

**Southeastern Fishes Council 44<sup>th</sup> Annual Meeting**  
**Hickory Knob State Park, McCormick, SC**  
**November 7-10, 2018**  
**PRESENTATION ABSTRACTS**

**Caleb A. Aldridge<sup>1</sup>, Bradley M. Richardson<sup>1</sup>, David A. Schumann<sup>1</sup>, and Michael E. Colvin<sup>1</sup>**

Identifying barriers to the detection of passive integrated transponder (PIT) tags in Southern Brook Lamprey *Ichthyomyzon gagei* ammocoetes

The southern brook lamprey (*Ichthyomyzon gagei*) is a primitive, nonparasitic, filiform fish that inhabits streams of the Southeastern USA. Little is known about the species, especially in their cryptic larval form (i.e., ammocoetes) which burrow into fine sediment. The presence of southern brook lamprey populations suggest good stream quality; they may also help maintain stream integrity (e.g., nutrient cycling). As part of a comprehensive study of southern brook lamprey ecology in Mississippi, we surgically implanted passive integrated transponder (PIT) tags into the peritoneal cavity of ammocoetes. Although short-term survival and tag retention was high (100%), the percentage of released individuals detected in subsequent sampling efforts was low compared to hidden PIT tag analogs ( $5.36 \pm 0.04$  % and  $66.07 \pm 0.10$  %, respectively). To understand, in part, this discrepancy, we varied sediment depth (0-30 cm; 3 cm intervals) above analogs *in laboratorio*. At each interval we measured the response of each analog, detected (1) or not (0), with a PIT tag reader. The analogs were then measured at the same depth intervals but without sediment (i.e., control). We modeled analog detection as a function of substrate type and depth to describe the influence of ammocoete burrowing behavior on the detections of tagged individuals. Substrate type ( $e^{\beta} = 0.40$ , Wald's  $\chi^2 = 4.09$ ,  $p = 0.04$ ) and depth ( $e^{\beta} = 0.73$ , Wald's  $\chi^2 = 16.53$ ,  $p = <0.01$ ) affected the detection probability of analogs. The estimated detection probability of analogs at 12 cm (typical ammocoete length) in sand was estimated at 42.6% compared to 97.1% in no substrate. Further investigation into ammocoete burrowing habits will improve expected detection probabilities and sampling approaches. This experiment provides a small but needed piece of information when using PIT tags in studying and conserving this unique species.

<sup>1</sup>Mississippi State University, Department of Wildlife, Fisheries and Aquaculture

**Sara Barrett<sup>1</sup>, Jake Schaefer<sup>1</sup>, and Scott Clark<sup>2</sup>**

Alternative stable state driving changes in fish assemblage within the Pascagoula River

Stable states are thought to represent alternative assemblages of species that may exist in stable equilibrium over time. Such states are defined as discrete temporal or spatial patterns in abundance of resident species. Theory predicts that shifting from one stable state to another may be facilitated by perturbations that may be either natural, anthropogenic or a

combination of both. The Pascagoula River in southeastern Mississippi is the largest remaining un-impounded river system in the contiguous United States with a discharge of over 2.4 cu mi per year. Examination of long term fish assemblage data show that the Pascagoula River, and its two major tributaries (Leaf and Chickasawhay Rivers) have been dominated by five abundant taxa that comprise 71% of individuals sampled. Within the last five years, a change in the Pascagoula River (but not Leaf and Chickasawhay) was seen to an alternate assemblage where three different taxa dominate (67% of assemblage). Thus, a shift in stable states seems to have occurred in one portion of the drainage but not the other. We explore potential drivers of this shift and whether or not it may in fact be stable.

<sup>1</sup>University of Southern Mississippi

<sup>2</sup>University of New Mexico

**Cori Black**<sup>1</sup>, Eric Bauer<sup>1</sup>, David Werneke<sup>1</sup>, Jon Armbruster<sup>1</sup>, Brian Helms<sup>2</sup>

Drought effects on ecological endpoint curves in a biodiversity hotspot

Regional geomorphic and ecological endpoint curves are valuable tools for effective stream restoration. In 2013 these tools were developed for the Piedmont of Alabama and in 2015 for the Appalachian Plateau of north Alabama, both of which are situated within the Mobile River Basin which harbors some of the richest freshwater diversity in the world. In 2016, this region was under one of the most extreme droughts in the last 10 years. How aquatic organisms respond to droughts and how natural disturbances influence restoration tools have been unclear. Our objective was to determine local community compositional shifts in response to drought and evaluate the effect of disturbance on ecological endpoint curves. In Summer 2017, fish and crayfish were collected post-drought within representative reaches of 18 Piedmont and 17 Appalachian Plateau streams ranging from 0.05-261 km<sup>2</sup> drainage area using a Smith-Root LR-24 backpack electrofisher. Data suggest that fish assemblage structure and ecological endpoint curves were not different post-drought, although maximum catch per unit effort was lower in 2017. These preliminary findings suggest that fish were minimally influenced by drought and that regional ecological endpoint curves are robust to such disturbances.

<sup>1</sup>Auburn University

<sup>2</sup>Troy University

Katelyn A. Bockwoldt<sup>1</sup> and **Steven L. Powers**<sup>1</sup>

Georeferenced electronic database for the Roanoke College ichthyological collection

The Roanoke College Ichthyological Collection (RC) has a long history as a regionally important collection. Despite this, few records included latitude/longitude coordinates and no electronic database existed for the collection. Beginning in August 2013, information from jar labels in the RC were transcribed into an Excel spreadsheet. Each entry included genus, species, number of individuals, preservative, state, county, water body, locality,

drainage, collection date, collector number, collected by, secondary collector number, and comments when available. For each locality, latitude and longitude were found and entered into the spreadsheet. Upon completion of data entry for non-problematic collection lots, data from Virginia, North Carolina, and Tennessee were imported into an Arc GIS project. Land cover, 8-digit watershed boundaries, mineral resources, stream data, and elevation datasets were downloaded from the United States Geologic Survey and also imported into the project. A total of 40,302 individual specimens in 5,124 lots from 31 states and five countries dating to July of 1941 comprise the complete database. As the overwhelming majority of these specimens are from localities in Virginia, with substantial but fewer specimens from North Carolina, and Tennessee, data from these three states were included in the Arc GIS project and represent 36,468 individual specimens in 4,634 lots. The web interface for this project and other information regarding the RC can be found in a Google search for Roanoke College Ichthyological Collection.

<sup>1</sup>Roanoke College, Biology Department

**Tyler M. Brown<sup>1</sup>**, Lindsey A. Martin<sup>1</sup>, and Brook L. Fluker<sup>1</sup>

Effects of black-spot disease on the body condition of Bleeding Shiners *Luxilus zonatus*

Black-spot disease is common in freshwater fishes and results from encystment of digenetic trematodes into the fins and flesh of the fish. The fish serves as an intermediate host in the life cycle of the trematode, and deposits melanin around the cyst as an immune response, producing the black spots for which the disease is named. Several studies have documented the occurrence of black-spot disease on game fishes, but little is known about how the trematode infestations affect the health or body condition of small stream fishes. The objective of this study was to evaluate the prevalence of black-spot infection in the Bleeding Shiner (*Luxilus zonatus*) throughout Myatt Creek, a tributary to the Spring River in northeastern Arkansas, and compare it with body condition. Specimens collected in the 1970s were obtained from the Arkansas State University Museum of Zoology (ASUMZ) and examined for abundance and location of black-spot infection. Infection rates were compared to coefficient of condition (K). Preliminary results revealed an infection rate of approx. 82%, with a mean of 16.5 encystments per individual. Coefficient of condition ranged from 1.29-2.09, and there was a general trend of decreasing number of encystments with increasing body condition; those with  $K > 1.7$  had no more than one encystment. Future work will incorporate more individuals from 1970s collections of Myatt Creek. These data will be compared to data from freshly collected specimens from Myatt Creek to evaluate a 40-year change in infection rate.

<sup>1</sup>Arkansas State University, Department of Biological Sciences

**Jacob Brumley<sup>1,2</sup>** and Philip Lienesch<sup>1</sup>

Use of dead mussel shells by madtom catfish in the Green River

The Green River in Kentucky has high fish and macroinvertebrate diversity. As both fish and macroinvertebrates have evolved together in this system, symbiotic relationships have developed between species. One type of relationship that has been observed is between madtom catfish (*Noturus* spp.) and mussels in the Green River, where madtoms use dead mussel shells as cover when not actively hunting. In the fall of 2016 and 2017, surveys were conducted to determine if madtom catfish prefer hiding under dead mussel shells or rocks of similar size. Three 12-meter by 12-meter plots were sampled at four separate sites along the Green River, once per year, by snorkeling in an upstream direction and searching for madtoms in dead mussel shells and under the rock substrate. An equal amount of effort was used searching for madtoms under rocks and in mussel shells. Significantly more madtoms were found under mussel shells than under rocks of similar size. These results support the hypothesis tested in this study that madtoms prefer the cover of mussel shells rather than rocks. The decline of mussel populations, and resulting decline in available mussel shells in rivers and streams, may have negative effects on madtom populations in the future.

<sup>1</sup>Western Kentucky University

<sup>2</sup>Austin Peay State University

**Hilary K. Canada<sup>1</sup>**, Brittany L. McCall<sup>1</sup>, and Brook L. Fluker<sup>1</sup>

Phylogeographic analyses suggest cryptic diversity within the Bluntnose Darter *Etheostoma Chlorosoma*

Previous morphological studies of the Bluntnose Darter (*Etheostoma chlorosoma*) revealed little variation among populations across the Gulf Coastal Plain. Although some western populations (e.g. Colorado River, Texas) showed significant divergence from other populations, there was little support for taxonomic recognition of these populations. In this study, we sampled *E. chlorosoma* from multiple river drainages across the southeastern United States to examine patterns of phylogeographic structuring among populations throughout its distribution range. Phylogeographic reconstructions and species tree estimations were conducted using the mtDNA cytochrome *b* gene and six nuclear DNA loci of sampled individuals. Preliminary results from phylogenetic analyses of nuclear DNA markers revealed a pattern of divergence between two clades of *E. chlorosoma*; a “western” group including all populations in and west of the Sabine River, and an “eastern” group including populations east of the Sabine River. Preliminary analyses of mtDNA revealed a deep phylogeographic break (TMRCA approx. 8 mya) among the eastern and western haplogroups of *E. chlorosoma*. However, the mtDNA-based patterns suggest multiple instances of mtDNA introgression among eastern and western haplogroups since their initial divergence. Despite this pattern of mtDNA introgression, the deep divergence among eastern and western clades of *E. chlorosoma* suggests previously unrecognized cryptic diversity within the species. Increased sampling across the distribution of *E.*

*chlorosoma* will need to be incorporated into this framework in order to fully understand the taxonomic status of these unique clades.

<sup>1</sup>Arkansas State University, Department of Biological Sciences

Mollie F. Cashner<sup>1</sup> and **Laurel Y. Hansen<sup>1</sup>**

Development of informative microsatellite loci for population genetic analysis of the Yellowfin Shiner *Notropis lutipinnis*

Freshwater fishes are restricted to linear habitats, and therefore, tracking populations across the landscape appears to be a simple process: follow the waterways. However, streams change over time, and areas which seem to be disconnected may, in fact, have been connected in the recent (geological) past. Moreover, patterns of gene flow within species are influenced by more than the environment: breeding systems, climate, demography, etc. all influence movement patterns of animals in the wild. One way to track, characterize, and assess overall contemporary gene flow within a species is the use of microsatellites: small, neutral, repeating segments of DNA dispersed throughout the genome. In a previous study, over 1000 potential microsatellite loci were identified for the Yellowfin Shiner. This fish is common in its native range, however, it has a distinctive breeding system (nest association), has relatively recently expanded its range, and exhibits high levels of color variation among populations. Microsatellite loci would be useful for population-level investigations. We set out to identify ~20 microsatellite loci that reliably amplify, occur in multiple populations, and exhibit at least 3-5 alleles among populations. We have successfully identified 18 viable loci with 5-8 alleles among specimens from three populations. We will use these loci to generate data for one population of Yellowfin Shiner and test for null alleles, irregular signals, and basic population genetic statistics. Future investigations of the species, or general questions about dispersal, range expansion, and population trends will benefit from the use of these markers.

<sup>1</sup>Austin Peay State University

**William Commins<sup>1</sup>** and William Ensign<sup>1</sup>

Using instream stationary antennas to monitor the movements of warm water fishes

Populations of riverine fishes can be divided into stationary (stayers) and mobile (movers) components. The importance of movement for many stream fishes is supported by reductions in fish diversity within watersheds where movement barriers have been introduced. In this study we investigate the variation in the proportions of stayers and movers in a stream fish community. This study took place between June 14, 2018 and August 2, 2018 in a 590-meter stream reach of Raccoon Creek in Paulding County, Georgia bisected by a box culvert. We used 12mm passive integrated transponder (PIT) tags and four instream stationary antennas to monitor six species of fish (221 individuals). Multiple detections of the same individual were grouped by day and considered to be a single daily

detection event. There were 1365 daily detection events during the study and the percent of marked individuals detected by species ranged from 33% (*Camptostoma oligolepis*) to 64% (*Micropterus coosae*). Larger fish were more frequently detected for four species (*C. oligolepis*, *M. coosae*, *Lepomis megalotis*, *L. auritus*), while two species had greater detection percentages for smaller fish (*Moxostoma duquesnei*, *Hypentelium etowanum*). We also examined the movement of 111 fish throughout a 320-meter reach of unimpeded stream (six riffle-pool sequences) above the culvert using three of the four instream stationary antennas. Within this reach, 58 upstream and 33 downstream movement events were detected. The proportion of movers in each population ranged from 14% (*M. duquesnei*) to 50% (*M. coosae*) and 28% of the tagged fishes within the reach made movements greater than 150- meters. The preliminary results from this study indicate that an array of instream stationary antennas can be used to examine the differential movements of PIT tagged fishes, and in turn potentially inform conservation and management decisions.

