



Thursday, 18 November 2021

9:00 Introduction to meeting, meeting chairs

Student talks, In Person, Moderator Rebecca Blanton Johansen

- 9:15 Do sedimentary processes have nonlocal consequences for metapopulation and metacommunity dynamics? Loren Stearman and Jake Schaefer
- 9:30 Thermal tolerance of fishes in an urban and non-urban stream in relation to environmental temperatures. Robert Remy, Reid Adams, Ginny Adams, and Matthew Gifford
- 9:45 Thermal tolerance of eggs of *Cottus paulus* (Pygmy Sculpin). Rachel Moore and Carol Johnston
- 10:00 Finding the freckled: focusing efforts to find Freckled Darter (*Percina lenticula*) in Mississippi. Noah Daun and Jake Schaefer

10:15 Break

Student talks, In Person, Moderator Brett Albanese

- 10:45 Parentage assessment of the Egg-mimic Darter (Percidae: *Etheostoma pseudovulatum*) demonstrates complex patterns of allopaternal care behavior. Nastasia T. Disotell, Zachary L. Wolf, Mollie F. Cashner, and Rebecca E. Blanton
- 11:00 Acoustic modulation of reproductive hormones in the Blacktail Shiner (*Cyprinella venusta*), a soniferous cyprinid. Jenna Crovo, Mary Mendonca, and Carol Johnston
- 11:15 Relationships between constructed waterbodies and homogenization of fish assemblages in the Black River watershed of Arkansas. Grace Davenport, Jennifer Main, George Gavrielides, Calvin Rezac, Ginny Adams, and Reid Adams
- 11:30 Habitat associations of fishes across a gradient of pool size and structure in an Ozark River. David Adams, Ginny Adams, Reid Adams, and David Mitchell
- 11:45 Modeling habitat suitability for the globally imperiled Etowah Darter (*Etheostoma etowahae*). Clayton W. Hale and Brittany L. McCall

12:00 Lunch

Student talks, In Person, Moderator Dan Holt

- 13:30 Using ecological niche modeling and genomic analysis to investigate established populations of the Green Swordtail, *Xiphophorus hellerii*, in north Florida. Anna N. Eastis, Zachary W. Culumber, Carla Gutiérrez-Rodriguez, and Michael W. Sandel
- 13:45 How to color a fish: examining male nuptial coloration gene expression patterns in Rainbow Darters (*Etheostoma caeruleum*) using TagSeq. Andrew N. Sherman and Kyle R. Piller
- 14:00 Distribution, abundance, and occupancy of the Striated Darter (*Etheostoma striatum*) in the Duck River. Abbey Holsopple and Kit Wheeler
- 14:15 Assessing the validity of three currently recognized subspecies of the Blacktail Shiner (*Cyprinella venusta*) through the use of next generation sequencing. Soren Johnson and Kyle R. Piller
- 14:30 Population dynamics of the Western Blacknose Dace (*Rhinichthys obtusus*) in Alabama. Courtney A. Weyand and Jonathan W. Armbruster
-

14:45 Break

Student talks, In Person, Moderator Duncan Elkins

- 15:15 An evolutionary analysis of lineage diversification among madtom catfishes (Siluriformes: Ictaluridae: *Noturus*). Brittany L. McCall, Jacob Egge, and Brook L. Fluker
- 15:30 Development of an environmental DNA (eDNA) assay to delineate the distribution of the imperiled Striated Darter (*Etheostoma striatum*, Page and Braasch 1977) in the Duck River, Tennessee. Adam L. Walker, Kit Wheeler, and Carla R. Hurt

Student talks, Virtual

- 15:45 Salmon of the south: suckers in Citico Creek. Mack White and Wit Wheeler
- 16:00 The effects of man-made barriers on present and historic site occupation of Arkansas *Etheostoma cragini* and Least Darters *Etheostoma microporca*. Alyssa Mostrom, Anthony Zenga, and Susan Colvin
- 16:15 Phylogenomic diagnosis of a recently discovered population of Tennessee Dace (*Chrosomus tennesseensis*) in Alabama. Julia E. Wood, David A. Neely, M. Worth Pugh, Phillip M. Harris, Michael W. Sandel
-

16:45 Business Meeting

18:00 – 21:00 Poster Session

Posters listed at end of schedule

FRIDAY, 19 November 2021

Virtual talks, Moderator Elizabeth Marchio

- 9:00 Are weight-length parameters of coastal Alabama stream fishes linked with life history traits and environmental variables? S. A. R. Colvin, Russell A. Wright, D. R. DeVries, and J. W. Feminella
- 9:15 Life history theory for environmental analysis of stream fish communities near the Potomac River. Nathaniel P. Hitt, Andrew P. Landsman, and Richard L. Raesly
- 9:30 Outmigration dynamics of American Eels in the Ouachita-Black-Red-Atchafalaya River System. Jeffrey Quinn, Kelly Winingham, Maxwell Hartman, Eric Brinkman, Todd Slack, Robby Maxwell, Sean Kinney, Brac Salyers, and Kayla Kimmel
- 9:45 Pinpointing biodiversity hotspots: local habitat and regional connectivity shape fish richness along rivers with contrasting habitat diversity. Corey Dunn and Craig Paukert
- 10:00 Re-tracing Edward Drinker Cope's travels through North Carolina and his contributions to North Carolina ichthyology. Bryn H. Tracy and Robert E. Jenkins
-

10:15 Break

Lightning Virtual talks, Moderator Brook Fluker

- 10:45 Genetic assessment of Southern Appalachian Brook Trout reintroductions. Rebecca J. Smith, Dave Kazyak, Matt A. Kulp, and Benjamin M. Fitzpatrick
- 10:50 Morphological differences and associated habitat partitioning among three species of *Percina* (Percidae: Actinopterygii) in the Roanoke River, Virginia. Michael M. Calvert and Steven L. Powers
- 10:55 Restoration of the Georgia College Fish Collection. Jordan Sorrells and Gregory Glotzbecker

Lightning In Person talks

- 11:00 Where did you find that? New records of mussels in Shoal Creek (Etowah River, Cherokee Co., GA). C. Keith Ray and Zach Felix
- 11:05 Phylogenetic and taxonomic evaluation of the Least Darter (*Etheostoma micropurca*) complex. Alexis M. Mross and Brook L. Fluker
- 11:10 An updated distribution of Trispot Darter breeding habitat. Anakela Escobar, Rebecca A. Bearden, Stuart W. McGregor, Daniel A. West, Michael W. Sandel, Kayla M. Fast, and Gary A. Hastert
- 11:15 Status survey for Saltmarsh Topminnow in Mississippi with notes on the effectiveness of boat electrofishing on coastal waters. Calvin R. Rezac, Robert J. Ellwanger, and Benjamin H. Chaffins
- 11:20 Occupancy of the Caddo Madtom: the good, the bad, and the unknown. Brittany L. McCall and Brook L. Fluker
- 11:25 Status survey of freshwater mussels in the Big Black River, Mississippi. Robert J. Ellwanger, Calvin R. Rezac, and Benjamin Chaffins

Final talks, In Person

- 11:30 The clutch concept and the reproductive biology of small fishes. David C. Heins and Nancy J. Brown-Peterson
- 11:45 Cryptic extinction in America's Amazon: genomic homogenization among fishes of the Mobile River Basin. Michael W. Sandel, Kayla M. Fast, Joshua Millwood, Kenny Jones, Kiersten Schellhammer, John Larrimore, Julia Wood, Alex Rakestraw, and Zach Alley
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- 12:00 Awards and adjourn.
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Poster Presentations

- 1 Improving collections and developing a public-facing persona: The BoneSheaux at Southeastern Louisiana University's Vertebrate Museum. Elizabeth Marchio and Kyle R. Piller
- 2 What's going on down south: re-examining the distribution of two species of *Labidesthes* across Mississippi using preserved collections, Benjamin H. Chaffins, Robert J. Ellwanger, and Calvin R. Rezac
- 3 Personality traits and colonization decisions by the Creek Chub (*Semotilus atromaculatus*). Jacob Barrett and Mollie F. Cashner
- 4 Fishes of Butler Creek, Tennessee River drainage, a biodiversity hotspot. David Pounders, Dalton Wright, Joshua Fitts, Gregory Gilmore, Jeffery Ray
- 5 Changes over two decades in the diversity, distribution, and conservation status of southeast U.S. native freshwater fishes. Bernie Kuhajda
- 6 Reproductive timing in *Percina aurora* and other *Percina* sp. in the Pascagoula River watershed. Malia Davidson, Noah Daun, Scott Clark, Brian Kreiser, and Jake Schaefer
- 7 Is red coloration in *Chrosomus erythrogaster* an honest signal? Julie Kastanis and Mollie Cashner

Student Posters

- 8 Effects of land use and instream barriers on population connectivity of the Kentucky Arrow Darter. River A. Watson, Alexis V. Culley, Rebecca E. Blanton, Matthew R. Thomas, Stephanie L. Brandt, and Michael A. Floyd
- 9 The effects of surface mining on population connectivity and genetic diversity of *Etheostoma sagitta spilotum*, the Kentucky Arrow Darter. Alexis V. Culley, River A. Watson, Matthew R. Thomas, Stephanie L. Brandt, Michael A. Floyd, and Rebecca E. Blanton
- 10 Nutrient subsidies from migratory fishes: evaluating drivers of ammonium excretion rates in multiple catostomids. Ryan Hudson and Kit Wheeler
- 11 Comparative population genetics of a rare, imperiled and a common, non-imperiled darter from the Big South Fork Cumberland River. Matthew Scott, Jacob F. Brumley, Abigail Etherton, and Rebecca E. Blanton
- 12 Assessing the efficacy of a barrier passessment method and the connectivity of headwater fish: an experimental approach. Langston Haden, Jake Schaefer, and Scott Clark

- 13 Does diet of *Luxilus pilosbryi* vary in response to stream drying? Rebeka Bradford, Sahara Morgan, Jessica Rath, Chance Garrett, Ginny Adams, and Reid Adams
- 14 Comparison of field acclimatization and lab acclimation approaches to measuring fish thermal tolerance. Cade Richeson, Canyon Vickers, Ginny Adams, Matthew Gifford, and Reid Adams
- 15 Variation in fish communities of Boston Mountain Streams in the Ozark National Forest. Jackson Pav, Ginny Adams, and Reid Adams
- 16 Mycobacterium presence in the dermal microbiome of freshwater fish in the southeastern U.S. Alex Rakestraw, Kayla Fast, Magdalene Dogbe, Heather Jordan, Sophie Picq, Joe Receveur, Alexandra Bauer, Christine Chevillion, Jean-François Guegan, Jennifer Pechal, Eric Benbow, and Michael Sandel
- 17 Influence of land-use on fish assemblage patterns across the South-Central Plains of Arkansas: a preliminary analysis. Ryne Lehman, Molly Wozniak, Hal Halvorson, Ginny Adams, and Reid Adams
- 18 Characterizing variation in black-spot disease among small stream fishes using historical collections from the Spring River drainage (Arkansas and Missouri; 1970s). Benjamin Brown, Landen Ho, Tyler B. Brown, Lindsey A. Martin, Amelia Atwell, Dylan DeRouen, Crystal Griffin, Alexis Mross, Clayton Vondriska, Jacob Wessels, and Brook L. Fluker
- 19 Population genetic assessment of the endangered Cumberland Darter (*Etheostoma susanae*). Hilary K. Canada, M. Taylor Perkins, Anna L. George, Bernard R. Kuhajda, and Brook L. Fluker
- 20 Effects of stream gradient on darter functional morphology in the Pomme de Terre River. Topher Hockaday and Aaron Geheber
- 21 Genotypic and phenotypic variation in the Rainbow Shiner (*Notropis chrysomus*). Zachariah Alley, Kayla Fast and Michael Sandel
- 22 The distribution and habitat status of freshwater mussels in the Wolf River, TN. Jack Fetter, Amanda Rosenberger, and Anthony Ford





ABSTRACTS

Habitat associations of fishes across a gradient of pool size and structure in an Ozark river

David Adams¹, Ginny Adams¹, Reid Adams¹, and David Mitchell²

¹The University of Central Arkansas, Department of Biology

²Ozarka College, Division of Applied Science Technology

Presentation Type: In Person, Student

11:30, Thursday, 18 November 2021

Streams in the Ozark Mountains have experienced an extended period of gravel aggradation, which has been exacerbated by changes in land use. The input of gravel into Ozark streams has resulted in the shallowing and widening of streams along with changes in substrate composition. These changes in stream geomorphology have likely had an impact on fish community structure; however, due to limitations in sampling methodology, few data are available on the abundances of fishes inhabiting pools, particularly in deep, non-wadable habitats. We hypothesized deeper pools in the Kings River with boulder and wood would be optimal habitat for many species, including Smallmouth Bass (*Micropterus dolomieu*). We conducted snorkel surveys, with four to eight snorkelers moving from downstream to upstream, to determine relative abundances of 14 target fish species/life stages. We snorkeled one pool/run reach at each of 20 sites. Community assemblage structure varied across pool/run reaches (NMS) along a gradient of habitat variables with some reaches being deeper with more percent boulder substrate and others shallower with higher percent sand substrate. Associations between habitat variables and individual fish relative abundances and raw abundances were evaluated using regression tree analyses. For example, higher relative abundances of quality-sized Smallmouth Bass (*M. dolomieu*) were associated with boulder volumes equal to and greater than 36.93 m^3 , whereas higher relative abundances of juvenile and young-of-year *M. dolomieu* were associated with average depths less than 0.43 m. Regression tree analysis results for other species will be discussed. Increased depths were positively associated with 11 of the 14 target species/life stages examined. Structure (boulder) and substrate were also significantly correlated with multiple species/life stages. Our data

highlight the value of deep pools for the maintenance of fish diversity in the Kings River and the potential impacts of continued gravel aggradation.

