located near the center is not strongly correlated with any of the habitat variables; this is the case for Blacknose Dace, which was one of the most abundant species in all samples and this shows no strong association with any habitat gradient. Likewise, Longnose Dace are similar to this, but associate with sites that have more forest cover. Common Shiner and the two darter species exhibit association with habitats that are warmer and lower elevation.

Monte Carlo permutation tests accepted the hypothesis that the sites/species data are linearly related to the sites/variables data (p<0.0001). This CCA explains 43.4% of the variation among species assemblages.

Table 5. Reach habitat and landscape level variables used in CCA analysis, calculated for 21 East Branch Ausable River tributaries, New York, 2016

<table>
<thead>
<tr>
<th>Variable name</th>
<th>Description</th>
<th>Data Source</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Sample reach habitat</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TEMP</td>
<td>water temperature, degrees C</td>
<td>field sampling</td>
</tr>
<tr>
<td>pH</td>
<td>pH</td>
<td>field sampling</td>
</tr>
<tr>
<td>DO</td>
<td>dissolved oxygen, percent saturation</td>
<td>field sampling</td>
</tr>
<tr>
<td>COV</td>
<td>percent canopy cover, estimated from densiometer</td>
<td>field sampling</td>
</tr>
<tr>
<td>DEP</td>
<td>maximum water depth (cm)</td>
<td>field sampling</td>
</tr>
<tr>
<td>ELEV*</td>
<td>elevation, m</td>
<td>GAIA GPS</td>
</tr>
<tr>
<td><strong>Landscape variables (calculated for each drainage basin)</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DRNAREA</td>
<td>Area that drains to a point on a stream, sq. mi.</td>
<td>STREAMSTATS</td>
</tr>
<tr>
<td>FOREST*</td>
<td>Percentage of area covered by forest</td>
<td>STREAMSTATS</td>
</tr>
<tr>
<td>LC11DEV</td>
<td>Percentage of developed (urban) land from NLCD 2011 classes 21-24</td>
<td>STREAMSTATS</td>
</tr>
<tr>
<td>LC11IMP*</td>
<td>Avg % of impervious area determined from NLCD 2011 impervious dataset</td>
<td>STREAMSTATS</td>
</tr>
<tr>
<td>JUNMAXT*</td>
<td>Maximum June Temperature, in degrees F</td>
<td>STREAMSTATS</td>
</tr>
<tr>
<td>PRECIP</td>
<td>Mean Annual Precipitation, inches</td>
<td>STREAMSTATS</td>
</tr>
</tbody>
</table>

* denotes variables that were included in final CCA
Discussion

*Patterns of Community Structure*

Fish communities in near-river tributary habitats change markedly along the river continuum, and the data support the initial hypothesis that fish species richness and diversity
increase from the headwaters downstream. Several studies show common patterns in how fish assemblages change from headwaters along a longitudinal gradient (Sheldon 1968, Horwitz 1978, Schlosser 1982), including that species richness and diversity increase with stream size. Indeed, streams in the upper East Branch watershed reaches are mostly first order and these increase in size to fourth order tributaries or higher near the confluence with the West Branch. It is expected that the species dominance will change across each part of the river continuum. The dominant species in the headwaters exhibit adaptations to local biotic and abiotic conditions. This is supported by the observations of Brook Trout and other cold-water loving species in the upper reaches, with more ubiquitous species moving throughout, and more warm water species dominating lower reach sites. The species assemblages in the East Branch are generally agreeable with the River Continuum Concept (RCC), in that species distribution changes as you move downstream along a river gradient and is related to biotic factors such as nutrient input from autochthonous and allochthonous sources (Vannote et al. 1980). It is also possible that the shift in species composition of the East Branch itself is directly reflected in the species assemblages of the mouths of these tributaries, and that fish may be regularly moving from river to tributary habitats.

Despite the demonstrated importance of these influences in describing fish communities, Brook Trout were found across the entire longitudinal gradient of the East Branch, and in some unexpected places, which suggests that additional factors are influencing Brook Trout occupancy in the region. The elevation gradient and relationships with stream order are certainly acting on the structure of the fish communities, and this is characteristic of most of the region’s watersheds. Three upper reach tributaries had high diversity and richness however, suggesting that elevation and stream size alone are not acting on fish assemblage structure. Multivariate
analysis illustrated that additional landscape variables, such as forest cover and percent
impervious surfaces within each sub-watershed, drive the presence and absence of Brook Trout
and other species. These analyses showed that local physical habitat characteristics (dissolved
oxygen, pH) played a lesser role in structuring fish assemblages, followed by reach-scale habitat
conditions (depth and % forest canopy cover directly over the stream reach). The CCA analyses
explain only 43% of overall variation in fish communities; and the second axis represented a
gradient not explained well with the backward selected environmental variables. This
unexplained variation could be related to other variables that were not selected as a significant
for the final model, including temperature data collected from the site during habitat surveys,
which weighted heavily on axis 2 prior to back selection of variables. While a correspondence
analysis of species data did not show a strong relationship between species, it is possible that the
presence of nonnative species is acting with abiotic factors to influence Brook Trout occupancy.

Landscape-scale patterns of land use are driving fish community assemblage in this
watershed, as is apparent from the analysis of the variables that were measured in this study.
Brook Trout, which are indicative of cold oxygenated water, are most abundant in the protected
areas - public and private - of this watershed. For example, the Adirondack Mountain Reserve is
forested and protected and had the highest Brook Trout abundance. Likewise, all streams flowing
out of state forest preserve lands in the lower reaches had high abundance of Brook Trout. There
was a distinctive gap in Brook Trout occupancy in the mid-reaches near the town of Keene.
These streams had some of the highest values for STREAMSTATS indicators of development,
including decreased forest cover, increased proportion impervious surfaces, and increased
development. Many of these streams are flowing through areas with a higher density of private
residential homes. Housing density can negatively impact wildlife populations in areas of rural
development (Kretser et al. 2008). Rural private development can result in forest fragmentation and locally intense areas of poor land management, including land clearing for home sites, clearing streamside vegetation, and increased nutrient runoff from manicured lawns, landscaping, and septic systems. These practices can directly affect water quality in streams and contribute to higher water temperatures, which may limit Brook Trout presence/absence seasonally. Further, these streams without Brook Trout were some of the most visibly impacted by Hurricane Irene in 2011, and it is possible that habitat in the near-river tributary reaches has not recovered completely. It was also possible that high temperatures throughout late summer 2016 may be able to explain Brook Trout absence from these streams. This could be due to interannual variability in temperature and habitat suitability. Brook Trout were found in NYS DEC surveys here in the 1990s and early 2000s (NYS DEC 2016), so this underlines the importance and need for future surveys of the near-river reaches (seasonally or in colder years), to assess Brook Trout occupancy and determine how far upstream optimal habitat may be offered.

*Rpatterns of salmonid distribution*

There was a notable shift in salmonid distribution of near river tributary study reaches from the headwaters to Au Sable Forks. In some streams, Brook Trout were the only salmonid, and others were found to have sympatric species associations with nonnative salmonids – Brook Trout with Brown Trout, Brook Trout with Rainbow Trout, or all three salmonids occurring together. There were two allopatric populations of Brown Trout existing alone in downstream tributaries.