<sup>1</sup>Kennesaw State University

## **Tierra Curry<sup>1</sup>**

Progress and setbacks in ESA protections for southeast freshwater species

Since 2010, 36 freshwater species from the southeastern United States have gained Endangered Species Act protection, and 4 have been proposed for listing. Fifteen additional species are slated to receive final listing decisions in fiscal year 2018. If proposed Trump administration changes to the ESA are finalized, then it will become more difficult for species to be listed, species listed as threatened will not receive the same protections as endangered species, and critical habitat protections will be weakened. Trump guidelines have also bypassed take protections for recently listed species. Ten freshwater and terrestrial species from the Southeast have been declared extinct since 2010, and several additional species are likely extinct. More than 240 southeast freshwater species are still under status review for ESA protection. The outlook for increased listing and recovery funding for southeast freshwater species remains bleak.

<sup>1</sup>Center for Biological Diversity

## **Michael Cyrana<sup>1</sup>, Alexander Ledet<sup>1</sup>, and Henry Bart Jr.<sup>1</sup>**

Reproductive impairment in three groundfish species in and around the northern Gulf of Mexico hypoxic zone

Over the last few decades coastal hypoxia has emerged as a major seasonally chronic stressor on the northern Gulf of Mexico (GOMEX) benthic community. Coastal hypoxia has been shown to have a litany of negative consequences, at both the organismal and populations levels, for organisms impacted by it. A particularly profound consequence is reproductive impairment and ovarian masculinization. We detected varying degrees of

ovarian masculinization in nearly all specimens examined of three groundfish species, captured in trawl samples by the RV Oregon II in waters in and around the area where hypoxia seasonally develops in the GOMEX during the 2016 SEAMAP Summer Groundfish survey. This phenomenon, which was previously documented in specimens of *Micropogonias undulatus* from the GOMEX hypoxic zone, was detected in much higher proportions of specimens of this species and also observed in *Leiostomus xanthurus* and *Prionotus longispinosus*. Masculinization was observed at both hypoxic and normoxic sites. Our finding of similar reproductive impairment at the order level demonstrates how widespread the impact of coastal hypoxia is on the northern GOMEX fish populations. This work builds on previous studies that have linked ovarian masculinization to hypoxia and shows that the scope of the reproductive impairment is more pervasive than previously thought.

<sup>1</sup>Tulane University

**Noah Daun<sup>1</sup>**, Justin Kowalski<sup>1</sup>, Maxfield JonasKrueger<sup>1</sup>, Jeanne Thibodeau<sup>1</sup>, and Justin T. Sipiorski<sup>1</sup>

Morphometric variation of Iowa Darters *Etheostoma exile* in lotic and lentic environments in Wisconsin

The Iowa Darter (*Etheostoma exile*), native to the state of Wisconsin, is a member of Percidae and makes up an important part of the benthic community in many lakes and streams. Iowa Darters are also an important indicator species of good water quality and have a high index of biotic integrity (IBI) value. They are notable because they are one of a few Wisconsin darter species found in both lotic and lentic environments. Even though Iowa Darters are fairly common and widely distributed throughout the north-central United States and central Canada, little ecological research has been done concerning this species. Our past research on over 650 individuals collected throughout Wisconsin over the past 65 years, showed that Iowa Darters have length-based growth. We wanted to continue this research to determine if growth differs between lotic and lentic populations. We used standard truss measurements to determine if morphologies differed between the populations. We also calculated gonadal-somatic index (GSI) for each population. We then compared the GSI's of the lotic and lentic populations to determine if there was a difference in reproductive investment between populations. PCA analysis on the morphometric data also shows population-specific morphological differences. Understanding differences in growth between Iowa Darter populations in lotic and lentic environments could help us to further understand this important indicator species and help future managers understand what makes this species a potentially important member of aquatic foodwebs.

<sup>1</sup>The University of Wisconsin - Stevens Point, Department of Biology

Jessica L. Davis<sup>1,2</sup>, Mary C. Freeman<sup>1,3</sup>, and Stephen W. Golladay<sup>2</sup>

### Stream drying and fish occupancy dynamics in the Ichawaynochaway Creek basin

Stream drying is a natural process, and many aquatic species can maintain populations despite periods of intermittent flow. The point at which a disturbance, like stream drying, exceeds the ability of a community to recover or causes a shift in assemblages is not well understood. This study explores effects of stream intermittency and drying on the composition of diverse fish communities in the Ichawaynochaway Creek basin, southwestern GA. We tested whether faunal composition differed between perennial and intermittent streams and identified species that were strongly associated with each stream type using published and unpublished data. Species-specific occurrences in repeated surveys of intermittent streams were used to measure occupancy dynamics of adults and juveniles of commonly occurring fishes, while accounting for incomplete species detection. We explored differences among species in abilities to persist in isolated pools and to recolonize when streams resumed flow. We also tested for correlations between environmental conditions and species occurrences in isolated pools. Intermittent stream communities were found to be a subset of perennial stream communities, with all species observed found in perennial streams, but not in intermittent streams. Species with the lowest persistence rates in isolated pools as adults or juveniles were also more common in perennial than in intermittent streams. However, colonization after the resumption of flow did not significantly differ among species associated with perennial or intermittent streams. High concentrations of ammonia and low water depth decreased the probability of fish occurrence in isolated pools. The incorporation of a species-specific rates approach, via dynamic occupancy modeling, to stream intermittency can help advance the mechanistic understanding of flow-ecology relationships.

<sup>1</sup>University of Georgia, Athens GA

<sup>2</sup>Joseph W. Jones Ecological Research Center, Newton GA

<sup>3</sup>USGS Patuxent Wildlife Research Center, Athens, GA

Nastasia T. Disotell<sup>1</sup>, Zachary L. Wolf<sup>1</sup>, Mollie F. Cashner<sup>1</sup>, and Rebecca E. Blanton<sup>1</sup>

### Are neighbors pillaging nests: detecting spatial complexity of allopaternal care in the imperiled Egg-mimic Darter *Etheostoma pseudovulatum*

Alloparental care behavior has been documented in several clades of animals, including fishes. Despite the increased energy cost of caring for more offspring, this behavior of raising non-descendent young also has potential benefits, including attraction of mates or reduced egg predation by dilution effects. The Egg-mimic Darter, *Etheostoma pseudovulatum*, is an imperiled darter species restricted to only five tributaries of the Duck river where they occur in rocky pools of small to medium-sized streams. Male Egg-mimic Darters and those of other species of clade *Goneaperca* construct nests under rocks and guard eggs until hatched. Two species from this clade, *E. virgatum* and *E. olmstedii*, exhibit alloparental care; whether this is a common strategy to all members of the clade is not known. Furthermore, the potential benefits of kin-selection and how nest density or male size influences such behaviors have not been tested. We will use microsatellite loci to



obtain genotypes from the eggs in 15 nests from two localities, the guarding males of each nest, and other non-guarding males and females from each site to identify whether: (1) allopaternal care occurs in this species; (2) kin-selection is one benefit of allopaternal care; (3) male size correlates to the proportion of non-descendant eggs in a nest; and (4) distance between nests influences allopaternal care frequency. To date, eggs from 17 nests, the guarding male for each, and 15 other non-guarding males have been collected from one locality. DNA was extracted from non-target individuals from a second location and used as a template to optimize 14 microsatellite locus primers that were variable within the focal taxon. The resulting loci will be used to generate genotypic data for all focal individuals from both localities, which will be subjected to parentage analyses using COLONY (V2.0) to address our objectives.

<sup>1</sup>Austin Peay State University

### **Duncan Elkins<sup>1</sup>**

If you spilled it, will they come? Tracking fish recovery in Flat Creek near Dawsonville, GA

On March 22, 2018, a fish kill was reported in Flat Creek, a tributary of Shoal Creek in the Etowah River system near Dawsonville, Georgia. It was subsequently determined that a discharge from an industrial facility of Ferric Chloride during a rainstorm had lowered the pH in a headwater creek to 1.1-1.8. The pH depression was extensive and resulted in a complete kill of aquatic life throughout the 3.7 miles of Flat Creek. This system is of particular interest because it supported a fish assemblage that included federally threatened Cherokee Darters *Etheostoma scotti*. Although Shoal Creek is a source for recolonization, culverted road crossings have the potential to be barriers to aquatic organism passage at several points. Staff of the UGA River Basin Center have begun sampling Flat Creek and will track the recovery of the fish assemblage, particularly with respect to any differences above and below the largest presumed barrier. Our samples through September 2018 have documented very few fish in the upstream reaches with higher species counts only in the lowest section.

<sup>1</sup>The University of Georgia, River Basin Center

### **Robert Ellwanger<sup>1</sup>, Carol Johnston<sup>1</sup>, and Alexis Janosik<sup>2</sup>**

Potential decline of Bluestripe Shiner *Cyprinella callitaenia* from hybridization and environmental factors

Bluestripe Shiner populations have been steadily declining across its range in Alabama since the species was described in 1957. There is evidence that this decline has been greater in some Alabama streams along the Chattahoochee river, than in other areas of its native range in Georgia and Florida. To better understand this decline and determine potential catalysts, we have collected both environmental DNA samples and physical specimens

from across the species range. From these, a current distribution will be established, and genetic samples will be analyzed to determine the genetic integrity of several populations. The distribution and genetic information will be evaluated alongside historic flow and land use data to determine a potential catalyst for differences in population numbers and genetic integrity within Alabama streams compared to populations throughout their range. This analysis could offer insight into the effects of flow alteration and land use change on the genetic integrity and distribution of fluvial species, and aid in the management and protection of sensitive aquatic communities.

<sup>1</sup>The University of Auburn, School of Fisheries and Aquaculture

<sup>2</sup>The University of West Florida, Department of Biology

**Rachel Finigan<sup>1</sup>, Michelle Ruigrok<sup>1</sup>, Thomas Martin<sup>1</sup>, Michael LaVoie<sup>2</sup>, Luke Etchinson<sup>3</sup>, and Rachael Hoch<sup>3</sup>**

Feasibility study for restoration of freshwater mussels *Villosa iris* and *Lampsilis fasciola* into the upper Oconaluftee River in North Carolina

Anthropogenic influences have contributed to the decline of many freshwater mussel species, with many listed as endangered, threatened, or of special concern. Suitable water quality, proper substrate habitat, and the presence of fish hosts are needed for mussel survival. Freshwater mussels have not previously been recorded in the Oconaluftee River in North Carolina upstream of the Bryson Dam despite suitable water quality, proper fish hosts being present, and the historically rich mussel fauna of the Little Tennessee River drainage. Two species of freshwater mussel, *Lampsilis fasciola* and *Villosa iris*, were placed in enclosures at three locations along the Oconaluftee River. Growth and survival were monitored over the course of a growing season (March through October) to determine if the Oconaluftee River is suitable for restoration of these species. Throughout the experiment, two *L. fasciola* died, all *V. iris* survived, and both species grew at all three sites. Overall, both species flourished, suggesting the Upper Oconaluftee River is an ideal location for introduction of *L. fasciola* and *V. iris* and the water conditions associated with the river can be used as a reference for future restoration projects. As a secondary study, three tag types (i.e. Hallprint shellfish tags, laser etching, and queen bee tags) were evaluated to determine long term legibility. Hallprint shellfish tags were the only tag to remain readable throughout experiment, closely followed by the queen bee tags, indicating laser tags were the least effective.

<sup>1</sup>Western Carolina University

<sup>2</sup>Eastern Band of Cherokee Indians

<sup>3</sup>North Carolina Wildlife Resources Commission

**Robert Frierberthausen<sup>1</sup>, Carol Johnston<sup>1</sup>, and Daniel Holt<sup>2</sup>**

Physiological and behavioral impacts of acute anthropogenic noise on stream fishes

While the expansion of anthropogenic noise studies in aquatic habitats has produced many conservation-based results for marine organisms, little attention has been paid to the potential impacts on freshwater stream fishes. Recent work showed that Blacktail Shiner (*Cyprinella venusta*), a hearing specialist, exhibited multiple responses to road noise. However, assemblage-wide effects of anthropogenic noise pollution have not been studied. By examining eight metrics of stress on four ecologically and evolutionarily disparate species of stream fishes, this laboratory experiment aimed to describe the potential negative impacts of anthropogenic noise on these understudied organisms. Each species studied represents a unique combination of hearing ability (specialist or generalist) and vertical zonation within the water column (benthic or pelagic). The anthropogenic noise source used throughout this research was an underwater audio recording of a train crossing a stream via a beam bridge. Physiological and behavioral metrics were measured and compared across the presence and absence of noise playback. Noise playback had no effect on blood glucose levels, elicitation of a startle response or preference for quieter habitat within the testing environment, however, the presence of noise produced significant changes in opercular beat frequency, total swim distance, and both chronic and acute swimming velocity. In some metrics, effects of noise were observed in certain species contrary to what was hypothesized based on their historical hearing ability designations. These results demonstrate that predicting physiological or behavioral responses to this type of stressor cannot be accomplished by simply considering hearing ability or water column position. More importantly, we show that anthropogenic noise can disrupt a variety of behavioral and physiological processes and should be considered as an environmental stressor and a driver of habitat degradation to those species affected.