Genotypic and phenotypic variation in the Rainbow Shiner (*Notropis chrosomus*)

Zachariah Alley, Kayla Fast, and Michael Sandel

The University of West Alabama, Department of Natural Science and Mathematics

Presentation Type: Poster #21

Thursday, 18 November 2021

The Southeastern United States is home to some of the most charismatic freshwater fishes found anywhere in the world. Many of these organisms showcase extensive variation in physical attributes across their geographic ranges, especially in regard to nuptial coloration. *Notropis chrosomus* is a leuciscid species widely recognized for its brilliant colors, communal spawning behavior, and affinity for crystal clear spring runs. This study focuses on genetic and phenotypic variation across the geographic range of *N. chrosomus*. We documented nuptial males from each major sub-basin, sequenced the mitochondrial gene cytochrome B, and calculated meristic measurements in order to determine relationships between phenotypic and genotypic groupings across their geographic range. This study is ongoing, so we present data accrued so far showcasing relationships between geography, genetics and phenotypic variation, with emphasis on nuptial coloration.

Personality traits and colonization decisions by the Creek Chub (*Semotilus atromaculatus*)

Jacob Barrett and Mollie F. Cashner

Austin Peay State University, Department of Biology

Presentation Type: Poster #3

Thursday, 18 November 2021

An increasingly relevant topic in the field of behavioral ecology is the study of animal personality, or individual differences in behavioral traits that are consistent across time and contexts. Personality has been identified in a wide range of animal taxa and has been linked to several ecological characteristics, including dispersal, habitat use, and foraging activity. However, few studies have investigated personality-dependent colonization of discontinuous habitat types or whether personality mediates dispersal patterns by native fauna, and information regarding the existence of personality in fishes native to the southeastern United States is particularly lacking. To that end, we have the specific goals of characterizing personality traits and their relationship to colonization decisions for an important local minnow species, the Creek Chub (*Semotilus atromaculatus*). The Creek Chub presents a unique opportunity to investigate whether personality-dependent processes are important for stream communities more generally due to its piscivorous diet, the use of its nests by a number of nest-associating minnow species, and its status as a known colonizer of intermittent streams. We will measure sociability (tendency to shoal), boldness (latency to emerge from refuge), exploration tendency (movement in a novel environment), and aggression (socially aggressive

displays) from individuals collected from perennial and intermittent streams to compare personality traits between residents and recent colonizers, respectively. We will test the predictions that: (i) individual Creek Chub behave consistently; (ii) Creek Chub exhibit behavioral syndromes; and (iii) personalities of Creek Chub colonizers differ significantly from those of residents based on location of capture.

Does diet of *Luxilus pilsbryi* vary in response to stream drying?

Rebeka Bradford, Sahara Morgan, Jessica Rath, Chance Garrett, Ginny Adams, and Reid Adams
University of Central Arkansas

Presentation Type: Poster #13

Thursday, 18 November 2021

Intermittent streams, characterized by variability in water flow over lengthy periods of time, play an essential role in preserving nutrients and biotic diversity within an overall stream network. Adaptations of fishes to these unique environments include increased diet breadth and, in one study, changes in gut length during summer months when food quality and quantity decreased. However, studies on the effects of seasonal intermittency on diet have not been conducted. *Luxilus pilsbryi* is known to inhabit intermittent streams of the Ozarks, with its diet including invertebrates and vegetation. Individuals were collected during winter, spring, summer, and fall from Rockhouse Creek: an intermittent tributary of the Kings River. Previous research found body condition of *L. pilsbryi* to be significantly higher in spring compared to other seasons (ANCOVA, $P<0.01$) and gut length (adjusted for standard length) varied significantly across seasons. However, the underlying mechanism for this variation was still unknown. Gut contents from previously dissected individuals were examined and identified to the lowest possible taxon, enumerated, and weighed. Fish collected in spring (0.00956 g) consumed more food content (based on mass) relative to summer (0.00336 g), winter (0.00325 g), and fall (0.00477g). Winter and spring stomach contents consisted mostly of aquatic invertebrates; however, the bulk of stomach contents during summer and fall seasons were composed of amorphous material. Plant/detritus was predominantly consumed in summer and fall. The shift to a plant/detritus diet corresponded with a lower condition in individuals during those seasons. Our data suggest *L. pilsbryi* are unable to compensate during low/poor food periods through morphological adjustments of gut length and may reflect their facultative association with intermittent headwater streams compared to obligate headwater species.

Characterizing variation in black-spot disease among small stream fishes using historical collections from the Spring River drainage (Arkansas and Missouri; 1970s)

Benjamin Brown, Landen Ho, Tyler B. Brown, Lindsey A. Martin, Amelia Atwell, Dylan DeRouen, Crystal Griffin, Alexis Mross, Clayton Vondriska, Jacob Wessels, and Brook L. Fluker

Arkansas State University, Department of Biological Sciences

Presentation Type: Poster #18

Thursday, 18 November 2021

Freshwater fishes commonly exhibit “black-spot disease”, which results from encystment of digenetic trematodes into the fins and flesh of the fish. As an immune response, the fish deposits melanin around the encysted trematode, producing the black spots for which the disease is named. The fish serves as an intermediate host in the life cycle of the trematode, but little is known about the prevalence, timing, and consequences of trematode infestations on small stream fishes. The objective of this study was to evaluate the prevalence, timing, and body condition association of black-spot disease among several fish species throughout Myatt Creek, a tributary to the Spring River in northeastern Arkansas. Fish specimens collected seasonally from 9 sites in Myatt Creek in the 1970s were obtained from the Arkansas State University Museum of Zoology (ASUMZ) and examined for abundance of black-spot infection, mass, and Standard Length (SL). Infection rates were compared to body condition (i.e., the coefficient of condition [$K = W \times 10^5 / L^3$]), where W = mass in grams and L = standard length in millimeters. Preliminary results suggest that infection rates differ among the five species examined. Relationship of body condition and black spot infection rate also show varying patterns among species, with some having a positive relationship, and some showing no significant relationship. Spatial and temporal aspects of black spot infection among fishes from Myatt Creek will further be evaluated in the context of a better understanding of “black-spot disease” on small stream fishes.

Morphological differences and associated habitat partitioning among three species of *Percina* (Percidae: Actinopterygii) in the Roanoke River, Virginia

Michael M. Calvert and Steven L. Powers

Roanoke College

Presentation Type: Virtual, lightning

10:50 Friday, 19 November 2021

The upper Roanoke River has three species of *Percina* (*P. nevisense*, Chainback Darter; *P. roanoka*, Roanoke Darter; and *P. rex*, Roanoke Logperch). Resource partitioning appears to be a key component of maintaining diverse fish assemblages with habitat and food partitioning cited as especially important in communities containing closely related species. The diets of these species have been documented in the literature with only modest differences among them. Microhabitat data for these species have also been published revealing differences in habitat occupied by each with *P. roanoka* living in the fastest, shallowest water and *P. nevisense* in the deepest, slowest water. In an effort to correlate morphological adaptations to these different microhabitats, 18 body measurements were taken from specimens of each species. Fineness ratios were calculated and compared among species. Raw measurements were also included in a Principal Component Analysis. The highest mean fineness ratio was found in *P. nevisense*, and the lowest was found in *P. roanoka* with *P. rex* having intermediate values. Principal component two loaded heavily for body width, body depth, and dorsal fin height, while principal component three loaded heavily for anal fin length and caudal fin depth. Scatterplots of principal component scores showed little to no overlap among species and revealed more elongate body and taller spinous dorsal fin in *P. nevisense*, deeper caudal fin and longer anal fin

in *P. roanoka*, and generally intermediate PC scores for *P. rex*. These morphological variables appear to be adaptations to the habitats each of these species occupies.

Population genetic assessment of the endangered Cumberland Darter (*Etheostoma susanae*)

Hilary K. Canada¹, M. Taylor Perkins², Anna L. George², Bernard R. Kuhajda², and Brook L. Fluker¹

¹Arkansas State University, Department of Biological Sciences

²Tennessee Aquarium Conservation Institute

Presentation Type: Poster #19

Thursday, 18 November 2021

The Cumberland Darter (*Etheostoma susanae*) is an endangered species of freshwater fish endemic to the tributaries of the Cumberland River above the Cumberland Falls in Kentucky and Tennessee. Once recognized as a subspecies of Johnny Darter (*E. nigrum*), *E. susanae* was elevated to species level based on morphological and mtDNA variation. Habitat degradation and modification is a primary concern for the species with its preference for slow-flow streams. Fragmented populations increase the risk of disrupting historic gene flow between tributaries which could potentially result in genetically distinct populations. Fin clips were obtained from eight localities across the range of *E. susanae* for a total of 188 samples. An additional 86 samples were collected for comparative purposes from four localities for *E. nigrum*, two of which were thought to be potential hybridization zones for *E. susanae* and *E. nigrum* in the Cumberland and Upper Kentucky River drainages. Samples combined for both species totaled to 274 individuals obtained from 11 sample sites. To better understand the evolutionary history, patterns of genetic structure, and the potential for hybridization between *E. susanae* and *E. nigrum*, we analyzed data from both mitochondrial DNA (mtDNA) and microsatellite DNA loci. Microsatellites and mtDNA revealed no evidence of recent or ongoing hybridization or introgression between *E. susanae* and *E. nigrum*. Microsatellite data further revealed moderate to high levels of genetic structuring among several populations of *E. susanae*. These results will later be combined with ongoing RADSeq data analyses, providing a comprehensive genetic roadmap that will be useful for conservation and management strategies involving *E. susanae*.

What's going on down south: re-examining the distribution of two species of *Labidesthes* across Mississippi using preserved collections

Benjamin H. Chaffins, Robert J. Ellwanger, and Calvin R. Rezac

Mississippi Museum of Natural Science

Presentation Type: Poster #2

Thursday, 18 November 2021

The *Labidesthes* species complex is widely distributed throughout the freshwaters of the Midwestern and Southeastern United States. Prior to the 1950s, the genus *Labidesthes* was represented by the Brook Silverside (*Labidesthes sicculus*) and the Hardy Silverside (*Labidesthes vanhyningi*), but was synonymized under *L. sicculus* in 1954 (Bailey et al). In 2015, Werneke and

Armbruster re-described the *Labidesthes* complex elevating *L. vanhyningi* based on several phenotypic characteristics. *Labidesthes vanhyningi* was distinguished from *L. sicculus* by the presence of an anterolateral process of the post temporal that is wider than is long (vs. longer than it is wide), an anteriorly broadening midlateral stripe (vs. anteriorly thinning), and a ratio of thoracic length to abdominal length of less than two (vs. greater than two). Additionally, Werneke and Armbruster established that *L. vanhyningi* was found to primarily inhabit coastal drainages in the Southeastern United States, while *L. sicculus* was found to occur further inland. However, apart from within the Tombigbee and Tennessee river drainages, both species were found to be sympatric throughout Mississippi. Previous ichthyologists at the Mississippi Museum of Natural Science (MMNS) had not differentiated between the two *Labidesthes* species and had cataloged all *Labidesthes* as *L. sicculus*, warranting a re-identification of all *Labidesthes* specimens to better understand the distribution of *Labidesthes* throughout Mississippi. We re-identified 14,267 specimens from 1,161 lots using methods established by Werneke and Armbruster (2015), which resulted in 63% (732/1,161) of the MMNS lots re-identified as *L. vanhyningi*. Our findings support that *L. vanhyningi* is the prevalent species in Gulf of Mexico drainages and suggest a recent species exchange via the Tennessee-Tombigbee Waterway. This project not only updates the MMNS ichthyological collection to reflect contemporary taxonomy, but also adds to our knowledge of the distribution of the two species within Mississippi.

