

2017 Southeastern Fishes Council Meeting Schedule



Wednesday 15 November 2017

- 12:00 to 3:30 – Freshwater Information Network workshop
- 4:00 to 6:00 – Tennessee Aquarium Conservation Institute open house
- 4:00 to 7:00 – Meeting registration at hotel

Thursday 16 November 2017

- 7:15 to 8:00 – Registration
- 8:00 – Welcome
- 8:15 to 9:45 – 1st session morning talks
- 9:45 to 10:15 – Morning break
- 10:15 to 12:00 – 2nd session morning talks
- 12:00 to 1:30 – Lunch
- 1:30 to 2:45 – 1st session afternoon talks
- 2:45 to 3:15 – Afternoon break
- 3:15 to 4:30 – 2nd session afternoon talks
- 4:30 to 6:00 – SFC Business Meeting
- 6:30 to 6:45 – Poster setup
- 7:00 to 10:00 – Poster session Tennessee Aquarium
- 10:30 to 12:00 – Auction at hotel

Friday 17 November 2017

- 7:30 to 8:00 – Registration
- 8:00 to 9:45 – 1st session morning talks
- 9:45 to 10:15 – Morning break
- 10:15 to 12:00 – 2nd session morning talks
- 12:00 to 1:30 – Lunch
- 1:30 to 2:45 – 1st session afternoon talks
- 2:45 to 3:15 – Afternoon break
- 3:15 to 4:30 – 2nd session afternoon talks
- 4:30 to 5:00 – Awards Ceremony

Saturday 18 November 2017

- 9:00 to 12:00 – Field trip to South Chickamauga Creek in Georgia

Meeting Agenda: Day 2 – Thursday, November 16th

START	END	TYPE	PRESENTER	TITLE
8:00	8:15	Oral	Anna George	WELCOME ADDRESS
8:15	8:30	Oral	*Jessica Grady	1: FACTORS AFFECTING SCALE SHAPE VARIATION IN ETHEOSTOMATINAE DARTERS
8:30	8:45	Oral	*Kyler B. Hecke	2: MULTISPECIES OCCUPANCY MODELING OF TWO ETHEOSTOMA SPECIES IN THE STRAWBERRY RIVER DRAINAGE IN ARKANSAS
8:45	9:00	Oral	*Joshua G. Stonecipher	3: THE EFFECTS OF DAMS, DISTANCE, AND LARGE RIVERS ON DISPERSAL AND GENE FLOW OF THE SMALLSCALE DARTER, <i>NOTHONOTUS MICROLEPIDUS</i>
9:00	9:15	Oral	*Joshua Hubbell	4: INFLUENCE OF TWO TYPES OF ANTHROPOGENIC DISTURBANCE ON STREAM FISH METRICS
9:15	9:30	Oral	*Colt Holley	5: EVALUATION OF THE TRANSLOCATION SUCCESS OF A RARE DARTER SPECIES IN OKLAHOMA
9:30	9:45	Oral	*Brooke A. Washburn	6: THE SPATIAL SCALE OF GENE FLOW IN A DISPERSAL-LIMITED HABITAT SPECIALIST LIVING IN A LARGE RIVER ENVIRONMENT
9:45	10:15	MORNING BREAK		
10:15	10:30	Oral	*Davy Black	7: POPULATION DYNAMICS AND HABITAT USE OF THE BUCK DARTER (<i>ETHEOSTOMA NEBRA</i>) IN BUCK CREEK, CUMBERLAND RIVER DRAINAGE, KENTUCKY
10:30	10:45	Oral	*Kate Harriger	8: USE OF STRONG HABITAT-ABUNDANCE RELATIONSHIPS TO ASSESS POPULATION STATUS OF CRYPTIC FISH SPECIES: AN EXAMPLE USING HARLEQUIN DARTER <i>ETHEOSTOMA HISTRIO</i>
10:45	11:00	Oral	*Eric Malone	9: PRIORITIZING NATIVE FISH REINTRODUCTIONS IN THE GREAT SMOKY MOUNTAINS NATIONAL PARK
11:00	11:15	Oral	*Joshua Millwood	10: ENVIRONMENTAL AND PHYLOGENETIC EFFECTS ON THE DERMAL MICROBIOME OF MOBILE BASIN SCULPIN (TELEOSTEI: <i>COTTUS</i>)
11:15	11:30	Oral	*Courtney A. Weyand	11: PHYLOGEOGRAPHY OF THE ROSYSIDE DACE, <i>CLINOSTOMUS FUNDULOIDES</i> (TELEOSTEI: CYPRINIDAE)
11:30	11:45	Oral	*Brooke A. Bedal	12: POPULATION GENETICS OF THE BLACKSIDE DACE
11:45	12:00	Oral	*Brett Longwith	13: INVESTIGATION OF COLOR VISION IN A NUPTIALLY COLORED MINNOW, <i>CHROSOMUS ERYTHROGASTER</i>
12:00	1:30	LUNCH BREAK		
1:30	1:35	⚡	Ryan Crutchfield	14: FISHMAP.ORG USER OBSERVATION SUBMISSIONS PROCESS
1:35	1:40	⚡	Sarah Sweat	15: FRESHWATER INFORMATION NETWORK (FIN): A FRESHWATER SPECIES DATABASE FOR THE SOUTHEASTERN UNITED STATES
1:40	1:45	⚡	Duncan Elkins	16: PARKS, ARKS, AND REMARKS: CONSERVATION LANDS AND SOUTHEASTERN AQUATIC BIODIVERSITY PRIORITIES
1:45	1:50	⚡	Tierra Curry	17: ONE FISH TWO FISH DEAD FISH BLUE FISH: THE ENDANGERED SPECIES ACT UNDER TRUMP
1:50	1:55	⚡	Jeffrey W. Quinn	18: FISH CHANGES TO THE ARKANSAS WILDLIFE ACTION PLAN
1:55	2:00	⚡	Brett Albanese	19: CONSERVATION OF THE SICKLEFIN REDHORSE IN GEORGIA
2:00	2:05	⚡	Matthew D. Wagner	20: AN UPDATE ON RECENT NOTURUS CONSERVATION WORK IN MISSISSIPPI
2:05	2:10	⚡	Warren Stiles	21: INITIATION OF SPECIES STATUS ASSESSMENTS FOR 3 SOUTHEASTERN DARTERS: <i>ETHEOSTOMA FORBESI</i> , <i>E. CINEREUM</i> , AND <i>E. MAYDENI</i>
2:10	2:15	⚡	Shawna Mitchell	22: POPULATION STATUS AND MICROHABITAT PREFERENCES OF THE FEDERALLY ENDANGERED LAUREL DACE, <i>CHROSOMUS SAYLORI</i>
2:15	2:20	⚡	Bruce Stallsmith	23: SEASONAL VARIATION IN LIPIDS LEVELS OF TWO SYMPATRIC SPECIES OF SNUBNOSE DARTER
2:20	2:25	⚡	Leos Kral	24: PRELIMINARY ASSESSMENT OF ADAPTIVE VARIATION OF GENES IN DARTER SPECIES
2:25	2:30	⚡	Nathan V. Whelan	25: MITOCHONDRIAL GENOME SEQUENCING OF ALABAMA STURGEON (ACIPENSERIDAE: <i>SCAPHIRHYNCHUS SUTTKUSI</i>)
2:30	2:35	⚡	Rebecca L. Scott	26: WHAT DETERMINES WHO IS WHERE IN ATLANTIC COASTAL PLAIN STREAMS?
2:35	2:40	⚡	Amanda K. Pinion	27: A NEW TERMINOLOGY FOR CRANIAL TUBERCLES OF NORTH AMERICAN MINNOWS (TELEOSTEI: CYPRINIDAE)
2:40	2:45	⚡	Michael Sandel	28: A NEW PYGMY SUNFISH SPECIES FROM SOUTHERN ALABAMA AND WESTERN FLORIDA
2:45	3:15	AFTERNOON BREAK		
3:15	3:30	Oral	*Jessica L. Davis	29: LIFE HISTORY TRAITS OF FOUR COMMON CYPRINID SPECIES FOUND IN INTERMITTENT STREAMS OF THE COASTAL PLAIN OF GEORGIA.
3:30	3:45	Oral	*Seoghyun Kim	30: ENVIRONMENTAL AND BEHAVIORAL FACTORS AFFECTING VARIATION IN BLUEHEAD CHUB (<i>NOCOMIS LEPTOCEPHALUS</i>) NEST SIZE AND UTILIZATION BY A NEST ASSOCIATE, YELLOWFIN SHINER (<i>NOTROPIS LUTIPINNIS</i>)
3:45	4:00	Oral	*Sam Silknetter	31: YELLOWFIN SHINER DENSITY DETERMINES THE INTERACTION OUTCOMES OF NEST ASSOCIATION WITH A BLUEHEAD CHUB HOST
4:00	4:15	Oral	*Emily Judson	32: NESTING MICROHABITAT USE OF BARTRAM'S BASS IN THE UPPER SAVANNAH RIVER BASIN
4:15	4:30	Oral	Benjamin P. Keck	33: SPECIES DELIMITATION OF A BIOLOGICAL CONSERVATION ICON
4:30	6:00	BUSINESS MEETING		
6:15	7:00	POSTER SETUP AT TENNESSEE AQUARIUM		
7:00	10:00	POSTER SESSION AT TENNESSEE AQUARIUM		
10:30	12:00	SOCIAL/AUCTION AT HOTEL		

*Competing in student competition

Meeting Agenda: Day 3 – Friday, November 18th

START	END	TYPE	PRESENTER	TITLE
8:00	8:15	Oral	*Robert T. R. Paine	34: ENVIRONMENTAL DNA SURVEILLANCE OPTIMIZATION OF THE PYGMY MADTOM, <i>NOTURUS STANAULI</i>
8:15	8:30	Oral	*Meredith Harris	35: SIZE-SPECIFIC ADVANTAGE IN HABITAT COMPETITION BETWEEN MOUNTAIN MADTOMS (<i>NOTURUS ELEUTHERUS</i>) AND INVASIVE CRAYFISH (<i>ORCONECTES SPP.</i>)
8:30	8:45	Oral	*Jacob Brumley	36: USE OF DEAD MUSSEL SHELLS BY MADTOM CATFISH IN THE GREEN RIVER
8:45	9:00	Oral	*Brittany L. McCall	37: STABILITY AT LOW DENSITIES OR ENDANGERED? SPATIOTEMPORAL POPULATION DYNAMICS OF THE CADDO MADTOM (<i>NOTURUS TAYLORI</i>)
9:00	9:15	Oral	*Edward Stowe	38: ASSESSING FISH SPECIES DECLINES FROM 1996 TO 2016 IN THE CONASAUGA AND ETOWAH RIVERS, GA
9:15	9:30	Oral	*Joshua Vine	39: DETERMINING ENVIRONMENTAL CONDITIONS INITIATING ATLANTIC STURGEON SPAWNING MIGRATIONS IN THE SAVANNAH RIVER, SOUTH CAROLINA
9:30	9:45	Oral	*Cori Black	40: AQUATIC REFUGE AND RECOVERY IN THE FACE OF DROUGHT IN A BIODIVERSITY HOTSPOT
9:45	10:15	MORNING BREAK		
10:15	10:30	Oral	*Aaron Burgad	41: PATTERNS OF CHANGE IN FISH COMMUNITY COMPOSITION IN TWO OUACHITA RIVER SYSTEMS: TAXONOMIC AND FUNCTIONAL β -DIVERSITY REVEAL CONTRASTING PROCESSES
10:30	10:45	Oral	*Chelsey Sherwood	42: EXAMINATION OF FISH ASSEMBLAGE STRUCTURE OVER 45 YEARS IN THE BUFFALO NATIONAL RIVER, ARKANSAS
10:45	11:00	Oral	Loren Stearman	43: EXPLORING THE DYNAMICS OF LONGITUDINAL ASSEMBLAGE STRUCTURE IN AN OZARK HEADWATER STREAM SYSTEM
11:00	11:15	Oral	*Bradley Hartman	44: DEVELOPING A STANDARDIZED BOAT ELECTROSHOCKING SAMPLING PROTOCOL FOR LONG TERM MONITORING OF FISH COMMUNITIES IN KENTUCKY LAKE
11:15	11:30	Oral	*Anna Gruskiewicz	45: PHYLOGENOMICS OF LIVE-BEARING FISHES (POECILIINAE: POECILIIDAE)
11:30	11:45	Oral	David L. Bechler	46: LOG PACKING BEHAVIORS IN THE MANGROVE RIVULUS, <i>KRYPTOLEBIAS MARMORATUS</i>
11:45	12:00	Oral	*Geoffry Spooner	47: MIGRATION DYNAMICS OF OHIO SHRIMP, <i>MACROBRACHIUM OHIONE</i> , IN THE LOWER MISSISSIPPI RIVER
12:00	1:30	LUNCH BREAK		
1:30	1:45	Oral	Kit Wheeler	48: HOW WELL DOES THE FLOW-TRAIT FRAMEWORK PREDICT SHORT-TERM FISH COMMUNITY DYNAMICS IN UNREGULATED RIVERS?
1:45	2:00	Oral	Phillip M. Bumpers	49: HIGH SUMMER FLOWS CORRELATE WITH LOWER POPULATION GROWTH OF SHOAL FISHES IN THE CURRENT YEAR, BUT HIGHER GROWTH IN THE NEXT YEAR
2:00	2:15	Oral	Jeffrey W. Simmons	50: STATUS OF THE ENDANGERED TUXEDO DARTER, <i>ETHEOSTOMA LEMNISCATUM</i> , WITHIN REACHES OF THE BIG SOUTH FORK CUMBERLAND RIVER AFFECTED BY RETURN TO NORMAL OPERATIONS OF WOLF CREEK DAM FOLLOWING AN EXTENDED DRAWDOWN PERIOD.
2:15	2:30	Oral	J. Brian Alford	51: A HABITAT-BASED MODEL FOR PREDICTING BROOK TROUT BIOMASS IN THE CHEROKEE NATIONAL FOREST
2:30	2:45	Oral	W. Keith Gibbs	52: RANGE REDUCTION AND RESTORATION OF SPOTFIN CHUB, <i>ERIMONAX MONACHUS</i>
2:45	3:15	AFTERNOON BREAK		
3:15	3:30	Oral	Peggy Shute	53: BIOTIC AND ABIOTIC IMPACTS OF MINING AND RECLAMATION - A LITERATURE REVIEW
3:30	3:45	Oral	Tim O'Donnell	54: POPULATION GENETICS OF BLACKBANDED SUNFISH (<i>ENNEACANTHUS CHAETODON</i>) FROM NEW JERSEY TO FLORIDA
3:45	4:00	Oral	Brook Fluker	55: GENETIC STRUCTURE AND DIVERSITY OF DISJUNCT POPULATIONS OF RAINBOW DARTERS (<i>ETHEOSTOMA CAERULEUM</i>) AND SOUTHERN REDBELLY DACE (<i>CHROSOMUS ERYTHROGASTER</i>) THROUGHOUT THE MISSISSIPPI CORRIDOR
4:00	4:15	Oral	Rebecca E. Blanton	56: THE EFFECT OF POPULATION LOSS ON GENETIC DIVERSITY IN THE KENTUCKY ARROW DARTER, <i>ETHEOSTOMA SPILOTUM</i>
4:15	4:30	Oral	Jonathan Armbruster	57: PHYLOGENOMICS OF NOTROPIS AND RELATED SHINERS (CYPRINIFORMES: LEUCISCIDAE)
4:30	5:00	STUDENT AWARDS CEREMONY		