The presence of these nonnative species is known to impact Brook Trout behavior, including competition for feeding and resting positions, redd superimpositions, and competitive
exclusion from areas of thermal refuge (Fausch & White 1981, Essington et al. 1998, Kanno et al. 2014, Huntsman & Petty 2014), and can lead to declines in Brook Trout populations (Fausch & White 1981). Hitt et al. (2016) found that Brown Trout affect Brook Trout use of foraging habitat outside of cold-water refugia. The presence of Brown Trout may limit the ability of Brook Trout populations to adapt to warmer temperatures and may prove problematic for the long-term adaptation of Brook Trout to climate change.

Natural reproduction of trout is expected to be minimal in the East Branch Ausable River watershed due to habitat heavily impacted by sediment (NYS DEC 2009). All trout stocked into the East Branch Ausable River since 2011 were in the size range of 200 mm; there was no fingerling stocking (NYS DEC 2018). With the exception of a single Brown Trout at Lewis Brook (217 mm), total length of all captured Brown Trout and Rainbow Trout in this study was much less than the size range at which fish are stocked into this system (Brown Trout were 70 to 198 mm, mean = 98; Rainbow Trout 55 to 80 mm, mean 66 mm). This suggests that natural reproduction of Brown Trout and Rainbow Trout may currently be occurring in six streams. Brook Trout are likely reproducing in all streams in which they were present. Given that the presence of Brown Trout and Rainbow Trout can have negative effects on Brook Trout populations, the presence of natural reproduction may be further limiting the ability of Brook Trout to occupy these habitats.

Conservation of cool, groundwater-fed habitat areas provided at tributary confluences and sites immediately downstream in main stem rivers will help protect critical habitat and thermal refuge for Brook Trout (Kiffney et al. 2006, Petty et al. 2012, Baird & Krueger 2013, and Al-Chokhachy et al. 2013). Given ample evidence that Brook Trout use a variety of habitats, and possibly multiple tributaries in their lifetime, (Curry et al. 1997, Warren et al. 2012,
Petty et al. 2012, Kanno et al. 2014, Huntsman & Petty 2014) it is important to identify stream reaches that provide critical habitat for Brook Trout. Further, Hitt et al. (2016) have highlighted the importance of maintaining habitat in lower reaches that seem unsuitable for Brook Trout. These areas can offer thermal refugia for river dwelling trout, and stream-dwelling Brook Trout may need to move through areas of suboptimal habitat to access better thermal or feeding conditions (Hitt et al. 2016). The tributary habitat near the confluence with the East Branch Ausable River should be prioritized for habitat improvement projects to maintain these refugia. Finally, the effects of stocking nonnative fish into the river on the Brook Trout populations in the lowest reaches of these tributaries deserve further consideration.

**Brook Trout distribution and habitat use of headwater reaches**

A primary goal of this study was to characterize the Brook Trout population of the headwaters at the AMR. The tributaries here provide excellent Brook Trout habitat, with cold water, high dissolved oxygen, plenty of pools, lower conductivity than downstream sites, and ample forest cover. Characteristic of high elevation first order headwater tributaries, production potential may be reduced here (Schlosser 1982). Production could be limited here by the flashy nature of extreme gradient first order streams and their tendency to flood easily after extensive rainfall events (Vannote et al 1980). Further, the low nutrient inputs found in headwaters of a watershed may impact food availability and the ability of these streams to support a diverse array of invertebrate and fish species (Vannote et al. 1980).

While Brook Trout were present in and abundant in all four AMR tributaries, the lake population estimate was lower than expected. Limited access to the property and sample gear restrictions in 2016 made documenting the use of tributaries by lake-dwelling Brook Trout difficult. Further, a low recapture rate of marked Brook Trout during trap net surveys of Upper
Ausable Lake resulted in an uncertain population estimate. In future studies, a multiple-mark-recapture study using permanent and unique marks or tags for each recapture event could be more appropriate for studying lake population size and fish movement in the system. Overall, the hypothesis stating that the population of Brook Trout in Upper Ausable Lake is self-sustaining, consisting mostly of wild fish was supported. Of all the Brook Trout captured here, there were no fish with hatchery fin clips, suggesting that natural reproduction is occurring in the lake. It is unclear based on these results, however, whether hatchery fish experience high rates of natural or angling mortality, whether the captured fish are all wild, or if hatchery fish are leaving a lasting impact on the genetics of this system. Fin tissue samples were collected from all Brook Trout in AMR tributary and lake sampling events. Genetic analysis presented in Chapter II provides answers to some of these questions and elucidates new information about the population status of the AMR Brook Trout population.

Brook Trout distribution and habitat use of upper, mid-river, and lower reaches

Brook Trout have been documented in all but one of the tributaries that flow into Upper Ausable Lake and the portion of the East Branch Ausable River on AMR and Ausable Club property (Josephson et al. 2014). Outside of the AMR, Brook Trout are most concentrated in the upper watershed reaches, but are present in tributaries adjacent to the river confluence from the AMR downstream to Keene. In the lower reaches, from Keene Valley to Au Sable Forks, Brook Trout were present in four of ten tributaries to the East Branch, Brown Trout were captured in five tributaries, and Rainbow Trout were captured at two sites. It is likely that habitat variables limit Brook Trout occupancy of open, low gradient stream reaches near the river.
Conclusions

This study provides information on the current distribution and status of Brook Trout in near-river tributary reaches within the intact East Branch Ausable River watershed. Many of the tributaries across the elevation gradient provide important habitat for young Brook Trout. Brook Trout occupancy and fish community assemblages in the East Branch Ausable tributaries are structured not by elevation gradients of the river itself, but by multiple interacting biotic and abiotic variables. This preliminary assessment of the East Branch Ausable River will allow for future comparisons of fish community and habitat change will provide valuable information to any future studies of Brook Trout movement and use of thermal refugia in the river and tributaries.

Community assemblage structure in the East Branch Ausable River watershed is influenced by landscape scale habitat variables and elevation gradients. The habitat associations demonstrated by species abundance data and corroborated by CCA analysis offer insight to the ecological status of the East Branch Ausable River corridor, and may aid in future land management, conservation action, and fisheries management for the region.

Protection and management of native species assemblages will maintain ecological integrity and functional food webs. Management priorities, as laid out by the Eastern Brook Trout Joint Venture include protection of intact populations, collecting finer scale catchment level data, improving water quality and reducing habitat fragmentation, and building partnerships for research and conservation (EBTJV 2011). The tributaries of the East Branch have been identified by the EBTJV as intact, resilient to climate change, and a priority for protection. These tributaries offer refuge to Brook Trout across the length of the watershed due to their physical and chemical characteristics, their high amounts of intact and well connected forest blocks, and
cool temperatures fed by extensive groundwater. Such characteristics make the East Branch Ausable River less vulnerable to increased stressors projected with climate change, and by protecting these tributaries, it will be possible to maintain high water quality and Brook Trout populations into the future. Continued efforts to connect stream fragments that offer optimal habitat conditions will ensure populations can be reestablished. The higher resiliency of the forests and streams of this watershed give a reasonable assurance that Brook Trout populations will be maintained in the East Branch Ausable River watershed into the future.
Abstract: In the Northern Forest region of the northeastern United States and eastern Canadian provinces, Brook Trout *Salvelinus fontinalis* are an iconic native stream-dwelling salmonid and have been stocked extensively since the 1800s to restore and supplement a recreational fishery. Brook Trout from tributary streams and a lake that form the headwaters of the Ausable River in the Adirondack Mountains of New York State were examined for genetic variability and influence of past stocking. Tissue samples were collected (*n* = 136) from the study site and a hatchery (*n* = 35) and analyzed using 13 microsatellite loci to determine individual genotypes, which were compared to additional hatchery genotypes to assess population structure and within-population genetic variability. The primary goal was to evaluate whether tributary habitat availability or past stocking efforts influence reproduction of wild fish in the lake. Levels of hatchery introgression with resident fish are presented and this knowledge will add to a growing body of research on the full impact of historical stocking efforts across New York State. Brook Trout in the headwaters of the Ausable River are an admixed population of wild and domestic-Temiscamie fish, and results show lasting effects of fish stocking on the genetic diversity and population status of this system.