Are weight-length parameters of coastal Alabama stream fishes linked with life history traits and environmental variables?

S. A. R. Colvin^{1,3}, Russell A. Wright², D. R. DeVries², and J. W. Feminella¹

¹Department of Biological Sciences, Auburn University, Auburn, AL

²School of Fisheries, Aquaculture, and Aquatic Sciences, Auburn University, Auburn, AL,

³Department of Biological Sciences, Arkansas Tech University, Russellville, AR

Presentation Type: Virtual, Oral

9:00 Friday, 19 November 2021

Weight-length relationships (WLRs) are foundational elements in fisheries research but have infrequently been investigated for non-game species or across environmental gradients. We quantified WLR patterns of 17 Alabama coastal stream fish species in both clearwater and blackwater streams to assess if they differed between stream types, life history traits, and environmental variables. We used a log¹⁰-transformed length-weight regression for each species and used multi-level mixed models within and across species to determine if WLR differed between stream types and to quantify correlations between log W and measured environmental and biotic factors. We also compared differences in size-related shifts in growth stanzas between blackwater and clearwater populations, across feeding trait types, and quantified whether levels of longevity and fecundity influenced at what size these shifts occur by examining differences in inflection points in weight-length plots. We found a lower WLR slope across all species in lower-benthic macroinvertebrate (vs. blackwater) clearwater streams. Log weight across species was positively related to benthic invertebrate density, discharge, coarse woody debris abundance, and negatively correlated with dissolved organic

carbon concentration. Inflection points (shift in growth stanzas) were lower for clearwater stream indicator species and surface/water column feeders. Inflection points increased with an increase in species longevity and decreased with increasing fecundity. Overall, our results indicate that environmental and life history parameters, stream type, and traits all influenced WLRs. Our work provides a baseline for understanding WLR relationships for species in these ecosystems and an approach that can be applied to this and additional systems to identify potential mechanisms in changing emergent properties such as species rearrangement and declining biodiversity in stream ecosystems.

Acoustic modulation of reproductive hormones in the Blacktail Shiner (*Cyprinella venusta*), a soniferous cyprinid

Jenna Crovo¹, Mary Mendonca², and Carol Johnston¹

¹Auburn University, School of Fisheries, Aquaculture, and Aquatic Sciences

²Auburn University, Department of Biological Sciences

Presentation Type: In Person, Student

11:00 Thursday, 18 November 2021

Animal communication networks consist of multisensory signals and often include an acoustic element. A large number of freshwater fishes, including the blacktail shiner (*Cyprinella venusta*), produce specific vocalizations during courtship and agonistic behaviors. Similar to other vocal taxa, fish communication networks are vulnerable to noise pollution. The dominant frequencies of anthropogenic noise often overlap spectrally with animal acoustic signals. To investigate the role of acoustic signaling in breeding soniferous fishes in a physiological context, we conducted a series of acoustic playback trials. We measured waterborne levels of estradiol (E2) and prostaglandin F2-alpha (PGF) in gravid females exposed to courtship calls, and levels of 11-ketotestosterone (11KT) in males exposed to agonistic calls. In a separate series of trials, we exposed individuals to calls masked with bridge traffic noise. Hormone levels were quantified using enzyme-linked immunosorbent assays (ELISA) and analyzed using repeated measures ANOVAs. Gravid females exhibited a significant drop in E2 ($p = 0.023$) and an increase in PGF during courtship calls ($p = 0.01$). Our research suggests that growl signals contribute to the onset of spawning behaviors in female *C. venusta* and this response may be dampened by anthropogenic noise pollution.

The effects of surface mining on population connectivity and genetic diversity of *Etheostoma sagitta spilotum*, the Kentucky Arrow Darter

Alexis V. Culley¹, River A. Watson¹, Matthew R. Thomas², Stephanie L. Brandt², Michael A. Floyd³, and Rebecca E. Blanton¹

¹Austin Peay State University, Department of Biology and Center of Excellence for Field Biology, Clarksville, TN

²Kentucky Department of Fish and Wildlife Services, Frankfort, KY

³United States Fish and Wildlife Service, Frankfort, KY

Presentation Type: Poster #9

Thursday, 18 November 2021

The Kentucky Arrow Darter (KAD), *Etheostoma sagitta spilotum*, is endemic to first and second order headwater streams in the Upper Kentucky River Basin. This species was listed as threatened under the Endangered Species Act by the United States Fish and Wildlife Service in 2016 due to declines in occurrence and population size attributed to extensive habitat degradation, particularly from mining activities, across its range. Blanton et al. 2019 (using samples from 2014) used mitochondrial and microsatellite markers to examine historic and contemporary levels of genetic diversity and population isolation. They found that historically (pre-human influence), populations of KAD maintained some level of gene flow across its range, while all contemporary populations were genetically isolated and showed signatures of recent reduction in genetic diversity. Our objectives were to use the same 11 microsatellite markers of Blanton et al. (2019) to assess the impacts of surface mining on population connectivity and genetic diversity in KAD and to describe any changes in these metrics that may have occurred over the past 6 years. A total of 130 KAD tissue samples have been collected from seven of the ten localities examined by Blanton et al. (2019); DNA was extracted from all individuals and genotyping of microsatellite loci is ongoing. Spatial analyses were used to identify and quantify surface mines that impact targeted KAD populations. These mining data will be used to build resistance models in Circuitscape to examine the impact of mining on population level genetic diversity and the degree of population isolation observed in this species. Preliminary results of this ongoing study will be presented and discussed.

Finding the freckled: focusing efforts to find Freckled Darter (*Percina lenticula*) in Mississippi

Noah Daun and Jake Schaefer

The University of Southern Mississippi, Department of Biological Sciences

Presentation Type: In Person, Student

10:00 Thursday, 18 November 2021

Understanding the status of a species can be influenced by the ease in which their preferred habitat can be effectively sampled through general sampling means. The Freckled Darter (*Percina lenticula*) is a species of concern in Mississippi due to the low number of historical collections. Native to the Pascagoula, Pearl, and Mobile drainages, this large darter species is known to inhabit deep, fast-flowing water and is associated with Coarse Woody Debris (CWD). As such, Freckled Darter are not frequently caught in seines. Our primary objectives for this study was to sample individual CWD patches in these mainstem rivers and their large tributaries using electrofishing techniques to better assess the status of the species in the Pearl and Pascagoula drainages, with a focus on resampling historical localities. Our secondary objective was to analyze environmental and assemblage data to better understand variables associated with presence of Freckled Darter. In addition to electrofishing, eDNA detection was also used to verify presence of the species in 12 sites in the Pearl and Pascagoula drainages. We sampled 82 CWD patches and caught 21 individuals among 10 different patches. This study will provide information to make an accurate assessment of the populations of Freckled Darter in

Mississippi and help us better understand the importance of the under-sampled habitats that they occupy.

Relationships between constructed waterbodies and homogenization of fish assemblages in the Black River watershed of Arkansas

Grace Davenport¹, Jennifer Main², George Gavrielides³, Calvin Rezac⁴, Ginny Adams¹, and Reid Adams¹

¹University of Central Arkansas, Department of Biology, Conway, AR

²University of Arkansas, Department of Education, Fayetteville, AR <

³Southern Ute Indian Tribe, Water Resources Division

⁴Mississippi Department of Wildlife, Fisheries, and Parks, Research Department of Mississippi Museum of Natural Science

Presentation Type: In Person, Student

11:15 Thursday, 18 November 2021

Although many studies have focused on the impacts of large reservoirs on stream fish assemblages, few data have been published on the influences of farm ponds and small impoundments. Impoundments are often negatively correlated with stream fish diversity and may lead to homogenization of fish assemblages due to species introductions and extirpations. Previous research suggests fishes typically associated with farm ponds and impoundments (referred to collectively as constructed waterbodies, or CWs) have increased in some rivers within the Black River watershed. This study investigates relationships between CWs and fish assemblages in the Strawberry, Eleven Point, Spring, and Fourche rivers. The USGS StreamStats program was used to delineate upstream catchments of each site, and Google Earth Pro was used to quantify a suite of variables, including distance of CWs from the stream, area of CWs, and whether connectivity between CWs and the stream was evident. We measured 812 CWs across 23 sites in the Strawberry River, 234 across 13 sites in the Eleven Point River, 1,801 across 23 sites in the Spring River, and 243 across 9 sites in the Fourche River watersheds. Using historical and contemporary fish assemblage data at 68 sites, stability was positively correlated with mean distance of CWs to the stream ($\rho = 0.29$). Redear sunfish relative abundance (RA) was positively correlated with number of CWs in the upstream catchment ($\rho = 0.30$). Increase in largemouth bass RA was negatively correlated with mean distance of CWs to the stream ($\rho = -0.31$). Mean area of CWs was positively correlated with contemporary RA of bluegill ($\rho = 0.33$) and increase in bluegill RA ($\rho = 0.27$). Catchment-scale analyses suggest CWs could be influencing fish assemblages in the Black River watershed. Analyses conducted at a finer spatial scale will also be discussed.

Reproductive timing in *Percina aurora* and other *Percina* sp. in the Pascagoula River watershed

Malia Davidson¹, Noah Daun¹, Scott Clark², Brian Kreiser¹, Jake Schaefer¹

¹University of Southern Mississippi, Department of Biological Sciences

²U.S. Fish and Wildlife Service, Baton Rouge Fish and Wildlife Conservation Office

Presentation Type: Poster #6
Thursday, 18 November 2021

Understanding the timing, duration and effort put into reproduction is vital to successful management of any species. The southeastern US is home to tremendous levels of aquatic biodiversity. The region was recently named one of the Earth's biodiversity hotspots. Within this region, growing human populations continue to put pressure on aquatic ecosystems and the resident species. Within freshwater fishes, darters represent a large proportion of the diversity in the southeastern US. However, for some species the fundamentals of reproduction timing, effort and ecology remain poorly understood. The purpose of this project was to examine the reproductive ecology of Pearl Darters (*Percina aurora*), and other coexisting *Percina* species in the Pascagoula River basin. To do this, the gonadosomatic index (GSI) of four *Percina* species were examined to find the reproductive window of these species. Including *Percina aurora*, the other three species included were *Percina vigil*, *Percina sciera* and *Percina suttkusi*. Specimens were collected from the Pascagoula River Basin of southeastern Mississippi starting in late February through late June. The goal was to find the spawning window of each species as there may be some overlap with the Pearl Darter. This overlap could lead to larval competition for resources, placing another stressor on the threatened Pearl Darter. To include a baseline for the average gonad size away from spawning season Pearl Darters collected in the late summer; early fall were included. Some juveniles were also included for comparison.

Parentage assessment of the Egg-mimic Darter (Percidae: *Etheostoma pseudovulatum*) demonstrates complex patterns of allopaternal care behavior

Nastasia T. Disotell, Zachary L. Wolf, Mollie F. Cashner, and Rebecca E. Blanton

Austin Peay State University

Presentation Type: In Person, Student

10:45 Thursday, 18 November 2021

Alloparental care has been documented in several clades of animals, including fishes. Despite the increased energy cost of caring for more offspring, care of non-descendent young has potential benefits, including mate attraction or reduced egg predation. Male Egg-mimic Darters, *Etheostoma pseudovulatum*, like other members of clade *Goneaperca*, construct nests under rocks and guard eggs until hatched. Two species from this clade, *E. virgatum* and *E. olmstedi*, exhibit allopaternal care; whether this is a common strategy for the clade is not known. Furthermore, the potential benefits of kin-selection or how nest density or male size influence such behaviors have not been tested. We genotyped 352 eggs and 23 guarding males of *E. pseudovulatum* from 19 nests using 9 microsatellite loci; other non-guarding males and females were also genotyped to identify the following: (1) if allopaternal care occurs in this species, (2) if kin-selection is one benefit of allopaternal care, and (3) if male size or nest position correlates to the occurrence of non-descendant eggs in a nest. Parentage was estimated using Cervus (v 3.0). We found that allopaternal care occurred in 10 out of 19 nests examined. Male size was not correlated to the proportion of non-descendant eggs in a nest. Alloparent males were more related to non-sired eggs than the mean relatedness of the overall population, suggesting kin-

selection may be one benefit of this behavior. The complex alloparent patterns observed also suggest these fishes engage in strategies such as cuckoldry or nest takeovers. Our study reveals a potential selective benefit of allopaternal care and further suggests this behavior may be a trait shared by all *Goneaperca* clade members.