*Competing in student competition

Poster Presentations

PRESENTER	TITLE
*Matthew Fossett	1: GROWTH, REPRODUCTION, AND MICROHABITAT OF THE BIGEYE SHINER, <i>NOTROPIS BOOPS</i>
*Jennifer Main	2: CHANGE IN HISTORIC VS CONTEMPORARY FISH ASSEMBLAGES OF THE STRAWBERRY RIVER WATERSHED
*Jerry Kattawar III	3: COMPARATIVE POPULATION GENETICS OF THE RELICT DARTER AND GUARDIAN DARTER IN WESTERN KENTUCKY
*Jennifer Caudle	4: WATER DEPTH AND SUBSTRATE USE OF <i>NOTURUS ELEUTHERUS</i> IN THE CLINCH RIVER, TENNESSEE
*Lindsey Martin	5: EFFECTS OF BLACK-SPOT DISEASE ON THE BODY CONDITION OF BLEEDING SHINERS, <i>LUXILUS ZONATUS</i>
*Kyler B. Hecke	6: HISTORICAL OCCUPANCY MODELING OF NON-GAME FISHES IN THE CLINCH RIVER WATERSHED.
*Peter Grap	7: HABITAT AND COMMUNITY DIFFERENCES IN THE HISTORIC AND CURRENT RANGE OF THE BUCK DARTER (<i>ETHEOSTOMA NEBRA</i>)
*Aaron Burgad	8: CONTRASTING TAXONOMIC AND FUNCTIONAL β -DIVERSITY OF FISH COMMUNITIES IN A RIVERINE NETWORK ACROSS AN ENVIRONMENTAL TRANSITION ZONE
*Natalie Ellis	9: GENETIC DIVERSITY AT NEUTRAL AND ADAPTIVE LOCI IN THE BARRENS TOPMINNOW
*Sara Barrett	10: THE EFFECTS OF CUMULATIVE DRAINAGE AREA ON SPECIES VARIABILITY
*Isabel F. Papraniku	11: IMPACT OF WATER FLUCTUATIONS AND INTERMITTENCY ON STREAM FISH COMMUNITY STRUCTURE
*Samantha Holcomb	12: MICROHABITAT ANALYSIS OF THREE CO-OCCURRING SCULPIN SPECIES (COTTIDAE)
*Jacob Waymack	13: IMPACTS OF ANTHROPOGENIC LAND USE ALTERATION ON THE MORPHOLOGY OF STREAM FISHES IN ARKANSAS
*Nastasia Disotell	14: ASSESSING THE MITOCHONDRIAL GENETIC DIVERSITY OF THE SMALLSCALE DARTER, <i>NOTHONOTUS MICROLEPIDUS</i>
*Ethan Fite	15: ASSESSMENT OF BLACK (<i>MOXOSTOMA DUQUESNEI</i>), GOLDEN (<i>M. ERYTHRURUM</i>), AND SICKLEFIN (<i>M. SP.</i>) REDHORSE POPULATIONS IN THE UPPER OCONALUFTEE RIVER, QUALLA BOUNDARY, WESTERN NORTH CAROLINA
*William G. Wells	16: PRELIMINARY ANALYSIS OF AGE-CLASS STRUCTURE AND LONGEVITY FOR THE ENDANGERED PYGMY MADTOM, <i>NOTURUS STANAULI</i>
*Amanda K. Pinion	17: CEPHALIC AND BODY TUBERCULATION OF THE SHOAL CHUB <i>MACRHYBOPSIS HYOSTOMA</i> (TELEOSTEI: CYPRINIDAE)
*Zeina Sleiman	18: OBSERVATIONS ON THE REPRODUCTIVE BIOLOGY OF THE DARTER FISH <i>ETHEOSTOMA KENNICOTTI</i> IN RESPONSE TO GILL PARASITE INFECTIONS
*Shannon P. Murphy	19: TESTING DIEL FISH MIGRATIONS BETWEEN RIFFLE-POOL HABITATS
*Jackson Sibley	20: LINKING INTER-RIVER MOVEMENTS OF SAVANNAH RIVER STRIPED BASS, <i>MORONE SAXATILIS</i> WITH SPAWNING ACTIVITY IN THE NEARBY OGEECHEE RIVER.
*Dustin R. Thomas	21: ANALYSIS OF BODY SHAPE VARIATION AMONG RESTRICTED AND WIDESPREAD POPULATIONS OF THE SOUTHERN REDBELLY DACE, <i>CHROSOMUS ERYTHROGASTER</i>
*Chance Garrett	22: RESPONSE OF RIFFLE FISH COMMUNITIES TO MORPHOLOGY CHANGES RESULTING FROM STREAM DEGRADATION
*Kandria N. Driskill	23: BODY SHAPE VARIATION WITHIN AND AMONG LINEAGES OF THE RAINBOW DARTER, <i>ETHEOSTOMA CAERULEUM</i>
*Hilary Canada	24: PHYLOGEOGRAPHIC ANALYSES SUGGEST CRYPTIC DIVERSITY WITHIN THE BLUNTNOSE DARTER, <i>ETHEOSTOMA CHLOROSOMA</i>
Eric Bauer	25: WESTERN BLACKNOSE DACE IN THE BLACK WARRIOR RIVER DRAINAGE, ALABAMA
Laurel Hansen	26: WHO IS SPAWNING HERE? DEVELOPMENT OF AN RFLP LIBRARY FOR MINNOWS IN THE RED RIVER SYSTEM (CUMBERLAND RIVER DRAINAGE)
Steven L. Powers	27: MICROHABITAT OF THE CHAINBACK DARTER, <i>PERCINA NEVISENSE</i> (ACTINOPTERYGII: PERCIDAE) IN THE ROANOKE RIVER IN SALEM, VA
Mike Stegall	28: ALLOPATRIC SPECIATION OF <i>LEPOMIS MEGALOTIS</i> IN THE HILL COUNTRY OF TEXAS
Logan Phelps	29: A PRELIMINARY LOOK AT THE GREEN RIVER FISHES WITHIN MAMMOTH CAVE NATIONAL PARK FOLLOWING THE REMOVAL OF LOCK AND DAM #6
Elizabeth Cushman	30: DEVELOPMENT OF A MICROSATELLITE MARKER PANEL FOR GENETIC CHARACTERIZATION OF BLUEHEAD CHUB (<i>NOCOMIS LEPTOCEPHALUS</i>) IN SOUTH CAROLINA
Will Glenn	31: DIEL PATTERNS IN BENTHIC RIFFLE SPECIES DIVERSITY IN THE KING'S RIVER, ARKANSAS
Jon Skaggs	32: THE ECOSYSTEM ROLE OF SOUTHEASTERN STREAM FISHES: WHEN, WHERE, AND WHY DO THEY MATTER?
George Gavrielides	33: FRESHWATER INFORMATION NETWORK (FIN): A USER-FRIENDLY WEBPAGE FOR RECORDING AND SHARING FIELD DATA
Morgan E Raley	34: THE SIRAJÓ SHUFFLE: A SYSTEMATIC STUDY TO IDENTIFY RESIDENT SPECIES OF ENIGMATIC AMPHIDROMOUS WATERFALL-CLIMBING <i>SICYDIUM</i> GOBIES IN PUERTO RICO
Brittany L. McCall	35: STATUS SURVEY AND CONSERVATION GENETIC ASSESSMENT OF THE PALEBACK DARTER (<i>ETHEOSTOMA PALLIDIDORSUM</i>)

*Competing in student competition

For issues contact Bernie Kuhajda (205-792-1453) or Matt Wagner (610)-763-9074

2017 Southeastern Fishes Council Meeting Presentations

Presenters with an asterisk (*) in front of their name are competing in student competition. Titles with a lightning bolt (⚡) indicate a 5 minute lightning talk.

Oral Presentations

1. FACTORS AFFECTING SCALE SHAPE VARIATION IN ETHEOSTOMATINAE DARTERS

*Jessica Grady, C.M. Gienger, and Rebecca E. Blanton

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

The species-rich darter clade (Percidae: Etheostomatinae) has a vast research history. However, studies of variation in scale microstructure have been limited to a small number of species and variation in scale shape has not been previously studied. Because both phylogeny and environment are known to influence darter phenotypes, our goal was to evaluate the relative impact of phylogeny, environment, and behavior on darter scale shape. We generated scale shape data using geometric morphometrics. TPSDIG2 was used to digitize 7 homologous landmarks for 30 individuals from 92 species of darters representing all genera, subgenera, and terminal clades. Variables documenting species habitat use (e.g., flow, mesohabitat), spawning mode, burying behavior, and phylogeny were summarized from the literature. Procrustes superimposition and ordination methods were carried out in MORPHOJ 1.05f and tps software (Sunybrook). Scale shape variation was noted within and among genera and clades of darters due to allometry and phylogeny. Allometry and phylogeny-corrected analyses reveal additional variation in scale shape due to environmental variables. For example, darters occupying different flow rates, mesohabitats, positions in the water column, spawning modes, and burying behaviors had discernible differences in scale morphology. The shape differences observed generally follow patterns of increased streamlining in darters, which experience relatively higher rates of water flow; a trend also demonstrated in studies of body and fin morphology. Because scales aid in reducing drag and facilitating movement, understanding the relative impact these factors have on darter phenotypes will enhance knowledge of the response of this group of fishes to environmental changes and provide insights to factors promoting phenotypic diversification.

Keywords: darters; ecomorphology; geometric morphometrics; scales
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2. MULTISPECIES OCCUPANCY MODELING OF TWO ETHEOSTOMA SPECIES IN THE STRAWBERRY RIVER DRAINAGE IN ARKANSAS.

*Kyler B. Hecke^{1,2} and Steve E. Lochmann²

¹ University of Tennessee Institute of Agriculture, Department of Forestry, Wildlife, and Fisheries. ² University of Arkansas at Pine Bluff, Department of Aquaculture and Fisheries.

The Strawberry River contains one of the most diverse ichthyofaunas in Arkansas with over 100 species occurring in the drainage. This river system is also home to the endemic Strawberry Darter *Etheostoma fragi*. The species has been understudied, but recent studies have assessed its historical and current occupancy. A more comprehensive study was warranted to understand if other ecologically similar species co-occur with the Strawberry Darter. Multispecies occupancy modeling was used to assess co-occurrence between the Strawberry Darter and the Rainbow Darter *E. caeruleum* across multiple spatial scales. A new status survey of the Strawberry Darter was conducted during the summers of 2015 and 2016. Sixty-four sites (32 each summer) were sampled within the Strawberry River drainage. Site surveys were replicated 4 times each summer using a kick-seine. Data were analyzed using the software Presence, which estimates occupancy rate (Ψ) and probability of detection (p) for each species. Multispecies occupancy models within the package also estimate an occupancy interaction factor (ϕ) and a probability interaction factor (δ). A total of 920 Rainbow Darters and 236 Strawberry Darters were observed in this study. Rainbow Darters were captured at 56 of the 64 sites and Strawberry Darters were found at 24 of the 64 sites. The drainage-wide occupancy (mean \pm SE) and detection were 0.90 ± 0.04 and 0.77 ± 0.03 for Rainbow Darters and 0.41 ± 0.06 and 0.56 ± 0.06 for Strawberry Darters. In a drainage-wide model, the occupancy interaction factor was 0.95 ± 0.06 and the probability interaction factor was 1.02 ± 0.04 , suggesting possible avoidance or competitive exclusion between these two species. The results of this study provide a framework for designing a new study to assess which species is being competitively excluded and determine the limited resource (refugia, food, etc.).