<sup>1</sup>Auburn University, School of Fisheries, Aquaculture and Aquatic Science

<sup>2</sup>Columbus State University, Department of Biology

**Chance Garrett<sup>1</sup>, Ginny Adams<sup>1</sup>, and Reid Adams<sup>1</sup>**

Habitat associations of riffle fishes in an Ozark river having a dynamic gravel bed load

Streams of the Arkansas Ozarks have experienced extensive erosion and gravel intrusion due to changing land use. As a result, modifications to instream habitat have resulted in an increase in transverse and diagonal gravel bars along with associated transient, shallow, low velocity riffles. This study was conducted to determine if variation in riffle habitat quality (depth, velocity, substrate size) affects riffle fish communities. For this study, 37 riffles were sampled across fall and spring in the Kings River, Arkansas using seines and kick-set methods. Fishes were preserved in 10% formalin and identified in the laboratory and standard lengths of benthic fishes were measured. Habitat data were collected at each riffle including velocity, pebble count, depth, width, presence of structure, and water quality. Riffles in the Kings River exhibited a gradient in available habitat with two extremes, one being shallower, slower riffles with smaller substrate (unstable riffles) and the other deeper, faster riffles with larger substrate (stable riffles) (PCA). Unstable riffles shifted or disappeared after large rain events. Benthic species richness was significantly higher in stable riffles during both seasons. In the fall, *Etheostoma juliae* had higher mean relative abundance in stable riffles (42%) relative to unstable riffles (25%). Presence of

water willow, substrate size, and water depth were significantly correlated with relative abundance of multiple species. Additionally, *Etheostoma juliae* was strongly negatively correlated with *Etheostoma caeruleum* during both seasons (Spearman's  $r_s > -0.81$ ;  $p < 0.001$ ). Understanding variation in riffle habitat and how fishes are utilizing riffles is crucial to ensuring restoration efforts provide necessary habitats for fishes throughout their life.

<sup>1</sup>The University of Central Arkansas

**George Gavrielides<sup>1</sup>, Ginny Adams<sup>1</sup>, Reid Adams<sup>1</sup>, and Matt Connolly<sup>2</sup>**

Potential effects of land cover change on fish assemblages in the Eleven Point River basin

The Eleven Point River is a spring-fed, karst-dominated stream flowing through the Salem Plateau of the Ozarks ecoregion in southeast Missouri and northeast Arkansas. Limited research has been conducted on the Arkansas stretch of the river despite growing concerns about the existing and projected expansion of the poultry industry in the watershed. Land cover within the watershed is approximately 69% forest, 30% agriculture, and 1% development. Increased poultry production in the lower watershed may result in increased deforestation, water withdrawal and effluent which may negatively affect fish assemblages. Overall land cover change may also alter channel morphology and water chemistry of the stream. Johnson and Beadles (1977) collected 90 species of fish from 1976-1977 prior to the land cover change. In order to examine changes in fish assemblage, we replicated Johnson and Beadles' sampling method using similar seine dimensions and scope of habitat selection (riffles, runs, pools). NMDS of their historical fish collections will be compared with National Wall-to-Wall Anthropogenic Land Use Trends (NWALT) from 1974-2012 to examine changes in contemporary assemblages. Geomorphology data will be collected at each site to further our examination of physical change in the stream. Water table fluctuation and in-stream habitat alterations due to land use are expected to be the main causes of assemblage changes since the Johnson and Beadles study. However, analyses of future collections will determine how the land cover disturbances within the watershed have affected fish biota.

<sup>1</sup>The University of Central Arkansas, Department of Biology

<sup>2</sup>The University of Central Arkansas, Department of Geography

**Brooke Grubb<sup>1</sup>, John W. Johansen<sup>2</sup>, and Rebecca E. Blanton<sup>1</sup>**

Phylogeography of a small-stream adapted crayfish, *Cambarus pristinus*, from the Cumberland Plateau of Tennessee

Many North American crayfishes are considered imperiled due to habitat loss and fragmentation. Despite this, few phylogeographic studies have been conducted to aid conservation management decisions by assessing the impact of habitat fragmentation, delineating evolutionary significant management units, and identifying dispersal barriers, historical vicariance, and other factors that contribute to geographic structure. *Cambarus*

*pristinus* (Pristine Crayfish) is an imperiled crayfish endemic to the Cumberland Plateau in Tennessee where it occurs at low densities in headwater tributaries and lower order ( $\leq 4^{\text{th}}$  order) mainstem reaches of the Caney Fork and Sequatchie Rivers. Currently, two forms are recognized based on morphology: the nominate form (*C. pristinus*), restricted to the Caney Fork River system and the Sequatchie form (*Cambarus cf. pristinus*), found in the Sequatchie River system and one tributary to Cane Creek (Caney Fork River System). We examined phylogeographic relationships of *C. pristinus* populations to identify if any long-standing isolation among populations or between the forms had occurred by sequencing the mitochondrial cytochrome oxidase subunit I gene (COI) of five individuals from eight localities. Haplotype networks of sequences were constructed in TCS. (V. 1.21) and a phylogeographic tree was created using MEGA7. A total of 10 haplotypes were detected. *C. ambarus pristinus* exhibited low haplotype diversity (1-2 mutations), with at least one haplotype shared among all populations, suggesting that no long-standing isolation among examined populations occurred despite potential barriers to gene flow such as intervening large river habitats and elevational changes associated with the Cumberland Plateau. *Cambarus cf. pristinus* had two unique haplotypes recovered in a separate haplotype network that differed from *C. pristinus* by 14-15 mutational steps. The two forms were recovered as separate well-supported clades suggesting that *Cambarus cf. pristinus* has experienced long-standing isolation from *C. pristinus*, supporting its recognition as a distinct taxon.

<sup>1</sup>Austin Peay State University, Center of Excellence for Field Biology, Clarksville, TN, USA

<sup>2</sup>Tennessee Tech. University, Department of Environmental Science, Cookeville, TN, USA

### **Meredith Hayes Harris<sup>1</sup>**

Captive propagation of a federally endangered species, the Laurel Dace *Chrosomus saylori*

<sup>1</sup>Tennessee Aquarium Conservation Institute

### **Malorie M. Hayes<sup>1,2</sup> and Kyle R. Piller<sup>1</sup>**

The diversification of the Blackbanded Darter *Percina nigrofasciata* across the southeast

The Blackbanded Darter, *Percina nigrofasciata*, has historically been considered a single species across its broad range in the southeastern United States. Its distribution spans multiple recognized biogeographic barriers, yet an understanding of the diversity of the group has been lacking. Two putative species recently have been elevated from within *P. nigrofasciata*: *P. crypta* and *P. westfalli*; however, the validity of *P. crypta* has been questioned and no discussion of the distribution of *P. westfalli* has been proposed. This study includes a broad sampling of *P. nigrofasciata sensu lato* across the southeastern United States and determines the delineation of the three hypothesized species based on mitochondrial and nuclear markers. Using these molecular markers, we clarify the

distribution of *P. nigrofasciata* and *P. westfalli*. Furthermore, we find that *P. crypta* may not be a genetically distinct population of *P. westfalli*, but that there is ancestral hybridization between *P. nigrofasciata* and *P. westfalli* in the panhandle of Florida between Mobile Bay and the Apalachicola River. This study highlights regions where finer-scale studies of population dynamics should be focused and also contributes to the expanding evidence of unique biogeographic patterns occurring in the lower Apalachicola River region.

<sup>1</sup>Southeastern Louisiana University

<sup>2</sup>Auburn University

**Kyler Hecke**<sup>1</sup> and Brian J. Alford<sup>1</sup>

Ecological niche-modeling of the Sickle Darter *Percina williamsi* across multiple scales

The Sickle Darter *Percina williamsi* is a species of fish endemic to the upper Tennessee River drainage in eastern Tennessee and southwestern Virginia. Because of its narrow range and presumed decline in occupied sites over the last half century, it has been listed as threatened by the states of Tennessee and Virginia and is being petitioned for federal listing under the Endanger Species Act. The species' current distribution has not been assessed throughout its historic range. Microhabitat utilization, historic occurrence, and diet are known, but a new study was warranted to determine its current distribution, occupancy status, and ecological niche. During 2016, electrofishing with seining and snorkel sampling occurred for the Sickle Darter at historically occupied sites and previously un-sampled sites within its range. A total of 144 Sickle Darters were observed at 17 different sites. Niche-modeling was used to estimate the probability of stream segment occupation by the Sickle Darter in three primary drainages within its range: Emory River Little River, and Middle Fork Holston River. These data will be useful for determining future federal listing status and informing monitoring activities and conservation decisions for this species.

<sup>1</sup>University of Tennessee Institute of Agriculture, Department of Forestry, Wildlife and Fisheries, 274 Ellington Plant Sciences Bldg., Knoxville, TN 37996, USA

**Joshua Hubbell**<sup>1</sup> and Jake Schaefer<sup>2</sup>

Evidence for habitat filtering as a basis for the coexistence of three darters (*Etheostoma*) in a Gulf coastal plain drainage

Patterns of occurrence and co-occurrence among many North American freshwater fishes are poorly understood. In headwater systems, where abiotic forces drive patterns of occupancy and abundance, it is feasible that closely related species may be able to co-occur due to the harshness of local environmental conditions. We examined patterns of occurrence and co-occurrence among three darters, the Yazoo darter (*Etheostoma raneyi*), the goldstripe darter (*Etheostoma parvipinne*) and the redspot darter (*Etheostoma artesia*),

within the Little Tallahatchie River system. We used spatial replicates as a substitute for temporal sampling, and incorporated current (2015-2016) and historical (1999-2003) data within our analyses. Single-species and two-species occupancy models were used to examine patterns of occurrence and co-occurrence. Range models were built to predict and test the significance of the frequency of coexistence among species pairs, against the number of observed stream reaches from which species pairs were known to coexist. Darters were habitat-limited across multiple spatial scales. Habitat filtering may allow for coexistence among darter pairs, with groundwater input, and depth playing the largest roles in regulating patterns of co-occurrence.

<sup>1</sup>The University of Southern Mississippi, Department of Biological Sciences

<sup>2</sup>The University of Southern Mississippi, School of Biological, Environmental and Earth Sciences

**Karlie Jeffers<sup>1</sup>, Shawna Mitchell<sup>2</sup>, and Brian Alford<sup>1</sup>**

Using otoliths to age a population of Tennessee Dace in southeast Tennessee

There is currently ongoing research into the life history of Tennessee Dace (*Chrosomus tennesseensis*) in Southeast Tennessee. The Tennessee Dace is closely related to the federally endangered Laurel Dace (*Chrosomus saylori*). The Laurel Dace is historically known from only seven streams, but current field surveys indicate that there are only two streams that they are thriving in. Little is known about the life history of the Laurel Dace and its current status prevents the collection of some data needed to compile a complete life history study. The Tennessee Dace was chosen as a surrogate for the study as the species has a close relation to the Laurel Dace. The study will be collecting twenty Tennessee Dace for eighteen months. Currently five months of collection have occurred from May 2018- September 2018. Each month, otoliths from five individuals of different size classes are being used to determine age classes of the Tennessee Dace population. The otoliths are extracted by cutting the head to the base of the pectoral fin and then cutting the head in half. Using dissection probes and a dissecting microscope, the otoliths are extracted and mounted to the slides. After sanding down the otolith, two observers age each otolith separately. Tennessee Dace otolith ages have varied from one to five years old. Length-frequency graphs indicate that Tennessee Dace have four age classes. More otolith extractions and sample collections will allow for more age classes to be confirmed and knowing the timeline of growth and development of the Tennessee Dace will allow for better management practices to be created and implemented for the Laurel Dace.

<sup>1</sup>The University of Tennessee, Department of Forestry, Wildlife and Fisheries

<sup>2</sup>Tennessee Aquarium Conservation Institute

**Kenny Jones<sup>1</sup>, Michael Sandel<sup>1</sup>, and Bernard Kuhajda<sup>2</sup>**

Using genomics and eDNA methods to assess the conservation and future management of the endemic Coal Darter *Percina brevicauda*

The Coal darter *Percina brevicauda* (Suttkus et al 1994) is endemic to 3 watersheds in the upper eastern part of the Mobile basin in Alabama. It's restricted to the Cahaba, Coosa, and Locust Fork rivers and populations of *P. brevicauda* have been declining recently (Warren et.al 1997, 2000). The species stronghold is in the Cahaba river, and collections of *P. brevicauda* show that they're more commonly found in upland habitats north of Centreville, AL, an area that's undergoing increased urbanization and environmental change (Suttkus et al 1994). *P. brevicauda* inhabits a range of 64 miles in the Locust Fork mainstem, and is most likely extirpated from the Black Warrior at Tuscaloosa (Boschung and Mayden 2004). In the Locust Fork, problems such as river impediments, strip mine runoff, sedimentation, and toxic contamination are factors that impede aquatic fauna within the watershed (Shepard et al 2002). The most eastern population of *P. brevicauda* is found in a stream named Hatchet Creek, which supports the only extant population of Coal darters in the Coosa River watershed (Boschung and Mayden 2004). Our aims are to investigate and understand the endemism, population genetics, and conservation of the Coal darter. To do so, we're applying population genetics tools, whole genome sequencing, and phylogenetics to the subgenus in which the Coal darter belongs, *Cottogaster*. Our environmental DNA (eDNA) methodology will test for presence of this species in habitats of the Cahaba, Locust Fork, and Coosa Rivers by attempting to amplify DNA isolated from water samples with the COI (Cytochrome Oxidase Subunit I) gene in PCR based on the primers ability to serve as a standard for metabarcoding (Andújar et al 2018). By doing this research, we hope to inform federal and state agencies about the Coal darter and its status so that goals and plans can be made to protect and conserve this endemic species.