Pinpointing biodiversity hotspots: local habitat and regional connectivity shape fish richness along rivers with contrasting habitat diversity

Corey Dunn¹ and Craig Paukert²

¹U.S. Geological Survey, Mississippi Cooperative Fish and Wildlife Research Unit; Mississippi State University, Department of Wildlife, Fisheries, and Aquaculture

²U.S. Geological Survey, Missouri Cooperative Fish and Wildlife Research Unit; University of Missouri, School of Natural Resources

Presentation Type: Virtual, Oral

9:45 Friday, 19 November 2021

Connectivity and habitat diversity are generally regarded as important for structuring riverine assemblages, but their specific contributions to riverine fish richness are often unclear. We sampled fish assemblages along ≥ 200 km of nonsaleable mainstems (fifth–seventh orders) and tributary branches of the Grand (low habitat diversity) and Meramec (high habitat diversity) river systems (Missouri, USA). We asked whether habitat diversity and regional connectivity explained site-level fish richness of three stream-size preference guilds: core riverine species, large-river specialist (LRS) dispersers from the Mississippi and Missouri rivers, and headwater species dispersing from network branch streams (\leq third order). We defined biodiversity hotspots as sites with high fish richness ($\geq 75^{\text{th}}$ percentile) and examined whether occurrences of LRS and headwater species shifted hotspots longitudinally compared to hotspots defined solely by corespecies. Species richness peaked in mid- to lower-courses in both rivers (maximum richness = 39 species in Grand River, 73 species in Meramec River) but not at either river's mouth. Downriver connectivity (distance to Missouri/Mississippi rivers) and habitat diversity predicted LRS- ($R^2 = 0.44\text{--}0.91$) and core-species ($R^2 = 0.37\text{--}0.57$) richness, respectively. Densities of headwaters within 25 fluvial km of sites positively related to headwater species richness in the Grand River system ($R^2 = 0.85$) but not the Meramec River system, indicating rivers constrained headwater species pools differently. Biodiversity hotspots based on core species extensively spanned sites with high habitat diversity, covering 63% (Grand) and 50% (Meramec) of mainstem sites. When viewing all species collectively, contributions of LRS species (13–17 species) to hotspots outweighed those of headwater species (≤ 6 species), causing hotspot spatial extents to narrow and shift downriver. Overall, riverine assemblages contained downriver, core, and headwater constituents, and thus, conserving hotspots likely requires strategies that preserve both habitat diversity and connectivity to surrounding regional species pools.

Using ecological niche modeling and genomic analysis to investigate established populations of the Green Swordtail, *Xiphophorus hellerii*, in north Florida

Anna N. Eastis¹, Zachary W. Culumber², Carla Gutiérrez-Rodriguez³, and Michael W. Sandel¹

¹The University of West Alabama, Department of Biological and Environmental Sciences

²The University of Alabama in Huntsville, Department of Biological Sciences

³Instituto de Ecología A.C., El Haya, Xalapa 391070, Veracruz, México

Presentation Type: In Person, Student

13:30 Thursday, 18 November 2021

The Green Swordtail, *Xiphophorus hellerii*, is a Neotropical freshwater fish species that has been introduced to non-native watersheds worldwide through the aquarium trade. Introduced Green Swordtail populations are associated with the decline of native fish and invertebrate communities, some of which are protected by the Endangered Species Act. The Green Swordtail is now established in 15 US states and territories, with Florida reporting the most number of observations and occupied watersheds. We report three newly discovered Green Swordtail populations in North Florida, and provide results of population genetic analysis and Ecological Niche Models (ENMs) designed to investigate the geographic origin and potential range expansion of the species in the southeastern US. We used double-digest RADseq (DArTseq) to generate 19,578 single nucleotide polymorphisms (SNPs) for population genomic analysis. Results of phylogenetic and ancestry assignment analyses provide support for a monophyletic clade containing all invasive Green Swordtail populations, with negligible introgression from domesticated congeners (i.e. *X. maculatus*, *X. variatus*). Invasive populations were found to be most closely related to native populations in the Rio Coatzacoalcos watershed of northeastern Oaxaca and eastern Veracruz, Mexico. ENMs inferred from native climate data fail to predict suitable habitat for the North Florida populations, even though these populations have persisted for at least 14 years in a subtropical climate. Our research highlights the importance of conservation threats posed by the ornamental fish trade, as well as the limitations of Ecological Niche Modeling for freshwater taxa. Results presented here will aid in the development of management strategies for invasive freshwater fishes of Florida and similarly impacted regions.

Status survey of freshwater mussels in the Big Black River, Mississippi

Robert J. Ellwanger, Calvin R. Rezac, and Benjamin Chaffins

Mississippi Department of Wildlife Fisheries and Parks: Mississippi Museum of Natural Science

Presentation Type: In Person, Lightning

11:25 Friday, 19 November 2021

An updated distribution of Trispot Darter breeding habitat

Anakela Escobar¹, Rebecca A. Bearden², Stuart W. McGregor², Daniel A. West², Michael W. Sandel³, Kayla M. Fast³, and Gary A. Hastert²

¹Georgia Department of Natural Resources, Social Circle, Georgia

²Geological Survey of Alabama, Tuscaloosa, Alabama

³University of West Alabama, Livingston, Alabama

Presentation Type: In Person, Lightning

11:10 Friday, 19 November 2021

The distribution and habitat status of freshwater mussels in the Wolf River, TN

Jack Fettters¹, Amanda Rosenberger², and Anthony Ford³

¹Tennessee Technological University Cooperative Fisheries Unit

²U.S. Geological Survey, Tennessee Cooperative Fishery Research Unit

³U.S. Fish and Wildlife Service, Tennessee Ecological Services Field Office

Presentation Type: Poster #22

Thursday, 18 November 2021

Tennessee has the second most diverse freshwater mussel fauna in the United States, with 139 species of historical occurrence, most of which, have some form of conservation status. The Cumberland River system in Tennessee and Kentucky has one of the most diverse assemblages in the world, including several species that are federally listed as endangered. The Obey River system, a large tributary of the Cumberland River, once contained 35 species. Now most of these historical occurrences are inundated by Dale Hollow Lake and have been nearly eliminated due to acid mine drainage in the river headwaters. The Wolf River, the largest tributary of the Obey River, remains a critically important stronghold of the Cumberland River mussel fauna. In a previous study, a 31 km length of the Wolf River was surveyed in 2005-2006. Using visual and tactile methods, they located nine live mussel species, and 24 of 45 sites sampled contained mussels with signs of recruitment. For this study, we resurveyed all 45 previously investigated sites. We used similar, but more intensive methods, to determine current mussel assemblages with particular emphasis on the federally endangered Fluted Kidneyshell *Ptychobranchus subtentus*. We found seven of the nine species found in 2005-2006, with live mussels at 33 of the 45 sites. Moreover, we located several species rich sites with *P. subtentus* as the most abundant species. Future direction for this project will entail returning to areas with high species richness and local abundance, and resurvey with more intensive survey methods to determine densities and size-structure. Additionally, using remotely-sensed data, a basin-wide habitat assessment will be conducted to identify potential habitat for mussels or problem areas that could be targeted for restoration. These preliminary findings emphasize the importance of the Wolf River Mussel fauna due to its unique mussel assemblages and high potential for restoration.

Assessing the efficacy of a barrier assessment method and the connectivity of headwater fish: an experimental approach

Langston Haden¹, Jake Schaefer¹, and Scott Clark²

¹The University of Southern Mississippi, Department of Biological Sciences

²United States Fish and Wildlife Service, Baton Rouge Fish and Wildlife Conservation Office

Presentation Type: Poster #12

Thursday, 18 November 2021

The connectivity of populations particularly in dendritic networks is essential for the retention of genetic diversity, ample habitat, access to resources, and overall ecosystem function. Riverine ecosystems are dendritic networks which have become increasingly threatened by fragmentation due to in-stream barriers. Within riverine networks, culverts are the most common type of barrier to aquatic organismal passage (AOP). Studies on the effect of culverts on fish connectivity have been biased towards economically important species and primarily consist of small-scale mark-recapture and large scale modeling approaches. Barrier surveys have been developed to rapidly assess culverts for AOP, but consistent support and studies investigating the efficacy of these surveys are lacking. Additionally, more information is needed to understand the connectivity of small-bodied headwater fish which account for much of the freshwater biodiversity in the southeastern U.S. The goal of this study was to 1) use a novel experimental approach to assess the efficacy of a common barrier survey, and 2) to determine the connectivity of stream fish within the range of the federally threatened Louisiana Pearlshell Mussel (*Margaritifera hembeli*). We conducted SARP (Southeast Aquatic Resource Partnership) barrier assessments at all accessible sites across two watersheds. 6 sites with varying SARP AOP scores were selected to conduct mark-recapture studies over a 2-year study period. Of the 49 culverts surveyed, 11 (22%) were identified as moderate barriers and 9 (18%) were identified as significant or severe. Initial marking survey's resulted in the capture and marking of 3,162 fish across 29 species. The mean recapture percentage was relatively high (11.1%), but varied depending on the site. Further recapture samples are needed to make conclusions, but preliminary recapture results reflect varying AOP across the 6 sites.

Modeling habitat suitability for the globally imperiled Etowah Darter (*Etheostoma etowahae*)

Clayton W. Hale¹ and Brittany L. McCall²

¹University of Georgia, Integrated Plant Sciences

²Arkansas State University, Department of Environmental Sciences

Presentation Type: In Person, Student

11:45 Thursday, 18 November 2021

The Etowah Darter (*Etheostoma etowahae*) is a globally imperiled percid species endemic to the Etowah River system in northern Georgia, USA. Federally listed in 1994, the Etowah Darter faces a myriad of threats to its persistence including: impoundment, point and non-point source pollution, and inappropriate silvicultural management practices. In recent years, population trends have remained steady with a new population being discovered, potentially representing a range expansion for the species. However, little is known of other potential suitable habitats within the Etowah River system. Modeling a species' habitat suitability can allow conservationists to focus limited human and financial conservation resources on areas most likely to support the species. This study presents a habitat suitability model for the Etowah Darter across the Etowah River System utilizing maximum entropy (maxent) with eight biologically relevant hydrologic environmental factors and fifteen known occurrences. The map produced by the maxent model was then classified into bins for further spatial analysis. Overall,

only 0.3% of the study area was within the highest bin of habitat suitability (0.9-1), and 5% of the study area was within the two highest bins (0.8-1). Such a low percentage of the total study area within the highest bins of habitat suitability indicates the species is highly restricted, even within the watershed it occupies. The presented model could focus searches for new populations of the Etowah Darter, direct the protection of critical habitat, and, if ecologically appropriate, new populations could be established in river segments of high habitat suitability.

The clutch concept and the reproductive biology of small fishes

David C. Heins¹ and Nancy J. Brown-Peterson²

¹Tulane University, Department of Ecology and Evolutionary Biology

²The University of Southern Mississippi, Center for Fisheries Research and Development

Presentation Type: In Person, Oral

11:30 Friday, 19 November 2021

Application of the clutch concept in studies of the reproductive biology of small fishes will be reviewed. Direct macroscopic observations of stages of ovarian development, oviposition, clutch counts, clutch frequency, and estimates of fecundity traditionally used to estimate important reproductive metrics will be reviewed. Histological methods also have value for determining ovarian development and spawning interval (i.e., number of days between spawns) although histological methods have been used less commonly for examining the reproduction of small fishes. We will review the advantages of histological methods for determining the potential number of clutches fishes can produce.

Life history theory for environmental analysis of stream fish communities near the Potomac River

Nathaniel P. Hitt¹, Andrew P. Landsman², and Richard L. Raesly³

¹US Geological Survey, Eastern Ecological Science Center

²National Park Service, Chesapeake and Ohio Canal National Historical Park

³Frostburg State University, Department of Biology

Presentation Type: Virtual, Oral

9:15 Friday, 19 November 2021

We applied life history theory to evaluate local and regional influences on stream fish communities sampled near their confluence with the Potomac River mainstem (< 1 km). The dataset included 20 sites sampled in 2018-2019 and contained 51 species within 10 taxonomic families. Multivariate analysis of life history traits demonstrated trade-offs between fecundity, spawning season length, and parental care indicating opportunistic, periodic, and equilibrium-based strategies for survival and reproduction. Analysis of trait-environment interactions revealed effects of elevation, watershed size, and forest cover as well as the size of the mainstem river near stream sites, suggesting the importance of regional movement dynamics. Our results highlight the utility of life history theory for fish community analysis and the importance of management and conservation planning at the landscape scale.