Keywords: modeling; river; darters
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3. THE EFFECTS OF DAMS, DISTANCE, AND LARGE RIVERS ON DISPERSAL AND GENE FLOW OF THE SMALLSCALE DARTER, *NOTHONOTUS MICROLEPIDUS*

*[Joshua G. Stonecipher](#) and Rebecca E. Blanton

Austin Peay State University

The Smallscale Darter, *Nothonotus microlepidus*, occurs in four tributaries to the middle and lower Cumberland River System in Tennessee and Kentucky (Little, Harpeth, Red, and Stones rivers). These tributaries are separated by the large-river mainstem of the Cumberland River, which lacks habitat typical of *N. microlepidus*. Because *N. microlepidus* is small-bodied, benthic, and lacks a gas bladder, large-river habitats may limit dispersal and restrict gene flow among tributaries. Additionally, the Smallscale Darter's range has been fragmented by dams and alterations to the Cumberland River. The objective of this study was to describe patterns of genetic diversity, and assess the relative impacts of dams, distance, and intervening large-river habitat on dispersal and gene flow in this species. Tissues from 30 individuals from two localities in each river system were used as a template for amplification of twelve variable species-specific microsatellite loci. All pairwise FST comparisons were significant except for sites within the Harpeth and Stones systems, with the highest values recovered among sites separated by Percy Priest Dam. A significant positive correlation between geographic distance and genetic distance was observed ($p=0.0002$, $r^2=0.59$). STRUCTURE v2.3.4 recovered $K=4$ using the log-likelihood method, identifying four clusters corresponding to each tributary, and $K=2$ using Evanno's delta K , identifying populations from the Stones River as a distinct cluster. The Stones River has experienced population loss, has lower population sizes, and was identified as genetically distinct from other clusters in both clustering methods, indicating it may be particularly vulnerable. Although recovered as distinct clusters using the log likelihood method, we observed considerable admixture among the Harpeth and Red systems, which may reflect recent isolation associated with the construction of Cheatham Dam in 1957, but large population sizes especially in the Harpeth may be mitigating the impact of genetic drift.

Keywords: conservation, genetics, darter, *Nothonotus*
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4. INFLUENCE OF TWO TYPES OF ANTHROPOGENIC DISTURBANCE ON STREAM FISH METRICS

*[Joshua Hubbell](#), Peter Flood, Jake Schaefer

The University of Southern Mississippi

Habitat fragmentation, as a consequence of anthropogenic disturbance, influences species distribution patterns by disrupting the connectivity and structure of habitat patches. Landscape indicators can supplement other methods for measuring anthropogenic effects on river systems by assessing land use types. We used multivariate analyses and linear models to distinguish patterns in fish metrics as a response to either changes in anthropogenic land use or a community's distance to a reservoir as a function of both local scale (habitat and water quality) and landscape (% anthropogenic land use, stream size, and distance to reservoir) factors. Community data was collected from the Upper Yazoo River basin in North-Central Mississippi during the summers of 2015 and 2016. Within the upper Yazoo River basin, 45 sites were sampled within the Little Tallahatchie River system, whereas only 17 sites were sampled within the Yocona River system. Sites were distinguished based on their distance to a reservoir (DTR) and the % of anthropogenic land use (% ALU) within their upstream drainage areas. Both CCAs resulted in the constraining of scale-relevant variables and described a significant amount (23% = local, 13.98% = catchment) of the variation in fish metrics. The two best local scale linear models contained our habitat variable. There was a significant effect of habitat ($F_{1,50} = 4.48, p < 0.001$) on the proportional abundance of intolerant species. The two best catchment scale linear contained our ALU variable. Sites at which intolerant species were sampled were significantly different in the % ALU within their upstream drainage areas ($F_{1,50} = 2.51, p < 0.05$). It is apparent that changing land use patterns appear to have a stronger effect on driving patterns in community structure in the upper Yazoo River basin than the presence of either of the large-scale impoundments.

Keywords: anthropogenic disturbance; stream fish; ecology; reservoir; land use
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5. EVALUATION OF THE TRANSLOCATION SUCCESS OF A RARE DARTER SPECIES IN OKLAHOMA

*[Colt Holley](#)¹, [Jim Long](#)², and [Mona Papes](#)³

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Currently, little is known regarding the status of state-endangered Longnose Darter (*Percina nasuta*) within Oklahoma. Longnose Darters were known from two river systems in Oklahoma, but are believed to have been extirpated from the Poteau River system. Translocation efforts from Lee Creek into Blackfork Creek were made in 1991-92 with hopes of reestablishing a Poteau River system population, but whether this population currently persists is unknown. Our objectives were to sample these two systems thought to contain Longnose Darters in an occupancy modeling framework to evaluate the success of past translocation efforts and to examine differences in detection between systems. Between the two systems, a total of 31 stream reaches were sampled via backpack electrofishing in the summer of 2017. We failed to detect Longnose Darters within the stream where the translocations took place, but eight individuals from four reaches were detected in Lee Creek. Among co-occurring darter species, Longnose Darters had the lowest detection probabilities. The translocation of Longnose Darters in Oklahoma appears to have been unsuccessful and the species is now thought to be restricted within Oklahoma to a single stream. Results from this study will be used to further manage for this state-endangered stream fish.

Keywords: detection probability, endangered species, darter
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6. THE SPATIAL SCALE OF GENE FLOW IN A DISPERSAL-LIMITED HABITAT SPECIALIST LIVING IN A LARGE RIVER ENVIRONMENT.

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The federally endangered Tuxedo Darter, *Etheostoma lemniscatum*, occupies a 38.6 km reach of the Big South Fork Cumberland River, occurring in shallow, slow-moving water with large substrate, located near riffles. This habitat is patchily distributed and separated by long sections (>1 km) of deep pools believed to be unsuitable for the species. Additionally, there is a 10.7 km disjunction where little suitable habitat occurs that coincides with a high gradient rapid. Given intrinsic features of the species that suggest limited dispersal potential, we examined whether the intervening pools, distance, or rapids act as filters to gene flow. Fin clips were taken from 163 *E. lemniscatum* from 18 habitat patches encompassing its range. All individuals were genotyped for 20 variable microsatellite loci. Genetic diversity was low ($N_a=6.0$; $H_e=0.597$) overall, and the effective population estimate was 398 individuals, higher than the last census estimate. We found weak, but significant ($F_{ST}=0.011-0.040$), genetic structure among some sites, including those separated by the disjunction and rapid complex. However, the STRUCTURE analysis recovered all localities as a single cluster ($K=1$), with substantial admixture across the species range, suggesting *E. lemniscatum* is comprised of a single population. A significant isolation-by-distance relationship was found ($p=0.049$), but distance explained only 5.6% of the total genetic variation. Spatial autocorrelation analysis recovered a genetic patch size of 5.8 km, indicating that dispersal occurs at distances greater than most distances between localities. Together, data suggest *E. lemniscatum* is a single population and that extrinsic habitat features contribute to low levels of genetic structure among localities, but are not barriers to dispersal and genetic exchange. Although presumed to be dispersal limited, adaptation to movements through a large river environment may explain these observations.

Keywords: Tuxedo Darter; spatial genetic structure; genetic diversity; conservation
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7. POPULATION DYNAMICS AND HABITAT USE OF THE BUCK DARTER (*ETHEOSTOMA NEBRA*) IN BUCK CREEK, CUMBERLAND RIVER DRAINAGE, KENTUCKY

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The Buck Darter is a recently described fish species confined to the Buck Creek system of Kentucky's Cumberland River Drainage. A survey of Buck Creek by Kentucky Department of Fish and Wildlife Resources personnel found Buck Darters in 2 of 47 historical sites. Individuals were found in two spring-fed tributaries, Big Spring Branch and Stewart Branch, within the entire system. The objectives of this ongoing study are to: determine population size and habitat use of Buck Darters at Stewart Branch and Big Spring Branch; and monitor and compare water quality and fish communities at historical sites and presently occupied streams. Preliminary analyses indicate higher abundances of Buck Darters in the mid-reaches of each occupied stream, and no individuals observed in other Buck Creek tributaries. A total of 86 individuals were captured in Stewart Branch and 75 individuals were captured in Big Spring Branch. We estimate the population to be 868 ± 344 individuals in Stewart Branch and 887 ± 345 individuals based on extrapolation of sampled densities. Important habitat variables associated with their abundance include lower water temperatures and variable substrate. Occupancy and N-Mixture modeling are being used to determine patterns in occupancy and abundance relative to habitat parameters. Results will aid cooperating natural resource agencies in making decisions toward management and conservation of this imperiled species.

Keywords: fish; darter; population; modeling
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8. USE OF STRONG HABITAT-ABUNDANCE RELATIONSHIPS TO ASSESS POPULATION STATUS OF CRYPTIC FISH SPECIES: AN EXAMPLE USING HARLEQUIN DARTER *ETHEOSTOMA HISTRIO*

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Understanding trends in abundance is important to fisheries conservation, but techniques for estimating stream-wide abundance of cryptic fish that use complex habitat are not well established. We developed techniques to address this need using Harlequin Darter *Etheostoma histrio*, which is imperiled in Florida. This species is a small, cryptic freshwater fish associated with woody structure in streams where it occurs. Specifically, our objectives were to (1) determine how Harlequin Darter abundance and in-stream wood were related at sites, and (2) to use this relationship to estimate Harlequin Darter abundance stream-wide. We conducted mark-recapture studies using visual surveys to sample Harlequin Darter from Big Escambia and Pine Barren creeks in northwest Florida. In-stream woody debris abundance was quantified and mapped in both creeks using side scan sonar and GIS tools. These darter and wood data were used in a hierarchical Bayesian model to determine the effect of in-stream wood on Harlequin Darter site abundance, and to use this relationship to extrapolate darter abundance stream-wide. We found a strong positive relationship between wood and darter abundance in both creeks, and there was more wood in Pine Barren Creek than Big Escambia Creek. The extrapolated stream-wide abundance estimates were 7,223 darters (95% credible interval = 5,743-9,244) in Big Escambia Creek and 8,801 darters (95% credible interval = 7,666-10,141) in Pine Barren Creek. We believe our methods were effective for estimating stream-wide abundance of a cryptic fish with a strong habitat-abundance relationship, and they may have application for other fishes such as madtoms. Our findings will also benefit the conservation of Harlequin Darters in Florida and range-wide.

Keywords:habitat-abundance relationships, stream-wide abundance estimate, Harlequin Darter
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9. PRIORITIZING NATIVE FISH REINTRODUCTIONS IN THE GREAT SMOKY MOUNTAINS NATIONAL PARK

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Extirpated organisms are reintroduced into their former ranges to combat species declines and biodiversity losses. The growing field of reintroduction biology provides guiding principles for reestablishing populations, though criticisms remain regarding limited integration of initial planning, modeling frameworks, interdisciplinary collaborations, and multi-species approaches. We used a multidisciplinary, multi-species, quantitative framework to plan reintroductions of three fish species into Abrams Creek, Great Smoky Mountains National Park, USA. We first assessed the appropriateness of habitat at reintroduction sites for banded sculpin (*Cottus carolinae*), greenside darter (*Etheostoma blennioides*), and mottled sculpin (*Cottus bairdii*) using species distribution modeling. Next, we evaluated the relative suitability of nine potential source stock sites using population genomics, census counts, and multiple-criteria decision analysis (MCDA) based on known correlates of reintroduction success. Species distribution modeling identified mottled sculpin as a poor candidate, but banded sculpin and greenside darter as suitable candidates for reintroduction based on species-habitat relationships and the current habitat template of Abrams Creek. Genotyping by sequencing revealed acceptable levels of genetic diversity at all candidate source stock sites, identified population clusters, and allowed for estimating the number of fish that should be included in translocations. Finally, MCDA highlighted clear priorities among candidate source stock sites that were most likely to yield successful reintroductions based on differential weightings of habitat assessment, population genomics, and the number of fish available for translocation. Our integrative approach represents a culmination of multiple recent advancements in the field of reintroduction biology and highlights a recent paradigm shift away from simply choosing nearby populations for translocation to an information-based science with strong *a priori* planning coupled with several suggested *posteriori* monitoring objectives. Our framework can be applied to optimize reintroduction successes for a multitude of organisms and advances the science of reintroduction biology by simultaneously addressing a variety of criticisms of the field.