Key words: *Salvelinus fontinalis*, Adirondack Mountains, population genetics, genetic population structure, microsatellite loci, Ausable River, introgression

Introduction

In the Northern Forest region of the northeastern United States and eastern Canadian provinces, Brook Trout *Salvelinus fontinalis* are one of two iconic native stream-dwelling salmonids, and in New York State their range has contracted due in part to habitat fragmentation and water temperature increases (Carlson et al. 2016). In much of New York, the optimal habitats necessary for all life stages of Brook Trout are small and fragmented, with limited numbers of intact populations remaining across their native range (Hudy et al. 2008, Carlson et al. 2016). Climate change will likely play a role in amplifying existing pressures on Brook Trout, including increased water temperature and variable flow regime, with lower flows in summer and high flows at uncommon times during the growing season (Bassar et al. 2016, Lynch et al. 2016).
Across the northeastern United States, Brook Trout have been stocked extensively since the 1800s to restore and supplement a recreational fishery (Bowen 1970, Cooper 1970, Perkins et al. 1993). In New York, popular strains for stocking to improve recreational opportunities include domestic, Temiscamie, Little Tupper, and hybrids of these. Domestic fish propagated in New York hatcheries originate from native New York genetics and are prized for their disease resistance and adaptations to hatchery life.

Native strains tend to be better suited for survival and reproduction in their native waters than stocked fish of the same species (Lachance & Magnan 1990, Hayes et al. 1996, Christie et al. 2012). At least 15 unique strains of wild Brook Trout, endemic to the pond or region in which they were found, have been identified in lakes and ponds across the Adirondacks (Keller 1979, Perkins et al. 1993). These are collectively known as “heritage” strain brook trout, and they have been used as brood stock for hatchery restorative stocking in New York since the 1970s (Baird et al. 2002). Little Tupper Brook Trout - considered a heritage strain in New York that originated in Hamilton County - are widely raised in hatcheries as pure and hybrid strains for stocking in Adirondack waters; though they have some hatchery influence in their background (Keller 1979, Baird et al. 2002). Temiscamie fish originated from Lake Albanel, in northeastern Québec, and are known to have longer life spans and achieve better growth in the wild than domestic strain Brook Trout; they were introduced into New York hatcheries in 1965 and raised in reclaimed brood ponds at Brandon Park in the Adirondacks (Flick 1977, Van Offelen et al. 1993, Baird et al. 2002). This strain is also used to create F1 hybrids with domestic strain Brook Trout; these are one parent from each strain, and the first generation of these are stocked, often for fall fingerling stocking due to high survival and growth rates. Finally, various private hatcheries also
raise Brook Trout and provide fish for stocking on private lands; these are usually a mix of various strains.

It is questionable whether hatchery fish assist recovery of Brook Trout or leave lasting effects on wild genetics. Captive rearing and breeding of hatchery fish leads to inbreeding depression, genetic adaptation to captivity, and ultimately to loss of diversity and overall genetic deterioration (Frankham et al. 2002). Numerous studies provide evidence that Brook Trout stocking can cause direct and indirect genetic impacts on native stocks (Hayes et al. 1996, Marie et al. 2010). There is evidence that hybridization can occur resulting in admixture between stocked and wild strains of Brook Trout (McCracken et al. 1993, Neville and Bernatchez 2013, Harbicht et al. 2014), and that hatchery fish exhibit lower diversity and reproductive fitness in wild systems (Hallerman 2003, Christie et al. 2012). Here, reproductive fitness is defined as the number of fertile offspring that survive to reproductive age. Genetic admixture can occur when two or more previously isolated populations begin interbreeding; this results in the introduction of new genetic lineages into the population. Admixture has also been known to slow local adaptation by introducing foreign, maladapted genotypes, known as gene swamping (Frankham et al. 2002). Hybridization and outbreeding depression can lead to lower survival and reproduction and an unintentional loss of effective population size (Christie et al. 2012). Further, repeated stocking events and increased stocking intensity introduces more hatchery alleles into the system with lower diversity and maladapted traits, which can lead to a decrease in population size over time (Christie et al. 2012).

Studies of hatchery influence on lentic and lotic habitats have documented varying levels of these effects; some studies have found minimal influence of hatchery fish on genetics of tributary fish (Jones et al. 1996, Humston et al. 2012), where others have found significant
hybridization in both habitats (McCracken et al. 1993, Neville & Bernatchez 2013, Harbicht et al. 2014). In the Pacific Northwest, extensive impacts have been documented on the effects of Pacific salmon hatcheries on native strains, including loss of diversity, lower survival rates, and decreased reproductive success (Waples et al. 1991, Reisenbichler & Rubin 1999).

Certain anthropogenic and landscape variables are correlated with levels of introgression among populations and can be used to explain varying levels of hatchery influence (Harbicht et al. 2014), as well as time required for native stocks to recover from hatchery influence (Létourneau et al. 2017). Throughout the northeastern United States and Canadian provinces, recent studies have focused on genetic diversity of native fish and whether any long term genetic impacts from stocking have occurred (Harbicht et al. 2014, Valiquette et al. 2014, Bruce et al. 2018). Within New York, specific studies are examining trout populations in the Adirondacks and across the state, and are concluding widespread introgression of hatchery genetics in wild caught fish (Bruce et al. unpublished data). In contrast, a study of fish in the Dix Pond-Elk Lake system, just over a mountain from Upper Ausable Lake documented minimal impacts of supplemental stocking on wild populations (Bruce et al. 2015, Kelson et al. 2016).

Genetic diversity can be measured by inspecting the amount of heterozygosity in alleles across multiple distinct genetic markers, or microsatellite loci. A microsatellite is defined as a locus with a short tandem repeat sequence (i.e., AC repeated 10 times) and are found in many regions across a fish genotype. King et al. (2011) identified 13 microsatellite loci that can be used to create distinct genotypes for Brook Trout across their native range. Creating genotypes using microsatellite loci can be used to understand population and individual level genetic diversity, and to compare fish from sub-populations to each other. For example, large amounts of heterozygosity in a population is considered to have high diversity (Frankham et al. 2002). This
study assesses genetic diversity and population structure, or population differentiation in the remote headwaters of a large Adirondack river system in New York State and aims to understand whether tributary habitat availability or past stocking efforts influence wild reproduction of lake fish. Brook Trout have been stocked at a private reserve in the headwaters of the East Branch Ausable River to supplement a recreational fishery since 1972 (Field 2009); however, few stocked fish were reported each year from 2012-2016 in fisheries assessments and creel surveys (Josephson et al. 2014). Specific study questions include whether hatchery fish are reproducing in the system, whether introgression with wild fish genetics has occurred, and determining the geographical extent of hatchery influence in the upper Ausable watershed. Genetic analysis of tissue samples using microsatellite loci made it possible to produce distinct multi-locus genotypes of individual fish and compare them to hatchery genotypes and an un-stocked reference stream at the extreme watershed boundary. Further, data are used to assess population differentiation and within-population genetic variability.