Effects of stream gradient on darter functional morphology in the Pomme de Terre River

Topher Hockaday and Aaron Geheber

University of Central Missouri

Presentation Type: Poster #20

Thursday, 18 November 2021

Darters are a group of small benthic freshwater fishes endemic to North America that often occur in fast moving riffle habitats. Previous research has indicated that stream flow may impact darter morphology, possibly through plastic response and or natural selection processes. The goal of this study was to quantify the effects of stream gradient factors (i.e., related to flow) on functional morphological traits of *Etheostoma spectabile* (Orangethroat Darter) and *Etheostoma caeruleum* (Rainbow Darter) within the Pomme de Terre River, Missouri, USA. Using specimens collected from 11 distinct stream sites, we examined darter geometric morphometric data based on 15 homologous lateral landmarks and seven homologous dorsal landmarks. Moreover, we manually measured pectoral fin surface areas, scaled to body length, for all individuals. To explore environmental factors influential on darter morphology, we gathered abiotic stream data from each site including elevation, flow velocity, stream depth, and substrate type. Morphometric data were visualized using Principal Component Analysis to assess body shape differences among individuals. We then used regression to examine relationships between the resultant Principal Component scores and abiotic stream factors. Our analyses suggest that individuals of both species found in higher elevations had larger, broader heads, while individuals from lower elevations had longer and laterally compressed heads. The perceived functional benefits of such morphological alterations in relation to abiotic stream gradient features will be discussed.

Distribution, abundance and occupancy of the Striated Darter (*Etheostoma striatulum*) in the Duck River

Abbey Holsopple and Kit Wheeler

Tennessee Technological University, Department of Biology

Presentation Type: In Person, Student

14:00 Thursday, 18 November 2021

The Striated Darter (*Etheostoma striatulum*) is a species endemic to the Duck River system in Tennessee that is listed as state endangered and currently under review for federal listing. Historically, the species range included the mainstem Duck River and tributaries throughout Bedford, Coffee, Lewis, Marshall and Maury Counties. Previous species surveys in 1992 and 2006 noted low densities and high potential for local extirpations. We deployed similar sampling techniques in 2020-21 to better understand the current status of the species. We captured Striated Darters at 10 of 26 survey sites using seining, and subsequent snorkeling surveys produced detections at two additional sites. Collectively, we detected Striated Darters at 12 sites distributed over eight streams. We found Striated Darters at four sites where they

were undetected in 2006; however, three of the 11 occupied sites from 2006 did not produce individuals in our surveys. One occupied site from the 1992 survey did not produce individuals in either subsequent survey. Because the number of occupied sites is similar between our survey and the 2006 survey, we tentatively conclude that the distribution of the Striated Darter has not changed considerably over the past 15 years. We generated mark-recapture abundance estimates at two sites that were three to five times greater than 2006 abundance estimates. We used data collected during seining to construct candidate models and estimate probabilities of site-level occupancy (mean=40%) and detection (mean=71%). We modeled effects of land use, competition, and predation on occupancy, and effects off low and turbidity on detection. The top-fitting model had constant values of occupancy and detection but was not substantially better than all other fitted models. Among models considered credible, none included predation. Model-averaged estimates of covariate effects were imprecise but suggested that land use and competition may affect Striated Darter occupancy, and that discharge may impact detection slightly more than turbidity.

Nutrient subsidies from migratory fishes: evaluating drivers of ammonium excretion rates in multiple catostomids

Ryan Hudson and Kit Wheeler

Tennessee Tech University, Department of Biology

Presentation Type: Poster #10

Thursday, 18 November 2021

Ecologists recognize the capacity for animals to move substantial resource subsidies across spatial boundaries that can have profound effects on recipient ecosystems. Resource subsidies coming from fishes are usually represented as inputs of nitrogen (N) and phosphorus (P), as they are the two nutrients most commonly limiting primary production in freshwater ecosystems. Fishes can deliver a source of dissolved inorganic nitrogen directly, in the form of ammonium (NH_4^+), by excreting it through their gills as waste. However, there is a limited understanding of factors that influence N-excretion subsidies and the extent to which excreted N is retained by recipient ecosystems. Every spring, migrations of fishes known as redhorse occur throughout the Hiwassee River Basin in portions of Tennessee, North Carolina, and Georgia. In Brasstown Creek, the migration consists of Silver Redhorse (*Moxostoma anisurum*), Black Redhorse (*Moxostoma duquesnei*), Sicklefin Redhorse(*Moxostoma* sp.), Golden Redhorse (*Moxostoma erythrurum*), and River Redhorse (*Moxostoma carinatum*). Here, we assessed what independent variables affected rates of excretion in Brasstown Creek redhorses during the 2021 spawning migration. The variables evaluated in this study were species, sex, body size (as mass and length), and water temperature. Species and sex had no significant effect on excretion rate, whereas water temperature and body size were positively correlated with excretion rate. Moving forward, the results of these analyses will be used to estimate the quantity of NH_4^+ delivered to Brasstown Creek via redhorse excretion, and this will be compared with the total quantity of NH_4^+ exported from the Brasstown Creek watershed.

Assessing the validity of three currently recognized subspecies of the Blacktail Shiner (*Cyprinella venusta*) through the use of next generation sequencing

Soren Johnson and Kyle R. Piller

Southeastern Louisiana University, Department of Biological Sciences

Presentation Type: In Person, Student

14:15 Thursday, 18 November 2021

The Blacktail Shiner, *Cyprinella venusta* (Cypriniformes: Leuciscidae), is abundant throughout lotic systems in the southeastern United States. This species consists of three morphologically defined subspecies: *C. v. venusta*, *C. v. cercostigma*, and *C. v. stigmatura*. The validity of these subspecies has been challenged by mitochondrial genetic work which recovered four distinct clades that did not fully align with the ranges of the morphologically diagnosed subspecies. We used next generation sequencing to assess the phylogenetics and genetic population structure of *C. venusta* to help alleviate this incongruency. Tissue samples of *C. venusta* were obtained from across the range, representing all the subspecies and the four previously inferred mtDNA clades. Double-digest restriction site associated DNA sequencing (ddRADseq) was conducted with these samples and single nucleotide polymorphism (SNP) data was generated. The SNP data were used to infer a maximum likelihood phylogeny and to assess population structure using discriminant analysis of principle components (DAPC). The results from the inferred phylogeny do not align with the currently recognized subspecies and is similar to the inferred mtDNA phylogeny but not fully congruent. The DAPC generated four genetic clusters: populations east of the Mobile Basin, populations from the Mobile and west to the Mississippi drainage, populations from the Mississippi drainage and eastern Texas, and populations from western Texas. Based off the results of the inferred phylogeny and the population genetic analyses, the current taxonomic status of the three subspecies needs revision. These results also implicate the possibility of cryptic species within *Cyprinella venusta*.

Is red coloration in *Chrosomus erythrogaster* an honest signal?

Julie Kastanis and Mollie Cashner

Austin Peay State University, Department of Biological Sciences

Presentation Type: Poster #7

Thursday, 18 November 2021

Color can play a vital role in how fish interact within their environment by impacting social interactions, species identification, mate attraction, and predator-prey interactions.

Carotenoids are the source of red and yellow pigments in fishes, and are synthesized by organisms such as algae, plants, fungi, and bacteria, thus fish must obtain them through diet. Furthermore, they provide immune system support in a number of animals including fish. The Southern Redbelly Dace (*Chrosomus erythrogaster*) display red and yellow carotenoid-based coloration, most prominently during the breeding season. Red and yellow carotenoid-based coloration in both male and female *C. erythrogaster* may reflect species identification as well as mate quality (i.e. is an honest signal), but little research has been done to measure individual variation. The purpose of this ongoing study is to investigate red/yellow coloration in *C.*

erythrogaster as an indicator of overall individual health (i.e., is an honest signal) by comparing intensity and total coverage of carotenoid-based coloration, body condition, reproductive status, and presence of environmental stressors (i.e. external parasites, lesions, abnormal growths). We hypothesize that red/yellow coloration in *C. erythrogaster* acts as an honest signal of individual health. Determining the honesty of red/yellow coloration in this species may also provide evidence for the role of carotenoid-based coloration among other North American minnows.

Changes over two decades in the diversity, distribution, and conservation status of southeast U.S. native freshwater fishes

Bernie Kuhajda

Tennessee Aquarium Conservation Institute

Presentation Type: Poster #5

Thursday, 18 November 2021

The southeastern United States is a global hotspot for diversity of aquatic animals, and freshwater fishes are the largest group within this incredible biodiversity. The last comprehensive list of Southeastern freshwater fishes was compiled over 20 years ago. The current project updates and expands on the diversity, distribution, and conservation status of freshwater and diadromous fishes across 52 watersheds. These drainages cover all or part of 18 states and range from the Monongahela River in Pennsylvania and West Virginia to the lower Missouri River in Missouri, south to the Rio Grande River in Texas, east to Florida, and up the Atlantic Slope to the Potomac River in Virginia and Maryland. A total of 864 fish taxa in 43 families are found in the Southeast, including 736 described species and subspecies, 83 undescribed species, 35 distinct populations, and 10 hybrid zones. By far the most diverse families are the darters (Percidae, 263 native species) and minnows (Cyprinidae, 231). Alabama and Tennessee have the greatest number of native fishes (330+), and a watershed shared by these states, the lower Tennessee River, has the greatest fish diversity (205). Of the current 819 described species, subspecies, and undescribed species, over 60% (494) are endemic to the Southeast, and almost half of these endemics (230) are restricted to a single watershed. This contrast with only four fish species native to all 52 watershed. Almost 35% of Southeastern fishes are imperiled (274), extirpated (3), or extinct (4). This is an increase from the 28% in the previous list. Compared to the previous list, the current project recognizes 103 additional fish taxa, the conservation status of 9 species has improved, but 32 species are more imperiled. The largest numbers of imperiled fishes by family are 114 darters and 62 minnows, but the most imperiled families by percentage (at least five species in Southeast) are cavefishes (Amblyopidae, 92%) and sturgeons (Acipenseridae, 86%).

Influence of land-use on fish assemblage patterns across the South-Central Plains of Arkansas: a preliminary analysis

Ryne Lehman, Molly Wozniak, Hal Halvorson, Ginny Adams, and Reid Adams

The University of Central Arkansas, Department of Biological Sciences

Presentation Type: Poster #17
Thursday, 18 November 2021

Land-use changes are known to alter physical in-stream habitat, water quality, and community structure within aquatic ecosystems. Streams located across the South Central Plains Ecoregion of Arkansas are no exception. Sites were classified into three different types of land-use categories: agriculture, urban, and forest. These land-use classifications are based off landcover percentages calculated within the upstream catchment area of each site using USGS Stream Stats. Understanding the relationship between land-use and patterns of fish assemblage structure can provide insight into how fishes respond to potential disturbances. Eighteen out of thirty sites were sampled during summer 2021 with relative abundance data calculated for fishes at each site. Non-metric multidimensional scaling (NMDS) was used to examine how sites were distributed based on species relative abundances. A two-axis solution was generated with a final stress value of 10.4. We used Multi Response Permutation Procedure (MRPP) to test group differences between land-use based on species relative abundance across sites. Fish community structure varied across sites, but no differences were detected among agriculture, urban, and forest. However, a trend between urban and forestland-use was observed. *Ameiurus melas*, *Gambusia affinis*, and *Micropterus salmoides* were associated with urbanized streams, whereas *Erimyzon claviger*, *Etheostoma parvipinne*, and *Lepomis miniatus* were associated with forested and agricultural streams. These preliminary analyses suggest streams sampled at this point in time in the South Central Plains Ecoregion have overall similar fish assemblages across major land-use designations, but patterns were evident due to other variables (e.g., hydrology) that will be discussed.

Improving collections and developing a public-facing persona: The BoneSheaux at Southeastern Louisiana University's Vertebrate Museum

Elizabeth Marchio and Kyle R. Piller
Southeastern Louisiana University; Department of Biological Sciences, Hammond, LA 70402
Presentation Type: Poster #1
Thursday, 18 November 2021

The broader impacts of small to moderate -sized university biodiversity collections are often limited in scope and overshadowed by larger museum spaces. However, it is the smaller, regional museums that maintain the robust collections of local biodiversity and it is these collections that can be used to reach local community members and introduce them to our native biodiversity. In 2020, the Vertebrate Museum at Southeastern Louisiana University procured an NSF collection grant to re-curate and digitize our fluid holdings (herps and ichs). This presentation will focus on our ichthyology collection, which contains 8836 cataloged lots and over 124,500 specimens. Our ichthyology collection contains specimens from 27 states and 10 countries. Along with overall collection improvements, we are developing an outreach and education program called “*The Bone Sheaux*” which has various experiential educational activities. We will present several example modules that we have developed. In addition, we are working to improve our connectivity to the broader community in Tangipahoa Parish with

budding collaborations between various local schools as well as organizations such as the Regional Arts Center to bring natural science to the community. We have also widened our reach to the undergraduate population, which has shown an immense interest in volunteering for the museum. Currently, over a dozen undergraduates are active in the museum. Between January 2021 and October 2021, volunteers logged 387.5 hours in the museum. Within the last year, several graduates have moved onto graduate school or other research projects -which shows connecting to Southeastern's community helps the museum itself as well as the people embedded in our organization.