<sup>1</sup>The University of West Alabama, Department of Biological and Environmental Sciences

<sup>2</sup>Tennessee Aquarium Conservation Institute

**Valerie J. Jones<sup>1</sup>, Hayden T. Mattingly<sup>2</sup>, Samantha A. Allen<sup>2</sup>, and Jeffery W. Simmons<sup>3</sup>**

Distribution and abundance of the Bluemask Darter *Etheostoma akatulo* in the Collins River during summer 2018

*Etheostoma akatulo* is a federally protected stream fish endemic to the Caney Fork River (CFR) system in Tennessee. The species inhabits several CFR streams, with the Collins River representing the most robust population. We studied the distribution and abundance of *E. akatulo* in relation to stream habitat in the Collins River to inform reintroduction efforts in the Calfkiller River, another CFR stream where the species has been extirpated. The Collins River was divided into 46 segments using GIS and 21 of those segments were sampled by snorkeling during July-September 2018. Two 160-m<sup>2</sup> plots per segment were selected using criteria related to stream habitat features. A total of 144 *E. akatulo* individuals (124 adults and 20 juveniles) were observed during our survey, with 64% of plots being occupied by at least one individual. We also observed the species further downstream in the Collins River than previously documented. Our results suggest that *E.*



*akatulo* continues to maintain a strong presence in the Collins River. Next steps include identifying segments of the Calfkiller River that contain habitat features most likely to support reintroduction of the species.

<sup>1</sup>Tennessee Tech University, Department of Biology, Cookeville, TN 38505

<sup>2</sup>Tennessee Tech University, School of Environmental Studies, Cookeville, TN 38505

<sup>3</sup>Tennessee Valley Authority, Chattanooga, TN 37402

**Emily Judson<sup>1</sup>**, Yoichiro Kanno<sup>2</sup>, Matthew Walker<sup>3</sup>, Tanya Darden<sup>3</sup>, and Brandon Peoples<sup>1</sup>

Modeling distribution of endemic Bartram's bass in the Savannah River basin

Bartram's Bass *Micropterus sp. cf. cataractae* is an undescribed species of Shoal Bass endemic to the Savannah River basin of South Carolina and Georgia. Bartram's Bass is threatened by habitat alteration and hybridization with invasive Alabama bass (*M. henshalli*) and other co-occurring congeners. Determining the relative importance of abiotic factors and dispersal from reservoirs for predicting occurrence of pure individuals is critical for conserving Bartram's Bass. From March to November of 2017 and 2018, individuals were collected from 160 sites across the upper Savannah River basin. Sites represented a gradient of key abiotic variables – watershed- and riparian-scale land use types, ecoregions, stream gradient, and elevation. Genetic analysis of 241 individuals from 50 sites revealed Bartram's Bass were present at 33 sites, and hybrids were present at 21 sites. Conditional inference trees were used to predict the variables that drive Bartram's Bass distribution. Forested land cover at the watershed scale was the most significant predictor of Bartram's Bass presence ( $p=0.0236$ ). Pure individuals preferred sites of greater than 68% forested cover ( $p<0.001$ ). In less forested watersheds, there was higher probability of finding pure Bartram's Bass at sites with greater slopes ( $p<0.001$ ), or increased distance from reservoirs ( $p=0.005$ ). Even when forested land cover was greater than 68%, sites closer to reservoirs were less likely to harbor pure fish ( $p=0.022$ ). These results reflect the tradeoff between land cover and dispersal for facilitating spread and hybridization of invasive fishes.

<sup>1</sup>Clemson University, Department of Forestry and Environmental Conservation

<sup>2</sup>Colorado State University, Department of Fish, Wildlife, and Conservation Biology

<sup>3</sup>Marine Resources Research Institute, South Carolina Department of Natural Resources, Charleston, South Carolina

**Jerry W. Kattawar III<sup>1</sup>**, Kyle R. Piller<sup>1</sup>, Dan J. MacGuigan<sup>2</sup>, Richard C. Harrington<sup>2</sup>, and Thomas J. Near<sup>3</sup>

Phylogenetics of *Stigmacerca*: evolutionary resolution of the spottail darters

Darters (Percidae: Etheostomatinae) are one of the most diverse groups of fresh water fishes in North America with over 250 described species. The spottail darters (sub-genus *Stigmacerca*) are a group of 11 recognized species that are characterized by a reproductive

mode that includes egg-clustering and male nest guarding. Previous molecular phylogenies using concatenated nuclear markers as well as mtDNA, have shown some inconsistent results leaving the clade's evolutionary history unresolved and in need of further examination. The development of next generation sequencing technologies has allowed for thousands to hundreds of thousands of loci to be used to infer phylogenetic relationships. Here we take advantage of this technology, and use ddRADseq data to build a phylogeny of the 11 recognized species, and multiple populations, of *Stigmacerca*. The data were aligned using iPyrad and analyzed using a maximum likelihood approach in IQtree. The relationships of previously unresolved nodes of the *Stigmacerca* phylogeny, including the placement of *E. forbesi*, *E. olivaceum*, and the undescribed *E. cf. oophylax* from the Clarks River, Kentucky and Tennessee, are now resolved and highly supported. Our results highlight the effectiveness of ddRADseq data and its ability to tease apart the evolutionary relationships of closely related congeners within an extremely diverse family of fishes.

<sup>1</sup>Department of Biological Sciences, Southeastern Louisiana University, Hammond LA 70402

<sup>2</sup>Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT 06520

<sup>3</sup>Department of Ecology and Evolutionary Biology and Peabody Museum of Natural History, Yale University, New Haven CT 06520

**Lauren Kelley**<sup>1</sup>, Kayla Key<sup>1</sup>, and Amanda Rosenberger<sup>2</sup>

Life history strategies of freshwater mussels along longitudinal gradients in the Meramec River, Missouri

Life history theory provides insight to the adaptive significance of an organism's response to environmental pressures. Understanding the life history strategies within mussel communities can therefore help inform conservation and management actions for vulnerable assemblages. Prior work indicates that dominant life histories of mussel assemblages change with river size, between large and small rivers, and within rivers, from headwaters to downstream. Mid-sized streams act as a transitional zone of mussel life history dynamics between species found in small and large rivers. Our goal in this study was to examine upstream to downstream patterns of mussel life histories in the Meramec River drainage in Missouri, a high-priority conservation area. Using surveys from the Missouri Department of Conservation database and Haag's 2012 descriptions of life history strategies, we investigated proportional changes in life history strategies of freshwater mussels longitudinally in the Meramec River in Missouri, from headwaters to downstream. Our results can help to inform conservation of mussels by increasing the understanding of mussel species' habitat selection, essential information for successful propagation and reintroduction efforts.

<sup>1</sup>Tennessee Technological University, Tennessee Cooperative Fisheries Research Unit, Department of Biology, Cookeville, TN

<sup>2</sup>U. S. Geological Survey, Tennessee Cooperative Fisheries Research Unit, Department of Biology, Cookeville, TN

**Jennifer Main**<sup>1</sup>, Ginny Adams<sup>1</sup>, and Reid Adams<sup>1</sup>

Fish assemblage dynamics over a 30-year period in the Strawberry River in relation to land use

The Strawberry River watershed (SRW) is a highly speciose river in Arkansas having 107 documented fishes. Historical SRW fish assemblage data from Robison (1974 and 1976) and Hilburn (1986) were compared to contemporary data (2017-2018) to determine if changes in fish communities have occurred across 16 sites. SRW contains two distinct land use types: forest (64%) and pasture (33%). Between 1982 and 2012, a 2.1% decrease in percent forest and a 1.3% increase in percent pasture occurred (NWALT 1982 and 2012). A total of 5,285 individuals (65 species) were collected from 1974-1986, and a total of 7,685 individuals (63 species) were collected during 2017- 2018 across the 16 sites. An ordination, NMDS based on relative abundances, revealed contemporary collections were nested within historic collections, and dispersion of the two groups of sites was not significantly different (perMANOVA  $p = 0.06$ ). Stability (0.20-0.68) and persistence (0.43-0.83) were highly variable in tributary catchments compared to mainstem. Variation in catchment size and pasture land use may be correlated with stability and persistence in tributary catchments. Despite little change in catchment land use over the study period, persistent stress from pasture and associated perturbations (e.g., stream bank degradation and sedimentation) may have impacted fish assemblages. By monitoring fish assemblages within the SRW, impacts of additional anthropogenic perturbations on fish assemblages can be better understood and provide a framework for understanding how fishes in the Ozarks respond to disturbance.

<sup>1</sup>University of Central Arkansas, Department of Biology

**Zach Martin**<sup>1</sup> and Paul Angermeier<sup>1,2</sup>

Testing effects of embeddedness on nest-site choice and oviposition by a cavity-nesting stream fish

Behaviors in many stream fishes tie their reproductive success to unembedded, stable substrates. Excess sedimentation is often implicated in fish extirpations and assumed to negatively affect fitness. For example, embeddedness may limit reproductive success of cavity-nesters by reducing available nesting space underneath rocks. However, few studies examine how fine sediment affects behavioral aspects of individual fitness and spawning success. We designed two laboratory experiments, using cavity-nesting fantail darters, to test effects of embeddedness on nest-rock choice, oviposition, and clutch size. We placed spawning pairs in Living Stream tanks for five-day trials with sand as a bottom substrate and 6-in x 6-in ceramic tiles as potential nest substrates. Four treatments of embeddedness (in increasing order) were represented: tile propped (~20mm on one side) with cavity

provided, tile flat on sand with cavity provided, tile flat with no cavity, and tile slightly covered in sand. One experiment presented spawning pairs (n=120; 30 per treatment) with one tile, one treatment; oviposition (0/1) and clutch size were responses. The second experiment (n=90) presented spawners with four tiles, one for each treatment, simultaneously; nest-rock choice, oviposition, and clutch size were responses. Overall, 52 fantail pairs spawned, including 15 in experiment one and 38 in experiment two. Spawners from both experiments oviposited on tiles of all but the most embedded treatment, and most commonly on tiles flat on sand with a cavity provided. Four spawning pairs excavated cavities and oviposited on tiles in the second-to-most embedded condition. Spawners also oviposited on tank walls; in experiment one, these instances coincided with the two most embedded treatments. Our observations suggest that fantail darters have limited ability to spawn in habitats smothered by fine sediments. Given that fantails are among the most sediment-tolerant darter species, we expect reproductive success of many other darters to be impaired by severe embeddedness.

<sup>1</sup>Department of Fish and Wildlife Conservation, Virginia Polytechnic Institute and State University, Blacksburg, Virginia 24061

<sup>2</sup>U.S. Geological Survey, Virginia Cooperative Fish and Wildlife Research Unit, Virginia Polytechnic Institute and State University, Blacksburg, Virginia 24061

**Katie E. McBaine**<sup>1</sup>, Paul L. Angermeier<sup>1,2</sup>, and Eric M. Hallerman<sup>1</sup>

Preliminary assessment of within-stream movement patterns of candy darter in Virginia

We examined movement patterns of Candy Darter *Etheostoma osburni*, an imperiled darter restricted to streams with cool, high-velocity, silt-free riffles in the New River drainage. Our analysis focused on potential effects of: a) habitat availability and distribution, and b) sex on the distance and direction moved. We used mark-recapture methods, based on visual implant elastomer tags, to characterize movement among suitable and unsuitable habitat patches in two streams differing in width and in spatial distribution of patches; width is a correlate of patch size and inter-patch distance. Preliminary results are based on 59 recaptures (21% of 286 marked fish) in Stony Creek and 38 recaptures (19% of 200 marked fish) in Laurel Creek from 2016 to 2018. Eight individuals were recaptured twice in Stony Creek (two marks); one individual was recaptured twice in Laurel Creek. Additional individuals were recaptured upstream of designated mark-recapture sites (Laurel Creek  $n = 6$ ; Stony Creek  $n = 1$ ). Most detected movements were upstream for both streams. However, most recaptured individuals in Stony Creek were found in the same riffle where they were initially captured, whereas most recaptured individuals in Laurel Creek moved at least one riffle from initial capture. Suitable patch size (i.e., riffle area), as well as overall habitat availability, was greater for Stony Creek than for Laurel Creek. These differences in habitat configuration may explain the tendency for Candy Darters to move less in Stony Creek. Both sexes of Candy Darter exhibited movements  $> 500$  m. In future work, molecular variation at eight microsatellite loci will be examined to characterize movement patterns of individual darters, including young-of-year and juveniles. Comparisons between molecular and mark-recapture results will help us assess effectiveness of mark-

recapture methods, identify the spatial extent of populations, and understand how individual movements contribute to demographic connectivity.