Specific hypotheses for the project include:

i. At the Adirondack Mountain Reserve, the population of Brook Trout in Upper Ausable Lake is self-sustaining, consisting mostly of wild fish,

ii. Lake and tributary fish are related, which suggests that lake fish use tributaries for fall spawning,

iii. There is little to no genetic introgression between lake fish and strains of fish previously stocked, given that fisheries surveys and anglers very rarely catch stocked (fin-clipped) fish.

Given recent projections of faster warming trends in the northeastern United States compared to the global average (Karmalkar & Bradley 2017), understanding the genetic diversity of Brook Trout in New York State is critical for conservation planning in the coming decade.
Further, this particular site is a priority habitat; subwatersheds within the Upper Ausable are predicted to have the highest probability of Brook Trout occupancy under the most severe climate scenarios across their entire native range (Hudy et al. 2008, Interactive Catchment Explorer 2017). Finally, since past studies show variable levels of hatchery influence on wild populations, there is a need to understand the extent of hatchery influence and what it may mean for the genetic diversity and status of this headwater population.

Methods

Site Description

The 132,000-ha Ausable River watershed comprises two branches that drain from the interior of the Eastern High Peaks Zone of the Adirondacks, join in the town of Au Sable Forks, and flow in a northerly direction to Lake Champlain (Figure 1). The headwaters of both branches of the Ausable are well protected; the West Branch located in a state wilderness area, and the East Branch located within the Adirondack Mountain Reserve (AMR), a 2,832-ha private reserve with an easement that grants extensive public access, which was created in 1887 to protect scenic lands and mountains of the Adirondacks from lumbering and environmental degradation (Figure 2). The streams and lakes that form the East Branch headwaters contain nearly pristine habitat that has remained intact since the AMR was created. The fish community composition within the 62.5-ha Upper Ausable Lake (UAL) and the tributaries of the AMR is entirely native, though Brook Trout have been stocked here for many years from a variety of hatchery sources.
Fig. 1. Map of Ausable River Watershed

Fish Capture and Tissue Collection

Brook Trout were collected ($n = 136$) from Upper Ausable Lake and four adjoining tributaries. Sixty of the wild fish were captured in four tributaries (Cedar, Otis, Crystal, and Sawtooth) in August 2015 using backpack electrofishing surveys, and an additional 76 fish were collected in Upper Ausable Lake in May and October of 2016 using trap net surveys (Figure 2). For all captured fish, fin clips were obtained using sterile technique and under IACUC approval from State University of New York College of Environmental Science and Forestry, (protocol 150801). A subset of Brook Trout fin clips was donated by the SUNY Morrisville hatchery ($n = 35$), a strain stocked in the system in 2010-11. Samples were stored in 90% ethanol, and frozen at
-20°C until analyzed in the lab. Additional genotype reference datasets were donated by Spencer Bruce of the University of Albany for Casey Brook and for strains of hatchery Brook Trout used to stock Upper Ausable Lake in 2012-14, (domestic, Temiscamie, domestic-Temiscamie F1 hybrids). The Casey Brook and hatchery strains were genotyped by Spencer Bruce at the New York State Museum in Albany, NY. Figure 2 shows relative position of tributaries and Upper Ausable Lake; it is notable that Casey Brook is an isolated outlier stream outside of AMR property and located in the true headwaters of the watershed, whereas Sawtooth Brook is downstream of Upper Ausable Lake, but is accessible to fish passage.
Genetic Lab Analysis

DNA extraction and Polymerase Chain Reaction (PCR) were performed at the Research & Collections Molecular Laboratory at the New York State Museum in Albany, NY. DNA were extracted from tissue samples using DNeasy Blood & Tissue Kit (QIAGEN Inc. Valencia, California) reagents, and the tissue protocol included in the kit was followed. After extraction, samples were eluted using a Qiagen TE buffer, which helps to re-suspend the DNA, and DNA
concentration was quantified using a NanoDrop 8000 spectrophotometer. If DNA was too concentrated, samples were diluted to a concentration of 100 ng/µl in deionized water as needed. PCR was used to amplify primers for 13 autosomal microsatellite loci: SfoB52, SfoC24, SfoC28, SfoC38, SfoC79, SfoC86, SfoC88, SfoC113, SfoC115, SfoC129, SfoD75, SfoD91, and SfoD100 created specifically for Brook Trout (King et al. 2012) (Table 1). PCR was completed using five multiple-loci and one single-locus 20-ul PCRs for each individual from optimized multiple T100 thermal cyclers (Bio-Rad), and conditions included an initial denaturing step of 2 minutes at 94°C, followed by 35 cycles each of 45 seconds at 94°C, 45 seconds at the annealing temperature of 56°C, and 2 min at 72°C, and a final extension step was performed for 10 min at 72°C; the PCR profile was the same for each primer set. Microsatellite primers were marked with fluorescent dye (NED, FAM, or HEX) to be detectable by PCR, and protocols from the King Lab at USGS were followed for consistency of analysis. Fish with poor amplification of microsatellites were processed a second time with PCR and genotyping. DNA fragment analysis was completed at the University of Albany Center for Functional Genomics using capillary electrophoresis and an internal size standard (Applied BioSystems 600 LIZ™) on an Applied BioSystems 3730XL DNA Analyzer. This enabled determination of individual genotypes, which were automatically scored and confirmed using GENEIOUS version 10.2.3 (https://www.geneious.com, Kearse et al. 2012), and were then compared to hatchery genotypes to assess within-population genetic variability and population genetic differentiation, or population structure. All automated genotype calls were confirmed for accuracy by eye prior to compilation for data analysis. DNA for domestic, hybrid, and Temiscamie hatchery fish and Casey Brook reference sample sets were extracted and quantified by Spencer Bruce at the New York State Museum and University of Albany using the same protocols.
Data Analysis

LOSITAN is a selection detection workbench based on $F_{ST}$ outlier methods, and enables understanding of the contribution of selection and molecular level adaptation. This was used to run outlier tests to find genes that have been affected by selection, and to ensure none of the microsatellite loci across all fish sampled showed non-neutrality (Anato et al. 2008). All genotypes were tested for Hardy-Weinberg equilibrium (HWE) (Guo & Thompson 1992) and expected and observed heterozygosity ($H_E$ and $H_O$) were calculated using ARLEQUIN version 3.5 (Excoffier & Lischer 2010).

Tests for linkage disequilibrium (non-random association of alleles), heterozygote deficiency and excess, and Wright’s inbreeding coefficient ($F_{IS}$) were completed using GENEPOP software (Raymond & Rousset 1995, Rousset 2008). $F_{IS}$ is defined as the proportion of the total inbreeding within the population due to inbreeding in sub-populations (Frankham et al. 2002). Heterozygote deficiency occurs when most individuals inherit the same gene from both parents and is a sign of low diversity or inbreeding (Frankham et al. 2002). If population level HWE is met, but populations are fragmented with restricted gene flow, heterozygote deficit can often occur (Frankham et al. 2002).