Keywords: Ecological restoration; population genetics; source stock prioritization; species distribution modeling; translocation

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10. ENVIRONMENTAL AND PHYLOGENETIC EFFECTS ON THE DERMAL MICROBIOME OF MOBILE BASIN SCULPIN (TELEOSTEI: *COTTUS*)

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The “slime” layer of fishes is of ecological and evolutionary importance, as it is inhabited by a co-evolving community of microbes, including commensals and potential pathogens. The diversity and dynamics of this community are influenced by the host genetics and the environment, but the relative contributions of these two factors remain largely unexplored. We are applying high-throughput molecular techniques to test for differential host and environment effects on the microbiome of Banded Sculpin (*Cottus carolinae*), a species with strong population structure and a broad geographic range. We focus on the Mobile River Basin, where the species occupies both upland and lowland habitats. Within the Mobile Basin there are two interesting populations. These two populations are distinct from each other, inhabiting different river drainages, and separated from upstream populations by over 100 miles. They are found to be inhabiting ecologically secluded areas at the southern reaches of their range. The microbiome analysis reveals possible effects of genes (clades) and environment, as well as an interaction effect. We discuss the relative importance of each, along with future directions involving the application of phylogenetic comparative methods to microbiome analysis.

Keywords: cottus; sculpin; microbiome; Mobile; slime
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11. PHYLOGEOGRAPHY OF THE ROSYSIDE DACE, *CLINOSTOMUS FUNDULOIDES* (TELEOSTEI:CYPRINIDAE)

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The genus *Clinostomus* (Teleostei: Cyprinidae) is an understudied genus of fishes in the order Cypriniformes. *Clinostomus* has a large geographic range occupying much of the eastern portion of North America. Currently, only two species are recognized within *Clinostomus*: *C. funduloides* and *C. elongatus*. A previous morphological study recognized three subspecies (*C. f. funduloides*, *C. f. estor*, and one undescribed subspecies). Given the broad distribution and disjunct geographic range, a phylogenetic assessment of *Clinostomus* is needed to further resolve the taxonomic uncertainty within this genus. The objectives of this study were to determine phylogenetic relationship and genetic variation within *Clinostomus*, using three unlinked DNA loci. Results of this study give insight on the phylogenetic relationships, genetic differentiation, taxonomic status, and distribution of *Clinostomus* across its range and suggests that there is a greater amount of species level diversity within this genus than is currently recognized. The current two species approach of *Clinostomus* appears to be an underestimate based on the genetic data recovered in this study. Therefore, a taxonomic re-evaluation is warranted.

Keywords: Phylogeography; *Clinostomus*; Rosyside Dace; Subspecies
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12. POPULATION GENETICS OF THE BLACKSIDE DACE

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The Blackside Dace (*Chrosomus cumberlandensis*) is a threatened cyprinid found in the Upper Cumberland River system in northeastern Tennessee and southeastern Kentucky, and was recently discovered in the Kentucky River system. Anthropogenic activities such as mining and logging are prevalent within the Blackside Dace range. Habitat fragmentation, caused by these anthropogenic activities, may lead to isolated populations with little or no gene flow among them. However, understanding historic gene flow among populations helps put contemporary patterns into perspective. The purpose of this study was to assess historic gene flow among populations of the Blackside Dace. We sequenced 1109 bp of the mitochondrial *cyt b* gene for individuals from 12 populations representing the species range. Populations found within both the Kentucky and Cumberland River systems contained shared haplotypes, suggesting historic connectivity between these systems. Haplotype diversity varied across drainages, but three populations had only one haplotype. Population expansion was detected for one population. Overall, our results showed widespread gene flow across the range of Blackside Dace, with evidence of historic isolation in the Jellico Creek drainage within the Cumberland River system. The low haplotype diversity observed in some populations may be evidence of recent bottleneck events but should be examined using contemporary-scale markers (e.g. microsatellites).

Keywords: mtDNA; conservation; genetics; cyprinidae; cytochrome b
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13. INVESTIGATION OF COLOR VISION IN A NUPTIALLY COLORED MINNOW, *CHROSOMUS ERYTHROGASTER*

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Research involving the visual systems of cyprinids is mostly limited to the capabilities of the rods and cones. The understudied area of visual filtering capabilities in stream fishes has the potential to elucidate more on their complex behavior and social interactions. Tennessee's freshwater streams offer a variety of colorful minnows, of which, 32% exhibit red coloration on their body, fins, or combination of the two. Our hypothesis is that highly ornamented fish exhibit coloration-driven behaviors. This led us to predict *Chrosomus erythrogaster* (Southern Redbelly Dace) will respond to and differentiate visual cues representative of their biology and environment. Southern Redbelly Dace was chosen due to its brilliant red body coloration during spawning and stable populations throughout most of its range. Southern Redbelly Dace individuals were trained via operant conditioning to one of four colors (red, blue, yellow, and green) based on the assumption of tetrachromy in cyprinids. Training was food-based, and movement towards expected food source along with overall increase in movement compared to a control was recorded for all individuals. Responses were averaged within a test school, and analyzed using an ANOVA. Individuals trained to red exhibited a significantly stronger response ($n=48$; $p < 0.001$) compared to other colors. Blue ($n=48$; $p=0.8193$), green ($n=48$; $p=0.5913$), and yellow ($n=48$; $p=0.0897$) trained individuals did not exhibit a significantly stronger response to their trained color. Southern Redbelly Dace exhibit a capability to distinguish red from all other colors based on hue alone, suggesting it plays a substantial role in the life history of the species.

Keywords: Behavior; Conditioning; Cyprinid; Tetrachromy
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14. ⚡ FISHMAP.ORG USER OBSERVATION SUBMISSIONS PROCESS

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Keywords: FishMap.org; submissions
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15. ⚡ FRESHWATER INFORMATION NETWORK (FIN): A FRESHWATER SPECIES DATABASE FOR THE SOUTHEASTERN UNITED STATES

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The Southeastern United States is a global biodiversity hotspot for freshwater aquatic organisms. Unfortunately, the Southeast also harbors some of the most imperiled aquatic species in the world. Thus the need for collaborative conservation efforts for southeastern aquatic organisms is more important now than ever. However, distributional and status data for these organisms are stored in a variety of platforms, including spreadsheets, museum records and databases, unpublished reports, and field notes. This can be exceptionally problematic for endangered species where recent sightings cannot be vouchered and accessed by others. The Freshwater Information Network (FIN) aims to combine all of these data sources into a single user friendly “living” database containing georeferenced locations and voucher photographs. We collected museum, institutional, and field note data and georeferenced records using the Guide to Best Practices for Georeferencing. Currently FIN includes 399 species of fishes within the Tennessee, Mobile, and Cumberland river drainages. This interactive website allows scientists and the public to submit new locality data and field photograph vouchers through a configurable application made with ArcGIS Solutions. Distribution maps, photo voucher galleries, a brief description of life history, and literature cited for each species will allow for a one stop webpage on information on all the species for both scientists and the public. Future additions to FIN will include other aquatic taxonomic groups in these drainages. With new addition of data from experts, conservation efforts in the Southeast can become a focused collaborative effort.

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16. ⚡PARKS, ARKS, AND REMARKS: CONSERVATION LANDS AND SOUTHEASTERN AQUATIC BIODIVERSITY PRIORITIES

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The southeastern United States is a global hotspot of freshwater biodiversity, supporting almost two-thirds of the country's fish species, over 90% of the U.S. total species of mussels, and nearly half of the global total for crayfish species. Many of these species are narrow endemics. Unfortunately, this region is also a hotspot for imperilment; the number of imperiled freshwater fish species in the Southeast has risen 125% in the past 20 years. While the causes of this imperilment, including habitat modification or loss, development, and introduced species, have been extensively documented, efforts to reverse these trends have been hampered by limited funding and lack of public awareness. In late 2016 we released the first version of Southeastern Aquatic Biodiversity Conservation Strategy, an analysis of historical presence records for fish, crayfish, and mussels at the 8-digit HUC level that combines species richness, endemism, and imperilment to derive conservation priorities. This talk will discuss recent updates to the strategy, including improved mussel and updated fish distribution data, and how the resulting priorities align with the existing network of protected lands in the Southeast. We convened a meeting of mussel experts to correct and improve our mussel maps, which in the 2016 dataset had higher error rates than for the other taxa. A comparison of landscape protection using two datasets of protected areas indicates a substantial mismatch between high-priority areas for freshwater biodiversity and existing public and private conservation lands, although certain highly protected areas, such as Choctawhatchee Bay in Florida, are nevertheless important strongholds for species protection.

Keywords: Conservation prioritization; multi-species conservation; protected lands
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17. ⚡ONE FISH TWO FISH DEAD FISH BLUE FISH: THE ENDANGERED SPECIES ACT UNDER TRUMP

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Keywords: Environmental Policy; Endangered Species Act
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18. ⚡ FISH CHANGES TO THE ARKANSAS WILDLIFE ACTION PLAN

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The Arkansas Game and Fish Commission revised the Arkansas Wildlife Action plan during 2015 (http://www.wildlifearkansas.com/strategy_2015.html), and this plan describes the Species of Greatest Conservation Need (SGCN) that may receive funding through the State Wildlife Grant Program. In this presentation, we review the State Wildlife Grant Program, how species were added and removed from the list, recent changes to the list of SGCN, and high-priority conservation issues that were identified. A total of 66 fish species were listed as SGCN. Twenty-one were added and three were removed. Most species added to the plan were infrequently collected, but some were newly described species. Leopard Darter *Percina pantherina*, Least Darter *Etheostoma microperca*, and Beaded Darter *Etheostoma clinton* are examples of highly-imperiled species with unique conservation challenges. Climate change may have unknown impacts on SGCN fishes. Thermal tolerances are generally unknown for SGCN species, and baseline stream temperature data are generally unavailable for many rivers. The 2015 plan will be used to prioritize projects that will receive State Wildlife Grant funding over the next decade.

Keywords: Conservation; Species; Plan; Arkansas

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19. ⚡ CONSERVATION OF THE SICKLEFIN REDHORSE IN GEORGIA

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Keywords: fyke net, PIT tag antenna array, mark-recapture, Candidate Conservation Agreement

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20. ⚡ AN UPDATE ON RECENT *NOTURUS* CONSERVATION WORK IN MISSISSIPPI

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Keywords: Madtom; *Noturus spp.*; gears; diet; status

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21. ⚡ INITIATION OF SPECIES STATUS ASSESSMENTS FOR 3 SOUTHEASTERN DARTERS: *ETHEOSTOMA FORBESI*, *E. CINEREUM*, AND *E. MAYDENI*

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Keywords: *Etheostoma*; Darters; status assessment

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22. ⚡POPULATION STATUS AND MICROHABITAT PREFERENCES OF THE FEDERALLY ENDANGERED LAUREL DACE, *CHROSOMUS SAYLORI*

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The Laurel Dace (*Chrosomus saylori*) is a federally endangered species endemic to the upper Tennessee River Basin in Tennessee. Laurel Dace historically occupied only eight streams on Walden Ridge of the Cumberland Plateau, however recent sampling indicates this species is only relatively common in two streams, Bumbee Creek and Youngs Creek. Previously, the northern population of Laurel Dace (Piney Creek system) appeared to be in relatively good shape, with high numbers of individuals in Bumbee and Moccasin creeks, but as of 2016 there have been no Laurel Dace found in Moccasin Creek. From 2016 to 2017 we saw a one-third decrease in abundance of Laurel Dace in Bumbee Creek due to the severe drought of 2016. The abundance of Laurel Dace in Youngs Creek was low when it was last sampled in 2013; however in 2017 the site was visited twice, with the second survey capturing hundreds of young of the year Laurel Dace. With heavy siltation and poor water quality from agriculture likely being the cause of population decline for this endangered fish, we also wanted to investigate specifically what factors could potentially be affecting them. We conducted a microhabitat habitat study and measured variables such as pool area, mean depth, substrate composition, mean silt depth and canopy cover. Laurel Dace seem to thrive in large, deep pools with a lot of canopy cover. Surprisingly, silt did not appear to be that much of a limiting factor for these fish. One of our most prominent observations was the introduction of invasive species (*Lepomis* sp.) to creeks that did not have invasives previously. The introduction of non-native competitors could potentially be a limiting factor on the population of Laurel Dace.

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23. ⚡SEASONAL VARIATION IN LIPIDS LEVELS OF TWO SYMPATRIC SPECIES OF SNUBNOSE DARTER

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Keywords: *Etheostoma*; *Ulocentra*; *duryi*; *simoterum*
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24. ⚡ PRELIMINARY ASSESSMENT OF ADAPTIVE VARIATION OF GENES IN DARTER SPECIES

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Determination of the conservation status of populations is usually carried out with neutral genetic markers. With the advent of inexpensive whole genome DNA sequencing, it should be possible to soon determine the actual adaptive variation in populations to better assess their conservation status. In preparation for that eventuality, the patterns of adaptive variation in protein coding genes is being explored in four species of darters for which genomic DNA sequences have been obtained. The genome of the Tallapoosa darter (*Etheostoma tallapoosae*) has been partially assembled and a number of scaffolds have been annotated. Annotated full genes identified in the Tallapoosa darter were then used as reference sequences for the assembly of orthologous genes from genomic DNA sequences of three other darter species (*Percina crypta*, *Etheostoma chuckwachatte* and *Etheostoma jessiae*). Adaptive variation of a total of about 100 orthologous genes has been assessed in these species and a number of genes that appear to have evolved under positive selection have been identified. The entire mitochondrial chromosome from these darters has also been assembled and annotated. Adaptive variation of all of the protein coding mitochondrial genes has been assessed in these species as well as a few other darter species that are available in GenBank. Interestingly, three mitochondrial genes show evidence of adaptive evolution and may be useful in assessing potential adaptive differences between populations of darters.