<sup>1</sup>Department of Fish and Wildlife Conservation, Virginia Tech, Blacksburg, VA

<sup>2</sup>U.S. Geological Survey, Virginia Cooperative Fish and Wildlife Research Unit

**Shawna M. Mitchell<sup>1</sup>** and Bernie R. Kuhajda<sup>1</sup>

Studying life history of the Tennessee Dace *Chrosomus tennesseensis* to determine the best conservation practices for the endangered Laurel Dace *Chrosomus saylori*

<sup>1</sup>Tennessee Aquarium Conservation Institute

**Alexis M. Mross<sup>1</sup>** and Brook L. Fluker<sup>1</sup>

Assessing species boundaries among clades of the Least Darter *Etheostoma microperca*, using multilocus species delimitation methods and morphological data

The Least Darter occurs in tributaries to the Hudson Bay, Great Lakes, and upper Mississippi River drainages, with additional disjunct populations in the Ozarks. Previous morphological and molecular studies revealed that Ozark populations of the Least Darter are differentiated from northern populations, yet the taxonomic status of the Ozark populations remains undetermined. This project examines morphological variation of Ozark populations in relation to northern populations with the goal of elucidating the taxonomic status of distinct Least Darter populations in the Illinois River Drainage in Arkansas. In combination with morphological data, DNA sequence data from multiple single-copy nuclear genes and one mitochondrial gene will be used with species delimitation and species tree methods to evaluate hypotheses of species distinctiveness among populations of the Least Darter. Results of this study will provide information about the taxonomic status of the Least Darter in Arkansas, which is currently considered a Species of Greatest Conservation Need.

<sup>1</sup>Arkansas State University, Department of Biological Sciences

**Robert T. R. Paine<sup>1</sup>**, Mark W. Rogers<sup>2</sup>, and Carla Hurt<sup>3</sup>

Environmental DNA (eDNA) tracking of the invasive silver carp *Hypophthalmichthys molitrix* in the Duck River, Tennessee

The Silver Carp (*Hypophthalmichthys molitrix*) is an invasive species to many rivers in the United States and poses a threat to native biodiversity. Since its escape from aquaculture ponds in the 1970s, tracking the continued dispersal throughout North American waterways has posed a major problem for resource managers. Traditional methods, like seining and electrofishing, are commonly used to monitor Silver Carp with much success. However, traditional methods can be invasive to non-target organisms in the same system.

Environmental DNA (eDNA) is a non-invasive tool that is sensitive for tracking the leading edge of invasive species. In this study, we tracked the dispersal of Silver Carp in the Duck River, the most biologically diverse river in the United States. Water samples were collected from fourteen sites in winter 2017, and ten sites in summer 2018. Silver carp signals were detected in 9 of 14 sites from winter 2017 below Columbia Dam (non-functioning), the putative barrier to further upstream dispersal. However, traditional methods detected Silver carp upstream of Columbia Dam in August 2018, indicating that the leading edge has shifted. Further eDNA sampling from summer 2018 is currently being conducted to help re-assess the leading edge. Environmental DNA sampling can be used as an early warning system to monitor the dispersal and presence of invasive species, and thus, allow managers to develop and implement strategies to prevent further dispersal.

<sup>1</sup>School of Environmental Sciences, Tennessee Technological University, 200 W. 10th Street, Cookeville, TN 38505, United States

<sup>2</sup>U.S. Geological Survey, Tennessee Cooperative Fishery Research Unit, Tennessee Technological University, Box 5114, Cookeville, TN 38505, United States

<sup>3</sup>Department of Biology, Tennessee Technological University, 1100 N. Dixie Ave, Box 5063, Cookeville, TN 38505, United States

**Michael J. Pinder**<sup>1</sup>, Paul E. Bugas Jr.<sup>1</sup>, Donald J. Orth<sup>2</sup>, Corbin D. Hilling<sup>2</sup>, Valerie A. Kells<sup>3</sup>, Derek A. Wheaton<sup>4</sup>

A field guide to the freshwater fishes of Virginia

A Field Guide to the Freshwater Fishes of Virginia will fulfill a longstanding need in nature education. Central and Southern Appalachians are unrivaled in the U.S. for aquatic species diversity, which makes this regional field guide extremely important. Most authoritative information is contained in an extensive (6.6 pound) reference or online databases that are not useful for the beginning naturalist nor a field biologist. Furthermore, biologists worldwide are clamoring for more natural history skills to prepare young biologists for future challenges. We are creating a 5 x 7.5-inch, field guide on water-resistant paper. The book will teach the beginner how to identify fish families and reliably identify Virginia fish species with field characteristics. The taxonomy of family and common names will follow recent authoritative references. The field guide will include introductory chapters on how to use the field guide, fish diversity, river drainages, and freshwater habitats of Virginia. It will also contain brief sections on how to observe fish in the wild and captivity, and essential messages of fish conservation. Distribution maps will be based on recent distributional databases. Color illustrations will be incorporated to provide easy identification. Select illustrations will provide most reliable diagnostic characteristics (e.g., snout shape, pigment patterns, mouth morphology) for field identifications.

<sup>1</sup>Virginia Department of Game and Inland Fisheries

<sup>2</sup>Virginia Tech University

<sup>3</sup>Val Kells Marine Science Illustration

<sup>4</sup>Conservation Fisheries, Inc.

**Amanda K. Pinion<sup>1</sup>**, Daemin Kim<sup>2</sup>, and Kevin W. Conway<sup>3</sup>

Phylogeography of the Sand Shiner *Notropis stramineus* (Teleostei: Cyprinidae)

*Notropis stramineus* (Cope, 1865), the Sand shiner, is a small minnow that is a likely candidate for harboring cryptic diversity due in part to an expansive range. It is distributed across much of the North American continent to the east of the Continental Divide, from northern Mexico (Rio San Juan and Rio Salado) to southern Canada (upper St. Lawrence River to the east and the Red-Assiniboine River system to the west). This range spans regions commonly recognized as phylogeographic barriers. Despite early taxonomic work on the Sand shiner, including the recognition of two subspecies (*N. s. stramineus* and *N. s. missuriensis*), it continues to be recognized as a single widespread species. To test the hypothesis that the widespread *N. stramineus* represents a single species, we gathered one mitochondrial gene (*Cytb*) and two nuclear loci (*S7* and *RAG1*) representing the breadth of the range. Preliminary analysis of this data suggests that *N. stramineus* represents several genetically distinct and geographically isolated lineages. Additionally, the current subspecies designations may not accurately represent the true evolutionary history of this species complex.

<sup>1</sup>Department of Wildlife and Fisheries Sciences, Texas A&M University, College Station, TX 77845, USA

<sup>2</sup>Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT 06511, USA

<sup>3</sup>Department of Wildlife and Fisheries Sciences and Biodiversity Research and Teaching Collections, Texas A&M University, College Station, TX 77845, USA

**Worth Pugh<sup>1</sup>**, Julia Wood<sup>1</sup>, and Phillip Harris<sup>1</sup>

Shining a light on a treasure of natural history: modernization and digitization of the geological survey of Alabama Ichthyology Collection

Natural history collections have served as the foundation for the studies of ecology, evolutionary biology, systematics and conservation. Despite the importance of these collections many robust examples remain largely hidden due to lack of publicly available electronic data. The Geological Survey of Alabama Ichthyology Collection was created in the late 1970s as part of the enactment of the GSA's state-wide biological inventory assessments. In 2014, the GSA began to turn over their holdings to the University of Alabama Ichthyology Collection as part of an acquisition funded by the NSF Collections in Support of Biological Research program. Our goals are to incorporate this collection into the UAIC and then make all associated data available online (i.e., GBIF, VertNet, iDigBio). Thus far, we have cataloged >20,000 lots from the GSA collection and estimate that we are ~85% finished assimilating all lots. Preliminary results of the project show strong numbers of a variety of freshwater taxa from nearly every major tributary in the

state of Alabama as well as parts of Florida, Georgia, Mississippi, and Tennessee with shared watersheds. While the sheer volume of specimens is astounding and likely fills many gaps in geographic distribution, the true significance of this collection lies in the data it contains which were collected using standardized survey methods and includes environmental data across extensive spatial and temporal scales (1979-2010s). Future studies utilizing the GSA collection could examine a variety of research topics related to shifts in fish abundance, biomass and diversity in response to land-use change, water-quality and climate change.

<sup>1</sup>The University of Alabama, Department of Biological Sciences

**Calvin Rezac<sup>1</sup>**, Ginny Adams<sup>1</sup>, Reid Adams<sup>1</sup>, and Matt Connelly<sup>1</sup>

Temporal variation of fish assemblages in the Spring River, Arkansas, in relation to land-use change and geomorphology

The Spring River, located in the Ozark Highlands of northern Arkansas, is a spring fed system supported by the 7th largest spring in the United States (Mammoth Spring). The constant flow makes the Spring River one of the most dependable and important recreational rivers in Arkansas. With increasing residential and recreational development since the 1970's, it is critical to evaluate the anthropogenic influences in the watershed. In addition, legacy effects of timber clearing in the Ozark Region during the past century also continues to threaten stream channel stability through an influx of gravel substrate. A lack of data concerning Species of Greatest Conservation Need and baseline stream habitat parameters prompted a need for further study. We compared historical fish surveys (1978-1980) to contemporary fish assemblages (2018). We also performed geomorphic stream surveys and analyzed land-use change using ArcGIS. In 2018 we collected 6,863 individual fishes representing 43 species across 10 sites compared to 5,561 individuals and 43 species collected historically. Nonmetric multidimensional scaling (NMDS) was used to compare assemblage composition between time periods. Stability and persistence were calculated, and nine of the ten site assemblages were considered to be highly persistent (>0.6). Preliminary findings indicate species composition of the historical surveys remain similar to current surveys. Future fish and geomorphic surveys will help to improve understanding of the entire drainage.

<sup>1</sup>The University of Central Arkansas, Department of Biology

**Michelle S. Ruigrock<sup>1</sup>**, Rachael Finigan<sup>1</sup>, Luke Etchison<sup>2</sup>, Rachael Hoch<sup>2</sup>, Michael J. LaVoie<sup>3</sup>, and Thomas Martin<sup>1</sup>

In-situ feasibility study of freshwater mussel reintroduction: survival and growth of the Slippershell *Alasmidonta viridis* in the upper Oconaluftee River, NC (Swain Co.)

North American freshwater mussels are an imperiled group of organisms, with 29 of the 102 species in the Tennessee River basin listed as federally endangered or threatened, and



another 11 believed to be extinct (Fraley 2002). The Slippershell mussel (*Alasmidonta viridis*) has a widespread distribution but is protected as an endangered species in North Carolina. We monitored survival and growth of juvenile *A. viridis* in enclosures placed in the upper Oconaluftee River near Cherokee, NC to determine if the species may be successfully reintroduced on Eastern Band of Cherokee Indians tribal land. We also compared two enclosure designs, concrete enclosures modified from a design originally described by Chris Barnhart, and mesh enclosures that allow access to the substrate, modified from a design used by Rachael Hoch. Timed snorkel surveys were also conducted to confirm the presence of the appropriate fish host, Mottled Sculpin (*Cottus bairdii*). Between March and September of 2018, *Alasmidonta viridis* experienced significant mortality at all sites and in both enclosure designs. There was also no evidence of growth among survivors. *Alasmidonta viridis* may be sensitive to handling, as the cohort of mussels used in this study experienced increased mortality after tagging in captivity and prior to the experiment.

<sup>1</sup>Department of Biology, Western Carolina University, Cullowhee, NC

<sup>2</sup>Division of Inland Fisheries, NC Wildlife Resources Commission, Marion, NC

<sup>3</sup>Department of Natural Resources, Eastern Band of Cherokee Indians, Cherokee, NC

## **Michael Sandel<sup>1</sup>**

### Phylogenomic Interrelationships of the Southernmost Sculpins (Perciformes: Uranidea)

The genus *Uranidea* includes freshwater sculpins endemic to North America, previously considered congeneric with Eurasian sculpins of genus *Cottus*. Taxonomic resolution of species limits within *Uranidea* has been impeded by plesiomorphic (homoplastic) morphology, which is specifically evident among species of the southeastern United States. Within this region, the Mobile River basin is renowned for a relatively high proportion of freshwater endemic species, to include molluscs, crustaceans, amphibians, and teleost fishes. The genus *Uranidea* is currently represented by three species in the Mobile River basin, but previous studies have provided insufficient resolution to address taxonomic diversity among all populations. We analyzed single nucleotide polymorphisms (SNPs), mtDNA barcodes, and complete mitochondrial genomes to assess interspecific relationships among described and undescribed sculpins of the Mobile River Basin. Results reveal the Mobile River Basin sculpins to comprise a paraphyletic assemblage, which suggests multiple colonization events have occurred involving diverse ancestral populations. Concordant phylogenetic patterns inferred from nuclear and mitochondrial genomes provides support for an additional three sculpin species from the Mobile River Basin. Two of the new species occupy the uppermost and lowermost reaches of the Tombigbee River, and a third species occupies the Alabama River. Two new species that occupy the Tombigbee River basin are geographically restricted to specific geological formations, including the Tallahatta Red Hills and the Cumberland Plateau. This information will assist conservation agencies with prioritization of restoration efforts

within strategic habitat units. Results also provide a roadmap for reappraisal of “cryptic” morphological variation within and among sculpins occupying the Mobile River Basin.