Previous work on hatchery strains and Casey Brook fish demonstrate HWE and linkage equilibrium (Bruce et al. 2018, S. Bruce, unpublished data). NeEstimator V2.1 (Do et al. 2014) was used to estimate effective population size ($N_e$) from the molecular coancestry method of Nomura (2008). $F_{ST}$ is a measure of variance, and it describes genetic differentiation among sub-populations. Pairwise tests of differentiation ($F_{ST}$) were completed, and population level allelic richness ($A_R$) and allele frequencies were calculated using FSTAT 2.9.3.2 (Goudet 1995).
Tbl. 1. Thirteen microsatellite DNA loci developed for Brook Trout, after King et al. 2012.

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<th>Microsatellite locus</th>
<th>Repeat motif</th>
<th>Number of Alleles</th>
<th>Allelic size range</th>
<th>Primers (5’ – 3’)</th>
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<tr>
<td>SfoD100</td>
<td>(TAGA)$_{11}$</td>
<td>12</td>
<td>206-246</td>
<td>Forward: ACC TTT GAC CTG TAC ATC GTG &lt;br&gt; Reverse: CAG ACC TAG ACT AAA GCA TCC G</td>
</tr>
</tbody>
</table>

Testing for isolation by distance (IBD) was completed as per Rousset (1997), where a Mantel test was performed and the relationship between the genetic differences of sampling locations $[F_{ST}/1- F_{ST}]$ to the geographic waterway distance between sample sites were plotted.

A model-based Bayesian cluster analysis was completed using STRUCTURE 2.3.4 software (Pritchard at al. 2000) to determine the most likely number of populations. The model was first run on the Ausable samples alone to assess population differentiation, or genetic structure across sampling locations, and then was run again with wild caught and hatchery fish to assess hatchery ancestry in wild fish. For both model runs, ten iterations each for $K=1$ to $K=10$
putative populations (where \( K \) represents the number of populations or clusters) were run for 500,000 cycles, with a burn-in of 100,000 cycles. Model output was first processed with STRUCTURE HARVESTER to assess support for the most likely numbers of distinct populations and patterns of admixture (Dent & vonHoldt 2012) and then was processed with CLUMPAK (Kopelman et al. 2015) to create visual output including all bar chart plots using DISTRACT (Rosenberg 2004). To determine the most likely number of actual populations, the Evanno method was used to estimate delta-\( K \) (Evanno et al. 2005) and mean and log-likelihood of \( K \), which assists in identifying the highest level of genetic population structure. Additionally, a Bayesian Information Criterion (BIC) using a \( k \)-means clustering algorithm to identify the number of genetic clusters that explain the most variation in the data was calculated using \( R \) package ADEGENET (Jombart 2008) to show similarities among individuals and clusters and independently assign hierarchical structure. All tests were completed for wild samples, then run comparing wild and hatchery strains.

Results

DNA from Brook Trout was extracted from 136 wild fish collected at five samples sites and from 35 hatchery fish. All individuals were genotyped for 13 microsatellite loci, and deviations from HWE were only found for one loci; all loci were retained for the analyses. Neutrality testing using the \( F_{ST} \) outlier method LOSITAN showed all loci as neutral and ensured they were appropriate for additional analysis (Figure 3).
**Genetic Diversity of Populations**

Average levels of genetic variation in Upper Ausable Lake and adjoining tributaries (AMR sample), as measured by expected heterozygosity and allelic richness, \( (H_E = 0.605, AR = 5.439) \) are within the upper range seen in the hatchery fish (Table 2). Hatchery fish from SUNY Morrisville show the highest allelic richness \( (AR = 5.01) \), followed by the Domestic/Temiscamie F1 hybrid fish \( (AR = 4.651) \). \( H_E \) and \( H_O \) are the predicted and actual level of heterozygosity measured in the populations; when random mating (panmixia) occurs, these are expected to be similar. This is true for Casey Brook and the AMR sample (Table 2). Additionally, \( F_{IS} \) is calculated based on comparisons between observed and expected heterozygosity within a population, and both measure relative levels of inbreeding. An index value of zero would show no inbreeding, and a value of one would be completely inbred. The \( F_{IS} \) value for the AMR sample is 0.05, which suggests that there is a level of inbreeding occurring in the Upper Ausable Lake subpopulation. Given that the \( F_{IS} \) value for Casey Brook is less than this, it suggests this population is not inbred. Within the combined sample, fish from Upper Ausable Lake (October sample), Otis, and Sawtooth showed the highest Fis values.

![Fig. 3. LOSITAN output of neutrality test results.](image-url)
The samples were also tested for heterozygote deficiency. Most notably, the AMR sample, which does not include Casey Brook, tested most significant for heterozygote deficiency \((p = 0.0004)\), and we conclude the genetic diversity of the population in Upper Ausable Lake and adjoining tributaries is contracting. When populations are fragmented and have restricted gene flow, but HWE is met for the population, heterozygote deficit can often occur (Frankham et al. 2002).

Ne is a measure of all the breeding adults in a population, or the population that contributes genes to the next generation, and is strongly affected by fluctuating population sizes, sex ratios, and spatial distribution of breeders. The results for the hatchery domestic and Temiscamie fish were expected, and this number is high for Morrisville, further suggesting the high diversity of this population (Table 2). Effective population size for the AMR sample is 75.9 individuals, with a 95% confidence interval of 63.7 to 91.7. This is much lower than expected, especially given the large size of this population area.

### Tbl. 2. Summary statistics for all fish included in the study from hatchery and wild caught stocks.

| Sample site                  | N   | \(H_E\) | \(H_O\) | \(AR\) | \(H_{EXCESS}\) | \(H_{DEFICIENT}\) | \(F_{IS}\) | \(N_e\) | \(N_e\) \(w/95\% CI\) |
|-----------------------------|-----|---------|--------|-------|---------------|----------------||---------|--------|-----------------|
| Temiscamie                  | 30  | 0.65858 | 0.62919| 4.282154 | 0.032 | 0.968 | -0.0481 | 26    | 17.6-43.0       |
| Domestic                    | 31  | 0.44634 | 0.46501| 2.800615 | 0.9287 | 0.0713 | 0.041  | 25.3  | 13.4-63.4       |
| Domestic/Temiscamie F1 Hybrid | 31  | 0.69975 | 0.63487| 4.651385 | 0.0004* | 0.9996 | -0.1041 | 64.6  | 37.5-167.5      |
| SUNY Morrisville            | 35  | 0.68668 | 0.69392| 5.012231 | 0.512 | 0.488 | 0.0104  | 110.9 | 56.1-707.9      |
| Casey Brook                 | 15  | 0.45128 | 0.46684| 4.076923 | 0.7853 | 0.2147 | 0.0345  | infinite | 68.5-Inf       |
| **AMR Wild Sample**         | **136** | **0.60469** | **0.63781** | **5.438769** | **1** | **0** | **0.0522** | **75.9** | **63.7-91.7** |

\(N\) = number of samples, \(H_E\) = mean expected heterozygosity, \(H_O\) = mean observed heterozygosity, \(AR\) = mean allelic richness (based on min. sample size of 15 individuals), \(F_{IS}\) = Wright's inbreeding coefficient, \(N_e\) = effective population size, with 95% CI. All sample sites meet expectations of Hardy-Weinberg equilibrium across all 13 loci.