Keywords: darter; genomic sequencing; adaptive variation; conservation
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25. ⚡ MITOCHONDRIAL GENOME SEQUENCING OF ALABAMA STURGEON (ACIPENSERIDAE: SCAPHIRHYNCHUS SUTTKUSI)

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Found only in the Mobile River Basin in Alabama and Mississippi, *Scaphirhynchus suttkusi* is one of the most imperiled fish species in the southeastern United States. The species was last collected in 2007, and the last reliable visual report of the species was in 2009. This has led to fears that *S. suttkusi* may be functionally extinct. Recently, *S. suttkusi* was reported to have been detected throughout the lower and mid Alabama River using environmental DNA assays (eDNA). However, these assays relied on conventail PCR and a single marker, a small fragment of the mitochondrial cytochrome oxidase B gene (cytB); using only one marker could have led to false positives in *S. suttkusi* detection. Furthermore, expected differences in cytB among closely related Sturgeon species have not been well characterized, potentially limiting the ability of an assay based only on cytB to distinguish between *S. suttkusi* and other species. Here, we sequenced the complete mitochondrial genome of two *S. suttkusi* individuals from archived tissues that were stored frozen at the U.S. Fish and Wildlife Service Forensics Lab. A long-range PCR approach, combined with Illumina sequencing, produced two identical mitochondrial genomes. We found limited mitochondrial genetic diversity among all three *Scaphirhynchus* species, and gene order on the mitochondrial genome was conserved across Acipenseridae. Mito-phylogenomic analyses recovered a well-supported phylogeny of Acipenseridae with all three *Scaphirhynchus* species nested within Acipenser. However, none of the *Scaphirhynchus* species were recovered as reciprocally monophyletic, and overall genetic diversity among all three *Scaphirhynchus* was less than that observed within some other species like *A. fulvescens* (Lake Sturgeon). Mitochondrial genomes sequenced here could serve as a tool for designing effective eDNA assays for *S. suttkusi*. Given mitochondrial genome similarities among *Scaphirhynchus* species, care would need to be taken to design an assay that could unambiguously distinguish *S. suttkusi*.

Keywords: Mitochondrial genome; Alabama Sturgeon; *Scaphirhynchus*; Mobile River Basin
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26. ⚡ **WHAT DETERMINES WHO IS WHERE IN ATLANTIC COASTAL PLAIN STREAMS?**

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Atlantic coastal plain (ACP) streams exhibit pronounced environmental variation over time and space, yet influences of these dynamic conditions on fish community composition are poorly understood. We hypothesized that (1) ACP fish communities would be more influenced by local- than landscape-scale habitat conditions, but that (2) at the landscape scale, biogeographic factors such as basin, ecoregion, and stream size would be more influential than anthropogenic land use. We tested hypotheses with fish-community, local-habitat, and landscape data collected for two summers at wadeable ACP streams in the Ogeechee, Altamaha, and Savannah basins of Georgia. Species richness varied among sites from 5 to 24 species, and primarily was influenced by one landscape (stream size) and three local factors (woody debris, pH, and width:depth ratio). In contrast, multivariate assemblage composition primarily was influenced by local factors (woody debris, pH, depth, and water velocity). Sites sorted into two distinct groups, characterized either by “fluvial” or “non-fluvial” fish communities. The faunal and environmental characteristics of these site-groups were highly persistent, despite significant inter-annual variation in regional discharge patterns. Our findings suggest that ACP fish communities primarily are structured by local habitat conditions, which are strongly interdependent with local hydrology. This information helps refine predictions about the potential biological effects of channelization, water abstraction, and climate change in ACP streams.

Keywords: coastal plain; species composition; community; multivariate; hydrology
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27. ⚡ **A NEW TERMINOLOGY FOR CRANIAL TUBERCLES OF NORTH AMERICAN MINNOWS (TELEOSTEI: CYPRINIDAE)**

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Keywords: tubercles;sexual dimorphism;nuptial;cyprinidae
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28. ⚡ A NEW PYGMY SUNFISH SPECIES FROM SOUTHERN ALABAMA AND WESTERN FLORIDA

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The Pygmy Sunfishes are a morphologically distinctive, but poorly understood genus of freshwater fishes endemic to the southeastern United States. The Everglades Pygmy Sunfish (*Elassoma evergladei*) was described in 1884, but intraspecific morphological and molecular variation remains undescribed. This geographic distribution of *E. evergladei* includes the Cape Fear River drainage of North Carolina, the Mobile River drainage of Alabama, and all intervening rivers south to the Florida Keys. This distribution covers diverse physiographic subprovinces, including numerous karst plains, Pleistocene alluvium, Carolina Bays, and the Mid-Florida Ridge. Previous research on codistributed species has revealed strong population genetic structure associated with the same watershed divides and physiographic features. We characterized morphological and molecular variation among populations of the Everglades Pygmy Sunfish, including representatives from all major watersheds and physiographic provinces within the species range. Mitochondrial sequence data was used to construct a novel molecular phylogeny, which revealed two well-supported and geographically restricted clades (North Carolina and Alabama), which were basal to a broadly distributed and unresolved clade. Morphometric analyses revealed wide variation in body shape, but no significant differences among the three groups. Meristic analyses revealed a single character (head scale count) which distinguished populations from Alabama and extreme west Florida from all other populations. Morphological and molecular data provide evidence for a monophyletic and diagnosable clade within the range of *E. evergladei*, which satisfies criteria for the phylogenetic species concept 3 (PSC3). We propose a new species of Pygmy Sunfish, which is geographically restricted to the Mobile and Perdido River drainages of southern Alabama and western Florida.

Keywords: *Elassoma evergladei*, pygmy sunfish, cytochrome b, Mobile River, head scales, msandel@uwa.edu

29. LIFE HISTORY TRAITS OF FOUR COMMON CYPRINID SPECIES FOUND IN INTERMITTENT STREAMS OF THE COASTAL PLAIN OF GEORGIA

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Life history traits of stream fishes partly reflect adaptations to natural disturbance regimes, which in turn shape assemblage composition via environmental filtering on species persistence. Thus, trait-based approaches, including the trilateral life history model, have been useful for understanding species responses to streamflow alteration. In this study, we focused on life history traits of four closely related cyprinid species in a coastal plain stream system of southwest GA that is shifting from historically perennial streamflow to intermittency. Native fishes, including these four species, vary in how commonly they occur in intermittent streams. We evaluated differences among these four cyprinids in reproductive timing (based on ovary and oocyte development), sex ratio, and body size at maturity and reproductive investment (gonadosomatic index (GSI), gonad weight and egg diameter), traits hypothesized to influence the ability of species to persist in intermittent streams. We captured periodically sampled individuals in 14 streams over the duration of a year (May 2016-April 2017). We found that for *Notropis harperi*, the species with high persistence rates, reproductive timing did not overlap with typical seasonal stream drying. *N. harperi* also had the significantly smallest minimum length at maturation, greatest GSI and gonad weight, and, a tendency towards large average egg diameter. Species with low persistence rates in isolated pools (*Notropis petersoni*, *Notropis texanus*, and *Pteronotropis grandipinnis*), had at least a portion of their reproductive timing overlapping with times when streams were likely to dry down, and had similar and significantly lower GSI and relative gonad weight than *N. harperi*. All four of these species would be considered opportunistic, rather than periodic or equilibrium, strategists. Our results suggest, however, that some the life history traits used to define the trilateral life history model may be useful for understanding differences in how even closely related species respond to changing environments, with smaller body size at maturity along with appropriate reproductive timing promoting greater persistence given more frequent and intense disturbances.

Keywords: reproduction; functional trait ; flow-ecology; intermittent streams
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30. ENVIRONMENTAL AND BEHAVIORAL FACTORS AFFECTING VARIATION IN BLUEHEAD CHUB (*NOCOMIS LEPTOCEPHALUS*) NEST SIZE AND UTILIZATION BY A NEST ASSOCIATE, YELLOWFIN SHINER (*NOTROPIS LUTIPINNIS*)

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Yellowfin Shiners *Notropis lutipinnis* spawn on nests built by adult male Bluehead Chubs *Nocomis leptocephalus*. These reproductive interactions play a key role in maintaining community structure and biodiversity. In this study, we studied nest size variation of Bluehead Chub and nest utilization by Yellowfin Shiner in the upper Piedmont region of South Carolina. We conducted 89 consecutive days of field observations in April-July 2016 and recorded spawning activities, nest size, the number and sizes of male Bluehead Chub, the number of Yellowfin Shiners on each nest, and several environmental variables. Structural equation modeling was applied to identify networks of direct and indirect relationships among terminal variables, nest size and the number of Yellowfin Shiner, and environmental and behavioral factors. We located a total of 90 nests in three streams, and spawning was observed on 71 nests. We defined six types of nest based on nest resources, such as pebbles and location, were re-used by Bluehead Chub. All paths in models were significant and models were fitted with data based on the results of global significance tests. Photoperiod and water temperature were important environmental variables accounting for size of male Bluehead Chub. Nest size was influenced by the number, size, duration of nest construction, and their re-use of nest resources. The number of spawning days, nest size, the number and size of male Bluehead Chubs were important factors for attracting more Yellowfin Shiners to nests. The number of male was the most important direct factor affecting both nest size and the number of Yellowfin Shiner. The major indirect factor influencing behavioral variations of Bluehead Chub was the male size. This study suggests that nest size and interaction with associates is influenced by environmental variables and behavioral variations, which can be a key factor for reproductive success and evolution.

Keywords: behavior, nest association, reproductive ecology, reproductive success, structural equation modeling
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31. YELLOWFIN SHINER DENSITY DETERMINES THE INTERACTION OUTCOMES OF NEST ASSOCIATION WITH A BLUEHEAD CHUB HOST

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A major goal of ecology is to examine how abiotic and biotic context determine the outcomes of positive biotic interactions (mutualism, commensalism, and facilitation). One such interaction is nest association, in which ‘associate’ species such as Yellowfin Shiner *Notropis lutipinnis* deposit eggs in the nests built by host species such as Bluehead Chub *Nocomis leptocephalus*. The interaction is always advantageous for shiners, which benefit from parental care and clean gravel substrate provided by male chubs. Chubs benefit from a brood dilution effect, whereby adding associate eggs decreases the per-capita effects of predation on chub eggs. Though this interaction is usually mutualistic, low associate density may weaken the dilution to the point of being non-beneficial to the host. In an *in situ* experiment, we manipulated Yellowfin Shiner density (absent, low₁₅, high₈₀) at constant chub density (two adult males and 15 adult females) and quantified chub reproductive success (indexed by egg abundance, identified by molecular tools). We constructed 12 experimental units during the 2017 spawning season in a second-order stream in Pickens County, South Carolina, with 8 replicates of each treatment among two blocks (early- and mid-spawning season). We hypothesized chub reproductive success would respond positively to increased shiner density (absent < low < high) as a result of brood dilution. As hypothesized, chub reproduction was highest at high associate densities ($p = 0.03$). Surprisingly, chub reproductive success in the absence of associates was higher than at low associate densities ($p = 0.048$), suggesting that reduced associate abundance does not provide a strong enough brood dilution benefit to outweigh the costs of the interaction for the host (i.e. egg predation). These results suggest that changes in biotic context can shift interaction outcomes in this nest association from mutualistic to parasitic. Interspecific spawning may not necessarily always be advantageous.

Keywords: context; mutualism; nest association; *Notropis*; *Nocomis*
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32. NESTING MICROHABITAT USE OF BARTRAM'S BASS IN THE UPPER SAVANNAH RIVER BASIN

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Bartram's Bass (*Micropterus sp. cf. cataractae*) is an undescribed species of Shoal Bass endemic to the Savannah River basin of South Carolina and Georgia. Bartram's Bass populations are threatened by habitat alteration and hybridization with the invasive Alabama bass (*M. henshalli*), which were introduced into several Savannah River impoundments in the 1980s. Identifying the reproductive isolating mechanisms that have broken down to facilitate hybridization will be critical for conserving Bartram's Bass. In spring/summer 2017, snorkel surveys were performed in eight tributaries to the upper Savannah to quantify nesting microhabitat use of Bartram's Bass. Egg samples were collected for genetic analysis, and microhabitat parameters (depth, velocity and substrate) were recorded at each of the 34 nests detected. Habitat transects were used to quantify available habitat. Average velocity of the 34 nests observed was 0.12 m/s, and average available velocity in the transects was 0.23 m/s ($P=0.0184$). Average depth of the nests was 0.75m, and average available depth was 0.80m ($P=0.7736$). Depth selection ranged from 0.5m to nearly 1.5m, where velocity was observed below 0.5 m/s. The preferred substrate was primarily silt (35%) and cobble (44%), with some nests composed of gravel (6%) and bedrock (15%), whereas the most available substrate observed was sand (18%), cobble (21%) and bedrock (21%) ($P<0.0001$). The preliminary results indicate that the nesting Bartram's bass are selecting more for velocity than depth and substrate, and although there is a relationship between substrate use and availability, we believe the main factor driving substrate use is velocity. Genetic analyses of eggs and individuals are underway to confirm species identity, hybrid presence, and the extent of hybridization throughout the range in the upper Savannah River basin.