<sup>1</sup>The University of West Alabama, Department of Biological and Environmental Sciences

**Annie E. Savage<sup>1</sup>**, Jennifer C. Taylor<sup>1</sup>, Kari M. Harris<sup>1</sup>, and Brook L. Fluker<sup>1</sup>

Project Macroinvert: bringing mayfly (Ephemeroptera) collections out of the dark at Arkansas State University

The Arkansas State University Museum of Zoology (ASUMZ) Aquatic Macroinvertebrate collection at the Arkansas Center for Biodiversity Collections (ACBC) houses approximately 130,000 specimens (17,000 lots) collected by George L. Harp and his students from the early 1970s to his retirement in 1999. Since then, the collection has been stored and not well curated. In fall of 2016 two undergraduate honors students started Project Macroinvert with the task of restoring, databasing, and georeferencing the collection. As a part of Project Macroinvert, field notebooks containing the only record of specimen data were imaged and specimen data were digitally databased and georeferenced. Currently, specimens are being unpacked from storage, inventoried, relabeled, and reorganized in new containers. This project focuses on ASUMZ Mayfly collection data that may be of particular interest to aquatic biologists in Arkansas and the southeastern United States. Specifically, we map and describe distributional data of ASUMZ Mayfly collections, which may serve as important baseline data for contemporary stream assessment studies utilizing Index of Biotic Integrity (IBI) or EPT (Ephemeroptera, Plecoptera, Trichoptera) indices within the footprint of our collection's holdings.

<sup>1</sup>Arkansas State University, Department of Biological Sciences

**Jake Schaefer<sup>1</sup>**, Joshua Hubbell<sup>1</sup>, and Brian Kreiser<sup>1</sup>

Population genomics of two headwater specialist darters in the Yazoo River basin

Habitat fragmentation and changes to natural flow regimes are ongoing threats to aquatic biodiversity. The southeastern US is no exception with ongoing fragmentation isolating smaller populations in lower quality habitat resulting in reduced gene flow and diversity. The upper Yazoo River drainage in northern Mississippi is home to the endemic Yazoo Darter (*Etheostoma raneyi*) and the more broadly distributed Goldstripe Darter (*E. parvipinne*). Both species specialize in smaller headwater stream habitats. Given their limited distribution and persistent threats, Yazoo Darters are a species of conservation concern. The purpose of this study was to assess range wide population structure, genetic diversity, and broad patterns of connectivity for the Yazoo Darter. We sampled Goldstripe Darters to allow for comparison of these metrics between two ecologically similar species in the same drainage. We used Next Generation Sequencing (Genotyping by Sequencing) to generate a large SNP dataset for 160 Yazoo Darters (covering the entire range of the

species), and 150 Goldstripe Darters from the upper Yazoo River drainage. We present analyses comparing and contrasting population genomic patterns of these species.

<sup>1</sup>University of Southern Mississippi, School of Biological, Environmental and Earth Sciences

**Kiersten Schellhammer<sup>1</sup>** and Michael Sandel<sup>1</sup>

An aquatic melting pot: mapping genetic homogenization among fish populations of the Tenn-Tom waterway

The Tennessee and Mobile River Basins represent the two most biodiverse watersheds in North America, unfortunately, the same rivers are now recognized for their imperilment, as they are home to a number of threatened and endangered species. Many fish populations of the Mobile River Basin are recognized as distinct endemic species, but an influx of northern genes from fishes of the Tennessee River may threaten to erase this genetic distinction. Genetic homogenization, therefore, represents a threat to native biodiversity in Alabama by the loss of heritable variation the fuel for adaptation to environmental change. In 1984, with the completion of the Tenn-Tom waterway, the Mobile and Tennessee River basins united hydrologically, providing an opportunity for gene flow between fish populations that had been separated for at least 5 million years. Currently, no studies have measured the degree to which Tennessee and Mobile River basin fishes have interbred along the corridor, nor have any identified the genes that are most important in this process. Examining mitochondrial DNA variation in the Bullhead Minnow (*Pimephales vigilax*) across in the Tennessee River, Mobile River, and neighboring watersheds along the Gulf Coast we find evidence for distinct native haplogroups with genetic exchange along the Tennessee-Tombigbee waterway. Ongoing research will incorporate Single Nucleotide Polymorphisms (SNPs) from the nuclear genome, which will provide a more complete picture of gene flow among populations. This research will advance the field of conservation genomics, by investigating impacts of the most extensive watershed boundary diversion in North America and identifying genes that are most important in genetic homogenization.

<sup>1</sup>The University of West Alabama

**Kurtis Shollenberger<sup>1</sup>**, Carol Johnston<sup>1</sup>, and Alexis Janosik<sup>2</sup>

Current distribution and habitat use of the threatened snail darter *Percina tanasi* in Alabama

The Alabama portion of the Tennessee River system is home to over 175 species, and among these are many endemics that are being threatened with extirpation due to habitat loss and other factors. This has increased the need for the monitoring and conservation of these fishes. The snail darter (*Percina tanasi*) is a federally threatened species endemic to the Tennessee River drainage. Recent surveys have identified snail darters outside of their

known range in Alabama, and it is apparent that the species is dispersing via the mainstem Tennessee River. Our goal is to locate populations of Snail Darter throughout the Alabama portion of the Tennessee River and major tributaries and to characterize habitat where populations are found. We used environmental DNA to assess *P. tanasi* presence throughout the study area. A total of 57 unique sites were sampled via water collection. Twenty-nine, (51%) sites came back positive for *P. tanasi* DNA, indicating their presence at those locations. These positive detection sites include the known localities of *P. tanasi* in Bear Creek, Elk River, and Paint Rock River. This study has also discovered several new localities throughout the mainstem Tennessee River and in Shoal Creek, near Florence, Al. Side scan sonar techniques are being applied to compare habitat availability surrounding negative and positive eDNA sites. These results will allow us to determine critical localities and habitat types in which conservation efforts should be focused and could lead to studies assessing movement and relatedness between populations in this system.

<sup>1</sup>Auburn University, School of Fisheries, Aquaculture and Aquatic Sciences

<sup>2</sup>University of West Florida, Department of Biology

**Sam Silknetter<sup>1</sup>**, Bryan Brown<sup>2</sup>, Robert Creed<sup>3</sup>, Emmanuel Frimpong<sup>2</sup>, James Skelton<sup>4</sup>, and Brandon Peoples<sup>1</sup>

Positive biotic interactions in freshwaters: a research directive

Positive interspecific interactions (mutualism, commensalism, and facilitation) are ubiquitous in nature, but understudied in freshwater ecosystems. This review assesses the state-of-the-knowledge of positive interactions in freshwaters, and provides direction for future research. A few mutualistic relationships have received some research attention, namely seed-dispersing fishes, crayfishes and their branchiobdellidan symbionts, and communal-spawning stream fishes. Facilitative effects of a few habitat-modifying species have also been identified, as well as positive indirect trophic interactions. However, less is known about interactions in which participants directly exchange nutrients or protection. Most studies in freshwaters have been conducted using observations or experiments at small spatial scales. However, a cross-scale approach is necessary for a full understanding of how positive interactions operate. Likewise, research must seek to understand context dependency in positive interactions – how biotic (e.g. species or traits) and abiotic factors determine outcomes of positive interactions. Lastly, research on positive interactions must progress from a perspective of pairwise interactions, to a broader community context. A firm understanding of positive interactions will yield better predictions for managing freshwater ecosystems.

<sup>1</sup>Clemson University

<sup>2</sup>Virginia Tech

<sup>3</sup>Appalachian State University

<sup>4</sup>University of Florida

**Jeffrey W. Simmons<sup>1</sup>** and David C. Matthews<sup>1</sup>

Going with the flow- discovery of the Snail Darter *Percina tanasi* throughout the mainstem Tennessee River

The Snail Darter, *Percina tanasi*, was first discovered in the Little Tennessee River in August 1973 and the formal species description was published in January 1976. At this time, the only known habitat of the Snail Darter was slated for inundation by construction of Tellico Dam on the Little Tennessee River. Due to this impending threat, the species was listed as endangered under the newly formed Endangered Species Act in October 1975. In 1976, Tennessee Valley Authority (TVA) biologists transplanted individuals into the Hiwassee River in an attempt to avoid extinction prior to completion of Tellico Dam. Additional individuals were introduced into the Nolichucky, Holston, and Elk Rivers shortly thereafter. Of these, the Holston and Hiwassee transplants were the only ones believed to be successful. From 1980 to 1983, additional survey efforts found Snail Darters in the Little River, Big Sewee Creek, South Chickamauga Creek, and in the Sequatchie and Paint Rock Rivers, which prompted down-listing of the species to a threatened status. No additional populations were found until an individual was collected in the Flint River by TVA biologists during 2012, representing the most downstream occurrence within the Tennessee River system. In July 2015, we collected Snail Darters at two separate locations in Bear Creek, a tributary to the lower Tennessee River in Mississippi and Alabama. Three weeks later, we collected individuals in the Elk River which also drains to the lower Tennessee River. These were surprising discoveries since the Flint River was 152 river miles from the nearest Bear Creek collection site and 108 river miles from the Elk River locale. Furthermore, distances between the Elk River and Bear Creek locations were > 128 river miles and are separated by two large Tennessee River reservoirs. It was assumed that these previously undetected tributary populations were a result of larval drift through Tennessee River reservoirs and that there was potential of reproducing populations in the mainstem. During 2017 and 2018, we began sampling for Snail Darters in the Tennessee River using a benthic trawl. To date, we have detected individuals in sections of five Tennessee River reservoirs which span 272 river miles. In each reservoir, at least two age classes were collected. Flowing males and gravid females were collected during the spring, indicating that reproduction is occurring in the Tennessee River.

<sup>1</sup>Tennessee Valley Authority

**Zachary Sperstad<sup>1</sup>**, Peter Berendzen<sup>1</sup>, Andrew Simons<sup>2</sup>, Jonathan Armbruster<sup>3</sup>, Carla Stout<sup>4</sup>, Emily Moriarty Lemmon<sup>5</sup>, and Alan Lemmon<sup>6</sup>

Resolving the evolutionary history of the freshwater suckers using anchored enrichment (Cypriniformes: Catostomidae)

Reconstructing the evolutionary history of the Catostomidae, the freshwater suckers, using molecular data has proven challenging. This challenge stems from the occurrence of hybridization and tetraploidy in the family. Because of these issues, no robust phylogenetic hypothesis has been made for subfamilial relationships within the Catostomidae. We

present a hypothesis for the evolutionary history of the Catostomidae using 267 anchored hybrid enrichment loci representing 43 catostomids. Two disparate topologies were recovered depending on the method of analysis used: concatenation (maximum likelihood and Bayesian inference) and a coalescent-based species tree summary method (ASTRAL-II). We use a dataset filtration approach based on phylogenetic informativeness to select appropriate loci for resolving deep nodes in the catostomid phylogeny to infer the sister taxon relationships of subfamilies within the Catostomidae. The results supported a monophyletic Catostomidae, with the Asian Myxocyprinae sister to the North American catostomids. Within the North American clade, Cycleptinae is sister to Ictiobinae plus Catostominae. The sister relationship between Catostominae and Ictiobinae was recovered in this study with overwhelmingly strong support. We are unable to comment on many of the relationships within Catostominae; however, we corroborate previous hypotheses of paraphyly of *Catostomus* caused by recognition of the morphologically divergent taxa *Chasmistes*, *Deltistes*, and *Xyrauchen* as separate genera. Lastly, we find *Thoburnia* to be paraphyletic to Hypentelium. To regain taxonomic accuracy, we erect a new genus in which *Thoburnia atripinnis* can be subsumed.

<sup>1</sup>University of Northern Iowa, Department of Biology

<sup>2</sup>University of Minnesota, Bell Museum of Natural History

<sup>3</sup>Auburn University, Department of Biological Sciences

<sup>4</sup>California State Polytechnic University, Department of Biological Sciences

<sup>5</sup>Florida State University, Department of Biological Sciences

<sup>6</sup>Florida State University, Department of Scientific Computing

**Tammy St. James<sup>1</sup>** and Mollie F. Cashner<sup>1</sup>

The scarlet letters: detection of cross-species mtDNA between Scarlet Shiners and Striped Shiners

When developing an RFLP (restriction fragment length polymorphism) library for the Red River System of the Cumberland River in Tennessee, there was some evidence that Scarlet Shiner (*Lythrurus fasciolaris*) samples were exhibiting mtDNA sequences attributed to Striped Shiner (*Luxilus chrysocephalus*). Therefore, we conducted additional analysis of both species in an effort to determine the frequency of this hybridization. Ten to twenty individuals of each species were collected from two different streams in the Red River system. Fin clips were taken, and individuals were preserved for future morphological study. We extracted whole genomic DNA from the fin clips, amplified the mitochondrial *cytb* gene, then digested the amplicons with restriction enzymes to identify Scarlet Shiner and Striped Shiner genotypes. A subset of samples were sequenced for confirmation of RFLP findings. Our data suggests that hybridization between these species is rare, possibly fluctuating between locations and years

<sup>1</sup>Austin Peay State University

**Lauren Stoczynski<sup>1</sup>** and **Brandon Peoples<sup>2</sup>**

Understanding the elements of metacommunity structure in stream fish communities of the eastern United States

Community ecologists have always been interested in how species assemble themselves within their given environments. Metacommunity ecology offers a strategy for disentangling the spatial and environmental components for species assemblage. We investigated 190 stream fish metacommunity assemblages in the Eastern United States using the elements of metacommunity structure (EMS) in a qualitative and quantitative manner. Quantitatively, we used linear models to understand how different landscape level variables affect coherence, turnover, and boundary clumping from EMS calculations. Qualitatively, we used metacommunity structures to look for areas in the Eastern US where certain metacommunity structures seem to be more prevalent and make inferences for why these patterns are seen. Seven metacommunity patterns were observed with clementsian, quasi-clementsian, clumped species loss, and quasi-clumped species loss being the most prevalent patterns. Land use and dams showed significant ability to predict coherence, turnover, and boundary clumping, adding further meaning to the pattern assigned to the metacommunity. This research illustrates how additional factors can be used to explain metacommunity structures.