An evolutionary analysis of lineage diversification among madtom catfishes (Siluriformes: Ictaluridae: *Noturus*)

Brittany L. McCall¹, Jacob Egge², and Brook L. Fluker³

¹Arkansas State University, Department of Environmental Sciences

²Pacific Lutheran University, Department of Biology

³Arkansas State University, Department of Biological Sciences

Presentation Type: In Person, Student

15:15 Thursday, 18 November 2021

Madtom catfishes (Ictaluridae: *Noturus*) are the most speciose genus of North American catfishes. The species richness of *Noturus* has been attributed to a rapid diversification associated with a decrease in body size that has made resolving deep relationships within the genus difficult due to incomplete lineage sorting. Past phylogenetic hypotheses based on a combination of mitochondrial markers, nuclear markers, and morphology have resolved some relationships and served as the basis for identifying cryptic species. However, these same analyses inconsistently recover or report low support for several species groups and point to the potential for additional cryptic diversity. The objective of this study was to reevaluate genus-level phylogenetic hypotheses for *Noturus* to better resolve taxonomic relationships, assess additional cryptic diversity, and improve the available data on the genus. Tissue samples of *Noturus* species were obtained through a combination of field collection and gifted material from natural history collections. Restriction site associated DNA sequencing (RADseq) data was generated using a variety of data filtering approaches and analyzed with phylogenetic and species tree methods. Our resulting phylogenies recover novel relationships among taxa, corroborate previously identified patterns suggestive of cryptic diversity, and fail to recover some previously hypothesized subclades. This robust phylogenetic framework, combined with a relatively comprehensive understanding of the natural history of *Noturus* provides a unique opportunity to assess the response of a phenotypically conservative, yet genetically diverse clade to a changing environment through time.

Occupancy of the Caddo Madtom: the good, the bad, and the unknown

Brittany L. McCall¹ and Brook L. Fluker²

¹Arkansas State University, Department of Environmental Sciences

²Arkansas State University, Department of Biological Sciences

Presentation Type: In Person, Lightning
11:20 Friday, 19 November 2021

Thermal tolerance of eggs of *Cottus paulus* (Pygmy Sculpin)

Rachel Moore and Carol Johnston
Auburn University School of Fisheries, Aquaculture, and Allied Sciences
Presentation Type: In Person, Student
9:45 Thursday, 18 November 2021

The Pygmy Sculpin, *Cottus paulus*, is a federally threatened fish endemic to Coldwater Spring, Anniston, AL. The entire species range is a spring pool barely exceeding 1-acre, and around 800 meters of run flowing from the spring pool. As with many other specialist species, climate change is negatively impacting *C. paulus* – the average annual temperature of the spring in the 1970's was 16.7°C (62°F), in recent years the average annual temperature has been recorded as 18.3°C (65°F). The population estimates in recent years also reveal decreasing numbers of the species. To better understand and predict the future of the species, thermal tolerance tests were conducted on the eggs. Artificial nest tiles were used to collect eggs, transported to Auburn, and randomly placed into one of four temperatures. The temperatures included a control (16°C), and three treatment temperatures (18°C, 20°C, 22°C). Egg mortality was recorded daily until either hatching or total mortality in each treatment to determine percent mortality in each temperature. In the 16-20°C treatments, some clutches hatched in each system. At the highest temperature treatment, no eggs hatched, and few made it to the eyed stage of development.

The effects of man-made barriers on present and historic site occupation of Arkansas

Etheostoma cragini* and Least Darters *Etheostoma micropurca
Alyssa Mostrom, Anthony Zenga, and Susan Colvin
Arkansas Tech University, Department of Biological Sciences
Presentation Type: Virtual, Student
16:00 Thursday, 18 November 2021

Regionally endemic populations of Arkansas *Etheostoma cragini* and Least Darter *Etheostoma micropurca* populations are found in unique karst headwater streams and springs of NW Arkansas. In this rapidly urbanizing region these darters are currently threatened by declining habitat quality and stream connectivity due to man-made barriers such as culverts and low-water bridges. Barriers can alter habitat by increasing sedimentation, disturbing water quality, restricting fish passage, increasing pollution, and disrupting stream productivity. Using historic presence and absence data and ArcGIS Pro, we mapped current and historically occupied reaches as well as nearby barriers. We used simple linear regression to investigate any potential relationship between barrier presence and occupation status. We found a positive significant correlation between barriers and historic sites no longer occupied by either species. These efforts served as a pilot project to help us build hypotheses about the decline of these species

in historically occupied reaches. We will refine field methodology and spatial mapping approaches to further study these karst systems and Least and Arkansas Darter populations.

Phylogenetic and taxonomic evaluation of the Least Darter (*Etheostoma micropurca*) complex

Alexis M. Mross and Brook L. Fluker

Arkansas State University, Department of Biological Sciences

Presentation Type: In Person, Lightning

11:05 Friday, 19 November 2021

Variation in fish communities of Boston Mountain Streams in the Ozark National Forest

Jackson Pav, Ginny Adams, and Reid Adams

University of Central Arkansas, Department of Biology

Presentation Type: Poster #15

Thursday, 18 November 2021

The Boston Mountains of the Ozark-St. Francis National Forest have a rich history of conservation spanning hundreds of years. This Pennsylvanian aged mountain range yields high amounts of sandstone and shale, resulting in aquatic ecosystems unique to the state of Arkansas. Thirty-five sites among the Big and Littlefinger Creek, Illinois Bayou, and Lee Creek watersheds were analyzed using NMSTo determine fish community level differences using relative abundances data. Fish community composition was significantly different across watersheds (MRPP, $p<0.05$). Indicator species analysis identified eleven species of fish as significant($p<0.05$) indicators of watersheds. These fishes were *Semotilus atromaculatus* and *Etheostoma pulchellum* in Big Piney and Little Piney creeks; *Micropterus dolomieu*, *Etheostoma blennioides*, and *Etheostoma zonale* in Illinois Bayou; and *Luxilus cardinalis*, *Pimephales notatus*, *Fundulus catenatus*, *Lepomis macrochirus*, and *Etheostoma mihileze* in Lee Creek. Stream catchment size was one of the strongest drivers of variation in fish relative abundances across sites. Additional variation is likely related to abiotic factors such as differing substrate and water physicochemical properties. We are also interested in whether different forest management practices result in patterns of fish assemblage variation. This preliminary analysis provides useful insight into the community structure and habitat associations of fishes in streams of the Boston Mountains.

Fishes of Butler Creek, Tennessee River drainage, a biodiversity hotspot

David Pounders, Dalton Wright, Joshua Fitts, Gregory Gilmore, and Jeffery Ray

University of North Alabama, Department of Biology

Presentation Type: Poster #4

Thursday, 18 November 2021

Butler Creek is a tributary to Shoal Creek, which is considered a strategic habitat unit (SHU) due to high aquatic diversity and endemic taxa. Located in the southern bend of the Tennessee River and within the Western Highland Rim Ecoregion, Butler Creek has a drainage area of 61 mi² (158 km²). Although sampled as part of larger studies on Shoal Creek and for unique species such as Lollypop Darter, no in-depth survey or compilation of fishes had been conducted on the system. We determined landcover/land use for the watershed and compiled historical data (1956-2020) which includes 1,500 records from 37,000 individuals with 90 species reported. In 2018-2021, 36 collections were made from the headwaters to mouth, including all tributaries and multiple mainstem sites, plus remote localities not previously accessed. Collections included 66 species from 1,000 records and 14,000 individuals captured, with IBI sampling and analyses done at strategic locations. Land cover/land use changes were compared across decades. After the removal of erroneous records, the updated list for Butler Creek is a fish fauna of 85 species, with no loss of historically collected species, and multiple species having restricted distributions in Alabama.

Outmigration dynamics of American Eels in the Ouachita-Black-Red-Atchafalaya River system

Jeffrey Quinn¹, Kelly Winningham¹, Maxwell Hartman¹, Eric Brinkman¹, Todd Slack², Robby Maxwell³, Sean Kinney³, Brac Salyers³, and Kayla Kimmel⁴

¹Arkansas Game and Fish Commission

²U.S. Army Corps of Engineers,

³Louisiana Department of Wildlife and Fisheries

⁴U.S. Fish and Wildlife Service

Presentation Type: Virtual, Oral

9:30 Friday, 19 November 2021

The American Eel is a migratory, facultative catadromous species that spawns in the Sargasso Sea. We used ultrasonic telemetry to determine migratory chronology, escapement, and the impacts of multiple navigation damson migrations in the Ouachita-Black-Red-Atchafalaya River navigation system, Arkansas and Louisiana. A total of 83 American Eels (597-836 mm TL) were surgically implanted with acoustic tags from 2017 to 2020 at three rivers within the Ouachita River basin. A total of 17 VR2 stations was used to detect migrating eels. Receivers were deployed in the Atchafalaya River at Morgan City and the Wax Lake Outlet, and these stations were established to confirm outmigration from fresh water to the Gulf of Mexico. Migratory chronology was highly variable among years, migrations were triggered by high flow events, and long-range movements occurred from July to February. The percentage of tagged eels that migrated varied among years between 16% and 44%. The probability of outmigration was 18% at 700 mm, 63% at 750 mm, and 93% by 800 mm TL. For 2020-2021, 94% of migrants have been detected as they reached the Gulf of Mexico. Therefore, out-migration survival through the navigation system appears high despite the abundance of large apex predators, numerous tropical hurricane disturbances, and multiple navigation dams. Migration of eels through the Gulf of Mexico or along the Florida Coast has not been documented by iTag or FACT network collaborators. This case exemplifies the utility of maintaining a passive acoustic telemetry array and the importance of open communication between multi-agency researchers as a cost-

effective means for obtaining valuable biological information on species of interest over large spatial scales.

Mycobacterium presence in the dermal microbiome of freshwater fish in the southeastern U.S.

Alex Rakestraw¹, Kayla Fast¹, Magdalene Dogbe², Heather Jordan², Sophie Picq³, Joe Recever³, Alexandra Bauer³, Christine Chevillion⁵, Jean-François Guegan^{5,6}, Jennifer L. Pechal³, Eric Benbow^{3,7,8}, Michael Sandel¹

¹The University of West Alabama, Department of Biological Sciences

²Mississippi State University, Department of Biological Sciences

³Michigan State University, Department of Entomology

⁴Michigan State University, Ecology, Evolution, and Behavior Program

⁵Université de Montpellier, Ecologie, Génétique, Evolution et Contrôle, France

⁶Université de Montpellier, Animal, santé, territoires, risques et écosystèmes, Institut national de recherche pour l'agriculture, l'alimentation et l'environnement, France

⁷Michigan State University, AgBioResearch

⁸Michigan State University, Department of Osteopathic Medical Specialties

Presentation Type: Poster #16

Thursday, 18 November 2021

Mycobacterium species are the cause of some of the most medically important diseases in the recent human past, such as tuberculosis and leprosy. Presently, many tropical developing countries still struggle with these same diseases and many more caused by these microbes due to economic stress and climatic variables. In addition, these mycobacteria species cause disease in animals, many of which inhabit shared spaces with humans, such as aquatic environments and forests adjacent to urban and rural areas. Here we report the first evidence of the presence of the pathogenic species *Mycobacterium ulcerans* for both Alabama and Mississippi, as well as evidence of a previously unknown strain of this same species from Alabama. *Mycobacterium ulcerans*, the cause of the tropical skin disease Buruli Ulcer and the target of this study, is a known environmental pathogen in Western Africa, South America, Australia, and various other tropical countries. Its route of transmission to humans is unknown, although an aquatic zoonotic route is suspected. As part of a collaboration to investigate the ecology and geographic extent of this species, we sampled 9 sites in the Southeastern U.S. to collect the dermal microbiome of various fish species. We extracted the microbiomes of 512 individuals and used Sanger sequencing to isolate fragments of the *M. ulcerans* plasmid pMUM001 from these individuals. We then analyzed these fragments in comparison to known *M. ulcerans* strains and relatives. Identifying these microbes and the fish species that host them is crucial to understanding the ecology of these potential pathogens.