Keywords: Bartram's Bass, Black Bass, Nesting, Hybridization, Savannah River
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33. SPECIES DELIMITATION OF A BIOLOGICAL CONSERVATION ICON

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The Snail Darter, *Percina tanasi*, is an icon of biological conservation that provided an important legal test of the Endangered Species Act. *Percina tanasi* is distributed in the Tennessee River system from the Holston and French Broad Rivers in Tennessee downstream to the Bear Creek system in Alabama and Mississippi. When *P. tanasi* was described in 1976 it was determined to be closely related to *Percina uranidea*, which was described in 1887 and is currently distributed in the White and Ouachita River systems of Arkansas, southern Missouri, and northern Louisiana. The two species are reported to differ in the modal number of anal fin rays, the length and shape of pectoral fins, the length of pelvic fins, the width of dorsal saddles, and the distribution of tubercles on the pelvic fin. We investigated the distinctiveness of *P. tanasi*, relative to *P. uranidea*, using classical meristic trait morphology, mtDNA, and ~30,000 RADseq loci. Our analyses reveal that *P. tanasi* and *P. uranidea* share mtDNA haplotypes and that genomic clustering of RADseq SNPs do not correspond to the delimited species. In addition, the disparity of systematically important morphological traits is lower between *P. tanasi* and *P. uranidea* than observed in several other darter sister species pairs.

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34. ENVIRONMENTAL DNA SURVEILLANCE OPTIMIZATION OF THE PYGMY MADTOM, *NOTURUS STANAULI*

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A major challenge for freshwater biodiversity conservation is the identification and implementation of effective biosurveillance techniques. Many existing methods (e.g., traps, seining, electrofishing) lack the ability to reliably detect all species in a system, and may also be destructive to target and non-target organisms and their habitats. The utilization of environmental DNA (eDNA), the unseen genomic material in water, has proven to be a non-invasive and effective alternative for monitoring rare aquatic species, such as the Pygmy Madtom (*Noturus stanauli*). However, eDNA assays require optimization for each system and organism. Our objective was to determine where water samples should be collected in order to increase the detection probability of *N. stanauli* using eDNA surveillance. We sampled the type locations for the *N. stanauli* in both the Duck and Clinch rivers in order to determine the optimal sampling location in both rivers. We collected water samples from two points in both flowing water and slackwater areas from the surface, middle, and epibenthic water column strata in each river. Additionally, a 6-inch core sample was taken from each of the four points. All water samples were filtered and eDNA was extracted using standard techniques. Samples were PCR amplified using end-point PCR and quantitative PCR, using a species-specific primer set. Positive signals were confirmed using bi-directional Sanger sequencing. We found no signal from *N. stanauli* in the Duck River, however we did obtain multiple signals from Clinch River samples. Preliminary results indicate that detection probability is higher in flowing water compared to slackwater (66.41% vs 31.875%, respectively), and water samples taken at the surface yield higher detection probability compared to the middle, epibenthic or core (78%, 66%, 53%, and 69%, respectively). The results from this study will be used to improve detection of *N. stanauli* via eDNA surveillance and may inform the development of eDNA applications in other flowing river systems.

Keywords: environmental DNA; madtom; biosurveillance; molecular ecology; endangered species
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35. SIZE-SPECIFIC ADVANTAGE IN HABITAT COMPETITION BETWEEN MOUNTAIN MADTOMS (*NOTURUS ELEUTHERUS*) AND INVASIVE CRAYFISH (*ORCONECTES SPP.*)

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Nonindigenous crayfish have been implicated in the widespread decline of native fish populations where they have invaded. For example, in Little Chucky Creek, a tributary to the Nolichucky River in Tennessee, the population decline of the Chucky Madtom (*Noturus crypticus*) to the point of extirpation or even extinction has been partially attributed to the establishment of two nonnative crayfishes, the Kentucky River Crayfish (*Orconectes juvenilis*) and the Virile Crayfish (*O. virilis*). While it has been suggested that the crayfish exclude the cavity-dwelling fish from shelter, no studies have been conducted to demonstrate that crayfish directly outcompete madtoms for cover habitat. The objective of this study was to experimentally test the hypothesis that invasive crayfish competitively exclude the Mountain Madtom (*N. eleutherus*), a surrogate species for the Chucky Madtom, in a laboratory environment. Behavioral trials were conducted where shelter was the limited resource for the two potential competitors. The experiment was designed to test for the effect of crayfish density, territorial establishment, relative size difference, and length of exposure on a madtom's ability to occupy the cover object. For acute trials (48-h duration), effects of crayfish density and territory establishment were not significant (Fisher's Exact Test, $P=0.37$ and $P=0.24$, respectively), but average size difference significantly affected madtom occupancy of the shelter habitat (binomial logistic regression, $P=0.01$). Four chronic trials lasting 5 days were conducted on size-sorted treatments. Madtom occupancy and health (i.e. crayfish-induced disease, lesions, or death), were significantly affected by relative size ($P<0.001$ both), and mortality was 100% for juvenile madtoms. I concluded that the invasive Kentucky River and Virile crayfishes exhibit a size-specific competitive advantage over madtoms when habitat is limited, and that nonindigenous crayfish species can catalyze fish population declines at least partially through habitat exclusion and predation on juveniles.

Keywords: Madtom; Crayfish; Invasive species; Competition
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36. USE OF DEAD MUSSEL SHELLS BY MADTOM CATFISH IN THE GREEN RIVER

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The Green River in Kentucky, like many of the large rivers in the southeastern United States, has high fish and macroinvertebrate diversity. As both fish and macroinvertebrate have evolved together in this system, symbiotic relationships have developed between species. One type of relationship that has evolved is commensalism, where one individual benefits, while the other is not affected. Commensalism has been observed between madtom catfish (*Noturus* spp.) and mussels in the Green River, as the madtom individuals use dead mussel shells as cover while not actively hunting. In the fall of 2016 and 2017, surveys were conducted to determine if madtom catfish prefer hiding under dead mussel shells or rocks of similar size. The data was collected at four separate sites along the Green River, each sampled each year. Three 12-meter by 12-meter plots were sampled at each site by snorkeling upstream in the plot searching for madtoms in the dead mussel shells and under the rock substrate. Madtoms were found under a larger percentage of available mussel shells than under rocks of similar size. The density of madtoms was also higher at sites with higher density of mussel shells. Madtoms tend to prefer the shelter of dead mussel shells when the shells are abundant and competition between individuals for cover is low. When shells are not readily available, the madtoms gravitate toward using the rock substrate as shelter.

Keywords: madtoms; mussel shells; commensalism; cover
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37. STABILITY AT LOW DENSITIES OR ENDANGERED? SPATIOTEMPORAL POPULATION DYNAMICS OF THE CADDO MADTOM (*NOTURUS TAYLORI*)

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Approximately 20% of the genus *Noturus* (family Ictaluridae) are classified as federally threatened or endangered species. The Caddo Madtom (*Noturus taylori*) is an endemic of the Interior Highlands, historically known from three river drainages in the Ouachita River basin. However, *N. taylori* inhabits two of the river drainages presently, and a prior study found evidence suggesting population decline throughout its distribution. Additionally, the Center for Biological Diversity petitioned *N. taylori*, among other aquatic species from the southeastern U.S., for federal listing. Using microsatellite DNA loci, mitochondrial DNA, and extensive seasonal sampling, the objectives of this project were as follows: (1) determine the spatiotemporal population dynamics of *N. taylori*; and (2) evaluate potential genetic, habitat, and life-history differences among Caddo and Ouachita river populations of *N. taylori*. Together, these data will be useful for determining conservation needs and listing status for *N. taylori*. Phylogeographic analyses did not resolve Caddo and Ouachita river *N. taylori* populations as reciprocally monophyletic. Divergence among all individuals sampled was relatively shallow, having occurred during the late Pleistocene Epoch (approx. 0.15-Mya). Demographic analyses suggest that *N. taylori* populations are growing and expanding in both drainages from a historic bottleneck ($D^* = 3.30$ and $F^* = -3.35$, $P < 0.001$), despite low genetic diversity. Habitat parameters and water quality were assessed with a nonmetric multidimensional scaling ordination, which suggested different habitat usage by *N. taylori*, both within and among the Caddo and Ouachita river drainages. These results suggest that *N. taylori* populations are not heavily impaired; however, the endemic status and fragmented distribution of *N. taylori* populations merit conservation concern due to increased vulnerability to stochastic events, which could expedite extirpation or extinction.

Keywords: conservation, population genetics, habitat fragmentation, endemism
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38. ASSESSING FISH SPECIES DECLINES FROM 1996 TO 2016 IN THE CONASAUGA AND ETOWAH RIVERS, GA

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The highly diverse fish assemblages of the Conasauga River (Georgia and Tennessee) and Etowah River (Georgia) are threatened by land use changes, hydrologic alterations, and agricultural runoff. Annual surveys at multiple, fixed shoals sites have occurred in these rivers for 20 and 18 years, respectively. Previous analyses of occupancy data have shown that four shoal-dependent fish species have declined dramatically over the last two decades in the Conasauga River, but not in the Etowah River. In order to further investigate this difference in population trends, we used Poisson regression models to assess temporal changes in count data from the same surveys for 26 species in the Conasauga River and 28 in the Etowah River. As expected, negative trends in count data were strongest for the four taxa in the Conasauga River with declining occupancy. However, our analysis indicated that nine additional species may be declining in the Conasauga, while three species may be increasing there. In the Etowah River, we found that 13 species may be declining, while 6 species may be increasing in abundance. Our study highlights the value of using multiple types of analyses to assess population trends and demonstrates that regional factors affecting both rivers—as opposed to a strictly watershed-level phenomenon—may be contributing to population declines in these systems. The results underscore the extent to which fishes are imperiled in these important systems, and the importance of long-term datasets to identify these patterns.

Keywords: Population trends; long-term data; fish declines
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39. DETERMINING ENVIRONMENTAL CONDITIONS INITIATING ATLANTIC STURGEON SPAWNING MIGRATIONS IN THE SAVANNAH RIVER, SOUTH CAROLINA

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Atlantic Sturgeon (*Acipenser oxyrinchus*) are long-lived, anadromous fish historically inhabiting estuaries, rivers, and oceans along the Atlantic coast of North America from southern Canada to Florida. Atlantic Sturgeon are federally endangered and divided into five distinct population segments (DPS). This study sought to identify the cues initiating Atlantic Sturgeon spawning migrations in the Savannah River, South Carolina (South Atlantic DPS). Adult Atlantic sturgeon are internally implanted with Vemco V-16 transmitters, and movements are monitored using an array of Vemco VR-2W receivers extending from the mouth of the Savannah River, to the New Savannah Bluff Lock and Dam located at river mile 188. Two transmitted adult individuals in 2015-2016 were tracked upriver and used for this analysis. We used a generalized linear mixed model predicting whether or not the individual was on a spawning run, including the predictors temperature, dissolved oxygen, and river gauge height with each individual ID as a random effect. Temperature and dissolved oxygen were statistically significant in my model ($p < 0.0001$). Understanding conditions which initiate Atlantic Sturgeon migrations are important for making proper management decisions during vital periods of sturgeon movement in the Savannah River. Ongoing work will include more tagged individuals and other diadromous species.

Keywords: Atlantic sturgeon; spawning; migration, diadromous
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40. AQUATIC REFUGE AND RECOVERY IN THE FACE OF DROUGHT IN A BIODIVERSITY HOTSPOT

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The Southeastern US is a global hotspot for freshwater biodiversity with the Mobile River Basin harboring some of the richest freshwater diversity in the world. In 2016, this region was under one of the most extreme droughts in at least 10 years. In Alabama, exceptional drought conditions started in September 2016 and persisted unabated until late December 2016, drying numerous waterways with many large rivers reading 5% or less of historic flows. How aquatic organisms respond to atypical and quickly-occurring disturbances such as droughts has been unclear. We hypothesized that the ability to use a downstream refuge during drought is a bottleneck that varies in significance based on species' vagility and network position. Our objective was to determine local community compositional shifts in response to drought. Fish were collected within reaches using a Smith-Root LR-24 backpack electrofishing unit. Reaches were determined by multiplying the average wetted width of the stream channel by 20. A minimum of 150-meter and a maximum 300-meter reach was sampled if the calculated value was outside of these values. Using data collected during summer surveys in 2015 and 2016 from one of the most drought-stricken areas in Bankhead National Forest, we predicted drought effects across stream systems of different sizes. In the summer of 2017, we resampled all sites post-drought and compared the data to those of 2015-2016. Preliminary results will be presented.