<sup>1</sup>Clemson University, Department of Biological Sciences

<sup>2</sup>Clemson University, Department of Forestry and Environmental Conservation

**Edward Stowe<sup>1,2</sup>**, **Mary Freeman<sup>3</sup>**, **Seth Wenger<sup>1,2</sup>**, and **Bud Freeman<sup>1,4</sup>**

Assessing the status of the Amber Darter *Percina antesella* with multivariate state-space analysis

Under the U.S. Endangered Species Act, protected taxa require status assessments that evaluate their representation, resiliency, and redundancy, known as the three R's. Evaluators using the three R's framework assess extinction risk based on the number and spatial extent of the populations, as well as the degree of distinctiveness and long-term trajectory of each individual population. An important overlooked element may be the extent to which fluctuations in abundance of constituent populations are independent from other populations; higher positive correlations in stochastic population variation can increase the risk that catastrophic events or environmental shifts will lead to the extinction of a species as a whole. Multivariate autoregressive state-space modeling (MARSS) may be used to better understand non-independence in population fluctuations within a species, while also estimating other metrics commonly used in assessments of population viability, such as long-term growth rate. Using sampling data collected at 16 shoal sites in north Georgia from 1996 to 2017, we used MARSS analysis coupled with AIC-based model selection to assess the status of the federally endangered Amber Darter (*Percina antesella*) within its two known populations in the Conasauga and Etowah rivers. Our results indicate an overall decline in abundance of the Amber Darter over the last two decades within the study area but at differential rates: 12% annually in the Conasauga and 9% in the Etowah.

However, annual population fluctuations within the rivers were positively correlated, suggesting that the two populations experience synchronous environmental variation, and therefore reduced overall redundancy. Ultimately, this analysis indicates that the vulnerable status of the Amber Darter may be exacerbated by non-independent population fluctuations, and further demonstrates how MARSS modeling may augment the three R's approach when assessing the status of protected taxa.

<sup>1</sup>Odum School of Ecology, University of Georgia

<sup>2</sup>River Basin Center, University of Georgia

<sup>3</sup>U.S. Geological Survey, Patuxent Wildlife Research Center

<sup>4</sup>Georgia Museum of Natural History

### **Carrie A. Straight<sup>1</sup>**

Species status assessments and the use of decision analysis for recovery, listing, and conservation

The U.S. Fish and Wildlife Service has an increasing workload of Endangered Species Act decisions, including Listing, Recovery, and Consultations. These require an efficient process that uses the best available science to inform those decisions and fulfill our responsibilities. The Service needs to work with our conservation partners to assess the status of our trust resources, understand the threats to those species, and develop management and recovery plans for those species. The Service is using a common framework to bring a field of experts and the best science available to assess the viability and condition of a species called a Species Status Assessment (SSA). This new process places emphasis on the understanding the relationships between a species' life history needs, threats, and survival. By analyzing a species' resilience, representation, and redundancy, the SSA team can describe the viability of a species. This talk will review the Species Status Assessment Framework and structured decision-making tools currently used for species conservation in the Southeast, and how experts outside the Service are involved.

<sup>1</sup>U.S. Fish and Wildlife Service, Georgia Ecological Services

**Sarah Sweat<sup>1</sup>, Bernie Kuhajda<sup>1</sup>, George Gavrielides<sup>1</sup>, Justyn Patterson<sup>1</sup>, Christina Quinn<sup>1</sup>, Anna George<sup>1</sup>, Joe Powell<sup>2</sup>, Mack Lunn<sup>2</sup>, and Ryan Brown<sup>2</sup>**

Engaging scientists and citizen scientists using the Freshwater Information Network (FIN)

The Southeastern United States is a global biodiversity hotspot for freshwater aquatic organisms. However, distributional and status data for southeastern organisms are stored in a variety of formats, including spreadsheets, museum records and databases, unpublished reports, and field notes. Currently, data for endangered species cannot be vouchered using previous methods therefore data are not in an easily accessible database. The Freshwater Information Network (FIN) aims to combine all of these data sources into



a single user friendly “living” database containing georeferenced locations and voucher photographs. We collected museum, institutional, and field note data and georeferenced records. Currently FIN includes 402 native fish species within the Tennessee, Mobile, and Cumberland river drainages. This interactive website allows users to submit locality data and field photograph vouchers through a configurable application made with ArcGIS Solutions. Distribution maps, photo voucher galleries, and a brief description of life history will allow for a one stop website on information of all species for both scientists and the public. Future additions to FIN include other aquatic taxonomic groups in these drainages as well as relevant literature. With the addition of data from experts and citizen scientists, conservation efforts in the Southeast can become a focused collaborative effort.

<sup>1</sup>Tennessee Aquarium Conservation Institute

<sup>2</sup>Tennessee Technological University iCube

**Bernie Kuhajda<sup>1</sup>**, Sarah Sweat<sup>1</sup>, George Gavrielides<sup>1</sup>, Anna Geroge<sup>1</sup>, Justyn Patterson<sup>1</sup>, Christina Quinn<sup>1</sup>, Joe Powell<sup>2</sup>, Mack Lunn<sup>2</sup>, and Ryan Brown<sup>2</sup>

Sharing is caring: use the freshwater information network (fin) to share your southeastern fish encounters with others

The Southeastern United States is a global biodiversity hotspot for freshwater aquatic animals. Distributional data for southeastern freshwater fauna are stored in a variety of formats, including museum records and databases, spreadsheets, unpublished reports, and field notes. Imperiled species cannot typically be vouchered, therefore recent collection data are missing from museum databases. The Freshwater Information Network (FIN) aims to combine all of these data sources into a single user friendly “living” database containing georeferenced locations, museum catalog numbers, and other collection data, and voucher photographs for released specimens. We collected museum, institutional, and field note data, and georeferenced these records where needed. Currently FIN includes 402 native fish species within the Mobile, Tennessee, and Cumberland river drainages. This interactive website allows users to submit locality data and field photograph vouchers. Each fish species has a distribution map, photo voucher gallery, and a brief description that provides a one stop website on information for both scientists and the public. Future additions to FIN include other aquatic taxa in these drainages as well as relevant literature. With the addition of data from experts and citizen scientists, conservation efforts in the Southeast can become a focused collaborative effort.

<sup>1</sup>Tennessee Aquarium Conservation Institute

<sup>2</sup>Tennessee Technology University iCube

**Jennifer C. Taylor<sup>1</sup>**, Annie E. Savage<sup>1</sup>, and Brook L. Fluker<sup>1</sup>

Project Macroinvert: unlocking geospatial data of odonates from the aquatic macroinvertebrate collection at Arkansas State University

The Arkansas State University Museum of Zoology (ASUMZ) Aquatic Macroinvertebrate collection at the Arkansas Center for Biodiversity Collections (ACBC) houses approximately 130,000 specimens (17,000 lots). Most of the specimens were collected in Arkansas, but coverage includes North and Central America, and Australia. Project Macroinvert was initiated at the ACBC in fall of 2016, which involves restoration, digitization, and georeferencing of the collection by two undergraduate honors students. Until recently, specimen data were stored in handwritten catalogs, making query and locality mapping cumbersome and time consuming. Upon completion, these geospatial data will provide a very high-resolution picture of distributional patterns of aquatic macroinvertebrate taxa on smaller scales (e.g., regional, county, and/or drainage level) proximate to the institution. To date, approximately 95% of the collection has been digitally databased and georeferenced if locality descriptions were sufficient. This project focuses on Odonate collection data unlocked by Project Macroinvert. Specifically, ASUMZ Odonate collections were mapped and distributional patterns were compared to previous studies of Odonates within the regional footprint of ASUMZ collections. We expect that digitization and georeferencing of small collections, such as the ASUMZ collection, will contribute vastly to our knowledge of species distributions and our ability to accurately characterize biodiversity at fine scales.

<sup>1</sup>Arkansas State University, Department of Biological Sciences

**Matthew Thomas<sup>1</sup>** and Stephanie L. Brandt<sup>1</sup>

Status survey of the Redside Race *Clinostomus elongatus* in Kentucky

The Redside Dace is a Species of Greatest Conservation Need (SGCN) with a limited distribution in northeastern Kentucky. Fish community sampling at 92 sites in 77 streams in the Licking and Kentucky River basins during 2015-2016 detected Redside Dace at 38 sites in 36 streams. The species is more widely distributed and occupies more streams in the Licking River basin than the Kentucky River basin. Current centers of abundance are in the North Fork (Licking River), Beaver Creek (Licking River), and Upper Red River (Kentucky River) drainages, where forested land makes up over 70% of the watershed area. These populations represent the southernmost periphery of the species' range. The Western Allegheny Plateau has apparently served as a glacial refugium for the species based on high levels of genetic diversity documented within Licking and Kentucky River basin populations. Considering the evidence of high genetic structuring within Redside Dace populations indicating a general lack of gene flow among populations, maintenance and protection of Kentucky's populations is important for the overall conservation of the species. The continued persistence of Redside Dace in Kentucky is largely dependent upon the integrity of headwater habitats that support reproductively viable populations. Conservation objectives should include maintaining well forested watersheds (e.g., Daniel

Boone National Forest) and preventing further degradation of streams on private lands. Our survey results indicate that populations in the Licking and Red River drainages are generally stable, with additional stream occurrences than previously reported. Periodic surveys of Redside Dace populations in Kentucky should be continued every 5-10 years to monitor changes in distribution, abundance, and habitat conditions.

<sup>1</sup>Kentucky Department of Fish and Wildlife Resources

**Dustin R. Thomas<sup>1</sup>, Brook Fluker<sup>1</sup>, and Brett Timmons<sup>2</sup>**

Assessment of Walleye in the Eleven Point River, Arkansas, following a six-year stocking gap

The spring fed Eleven Point River contains a natural population of Walleye, *Sander vitreus*. Supplemental stocking of Walleye in Arkansas has occurred in the Eleven Point River since 1986. The river is managed for multiple sport fish species, but it was not until 2002 that researchers began to investigate the complexities of Walleye stocking programs in the Eleven Point River. Researchers discovered a unique mitochondrial DNA haplotype for the native population in the Black River drainage. The native haplotype is identified as haplotype C or Black River Strain Walleye. From 1986 to 2011, a non-native northern strain known as White River Strain Walleye or haplotype A were stocked into the Eleven Point River. This project will assess the Walleye stocking program in the Eleven Point River using haplotype frequencies, growth, and relative abundance. Population dynamics between strains of Walleye will be compared, and microsatellite data will be used to determine how prevalent the non-native genes are within the population. Additionally, Smallmouth Bass, *Micropterus dolomieu* relative abundance and annual growth will be assessed and compared to previous data. Preliminary data will be presented from 2017 sampling in the Eleven Point River, which follows a 6-year gap in Walleye stocking from 2011 to 2017. These data show a relative abundance of less than half in 2017 than in 2011.

<sup>1</sup>Arkansas State University, Department of Biological Sciences

<sup>2</sup>Arkansas Game and Fish Commission, District 3 Fisheries Supervisor

**Bryn Tracy<sup>1</sup>, Gabriela M. Hogue<sup>2</sup>, and Fritz C. Rohde<sup>3</sup>**

Ghost of ichthyologists past - the Longear Sunfish *Lepomis megalotis* in North Carolina

The Longear Sunfish, *Lepomis megalotis* (Rafinesque, 1820), was first reported from North Carolina by Cope in 1870 "from the upper waters of the French broad" (Cope 1870b), but vouchered specimens, collected by Cope, do not exist. In addition, nine lots (totaling 15 specimens) at various museums that were originally identified as Longear Sunfish were not. Four lots collected in the 1930s and 1940s from the North Fork Swannanoa River and the Swannanoa River in Buncombe County and from Pisgah Forest Lake in Transylvania County (ANSP Catalogue Nos. 61185, 61186, 61203, and 86937) were recently re-identified as Redbreast Sunfish, *Lepomis auritus* (Linnaeus 1758). Two

lots reported by Menhinick (1986) and Menhinick and Braswell (1997) collected in the 1940s from Richland Creek downstream from Lake Junaluska (Haywood County) were based upon material subsequently identified as Redbreast Sunfish (UMMZ Catalogue Nos. 131443 and 131444). Other lots from the 1960s-1980s (OSUM 59649, UF 64883, and INHS 27116) have also turned out to be Redbreast Sunfish. If Longear Sunfish ever occurred in North Carolina's (NC) western mountain river systems, these populations would have been on the extreme eastern edge of the species range (Bauer 1980). Various publications over the years have reported the Longear Sunfish as being extirpated from the state (e.g., Menhinick 1986; Menhinick 1991; Menhinick and Braswell 1997; NCNHP 2016), possibly because of competition with Redbreast Sunfish, which is non-indigenous to NC western mountain river systems. However, except for Cope's anecdotal record, there is no evidence that Longear Sunfish, historically or more recently, ever occurred in North Carolina. This presentation will expand upon the historical "ghost sightings", the propagation of these identification records through time because of similarities between species, and evidence supporting the true distribution of Longear Sunfish.