Where did you find that? New records of mussels in Shoal Creek (Etowah River, Cherokee Co., GA)

C. Keith Ray and Zach Felix

Reinhardt University

Presentation Type: In Person, Lightning

11:00 Friday, 19 November 2021

Mussels are not common in the Upper Etowah River Basin. In 2017, mussels were discovered downstream of Cline Lake on Shoal Creek in Cherokee County, GA. The mussel species identified include *Hamiota altilis*, *Vilosa nebulosus*, and *V. umbrans*. Subsequent trips and snorkel surveys revealed their distribution throughout other parts of the basin. Directly downstream of Cline Lake, mussel densities are highest, while many survey hours are needed to detect the mussels in other locations. We share our survey plans for the rest of the stream and discuss the other diversity within this area and efforts for conservation.

Thermal tolerance of fishes in an urban and non-urban stream in relation to environmental temperatures

Robert Remy, Reid Adams, Ginny Adams, and Matthew Gifford

University of Central Arkansas, Department of Biology

Presentation Type: In Person, Student

9:30 Thursday, 18 November 2021

Urbanization of watersheds may result in alterations to the thermal regime compared to non-urban watersheds, with higher daytime temperatures and lower nighttime temperatures. The altered thermal regime is due to degradation of riparian zones, warmer ground temperatures, and paved surfaces trapping heat and warming runoff water. Thermal tolerance (CTMax, Critical Thermal Maxima) of some species may allow them to survive in urban heat islands.

Temperature loggers were placed in the streams to record ambient temperatures in the two watersheds. Eight species were tested from Tucker Creek (mostly urban watershed) and twelve from Cadron Creek (55% forest, 35% pasture, and 5% developed). It was hypothesized that fishes that overlapped between the two systems, *Fundulus olivaceus*, *Campostoma spadiceum*, *Lepomis macrochirus*, and *Lepomis megalotis*, would have higher CTMax in Tucker Creek compared to Cadron Creek. Fishes were collected and held in containers overnight, and CTMax was measured the next day using Precision CIR 19 heated water baths that were increased 1 degree Celsius per minute until loss of equilibrium was recorded. No significant difference in CTMax was found between the four species occupying both Tucker and Cadron creeks: *F. olivaceus* ($p=0.99$), *C. spadiceum* ($p=0.23$), *L. megalotis* ($p=0.23$), and *L. macrochirus* ($p=0.74$). However, at a community level, there was a significant difference between the two stream systems ($p<0.001$) with Cadron Creek having overall lower CTMax. We will relate patterns of CTMax across species and streams to environmental thermal histories.

Status survey for Saltmarsh Topminnow in Mississippi with notes on the effectiveness of boat electrofishing on coastal waters

Calvin R. Rezac, Robert J. Ellwanger, and Benjamin H. Chaffins

Mississippi Department of Wildlife, Fisheries, and Parks, Research Department of the
Mississippi Museum of Natural Science

Presentation Type: In Person, Lightning

11:15 Friday, 19 November 2021

The Saltmarsh Topminnow, *Fundulus jenkinsi* (Evermann, 1892), is a marine-estuarine species found in Mississippi along the gulf coast and is dependent on the presence of saltmarsh habitat and dendritic tidal creeks located adjacent to main river channels. However, preferred marsh habitat is declining due to coastal development, sea-level rise, pollution, as well as levee and canal construction. The species is currently reported as rare and sporadic throughout the entire distribution from Texas to Florida and is presently under review for federal listing with a listing decision in 2022. The last targeted survey for *F. jenkinsi* in Mississippi was completed in 2010, leaving an information gap of over a decade for the species in the state. Additionally, in a range-wide assessment of the species, Peterson et al. (2016) noted the difficulty to accurately assess the status with commonly available gears which may have historically underestimated *F. jenkinsi* populations. However, a recent *F. jenkinsi* survey by Louisiana Department of Wildlife and Fisheries (LDWF) demonstrated that a custom electrofishing boat with the ability to sample in high conductivity waters produced higher catch rates when compared to traditional methods. Herein, we used the methods developed by LDWF to assess the status of *F. jenkinsi* along the Mississippi coast. In 2021, we collected 52 species, including 172 *F. jenkinsi* at 9 of 43 sites (21%). Compared to *F. jenkinsi* studies utilizing passive traps (0.03-1.44 fish/hour), our catch per unit effort was higher (21.5 fish/hour). These results indicate that *F. jenkinsi* populations are stable along the coast of Mississippi; although, future habitat loss is of concern. Additionally, our study supports the use of boat electrofishing as an effective gear targeting *F. jenkinsi* and other coastal species of interest during ideal sampling conditions (e.g., conductivity, tides).

Comparison of field acclimatization and lab acclimation approaches to measuring fish thermal tolerance

Cade Richesin, Canyon Vickers, Ginny Adams, Matthew Gifford, Reid Adams

University of Central Arkansas, Department of Biology, Environmental Science

Presentation Type: Poster #14

Thursday, 18 November 2021

Increased temperature may negatively impact fish in freshwater systems, particularly fish in urban streams. Measures of thermal tolerance, such as critical thermal maximum (CTMax), are often used to measure and indicate species' vulnerabilities to increased environmental temperatures. Historically, CTMax was commonly measured for fish acclimated to lab conditions over time. More investigation into protocols used to measure CTMax are needed to determine methods that best reflect fish CTMax measures in the field since laboratory

acclimation protocols might introduce confounding factors or other sources of variation. We measured CTMax of 150 Highland Stoneroller (*C. spadiceum*) and 150 Blackspotted Topminnow (*F. olivaceus*) individuals collected from an urban stream, Tucker Creek. Groups of fish were tested for CTMax using a field acclimatized approach on the same day of capture and after being held overnight. Groups of fish were also tested for CTMax following acclimation to ambient and constant temperatures after 10 and 20 days in the laboratory. Individuals of both species tested on Day 0 and Day 1 did not exhibit significant differences in CTMax. After ten days acclimation, both species exhibited differences in CTMax that were dependent on acclimation regime.

Cryptic extinction in America's Amazon: genomic homogenization among fishes of the Mobile River Basin

Michael W. Sandel, Kayla M. Fast, Joshua Millwood, Kenny Jones, Kiersten Schellhammer, John Larrimore, Julia Wood, Alex Rakestraw, and Zach Alley

The University of West Alabama

Presentation Type: In Person, Oral

11:45 Friday, 19 November 2021

The Mobile River Basin is recognized as a global hotspot of freshwater biodiversity, as it is inhabited by the greatest diversity of fishes, crayfishes, snails, mussels, and turtles among all watersheds of North America. Unfortunately, human activity has had disproportionate negative impacts on the viability of endemic species, to the extent that the Mobile River Basin also contains the greatest number of imperiled and extinct aquatic animal species in the United States. I review recent research conducted in my lab and those of collaborators to summarize prehistoric population genetic structure of aquatic organisms of the Mobile River Basin, and to highlight the risks posed by movement of non-native species across watersheds and geologic boundaries. Of particular concern is the potential for genomic homogenization among closely related populations of the Mobile and Tennessee River Basins, which were connected by the Tenn-Tom waterway in 1984. I also review recent discoveries of geographically restricted populations which may represent new species. On the whole, research suggests that the invasion of genomes across cryptic species boundaries represents an underappreciated threat to the endemic biodiversity of America's Amazon.

Comparative population genetics of a rare, imperiled and a common, non-imperiled darter from the Big South Fork Cumberland River

Matthew Scott, Jacob F. Brumley, Abigail Etherton, and Rebecca E. Blanton

Austin Peay State University

Presentation Type: Poster #11

Thursday, 18 November 2021

Population genetic studies of freshwater fishes have largely focused on imperiled species. A common inference from such studies is that the focal taxon has high or low genetic diversity.

However, most inferences are made from relative comparisons of diversity levels to other imperiled species. This is largely due to relatively few estimates of genetic diversity of common, abundant species. The Tuxedo Darter, *Etheostoma lemniscatum*, is restricted to the Big South Fork Cumberland River system and is listed as endangered due to past declines associated with mining effluent pollution and habitat inundation by Lake Cumberland. The conspecific and ecologically similar species, *Nothonotus camurus*, is syntopic with *E. lemniscatum*, and has a shared history of anthropogenic disturbance in the Big South Fork, but is more common and abundant and is not regarded as a species of conservation concern. We compared genetic diversity of *N. camurus* and *E. lemniscatum*, using a standard suite of genetic diversity metrics from a set of 8 shared microsatellite loci. Our goals were to determine if differences in genetic diversity exist between these two species and if so quantify those differences and evaluate how life history or other variables may contribute to different genetic outcomes between species with a shared history of habitat disturbance. Allelic richness, heterozygosity, effective population size, and measures of population structure were generated for 92 *E. lemniscatum* from 11 localities. To date, DNA from 87 *N. camurus* were collected from these same localities and have been extracted for genotyping. Genetic diversity and effective population size for *E. lemniscatum* was considered low in comparison to other imperiled species estimates, but little to no population structure was observed across localities examined. Genotypes and diversity metric data collection for *N. camurus* are ongoing, but preliminary results will be presented and discussed.

How to color a fish: examining male nuptial coloration gene expression patterns in Rainbow Darters (*Etheostoma caeruleum*) using TagSeq

Andrew N. Sherman and Kyle R. Piller

Southeastern Louisiana University

Presentation Type: In Person, Student

13:45 Thursday, 18 November 2021

Organismal coloration is an important phenotypic trait that serves a wide variety of functions. Coloration can be used for defensive purposes, such as those whose coloration mimic aspects of their environment to blend in, or warning coloration where individuals display specific vibrant colors or patterns toward off would-be predators. Coloration can also be vitally important for conspecific mating practices. Male darters of the genus *Etheostoma* are notable for the vibrant male nuptial coloration that they develop during the mating season that aid in mate-selection. A large body of work has been done to understand the mechanistic causes of coloration at the cellular level, but generally as it relates to adolescent coloration proliferation. However, the genetic basis of coloration proliferation for seasonal nuptial coloration has been understudied. *Etheostoma caeruleum*, the Rainbow Darter, is a widespread darter species found throughout the eastern half of the United States that exhibits brilliant blue and orange nuptial male coloration. Rainbow Darters represent an interesting model to examine the genetic basis for nuptial coloration proliferation. Thus, the goal of this study was to use TagSeq (3' mRNAQuantSeq) to characterize male nuptial coloration gene expression in Rainbow Darters across seasons. Our results showed that there are over 100 differentially expressed genes

across seasons for males (fall vs. spring) and that many of these genes are enriched for melanin and melanophore production pathways. Our result also showed that female sin the spring have a gene expression profile more similar to the spring males compared to fall females or fall males. Ultimately, our results indicate that nuptial coloration might not be as clear cut from a genotypic view as it is from a phenotypic view.

Genetic assessment of Southern Appalachian Brook Trout reintroductions

Rebecca J. Smith¹, Dave Kazyak², Matt A. Kulp³, and Benjamin M. Fitzpatrick¹

¹The University of Tennessee, Knoxville, Ecology and Evolutionary Biology Department

²United States Geological Survey

³National Park Service

Presentation Type: Virtual, lightning

10:45 Friday, 19 November 2021

In restoration ecology, reintroduction is a tool to re-establish native species to an area where they have been previously extirpated. However, identifying appropriate source populations for reintroductions can be a challenge because introduced genotypes may not be well suited for the target environment. In practice reintroductions are rarely preceded by detailed genetic evaluation. A threatened species in Southern Appalachia is the Southern Appalachian Brook Trout (*Salvelinus fontinalis*), which has been extirpated from its historical range due to anthropogenic impacts and competition with gone-native species. In the Great Smoky Mountain National Park (GRSM), brook trout are the only native salmonids but have been isolated in remote headwater systems since the early 1900s, exchanging little to no genetic information between populations. State and federal agencies have been strategizing to restore the unique Southern Appalachian Brook Trout strain to their native range and reintroduction efforts are ongoing in GRSM. Currently there are over 30 miles of reintroduced brook trout habitat in the National Park, which encompasses 13 different streams. Managers must use multiple source gene pools in one reintroduced habitat to prevent depleting source populations. However, recent studies have shown that source populations are extensively genetically differentiated from each other, and might not mix readily when brought together. The observed nonrandom admixture raises concerns about assortative mating or outbreeding depression. My research aims to address these concerns using next-generation sequencing to assess the genetic composition of the admixed populations. Additionally I will evaluate if there is evidence of bias favoring particular alleles from certain source stocks in an effort to help management determine the ‘right’ combination of gene pools in a given reintroduction site.

Restoration of the Georgia College Fish Collection

Jordan Sorrells and Gregory Glotzbecker

Georgia College and State University, Department of Biological and Environmental Sciences

Presentation Type: Virtual, lightning

10:55 Friday, 19 November 2021

Do sedimentary processes have nonlocal consequences for metapopulation and metacommunity dynamics?