* Heterozygote excess/deficit is significant at \(P < 0.05\) after sequential Bonferroni correction (\(\alpha = 0.008\) for Hatcheries and 0.007 for Ausable)
Analysis of population differentiation and genetic population structure

Measures of genetic diversity show the total amount of variation in the population, where population structure is used to explain how that variation is distributed across sub-populations. In other words, population structure occurs when genetic differentiation between sub-populations exists. When examining all wild-caught fish from Upper Ausable Lake and the tributaries in isolation using the program STRUCTURE, the maximum likelihood $\text{Ln}(K)$ values for $K=1$ to 10 showed $K=2$ as the best supported population model; results suggest a single, free-mixing population in the Upper Lake and tributaries (Figure 4). The Casey Brook sample was grouped as sharing similar genetics but being reproductively isolated in the upper part of the watershed.

![Graph showing mean likelihood Ln(K) values for STRUCTURE runs across all Ausable sampling locations, with corresponding STRUCTURE bar plots for K-values two through four. Each vertical line represents an individual. Note that additional K values fail to split the samples spatially, suggesting a single population in the AMR, with a separate population at the Casey Brook sample site. K=1 not shown, as it cannot be computed.](image-url)
Since little to no population structure or genetic differentiation was found for the lake and tributary populations, they are grouped for all further analyses (AMR sample). A second STRUCTURE run incorporated the hatchery strains, with Casey Brook treated as a separate population from the combined Ausable sample. STRUCTURE results using mean likelihood criteria indicate the most support for four genetically distinct clusters or populations (K=4), (Figure 5), and this is supported by a clear peak in delta-K at this value. Note that even though the Ausable Lake and tributary fish were combined and treated as one population, thin black lines still denote site differentiation (Figure 5).

Fig. 5. Average mean likelihood Ln(K) values for STRUCTURE runs across all hatchery and Ausable sampling locations, with corresponding STRUCTURE bar plots for K-values four through six. Each vertical line represents an individual fish, and colors represent the inferred ancestry of K=4 to 6 ancestral populations.
An independent analysis of genetic structure using DAPC using the ADGENET package in \( R \) produced similar results as STRUCTURE and suggested four separate genetic clusters in the sample. Recall that the use of a Bayesian Information Criterion (BIC) is a method of model selection in that the model that has the lowest BIC is preferred.

Further, \( k \)-means clustering algorithm partitions all observations into \( k \) number of clusters, and each fish belongs to the cluster with the nearest mean. The DAPC analysis designated all individuals from Casey Brook as one inferred population, while Ausable fish were assigned to an inferred grouping that was a mixture of Casey, Domestic, and Temiscamie ancestry, which suggests Upper Ausable Lake and adjoining tributaries are a strongly admixed population (Figure 6).

Casey Brook groups as a distinct population in all STRUCTURE and DAPC plots, and this sample is likely representative of the historic and mostly unaltered Ausable genetics. Perhaps the most important finding of these analyses is that a considerable number of samples in the remaining Ausable sites show varying amounts of introgression with hatchery strains (see Figure 7), including a significant amount of both domestic and Temiscamie heritage with very little Morrisville influence. The ancestry associated with the domestic fish in the Morrisville hatchery sample can likely be attributed to documented introgression from domestic fish in the heritage strain that Morrisville is derived from (Perkins et al. 1993, Bruce et al. 2018).
Fig. 7. STRUCTURE bar plots for stocked strains (on left), with the Upper Ausable Lake watershed samples (right), for K=4, the most strongly supported number of populations in the combined sample. Again, each vertical line represents an individual, and colors represent their inferred ancestry from 4K ancestral populations. Domestic-Temiscamie hybrid hatchery ancestry is apparent in much of the combined wild sample.

**Analysis of hatchery influence**

STRUCTURE results allow for an examination of the admixture proportions for all individuals within each population. There is a considerable amount of hatchery influence within the fish from the Ausable Lake and tributaries, but not in Casey Brook (Figures 5, 6, 7). When examining the proportions of hatchery membership within the populations of fish from the AMR sample, all fish exhibit a level of ancestry associated with hatchery samples at levels greater than 5% ($Q$-value > 0.05, $Q$-value represents the probabilistic membership to hatchery genetic clusters). Further examination of Q-values attributed to each hatchery stock at each site reveals more than 10% mean hatchery membership at all AMR sites (Figure 8). Here, sites with the highest level of hatchery membership are Cedar and Sawtooth Brooks, with 48% and 30% membership, respectively. When Upper Ausable Lake samples from May and October are combined, the mean hatchery membership is 24%. The maximum proportion of hatchery
membership among the entire sample was is 78%, found in a fish from Crystal Brook. No fish were determined to be directly from the hatcheries, and of the ten fish with the highest amount of hatchery membership, six were captured in the lake, three in Crystal Brook, and one in Cedar Brook. Notably, $Q$-values in the Casey Brook population ranged from 1% to 5% (mean = 2%), with values greater than 5% observed in two of 15 fish (Figure 8).

*Isolation by Distance*

Testing for IBD is another way to interpret population differentiation across the watershed. This measures genetic differentiation among sites, as measured by $F_{ST}$ ratios, and compares this relationship to the geographical waterway distance between sites in meters. The IBD test assumes that populations close to one another geographically will share many genetic similarities, and that populations spaced farther apart will not. Physical distance between Casey
Brook and Upper Ausable Lake is 6 kilometers; this relationship is significant, and the streams that are close to each other are genetically similar (Figure 9). Indeed, $F_{ST}$ ratios for all populations increase with geographical distance. The Brook Trout in Casey Brook exhibit genetic differentiation from all other sites, and this is correlated to geographic distance. Moreover, the results show less correlation of the downstream sites to each other. It is possible that Casey Brook is effectively cut off from the others due to a physical or geographic barrier among sites.

Fig. 9. The trend line in the isolation by distance scatter plot shows a significant relationship between genetic differentiation and geography ($p=0.0$, $R^2=0.8426$). Points represent relationship of genetic and geographic distance among sites. Colors represent the site that is being compared with the others.

Discussion

The landscape scale genetic structure of the East Branch Ausable River headwaters was investigated using 13 microsatellite loci, and the multiple model simulations created using program STRUCTURE strongly support that population structure, that is, population differentiation among the sampling sites is weak to non-existent. The independent cluster analyses showed similar results and the data demonstrate that the population of Upper Ausable
Lake and its tributaries is open to movement between lake and stream, both geographically and genetically. Tributary and lake fish were expected to utilize adjoining tributary habitat for spawning and to be related. This hypothesis was fully supported by the results; hatchery genes are widespread in this system.

When the fish from the Upper Ausable Lake watershed and Casey Brook are compared to fish from hatchery strains that were stocked in the system through 2015, it becomes apparent that the fish in the lake and study tributaries are genetically similar to Casey Brook, but have a significant amount of hatchery ancestry as well. The STRUCTURE and DAPC analyses demonstrate that overall, the fish in Upper Ausable Lake and Crystal, Sawtooth, Otis, and Cedar brooks are a mostly admixed population of resident Ausable and Domestic-Temiscamie hybrid parentage. Genetic admixture can occur when two or more previously isolated populations begin interbreeding; this results in the introduction of new genetic lineages into the population. The hypothesis that there would be little to no genetic introgression between lake and hatchery fish is not supported by the data, as fish from the lake and tributary systems show an average of 27% hatchery membership. Moreover, while these analyses show a significant amount of introgression of hatchery genetics among the Upper Ausable combined sample, fish from Casey Brook exhibit little to no hatchery introgression; the minor introgression that did occur appears to be attributed to genetics matching the SUNY Morrisville strain. This suggests that the long distance between sites may prevent exchange of genetics, or that there may indeed be a physical barrier to gene flow between the lake and this stream.