Keywords: fish, vagility, mobile bay, southeast, recolonization
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41. PATTERNS OF CHANGE IN FISH COMMUNITY COMPOSITION IN TWO OUACHITA RIVER SYSTEMS: TAXONOMIC AND FUNCTIONAL β -DIVERSITY REVEAL CONTRASTING PROCESSES

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Watershed alteration has resulted in the transformation of fish communities on a global scale, yet most studies have focused on taxonomic changes. Taxonomic and functional homogenization are highly dynamic, as the two do not occur simultaneously and vary in magnitude. Here, we examined temporal patterns of fish community composition and taxonomic and functional β -diversity using historical (Period I: 1969-1977, Period II: 1981-1982) and current (Period III: 2016-2017) datasets in the Saline River basin and Ouachita Headwaters basin, Arkansas. The Ouachita Headwaters basin has three major impoundments, whereas the Saline River is one of the longest unregulated rivers in Arkansas, but has been impacted by anthropogenic activities. At the largest temporal scale in the Saline River basin, fish community composition shifted with most change occurring in the lower mainstem. Changes in taxonomic β -diversity were scale dependent, with the mainstem showing less dissimilarity through time as indicated by tests for homogeneity of dispersion (PERMDISP: β_{sor} and β_{sim}). In contrast, functional β -diversity decreased through time at all spatial scales due to the loss of unique combinations of functional traits. Results in the Ouachita Headwaters basin indicated less taxonomic dissimilarity among sites between Period I and Period III, but functional dissimilarity did not change. Taxonomic dissimilarity decreased due to the convergence of tributary and mainstem fish communities. Two notable species (*Pimephales tenellus* and *Notropis perpallidus*), commonly reported during Period I, but never locally abundant, were not detected during Period III, likely due to a large reservoir downstream that disrupted metapopulation dynamics. Our results indicate fish community structure has changed through time, with a suite of specialist species declining and generalists (e.g. centrarchids) increasing in distribution and abundance. Furthermore, our results demonstrate the importance of incorporating taxonomic and functional β -diversity to provide a more holistic understanding of how communities change through time and space.

Keywords: retrospective analysis; beta diversity; biotic homogenization; watershed alteration
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42. EXAMINATION OF FISH ASSEMBLAGE STRUCTURE OVER 45 YEARS IN THE BUFFALO NATIONAL RIVER, ARKANSAS

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Long-term datasets are often lacking but critical to assess changes in community structure in relation to land use changes and to effectively conserve biodiversity. Historic anthropogenic activities (i.e. agriculture and logging) in the Buffalo watershed have altered landscapes which can have negative effects on aquatic biota. Buffalo National River is one of the last free-flowing rivers and is designated as an Extraordinary Resource Waterbody and Natural and Scenic Waterway. It has a diverse ichthyofauna (n=78) that includes ten species endemic to the Ozark Plateaus and seven Species of Greatest Conservation Need. We sampled 19 sites to compare to a study in the 1970s using the same sampling techniques. Highest species richness was found at the same site for both time periods (n=35 current, n=34 historic) as well as lowest species richness (n=6 current, n=8 historic). The four most abundant species were also the same in both time periods (*Luxilus pilsbryi*, *Notropis nubilus*, *Notropis percobromus*, and *Notropis boops*). We used nonmetric multidimensional scaling (NMDS) to compare changes in fish assemblage structure between the two time periods. No significant difference was found between historic and current fish assemblage structure (MRPP $p > 0.05$). *Fundulus catenatus*, *Fundulus olivaceus*, and *Semotilus atromaculatus* are good indicators of current assemblages (Indicator Species Analysis $p < 0.05$). *Etheostoma autumnale* and *Cottus hypselurus* were associated with historic, but were not significant. Site similarity was compared using Jaccard's similarity index and ranged from 0.27-0.80. Sixteen species showed a range expansion of three or more sites. Three of these species, *F. catenatus* (+6 sites), *F. olivaceus* (+9), and *Labidesthes sicculus* (+5) exhibited upstream expansion and could indicate changes to in-stream habitat. Land use and other fish metrics will also be examined.

Keywords: long-term datasets; fish assemblage structure; species richness; land use; watershed disturbance
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43. EXPLORING THE DYNAMICS OF LONGITUDINAL ASSEMBLAGE STRUCTURE IN AN OZARK HEADWATER STREAM SYSTEM

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Longitudinal change in stream fish diversity is a widespread yet poorly understood phenomenon. In the last decade, two hypotheses supported by data have emerged: hydrodynamic barriers and adventitious wandering. These two hypotheses, while not mutually exclusive, make different predictions. We test these predictions using a three-year dataset from Cedar Creek, a third-order tributary of the South Fork Little Red River, Arkansas. Fishes were sampled twice-yearly using quantitative three-pass depletion techniques from four reaches: two adventitious reaches, one reach with no proximal adventitious confluence, and one reach with a passage barrier downstream. Contrary to the predictions of the hydrodynamic barrier hypothesis, species richness and Shannon's H' showed a positive relationship with discharge at adventitious sample reaches ($F_{1,8} = 18.21$, $P = 0.003$, and $F_{1,8} = 42.16$, $P < 0.001$, respectively) and no relationship with discharge at nonadventitious reaches ($F_{1,9} = 2.32$, $P = 0.162$, and $F_{1,9} = 1.91$, $P = 0.201$, respectively). Adult body size and condition factor showed no relationship with discharge across ten resident taxa (Pearson's r , all $P > 0.05$). Nor were resident taxa in any reach more rheophilic than nonresident taxa ($F_{1,49} = 0.04$, $P = 0.959$). However, assemblage turnover as measured by Bray-Curtis dissimilarity was significantly higher at adventitious reaches ($F_{1,15} = 16.57$, $P = 0.001$). And the rate of species loss moving upstream from the base of the reach was significantly higher in adventitious reaches ($F_{1,19} = 6.85$, $P < 0.017$). Our results support the idea that the relationship between discharge and assemblage structure is complex and nonlinear, and that the patterns of ecotones in dendritic systems may well contribute, via adventitious wandering, to the patterns of longitudinal assemblage structure in stream fishes.

Keywords: Assemblage Structure, Longitudinal Change, Dendritic Ecological Networks

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44. DEVELOPING A STANDARDIZED BOAT ELECTROSHOCKING SAMPLING PROTOCOL FOR LONG TERM MONITORING OF FISH COMMUNITIES IN KENTUCKY LAKE

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Global aquatic ecosystems are negatively affected by numerous mechanisms including habitat destruction, fish overharvesting, climate change, and the introduction of invasive species. Long term monitoring of an ecosystem's fish community, along with abiotic and biotic factors that influence the fish community, is crucial in establishing effective management and conservation strategies. While there are existing fish community monitoring programs across the United States, a long-term monitoring program that includes non-game and non-commercial fish community dynamics has not been established within Kentucky Lake in Western Kentucky. The purpose of this research is three-fold: To establish a power based standardization of sampling effort using the boat electroshocking sampling gear, to determine which boat electroshocking settings are the most effective based on three key parameters (catch per unit effort, species diversity, total lengths), and to develop a standardized fish community sampling protocol using these most effective boat electroshocking settings. Four centrally located embayments within Kentucky Lake (Turkey, Anderson, Turner Hollow, and Ledbetter Bays) were sampled with a randomized block experimental design. Within each embayment, 6 separate electrofishing samples were obtained from randomly chosen 500-meter shoreline segments; each sample utilizing 1 of 6 different randomly selected electroshocking wave forms (15, 35, 55, 75, 95, and 115 Hz: 25% duty cycle). Each collected specimen was identified to species and total length of each specimen was obtained. Concurrently with Hancock Biological Station's bimonthly water quality/plankton surveys, this sampling protocol will be used for a long-term fish monitoring program that will track catch per unit effort, body condition, and species diversity of fish communities in Kentucky Lake.

Keywords: Invasive species, boat electroshocking, reservoir ecology, power based standardization, long term monitoring

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45. PHYLOGENOMICS OF LIVE-BEARING FISHES (POECILIINAE: POECILIIDAE)

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The subfamily Poeciliinae (family Poeciliidae) is a highly speciose (> 250 species) group of live bearing New World fishes found in the Americas from the southern US to southern regions of South America and the Antilles. Poeciliids typically inhabit small freshwater and brackish streams that can isolate populations, and limit dispersal and gene flow which readily promotes speciation. Several studies have examined the phylogenetic relationships within genera, subfamilies, or the entire family Poeciliidae, using Sanger sequencing methods for an array of mitochondrial and nuclear genes. The emergence of next-generation sequencing and target-capture techniques has made it possible to sequence hundreds to thousands of loci for phylogenomic studies. The use of ultra-conserved elements (UCEs) to generate phylogenies has become increasingly popular due to the recovery of remarkably well resolved trees at low relative costs. For this study, we used UCEs to produce a new phylogeny for the subfamily Poeciliinae. This data set includes 79 species, representing 24/29 genera of Poeciliinae. Whole genomic DNA was extracted from fin clips of specimens using the QIAGEN DNeasy tissue kit, enriched (1,000 UCE locus probe set), and massively parallel sequenced. The UCE data was run through the PHYLUCE software package pipeline and analyzed using RAxML. The inferred phylogeny was generally consistent with the most recently published Poeciliinae phylogeny, with a few exceptions. Bootstrap support values were 100 for most nodes. The implications of these results will be discussed.

Keywords: Poeciliid;UCE;phylogeny

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46. LOG PACKING BEHAVIORS IN THE MANGROVE RIVULUS, *KRYPTOLEBIAS MARMORATUS*

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Taylor, Turner and Davis first described log packing in *Kryptolebias marmoratus* in 2008, a behavior in which the mangrove rivulus moves into cavities and chambers inside logs and occupies them for extended time periods. Luke and Bechler subsequently provided a detailed description of behavioral interactions involving *K. marmoratus* dyads in an open water situation. This study, using an artificial log with chambers and passageways, examined the behaviors that occur when individuals enter, occupy and then leave a log as water levels fluctuate in an observation tank containing the artificial log. A total of 22 individual behaviors were observed and were composed of: (1) thirteen neutral behaviors, (2) four aggressive behaviors, and (3) five submissive behaviors. All neutral behaviors involved single fish that were either entering or leaving the log or adjusting position within the log. Agonistic behaviors (aggressive and submissive) involved two or more fish with the majority of the behaviors involving various means by which one fish moved via different mechanisms in order to secure a position in the log or avoid contact with another fish. A primary factor contributing to the diversity of behaviors was the presence or absence of water which required that fish move and interact with each other in different ways depending on the hydrologic conditions present at the time.

Keywords: Log Packing; Behaviors; Mangrove Rivulus; Laboratory Study; Artificial Log
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47. MIGRATION DYNAMICS OF OHIO SHRIMP, *MACROBRACHIUM OHIONE*, IN THE LOWER MISSISSIPPI RIVER

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The Ohio shrimp is amphidromous, serving as a trophic link between the Gulf of Mexico and inland reaches of coastal plain rivers. They feed primarily on basal food resources, transferring energy to predators within river channels such as pallid and shovelnose sturgeons. Current distribution, abundance, and life history of Ohio shrimp are relatively unknown upriver of Louisiana. Historical range included the Ohio River and Upper Mississippi River, but abundance upriver of Louisiana has reportedly declined. We collected shrimp monthly from March 2016 through November 2016 (N = 6984) with wire-meshed traps deployed along the mainstem Mississippi River and lower Arkansas, White, and St. Francis rivers. Total catch increased in May (N = 150), peaked in June (N = 2080), and declined from September (N = 1783) to November (N = 13). Male and female shrimp ≥ 7.5 mm carapace length (CL) were designated as Age 1+ after examining length frequency histograms from the sampling periods and consulting literature values. We captured an Age 1+ male-skewed population during May, a slightly Age 1+ male-skewed population in June, and then an Age 0 (≤ 7.4 mm CL) female-skewed population from July - October. Reproductive-sized females (≥ 7.8 mm CL) were caught during each sampling period, and shrimp with near-spawning ovaries were observed as early as March. The ratio was skewed toward early developing ovaries each sampling period. The largest proportion of near-spawning ovaries was observed in July, and no near-spawning ovaries were observed after September. Relatively fewer reproductive-sized females were observed in traps during peak migration and was possibly a result of downriver movement, indicative of an amphidromous life history. Despite declines from historic densities, Ohio shrimp likely remain important components of food webs in the Arkansas reach of the lower Mississippi River and its tributaries.

Keywords: Ohio shrimp; *Macrobrachium ohione*; amphidromy; Mississippi River; Arkansas
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48. HOW WELL DOES THE FLOW-TRAIT FRAMEWORK PREDICT SHORT-TERM FISH COMMUNITY DYNAMICS IN UNREGULATED RIVERS?