Loren Stearman and Jake Schaefer

University of Southern Mississippi, Department of Biology

Presentation Type: In Person, Student

9:15 Thursday, 18 November 2021

Altered fluvial sediment regimes have clear and deleterious effects on aquatic ecosystems. Researchers have exhaustively studied the short-term local effects of fine sediment deposition on fish communities, but growing evidence suggests that sedimentary processes may express over longer timescales in complex and often nonlocal manners. Notably, long-term geomorphic responses of river basins may include extended periods of instability in river mainstems, which may carry consequences for nonlocal ecological processes such as dispersal and source-sink dynamics for headwater forms across these mainstems. In this paper we explore whether such complex interactions shape metapopulation and metacommunity dynamics in streams of southwest Mississippi. We described sedimentary processes in river mainstems by a GIS-based approach, and quantified sedimentary processes in headwaters through both GIS and field-based approaches. River mainstems showed a range of apparent activity in sedimentary dynamics. Local channel morphology at sample stations varied across a gradient from stable (deep, narrow, sediment retention) to erosional (shallow, wide, bedrock exposure) forms. Correlation analysis found a strong relationship between geomorphic processes in headwaters and river mainstems. We measured gene flow and population structure in a widespread and common focal species, Blackspotted Topminnow, and we measured community and metacommunity structure via electrofishing surveys in headwater streams. Intra-basin F_{ST} showed a general trend to increase with increasing sedimentary activity. Multivariate analyses of fish communities suggested a complex relationship between whole-community beta diversity and degree of sedimentary activity in a river basin. Analyzed separately, darters (Percidae) increased in community dissimilarity with increasing sedimentary dynamics, while minnows (Leuciscidae) showed the opposite pattern. These data suggest that the complex and often nonlocal interacting sedimentary processes in river basins share a similarly complex interaction with metapopulation and metacommunity processes. We explore next steps with further focal taxa for genetic analyses.

Re-tracing Edward Drinker Cope's travels through North Carolina and his contributions to North Carolina ichthyology

Bryn H. Tracy¹ and Robert E. Jenkins²

¹Apex, NC

²Roanoke College, Roanoke, VA

Presentation Type: Virtual, Oral

10:00 Friday, 19 November 2021

Since 1870, ichthyologists have pondered Edward Drinker Cope's two publications: "On some Etheostomine Perch from Tennessee and North Carolina" and "A Partial Synopsis of the Fishes of the Fresh Waters of North Carolina", along with letters to his father while traveling in North Carolina. Transcriptions and annotations of these letters were searched for further knowledge regarding his field notebook(s) and original data (meristics, morphometrics, life coloration, etc.) from his travels during Summer and Fall 1869. Insights into who assisted with his collections were not achieved. The loss of some of larger specimens, e.g., *Carpioles*, *Ictiobus*, and *Moxostoma*, lead us to question if Cope hastily wrote some of the descriptions in the field, or wrote them from memory afterwards in his lodging, or did he write them in a field notebook? We did not discover the existence of his field notes. How was he able to successfully publish his results shortly after his trip? We concluded Cope must have been extremely impatient and consumed by his more important paleontological interests when writing two fish manuscripts within such a short time period. These publications laid a foundation for all ensuing studies of NC's freshwater fish fauna for the past 151 years. Of the 242 described species of freshwater fish in NC, Cope described 45 of them between 1865-1871. Cope described 25 species from NC of which 15 are considered valid. Cope recounted collecting 91 described and undescribed species during his trip and we accounted for all of the species and specimens he had collected. 139 lots, representing 63 species and 943 specimens were subsequently curated at Academy of Natural Sciences of Drexel University, the National Museum of Natural History, and the University of Michigan Museum of Zoology. Various type specimens are represented in 49 lots, with the remaining 89 lots representing non-type specimens.

Development of an environmental DNA (eDNA) assay to delineate the distribution of the imperiled Striated Darter (*Etheostoma striatulum*, Page and Braasch 1977) in the Duck River, Tennessee

Adam L. Walker, Kit Wheeler, and Carla R. Hurt

Tennessee Technological University, Department of Biology

Presentation Type: In Person, Student

15:30 Thursday, 18 November 2021

Striated Darters (*Etheostoma striatulum*) are small, uncommon darters endemic to the Duck River, Tennessee. Since their description, they have become increasingly rare within their range, which is limited to the Middle and Upper portions of the watershed. Historically, Striated Darters occupied 16 tributaries of the Duck River but, as of 2011, their known distribution declined to nine tributaries. Due to this documented decline, Striated Darters are currently under review for federal listing under the Endangered Species Act. Effective management and conservation of the Striated Darter will require information regarding their distribution. This study will delineate the current distribution of the Striated Darter through a species-specific environmental DNA (eDNA) assay. Aquatic species discard DNA fragments in many ways (e.g., urination, feces, and reproduction) into the water column, which can then be identified using well-established molecular techniques. Due to the Striated Darter's reclusive and cryptic behavior, conventional techniques are likely less effective for detection, requiring the use of much more efficient and sensitive eDNA monitoring techniques. At 30 historical sites in the

Duck River, three water samples will be taken and filtered for molecular analyses. A Multiplex qPCR assay will be designed to detect Striated Darters across all sampled sites and results will be analyzed using a hierarchical occupancy model to estimate the probability of detection at the levels of qPCR replicate, sample replicate, and individual sites. The development of this eDNA assay will enable the design of robust and cost-effective monitoring protocol while also facilitating the identification of critical habitat locations for the Striated Darter.

Effects of land use and instream barriers on population connectivity of the Kentucky Arrow Darter

River A. Watson¹, Alexis V. Culley¹, Rebecca E. Blanton¹, Matthew R. Thomas², Stephanie L. Brandt² and Michael A. Floyd³

¹Department of Biology, Austin Peay State University, Clarksville, TN, USA

²Kentucky Department of Fish and Wildlife Resources, Frankfort, KY, USA

³United States Fish and Wildlife Service, Frankfort, KY, USA

Presentation Type: Poster #8

Thursday, 18 November 2021

Anthropogenic habitat alteration and fragmentation are leading causes of imperilment of freshwater fishes globally. Habitat fragmentation contributes to population isolation by reducing or preventing gene flow, which contributes to declines in genetic diversity due to increased inbreeding and genetic drift. The Kentucky Arrow Darter, *Etheostoma sagitta spilotum* (KAD), is a federally threatened fish restricted to headwater streams of the Kentucky River system, an area heavily impacted by surface mining. Mining and other factors have contributed to extirpation of KAD from 45% of historic localities since the mid-1990's. Blanton et al. (2019) analyzed range-wide genetic diversity for the KAD from collections made in 2013-2014 and found evidence of low genetic diversity in and isolation of all populations examined. Populations located in close proximity to one another within the Daniel Boone National Forest (DBNF) had higher levels of genetic fixation than expected under an isolation-by-distance model. They hypothesized that recent human-mediated habitat fragmentation contributed to population isolation. We further explored the impact of instream anthropogenic factors including conductivity levels and culvert presence and type on population isolation within the South Fork Kentucky River in the DBNF. Eleven microsatellite loci will be used to analyze the impact of instream barriers and land use on gene flow at 15 sites within the Redbird District of the DBNF to assess the spatial scale at which populations of KAD are isolated. Nine culverts have been measured for a SARP barrier fish passability score across the sampling range, and conductivity levels have been measured at all sampling sites as well as seven corridors between sites. Preliminary results will be presented and discussed. Overall, this work will provide a novel, fine scale view of the barriers causing declines in connectivity among and genetic diversity within populations of highly imperiled fish.

Population dynamics of the Western Blacknose Dace (*Rhinichthys obtusus*) in Alabama

Courtney A. Weyand and Jonathan W. Armbruster
Auburn University, Department of Biological Sciences
Presentation Type: In Person, Student
14:30 Thursday, 18 November 2021

Within Alabama, the Western Blacknose Dace (*Rhinichthys obtusus*) is found within the Tennessee River and the Black Warrior and Coosa rivers of the Mobile River Basin. Based on infrequent and singleton collections, this species is hypothesized to be extirpated from the Black Warrior drainage. However, more recently, several populations have been documented from the Sipsey Fork and Locust Fork systems of the Black Warrior River. Additionally, other Tennessee endemics have been documented within the Mobile Basin, outside of their presumed range. Previous studies have noted a close relationship between Tennessee and Mobile endemics, and several hypotheses regarding a former connection have been suggested. Given the recent collections of *R. obtusus* within the Black Warrior, this suggests that the species is still occupying the drainage, but to what extent and source of entry are unknown. Using the genomic sequencing method 3RAD, the goals of this study were to identify the source population(s) of individuals within the Black Warrior River drainage and assess the genetic structure of *R. obtusus* throughout Alabama. Results will be used to determine if populations are the product of a recent or historical event, and to assess if gene flow is occurring between the Tennessee and Mobile River Basin.

Salmon of the south: suckers in Citico Creek

Mack White and Kit Wheeler
Tennessee Technological University, Department of Biology
Presentation Type: Virtual, Student
15:45 Thursday, 18 November 2021

The ability for migratory fishes to move limiting nutrients such as nitrogen (N) and phosphorous (P) between discrete freshwater environments may have pronounced effects on recipient ecosystem structure and function. However, the current scope of understanding about the ecological importance of nutrient delivery by migratory fishes is geographically and taxonomically limited due to a historical focus on Pacific salmonids in northwestern North America. As a result, fisheries management and conservation stands to improve with additional studies focused on the functional importance of fish movement. Here, we quantified the N and P contributions of an adfluvial sucker (Smallmouth Buffalo, *Ictiobus bubalus*) via excretion, eggs, and carcasses to Citico Creek in eastern Tennessee during their annual spawning migration. To get a sense of the ecological importance of buffalo-derived N and P, we compared these inputs to exported nutrient loads from the system. Across three migration waves, we estimated that 152,215 (95% CI: 150,245 – 154,222) buffalo delivered a mean 1,463 kg of N and 148 kg of P to Citico Creek as a result of their excretion and egg contributions. We estimated carcass inputs to be negligible due to rapid removal of carcasses from the system. The ratio of migrant nutrient inputs to system export varied among waves and compounds (i.e., dissolved inorganic nitrogen,

ammonium, and soluble reactive phosphorus); we observed values ranging from 0.25 to 10.85, which reflected the potential of buffalo-derived nutrient contributions to exceed nutrient export from the system under certain hydrologic conditions. Despite their iteroparous life history, our findings suggest that suckers like Smallmouth Buffalo have the potential to deliver large nutrient subsidies to their spawning habitats. We believe that the management and conservation of Southeastern freshwater biodiversity will benefit from understanding when and where migratory fish subsidies are ecologically relevant.

Phylogenomic diagnosis of a recently discovered population of Tennessee Dace (*Chrosomus tennesseensis*) in Alabama

Julia E. Wood¹, David A. Neely², M. Worth Pugh³, Phillip M. Harris³, Michael W. Sandel⁴

¹Yale University, Department of Ecology and Evolutionary Biology

²Tennessee Aquarium Conservation Institute

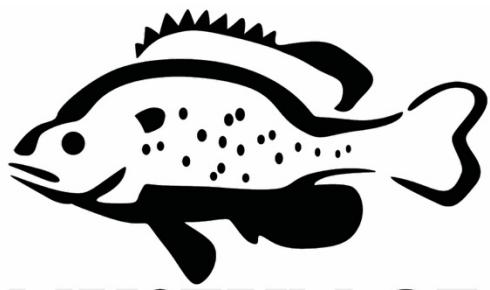
³The University of Alabama, Department of Biological Sciences

⁴The University of West Alabama, Department of Natural Sciences and Mathematics

Presentation Type: Virtual, Student

16:15 Thursday, 18 November 2021

An impressive degree of biodiversity is housed in the Southeastern United States and the mechanisms that promote and generate this biodiversity are worthy of investigation. In 2019, we collected Tennessee Dace (*Chrosomus tennesseensis*) from the Mobile River Basin, which is atypical as they were previously considered to be endemic to the Tennessee River Basin. *Chrosomus tennesseensis* occurs sporadically throughout its range and has been listed as vulnerable by the IUCN, making the collection in the Mobile River Basin more interesting. By using Next Generation sequencing techniques and population genetic analysis, we aimed to determine if the colonization of Graves Creek by *Chrosomus tennesseensis* reflects anthropogenic or prehistoric processes. Our results support the hypothesis that the colonization was not due to anthropogenic forces, and may instead have been a result of a natural interbasin transfer. By investigating the effects of isolation on populations in Graves Creek we can make inferences on the mechanisms generating biodiversity in the Southeastern United States.



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