It is probable that not all hatchery strains of Brook Trout are well suited to live in this system, and thus emigrate or are subject to natural or fishing mortality. Timing of angling mortality may be concentrated to the early spring season, when angling effort and success on
Upper Ausable Lake are highest (Field 2009). Natural mortality may occur due to predation by herons, osprey, or loons. Emigration of hatchery fish may be an important factor in this system. The analysis illustrates that fish with ancestry from the SUNY Morrisville hatchery made only a minor contribution to the genetics of the population of Upper Ausable Lake, but the Morrisville genetics did persist in the downstream tributary Sawtooth Brook. Given that this brook is downstream from Upper Ausable Lake, it suggests the possibility that the Morrisville fish emigrated from the lake after being stocked. A downstream bias in the movement of some strains of stocked Brook Trout has been documented (Van Offelen 1993), and this may help explain the presence of Morrisville strain genetics found at Sawtooth Brook. The propensity to wander that this strain demonstrates at Sawtooth may be further supported by minimal introgression of Casey Brook fish with Morrisville genetics.

It is also possible that anglers may catch stocked fish after fin clips have regenerated. Since no pure hatchery strain fish were captured among all 136 of the fish used for this study, it suggests the stocked fish themselves are not surviving long in the Upper Ausable Lake system. They are surviving long enough to mate with wild fish and influence the genetics of the system however. Further study should focus on documenting the full extent of hatchery influence in the full length of all subwatershed tributaries, whether there may be areas of genetic refuge within the headwaters of the East Branch Ausable River, and whether measures of fish genetic diversity from these sample sites change over time. If stocking were to occur here again, a tagging study may help explain the individual movements and final disposition of stocked fish.

The isolation by distance analysis comparing the relationship between genetic differentiation and waterway distance provides additional support for a current barrier to gene flow between Casey Brook and the rest of the watershed. While this analysis shows support for a
genetic gradient across sampling locations, the STRUCTURE results, in addition to insignificant $F_{ST}$ values among the downstream study sites, suggest that sampling locations do not represent discrete groupings. Casey Brook fish may be less genetically diverse than the hybridized fish downstream, but they mostly lack hybrid ancestry and inbreeding is not occurring within the sub-population; in fact, their $F_{IS}$ value suggests that the genetic diversity of the population may be expanding.

The data suggest that natural reproduction of hatchery and native fish is occurring in Upper Ausable Lake; however, the analyses on the genetic diversity and population status of the sampled fish show that the population of lake and adjoining tributaries is contracting, in terms of diversity and size. The fish in this system are not fully wild, but instead are an admixed population of wild and Temiscamie hybrids. The heterozygote deficit that was observed for Upper Ausable Lake and its tributaries was not observed at Casey Brook, and may reflect the introduction of Temiscamie hybrids into the system. It is possible that the native or resident strain were better adapted than the new admixed fish, but the extensive stocking here has caused admixture across the watershed and, is therefore, potentially catalyzing the population's decline.

The high levels of introgression found in the Upper Ausable system may be explained by anthropogenic and landscape-scale variables. Harbicht et al. (2014) correlated lake pH, elevation, distance to roads (as a relative indicator of fishing pressure), and seasonality of stocking events to levels of introgressive hybridization in Brook Trout in Canadian lakes. The study reported correlations between these variables, and suggests that introgression increases with elevation, decreasing pH, increases in lakes that are stocked in spring, and with increased fishing pressure (Harbicht et al 2014). Upper Ausable Lake is a high elevation (~600m) lake with an average pH of 6.7, was stocked annually in early June, and has moderate seasonal fishing pressure, which
may explain the high levels of introgression here. Further, Harbicht et al. (2014) hypothesize a density-dependent relationship in high elevation lakes. They suggest that high elevation headwater lakes with low densities of native fish may be more susceptible to introgression from the mere fact that there are repeated stocking events. Annual introductions of hatchery gametes to the system results in fewer native genes to compete with hatchery genetics (Harbicht et al. 2014). Relationships between similar variables have also been seen in Lake Trout Salvelinus namaycush populations in Québec (Létourneau et al. 2017). We can speculate that at the low densities of Brook Trout in Upper Ausable Lake, it was easy for the increased number of breeding hatchery fish in the system to contribute their genes to the system, and even artificially increase certain measures of diversity. But if the hatchery fish exhibit lower reproductive fitness and reproductive success, hatchery-wild hybrids could effectively break up native gene complexes tied to local adaptation. This could lead to a decrease in the overall effective population size and diversity of the system over time. Future study could compare the expected and observed heterozygosity of Brook Trout after stocking has been halted to the fish captured in this study. If the heterozygosity were to continue to decrease over time, it would strongly support the idea that hatchery genetics are not well suited for this wild system.

Moreover, Temiscamie and other hatchery fish -combined with their long history of being mixed in hatcheries and in this system - may have higher reproductive and colonization abilities in novel habitats (Neville & Bernatchez 2013), and may explain their success in colonizing and reproducing in the Ausable tributaries (Humston et al. 2012). Where Humston et al. (2012) found high colonization rates but low introgression in tributaries of headwater impoundments, this study also found some of the highest introgression in tributaries. Because different strains possess life histories that use a combination of lake and stream habitats, it may
be possible to explain where different strains are spawning in the system (Flick 1977, Keller 1979, Baird et al. 2012). Specifically, in their native habitat in Québec, Temiscamie fish spend much of the year in the lake but swim far up the Lake Albanel inlet, the Temiscamie River, to spawn (Flick 1977). The fish with the most hybridized Temiscamie and native ancestry at the AMR (nearly 80%) were caught in Crystal Brook. This is one of the largest tributaries that flow into the Upper Lake and lacks significant physical barriers; it seems that the propensity of Temiscamie fish to migrate into a river to spawn may be reflected in this. In contrast, Little Tupper Lake fish, of domestic and native hybrid ancestry are known to spawn on shoals within lakes (Keller 1979). Therefore, domestic strain fish may be using the lake outlet, tributaries, or spawning shoals within the lake. The highest proportion of domestic and Morrisville genetics were found in the lake, Cedar, and Sawtooth Brooks.

There are several management implications that arise from the results of this study. First, ample evidence supports the continued suspension of Brook Trout stocking in the watershed. Remarkably few of the stocked fish are ever caught. It is unclear whether a stocking cessation will allow the native population to recover and experience growth, or whether a population collapse may take place after stocking ceases. The managers of the AMR could work to maintain and improve local genetic diversity by improving habitat for wild-reproducing fish. Further, maintaining genetic diversity in areas like Casey Brook, and likely the other tributaries above waterfalls is advisable. This property and resource is of global importance for Brook Trout (ICE ECOSHEDS 2017), and this needs to be stressed to the Ausable Club. Conserving wild Brook Trout genetics here will assist with maintaining the genetic and biotic integrity of the entire watershed and the future of this species in the Adirondacks. It is possible that angling restrictions for club members could also improve the natural reproduction of fish without
supplemental stocking. This could include imposing a size limit or seasonal restrictions to
decrease fishing pressure on native Brook Trout in the early spring after ice out and the early fall
before spawning. It would also be interesting to consider the possibility of using restorative
stocking to add more native and resident genes into the population of the lake by collecting
brood stock from Otis Brook, Casey Brook or other places in the watershed above definitive
genetic barriers (Shanty Brook, Gill Brook, Marcy Brook). Additionally, it is possible that
“native genetics” may be able to recover without further sustained stocking influences
(Valiquette et al. 2014, Létourneau et al. 2017). Recent evidence suggests that over several
decades after stocking is ceased, the mean hatchery membership of fish will decrease until a pre-
stocking state is reached (less than 5% hatchery membership). In other words, the effects of
stocking effects could be reversible as selective processes in the wild may purge unfit alleles
over time (Létourneau et al. 2017).