<sup>1</sup>Apex, NC

<sup>2</sup>North Carolina Museum of Natural Sciences, Raleigh, NC

<sup>3</sup>NOAA, Beaufort, NC

**Joshua R. Vine<sup>1</sup>, S. Chad Holbrook<sup>2</sup>, William C. Post<sup>3</sup>, and Brandon K. Peoples<sup>1</sup>**

Identifying environmental cues for Atlantic and Shortnose sturgeon spawning migrations in the Savannah River

Quantitative understanding of the environmental factors that initiate reproductive activity are critical for conservation and recovery of imperiled fishes. We utilized generalized and linear mixed models to investigate the relationship between Atlantic Sturgeon (*Acipenser oxyrinchus*) and Shortnose Sturgeon (*Acipenser brevirostrum*) migration behavior and water temperature and discharge within the lower Savannah River from January 2013 - May 2018. Our generalized linear mixed model included a binary migration indicator as the dependent variable, which we calculated based on each sturgeon's maximum detection location (river kilometer, rkm) and movement direction each day. Our linear mixed models included each sturgeon's maximum daily rkm as the dependent variable. All models included individual ID and year as a random effect, as well as the previous days migration indicator or rkm as an offset to account for temporal autocorrelation. Throughout the duration of the study period, we detected six Atlantic Sturgeon attempt nine fall migrations (n = 918 records), four Atlantic Sturgeon attempt eight spring migrations (n = 257 records), and 15 Shortnose Sturgeon attempt 29 spring migrations (n = 3,542 records). Patterns of putative spawning migrations were affected primarily by shifts in water temperature, and secondarily by discharge. Cues for initiation of migration, as well as spatial position within the river during spawning migrations, were species-specific, and depending on the species and index of spawning, we observed significance in both water temperature and discharge for migration behavior. We also identified key times and locations of putative spawning aggregations. Greater understanding of the effects of water temperature and discharge

conditions that initiate and promote upriver movement by sturgeons will aid in the conservation of these species.

<sup>1</sup>Clemson University, Department of Forestry and Environmental Conservation

<sup>2</sup>Dennis Wildlife Center, South Carolina Department of Natural Resources

<sup>3</sup>Marine Resources Research Institute, South Carolina Department of Natural Resources

## **Matthew Wagner<sup>1</sup>**

The Comeback and the takeover: results from a 2018 survey of the Pearl River

The Frecklebelly Madtom, *Noturus munitus* (Suttkus and Taylor 1965), is found in the Pearl and Mobile River drainages and is currently petitioned for federal listing with a listing decision deadline of 2020. Populations of Frecklebelly Madtom are considered in decline throughout both the Mobile River and the Pearl River. The last targeted survey in the Pearl River drainage throughout Mississippi and Louisiana was completed in 1999, where the species was found at only 8 of 53 historical localities. In 2018, we sampled 16 mainstem Pearl River localities and 59 Pearl River tributary localities in Mississippi to assess the status of the species. Frecklebelly Madtom were collected at 14 of the 16 mainstem Pearl River localities, 21 of the 28 historic tributary localities, and at 7 of the 31 newly sampled tributary localities. Inadvertently, we also documented the presence of Rough Shiners, *Notropis baileyi* (Suttkus and Raney 1955), at 10 localities throughout the Pearl River, where they were not thought to occur previously. These results indicate that the status of *Noturus munitus* in the Pearl River drainage is stable and that *Notropis baileyi* is increasing its range throughout the drainage.

<sup>1</sup>Mississippi Museum of Natural Science

## **River A. Watson<sup>1</sup>, Brook L. Fluker<sup>1</sup>, and Bernard R. Kuhajda<sup>2</sup>**

Taxonomic evaluation of the Goldstripe Darter *Etheostoma parvipinne*, using species delimitation methods with molecular and morphological data

The Goldstripe Darter, *Etheostoma parvipinne*, inhabits shallow spring-fed streams in the Gulf Coastal Plain from the Colorado River drainage in Texas to the Altamaha River drainage in Georgia. A previous morphological study of *E. parvipinne* revealed a population above the fall line in the Black Warrior River drainage to be a distinct species; the Rush Darter, *E. phytophilum*. However, morphological variation of *E. parvipinne* populations across the Gulf Coastal Plain failed to reveal evidence for additional distinct populations. A previous unpublished study of mitochondrial and nuclear DNA sequence data for *E. parvipinne* across the Gulf Coastal Plain revealed a deep phylogenetic rift between populations east and west of the Mississippi River. The current study builds upon these molecular data by adding additional mitochondrial DNA data and novel nuclear DNA

markers, with the objective of providing finer resolution of the phylogenetic disconnection between populations east and west of the Mississippi River. Additional sampling of individuals and molecular markers, meristic and morphometric analyses, and species delimitation methods will be used to fully understand the cryptic diversity and taxonomic uncertainty within the species.

<sup>1</sup>Arkansas State University, Department of Biological Sciences

<sup>2</sup>Tennessee Aquarium Conservation Institute

**Seth Wenger**<sup>1</sup>, Mary Freeman<sup>2</sup>, William McLarney<sup>3</sup>, Edward Stowe<sup>1</sup>, Kelly Petersen<sup>1</sup>, Phillip Bumpers<sup>1</sup>, and Byron Freeman<sup>1</sup>

The critical importance of long-term fish monitoring

Fish ecologists employ multiple types of sampling and monitoring that serve different purposes. Synoptic and episodic sampling can yield valuable information about fish species status, distributions and habitat associations. In contrast, serial monitoring of abundances over time makes it possible to estimate population growth rates while accounting for stochasticity, which can reveal population trends that would not be otherwise apparent. Similarly, regular presence/absence monitoring at defined locations can detect range shifts associated with changing environmental conditions or the spread of introduced species with far greater sensitivity than episodic or rotating sampling. We illustrate the value of long-term serial monitoring with analyses of datasets from the Etowah and Conasauga Basins, Georgia, and the Little Tennessee Basin in North Carolina. We show evidence of declines in several species in the Conasauga and the Etowah and increased homogenization of fish communities in the Little Tennessee. We also show how some variability in fish abundances in the Etowah is explainable by flow patterns, illustrating the potential to find causal associations for trends. However, we cannot speak to the generality of our findings because of a paucity of comparable long-term monitoring programs in the Southeast. We call for the initiation of additional sustained, serial sampling programs in the region and a commitment for expanded funding for such programs by government agencies and non-governmental organizations.

<sup>1</sup>The University of Georgia

<sup>2</sup>US Geological Survey

<sup>3</sup>Little Tennessee Project / Asociación ANAI

**Nathan V. Whelan**<sup>1,2</sup> and Ashantye' S. Williams<sup>1</sup>

Lessons learned and new directions: long-term genetic monitoring of hatchery efforts in the southeastern United States

Genetic data are essential for both designing and evaluating hatchery efforts for freshwater fishes. At the front end of reintroduction efforts, genetic studies are important for informing

decisions about broodstock sources and for assessing if known populations should be treated as a single management unit. During multi-year propagation programs, genetic data are useful for evaluating program success and alerting managers to potential problems if reintroduced populations fail to have similar levels of genetic diversity as broodstock populations. However, long-term projects have unique challenges including turnover in staffing and changing technologies. Here, we examine the status of long-term genetic monitoring efforts for lake sturgeon reintroduction to the Tennessee River, gulf strain striped bass propagation to the Apalachicola-Chattahoochee-Flint River, and hatchery efforts for American shad in the Edisto River. Our experiences emphasize the need for informed study design that includes careful consideration of appropriate tools and realistic expectations of information genetic monitoring can provide. We find the quality control is essential to the success of long-term genetic monitoring studies, and projects must be structured so inevitable staff turnover does not prevent research continuity. In the future, genetic monitoring programs should embrace new technologies, but challenges associated with changes to the types of data being analyzed should not be understated. Looking forward, we will also discuss new population genomic projects on Sicklefin Redhorse and Spottfin Chub that will utilize genomic data to better understand natural populations and provide more detailed hatchery program evaluations than possible with traditional genetic tools such as microsatellites.

<sup>1</sup>Southeast Conservation Genetics Lab, Warm Springs Fish Technology Center, United States Fish and Wildlife Service

<sup>2</sup>School of Fisheries, Aquaculture, and Aquatic Sciences, Auburn University

**James D. Williams<sup>1</sup>**, Mark A. Cantrell<sup>2</sup>, and Judy A. Takats<sup>3</sup>

A vision for aquatic restoration for the Coosa River

We present an overview of the Coosa River basin, highlighting its diverse aquatic habitats and natural communities, synthesize the challenges facing aquatic conservation in the basin, and recommend next steps. The Coosa River basin drains over 10,000 square miles in Alabama, Georgia, and Tennessee. It is rich in aquatic diversity, with 112 fishes, 54 mussels, 92 snails, and other aquatic-dependent flora and fauna. Of these species, 69 are endemic and 62 are imperiled. The Coosa River also provides recreation, drinking water, and other environmental services to its human population. The need for dialogue is especially relevant now because the U.S. Court of Appeals for the District of Columbia Circuit reviewed Alabama Power Company's 30-year license to operate seven hydropower developments on the main stem of the Coosa River and determined that the Federal Energy Regulatory Commission (FERC) environmental review and a USFWS Biological Opinion it relied on "*were unreasoned and unsupported by substantial evidence*". In their July 2018 ruling, the Court vacated the licensing decision and remanded to the agencies. We conclude that this is an unprecedented time for a broad discussion to articulate clearly a comprehensive plan for the Coosa River basin, with an emphasis on the recovery of the globally unique, and valued, aquatic communities. Under the Federal Power Act, the FERC considers the extent to which a project such as the Coosa River hydroelectric development is consistent with federal or state comprehensive plans for improving or conserving a

waterway. We propose a process to convene stakeholders, including Alabama Power and the U.S. Army Corps of Engineers, to develop a comprehensive plan with a schedule for restoration and conservation of the significant aquatic resources of the Coosa River.

<sup>1</sup>Florida Museum of Natural History, Gainesville, FL

<sup>2</sup>U.S. Fish and Wildlife Service, Panama City, FL

<sup>3</sup>World Wildlife Fund, Nashville, TN

**Benjamin Wilson**<sup>1</sup>, Rebecca E. Blanton<sup>1</sup>, and Matthew D. Wagner<sup>2</sup>

Phylogeography of the Piebald Madtom *Noturus gladiator*

Past historical events, such as Pleistocene glaciations and associated sea level fluctuations significantly altered the fluvial morphology of the Mississippi Embayment. Alterations in drainage patterns and stream connections contributed to both dispersal and vicariant events that, in part, have shaped present day fish distributions and phylogeographic relationships in the region. Some taxa (including the genus *Noturus*) in the Embayment region have undergone shared historical events leading to similar phylogeographic relationships, while others have similar relationships that resulted from different historical events. To further understand historical factors that have contributed to geographic structure and diversity in this dynamic region, we examined phylogeographic relationships of populations of the Piebald Madtom, *Noturus gladiator*, a Mississippi Embayment endemic. Specifically, we examined whether the mainstem Mississippi River has been a long-standing barrier to gene flow among populations in each tributary system. To accomplish these objectives, we collected 60 tissues from 14 historic localities throughout the range of *Noturus gladiator* and generated mitochondrial cytochrome b sequence data for all individuals. Both a gene tree and haplotype network were used to evaluate diversity, degree of divergence, and phylogeographic relationships. Overall haplotype diversity was low and clades recovered were largely structured by tributary system, with the exception of two individuals. These findings suggest potential long-standing isolation among tributary systems, likely due to historical vicariance associated with the dynamic history of the Embayment region. More recently, the mainstem Mississippi River system may pose hostile conditions that prevent successful dispersal and has reinforced historical isolation events. Since the Piebald Madtom is currently under petition for federal listing, has been declared a species in need of management in Tennessee, and is listed as state endangered in Mississippi, understanding patterns of genetic structure is an important baseline for effective conservation. Additional work is underway to understand contemporary population dynamics.

<sup>1</sup>Austin Peay State University Center of Excellence for Field Biology

<sup>2</sup>Mississippi Museum of Natural Science

**Brian Zimmerman**<sup>1</sup> and S. Mazeika P. Sullivan<sup>1</sup>



## Successful translocation of Bluebreast Darters: A case study from the upper Licking River, Ohio

Aquatic ecosystems of Ohio historically supported diverse and abundant stream and river fish communities. Loss and fragmentation of high-quality aquatic habitat and impairments in water quality have led to significant alterations in the diversity, composition, and productivity of native fish communities. The Bluebreast Darter *Etheostoma camurum*, for example, was extirpated from many Ohio river systems over a century ago. In June of 2016 and 2017, 974 and 924 adult Bluebreast Darters, respectively, were translocated from the greater Muskingum River basin into the upper Licking River. Translocated individuals were marked with visible implant elastomer (VIE) tags. Translocated individuals from both events continue to be recaptured in follow-up surveys, most recently in late August 2018. VIE tags revealed minimal movement between release sites, however a few individuals have traveled as far as nine river kilometers following translocation. Natural reproduction by translocated fish has been documented by the capture of untagged individuals beginning in the first follow up surveys in 2016 and continues to be observed in subsequent years.

<sup>1</sup>The Ohio State University