The results of this study could potentially change the way fish are managed in the
watershed and promote habitat improvement for supporting a wild recreational fishery.
Economically, the Ausable River - known worldwide for its trout fishery and spectacular scenery
- attracts millions of dollars in fishing tourism to the region annually and supports four fly shops
and numerous private guides. Anglers from around the world travel to fish the Ausable River,
seeking legendary Brown Trout and Rainbow Trout in the East and West Branches, and
searching for wild Brook Trout in the tributaries. By understanding the genetic makeup of fish in
the lakes and streams within the headwaters of the Ausable River, we can apply this information
to understand fish populations downstream and inform future decisions about wild trout
management and the recreational fishing economy in Essex County and throughout the
Adirondack Park.
Conclusions

The application of conservation genetics to the fish data collected from the Upper Ausable Lake watershed was an effective way to understand more about the fish in this system. It clarified existing questions about this remote population that could not be answered using traditional fisheries techniques and elucidated valuable information about the genetic diversity and status of this population and the effects of historical management within the system. Additionally, it adds more data to the growing body of evidence that stocking different strains of fish across New York State has altered the genetics of resident fish substantially, including in remote and seemingly pristine habitats.
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Appendix A. Fish distribution in near-river habitats of East Branch Ausable tributaries, Adirondack Park, New York, 2015-2016
* denotes introduced exotic species, all others are native to NYS. All surveys were conducted in the first 50 to 100 meters upstream from the confluence with the East Branch Ausable River.

<table>
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<th>Latin Name</th>
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<th>Otis 1</th>
<th>Cedar</th>
<th>Sawtooth</th>
<th>Deer</th>
<th>Crystal 2</th>
<th>Mossy Cascade</th>
<th>Flume</th>
<th>Johns</th>
<th>Phelps 1</th>
<th>Porter</th>
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Appendix B. Local stream habitat variables and sub-watershed level stream statistics (USGS) for tributaries of the East Branch Ausable River, New York.

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<th>Variable</th>
<th>Minimum</th>
<th>Maximum</th>
<th>Mean</th>
<th>Standard Deviation</th>
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<td>pH</td>
<td>5.5</td>
<td>7.1</td>
<td>6.32</td>
<td>0.42</td>
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<td>% DO</td>
<td>71.3</td>
<td>80.4</td>
<td>75.0</td>
<td>2.93</td>
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<tr>
<td>% Saturation</td>
<td>45%</td>
<td>61%</td>
<td>52%</td>
<td>4.66</td>
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<tr>
<td>Width (m)</td>
<td>195</td>
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<td>350.1</td>
<td>247.5</td>
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<tr>
<td>Length (m)</td>
<td>1.15</td>
<td>2.37</td>
<td>1.72</td>
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<tr>
<td>Elevation (m)</td>
<td>0.29</td>
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<tr>
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* Descriptions of STREAMSTATS variables are found in Chapter 1, Table 5.

70
### Appendix C. In-stream habitat survey results.

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<tr>
<th>dominant substrate</th>
<th>mean % clay</th>
<th>mean % silt</th>
<th>mean % sand</th>
<th>mean % gravel</th>
<th>mean % cobble</th>
<th>mean % boulder</th>
<th>mean % bedrock</th>
<th>mean % canopy cover</th>
<th>Forest type - dominant species listed</th>
<th>In-stream boulders?</th>
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<tr>
<td>gravel, cobble, sand</td>
<td>0.0</td>
<td>4.0</td>
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<td>16.91</td>
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Appendix D. P-values from pairwise FST tests within Ausable sample sites.

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P-values obtained after: 21000 permutations
Indicative adjusted nominal level (5%) for multiple comparisons is: 0.002381

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<th>Crystal</th>
<th>UAL spring</th>
<th>UAL fall</th>
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<td>UAL spring</td>
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## Appendix E. Allelic richness by site at Ausable Only

### Allelic Richness per locus and population

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</table>
EDUCATION
SUNY Environmental Science and Forestry, M.S. Candidate in Environmental and Forest Biology, expected degree date: May 2018
SUNY Plattsburgh, Ecology, B.S., 2007 (Major GPA: 3.70 Cumulative GPA: 3.68, Magna cum Laude)
William H. Miner Agricultural Institute, Applied Environmental Science Program, 2006
North Tonawanda Senior High School, Advanced Regents Diploma, June 2003

AWARDS AND RECOGNITION
SUNY-ESF Graduate Student Association Travel Grant, Spring 2018
SUNY-ESF Graduate Student Association Research Grant, Fall 2017
Adirondack Garden Club Ellen Lea Paine Research Grant, 2017
NYAFS Student Travel Award, 2017
Edna Bailey Sussman Fellowship, 2016
George H. Disborough Trout Unlimited Research Grant, 2015
Adirondack Garden Club Ellen Lea Paine Research Grant, 2015
Saranac Lake Women’s College Scholarship Club Scholarship, 2014
SUNY Chancellor’s Award for Student Excellence, 2007
LCRI Undergraduate Research Award, 2007
CEES Outstanding Graduating Senior Award, 2007
New York State Galileo Award, 2007
LCRI Undergraduate Presentation Award, 2006
James A. FitzPatrick Memorial Scholarship/Miner Center, 2006
SUNY Plattsburgh Dean’s List (seven semesters)

EMPLOYMENT AND RESEARCH APPOINTMENTS
Science and Operations Associate, January 2017-present, Ausable River Association, Wilmington, NY
Operations Assistant, June 2014-December 2016, Ausable River Association, Wilmington, NY
Office Manager, 2008-Present, Wildlife Conservation Society, Saranac Lake, NY
River Steward, August 2014-February 2015, Ausable River Association, Wilmington, NY
Research Associate, 2007-2008, Lake Champlain Research Institute, Plattsburgh, NY
Undergraduate Research Assistant, 2004-2007, Lake Champlain Research Inst., Plattsburgh, NY
Research Assistant, 2006-2007, Windhorse, LLC, Beekmantown, NY
PUBLICATIONS


RESEARCH AND WORK EXPERIENCE
eDNA Pilot Study, Otis Brook, Ausable River Watershed, 2017
New York State Museum, Brook Trout population genetics, 2017
Summer 2016 Brook Trout tributary and habitat surveys, trap netting Upper Ausable Lake, Adirondacks
Summer 2015 Brook Trout tributary and habitat surveys, Upper Ausable Lake, Adirondacks
Streamside education and outreach to fly anglers and other river users about aquatic invasive species.
Bookkeeping, financial management of budgets; operations support at Ausable River Association and WCS
Administrative and financial management to the WCS Adirondack Landscape Program and the day-to-day managing of the Saranac Lake WCS Office, and coordination of the Annual Adirondack Loon Census
Black bear, small mammal, amphibian/reptile trapping research, vegetation studies of exurban development
Backcountry education and outreach to backpackers and hikers about human-black bear interactions.
Long-term zooplankton, phytoplankton, and water quality monitoring and research on Lake Champlain
Bat and insect abundance surveys at a potential wind farm site, Beekmantown, NY

PRESENTATIONS AT RECENT CONFERENCES