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Stream fish ecologists have recently emphasized interactions between hydrology and species' life-history traits as useful predictors of community composition and change, particularly across large geographic areas, in regulated rivers, and at coarse spatiotemporal scales. We evaluated the applicability of such an approach at a finer spatiotemporal grain that allowed an assessment of how flow and traits affected community dynamics via demographic responses (persistence and colonization) of individual species. Specifically, we tested hypotheses that (1) greater hydrologic variation leads to greater community variation, but (2) effects of increasing hydrologic variation on demography vary by life-history, being positive for opportunistic strategists and negative for equilibrium strategists. We tested hypotheses using data from intra- and inter-annual fish surveys collected over 21 years at shoals in the Roanoke and Conasauga rivers, two unregulated ridge and valley rivers with phylogenetically comparable fish communities. We used abundance data to examine correlations between taxonomic and functional community composition and variation in flow magnitude and the frequency of extreme high and low flows. We also analyzed presence-absence data in a dynamic occupancy framework to investigate the influence of these flow metrics and species traits on colonization and persistence. In both rivers, overall community composition was highly persistent over time, and contrary to expectations, interannual variation was poorly explained by hydrologic or trait variables. As expected, the influence of extreme-flow frequency on persistence varied among life-history strategists. However, contrary to our hypothesis, extreme flows were positively related to persistence of both opportunistic and equilibrium taxa. Thus, our results suggest a relatively weak influence of hydrology and traits on fish populations and communities in these rivers, over the range of conditions and years tested. Although this line of research is ongoing, our preliminary findings suggest limitations to the popular flow-trait framework for predicting short-term dynamics of fishes in unregulated rivers.

Keywords: flow ecology; Conasauga River; Roanoke River; life history
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49. HIGH SUMMER FLOWS CORRELATE WITH LOWER POPULATION GROWTH OF SHOAL FISHES IN THE CURRENT YEAR, BUT HIGHER GROWTH IN THE NEXT YEAR

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Understanding flow-ecology relationships is crucial to create management strategies that promote suitable habitat for riverine organisms. Humans are drastically altering natural flow regimes, yet we don't fully understand the relationship between natural flow variability and population dynamics of many riverine organisms. Extreme low flows or exceptionally high flows may affect survival and recruitment of fishes if those events coincide with spawning or recruitment periods. Using annual fish count data from the Etowah River, Georgia, U.S.A., we tested specific hypotheses of how high or low flows could affect population growth rates of fishes (as changes in relative abundance year to year). We evaluated four alternative hypotheses (including current and antecedent flow conditions) for 13 shoal-dwelling fishes using autoregressive population models that incorporated density dependence. We found broad support across our study species for a positive effect of high flow events in the preceding year on population growth rates, while high flow events in the current year (summer) generally negatively affected growth rates. We found little support for a broad effect of low flow events (3 of 13 species with a significant effect) or effect of high flows during the spring (no species with a significant effect). Our study suggest a synchronous response to flow variability of the shoal-dependent species used in our analysis. We hypothesize that the positive effect of high flow events in the previous year may be due to positive effects on fish habitat (e.g. flushing of sediment or stimulating primary production) while negative effects of high flows in the current year is likely due to increased mortality.

Keywords: Flow ecology; population models; shoal fishes; long-term data; flow variability
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50. STATUS OF THE ENDANGERED TUXEDO DARTER, *ETHEOSTOMA LEMNISCATUM*, WITHIN REACHES OF THE BIG SOUTH FORK CUMBERLAND RIVER AFFECTED BY RETURN TO NORMAL OPERATIONS OF WOLF CREEK DAM FOLLOWING AN EXTENDED DRAWDOWN PERIOD

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The Big South Fork is the largest tributary to Lake Cumberland, an impoundment of the Cumberland River. At full pool, Lake Cumberland affects the lower 70 river km of the Big South Fork. During January 2007, the U.S. Army Corps of Engineers (USACE) lowered Lake Cumberland to prevent possible dam failure from eroded limestone cavities beneath the dam. From January 2007 to spring 2014, lower reservoir elevations created free flowing conditions throughout a 16 km reach of the Big South Fork that had been previously inundated. Prior to raising reservoir elevations to normal operating levels, the U.S. Fish and Wildlife Service (USFWS) requested that the USACE conduct a survey for rare aquatic species that may have colonized this reach during the extended reservoir drawdown. During 2013, the USACE contracted with the Tennessee Valley Authority (TVA) to conduct these surveys, which resulted in the observation of the endangered tuxedo darter, *Etheostoma lemniscatum*, at eight shoals within this reach. Following this discovery, the USFWS issued a Biological Opinion which allowed the USACE to resume normal operations with a requirement for monitoring the effects of higher reservoir levels on tuxedo darters and their habitats for a minimum of five years. Data on tuxedo darter abundance, age class structure, and micro-habitat use were recorded annually during 2014 to 2017 to evaluate potential reservoir effects on their survivability within this reach. Additional fish community monitoring was conducted during this time to provide further insight into reservoir effects among shoal complexes that experienced varying degrees of inundation throughout the year. A rapid invasion of the non-native crayfish, *Orconectes rusticus*, was also documented which creates significant conservation concerns for native crayfishes and benthic nest building fishes such as the tuxedo darter. Compared to historical conditions within this reach of the Big South Fork, water quality conditions during the time of these surveys were greatly improved due to a decrease in active mines and improvements in water quality from acid mine drainage remediation which was reflected by the presence of an extremely diverse fish community and recovering mussel fauna.

Keywords: Big South Fork Cumberland River, Tuxedo darter, impoundment effects
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51. A HABITAT-BASED MODEL FOR PREDICTING BROOK TROUT BIOMASS IN THE CHEROKEE NATIONAL FOREST

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Population densities of native Brook Trout *Salvelinus fontinalis* have declined, and they have been extirpated from many streams in the southern Appalachian Mountains. Anthropogenic impacts, especially land cover change, restrict their distribution across much of their range. A large portion of Tennessee's streams that support Brook Trout streams are located within the Cherokee National Forest (CNF). The purpose of our research was to develop a predictive habitat model of Brook Trout biomass in the CNF to characterize the suitability of unoccupied streams for Brook Trout restoration. Thirty streams across the CNF known to support Brook Trout were evaluated by completing a three-pass depletion survey, quantifying instream habitat characteristics, and examining riparian forest structure. Habitat characteristics were modeled against Brook Trout biomass (kg/ha) to determine significant variables that characterized Brook Trout abundance. Ten additional streams on the CNF were sampled to validate the accuracy and precision of the models. A Random Forest model determined the significant habitat variables (n=11), then a multi-nomial logistic regression model predicted Brook Trout biomass based on these variables. For optimal biomass, values of the important variables in unoccupied streams should be: percent riffle area <25%, >350 m to the nearest road, >13% slope, elevation $\geq 1,000$ m, >55% boulder substrate, *Rhododendron* cover <10% or 25-40%, canopy cover 92-97% or $\geq 98\%$, dominant geologic rock type of gneiss, granite, or sandstone, <25% cobble substrate, total volume of 1.0-7.5 m³, and total dissolved solids >12 ppm. This model provides a technique for rapid habitat assessment to aid in the decision-making process for Brook Trout restoration. Based on these selected variables, efforts to improve Brook Trout habitat in the CNF should focus on four primary areas: reduction of riffle habitat (i.e., creating more pools), maintaining canopy closure, reducing *Rhododendron* cover, and preventing sediment run-off from nearby roads.

Keywords: Random Forest Model; Multinomial Logistic Regression; R; *Salvelinus fontinalis*; streams
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52. RANGE REDUCTION AND RESTORATION OF SPOTFIN CHUB, *ERIMONAX MONACHUS*

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The federally threatened Spotfin Chub, *Erimonax monachus*, is a small-bodied cyprinid endemic to the Tennessee River basin. Hydrologic alterations, specifically large impoundments, have resulted in a highly fragmented distribution. The purpose of our study was to analyze watershed characteristics and river fragmentation throughout the Tennessee River basin to identify potential large-scale spatial and temporal factors influencing the disjunction of Spotfin Chub populations. We conducted spatial analyses using GIS to compare watershed characteristics among natural, introduced, and extirpated populations. We developed a fluviality index of the Tennessee River basin to associate fragmentation events with distribution data. Geology, soil type, and land use patterns were highly variable across the Tennessee River basin and were not significantly different between watersheds with extant and extirpated Spotfin Chub populations. Most of the largest fragments that remain in the Tennessee River basin currently hold extant populations of Spotfin Chub. However, several large fragments, including the Duck and French Broad rivers, remain free flowing and represent possible additional reintroduction sites. Most river fragments where Spotfin Chub have been extirpated are <50 km in length. No obvious trends existed among large-scale watershed characteristics differentiating extant from extirpated populations, however, there does appear to be a size threshold that limits the number of available watersheds that can biologically support Spotfin Chub. From a large-scale perspective, persistent populations of Spotfin Chub exhibit a certain habitat plasticity and appear adapted to various abiotic conditions. However, local conditions and in-stream characteristics are still influential, yet have only been extensively studied in two of the five extant populations. The factors limiting populations at the watershed level need to be elucidated within all extant populations before additional watersheds can be prioritized for reintroductions. Local habitat suitability, interspecific competition, and predation are factors that still need to be assessed.

Keywords: Spotfin Chub, distribution, fragmentation, reintroduction, restoration
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53. BIOTIC AND ABIOTIC IMPACTS OF MINING AND RECLAMATION - A LITERATURE REVIEW

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Historically, impacts of surface coal mining considered pH, metals and sediment. However, impacts are more complex and persist longer than previously known. Surface coal mining can result in levels of salinity, measured as specific conductance, greatly elevated over baseline conditions under which native species evolved. In addition to coal mining, other activities contribute a variety of salts and ions affecting conductivity and stream water quality, including weathering of concrete infrastructure, runoff of salts from roads and other impervious surfaces, oil and gas exploration and extraction, agriculture, silviculture, and wastewater and industrial effluents. Recent studies indicate that areas with elevated conductivity contain altered aquatic invertebrate community composition and relative abundances, reduced species richness, and some taxa are eliminated. Conductivity change-points have been identified as predictors for abundance and persistence of various species. However, the various mechanisms of elevated conductivity's effects to various taxonomic groups are still under investigation. Some taxa (mayflies) may not properly osmoregulate at elevated salinities, while altered prey abundance or diversity may result in the observed changes in some fish species. Other research suggests potential energy requirements that allow aquatic organisms to eliminate environmental toxins could result in population-level effects because of competing energy requirements to produce gametes. Mining can alter the ability of affected areas to provide ecological services, possibly permanently, but at least for the long term. Additionally, impacts of surface mining far upstream in watersheds can affect stream water quality, community structure, and ecosystem functions downstream, and the impacts of multiple mining operations in watersheds can have cumulative downstream impacts. Yet accepted stream restoration practices fail to consider whether appropriate water quality and necessary ecological processes will be established in reclaimed streams. Permitting decisions should include the influence of mining on areas important for recovery of species of concern, and include appropriate mitigation and preservation.

Keywords: coal mining, conductivity, ecosystem services, reclamation
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54. POPULATION GENETICS OF BLACKBANDED SUNFISH (*ENNEACANTHUS CHAETODON*) FROM NEW JERSEY TO FLORIDA

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Blackbanded Sunfish (*Enneacanthus chaetodon*) is a member of the North American Centrarchid family that is distributed along the Atlantic coast from New Jersey to Florida, and is typically associated with shallow and heavily-vegetated blackwaters of herbaceous and forested wetlands. Blackbanded Sunfish have occurred historically in four distinct population centers including central Florida, southern Georgia, the Carolinas, and New Jersey. Despite repetitive efforts to sample Blackbanded Sunfish over the past decade throughout its southern range using traditional methods (seines, traps, electrofishing), surveys have provided evidence of only a few extant populations in GA and FL and a potentially fragmented distribution along the upper coastal plain in SC, indicating that southern populations are in decline. We have developed a qPCR-based eDNA detection tool for Blackbanded Sunfish and applied it in the field at a total of 60 sites throughout GA and SC (30 sites per state) with results showing Blackbanded Sunfish DNA present at five sites in GA and nine sites in SC. Revisiting all of the sites where Blackbanded Sunfish were detected with the eDNA tool and sampling with traditional fisheries gears yielded 193 fin clip samples (all from SC), which were supplemented with archived tissue samples for use in a population genetics study. We genotyped 386 Blackbanded Sunfish at eight microsatellite loci that were collected from 34 sites across the species range from NJ to FL. The genetic population structure across the range was evaluated using pairwise comparisons of F_{ST} , allele frequency distributions, and a model-based clustering method implemented in STRUCTURE. The genetic health of Blackbanded Sunfish was estimated by calculating various metrics of genetic diversity and effective population size. Having a better understanding of the genetic connectivity and diversity of Blackbanded Sunfish throughout its range will allow for more informed management recommendations concerning the conservation of the species.

Keywords: *Enneacanthus chaetodon*; genetics; eDNA
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55. GENETIC STRUCTURE AND DIVERSITY OF DISJUNCT POPULATIONS OF RAINBOW DARTERS (*ETHEOSTOMA CAERULEUM*) AND SOUTHERN REDBELLY DACE (*CHROSOMUS ERYTHROGASTER*) THROUGHOUT THE MISSISSIPPI CORRIDOR

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Conservation studies of North America's freshwater fish fauna frequently focus on recently fragmented species or species with naturally small ranges. Our grasp of how recent, natural isolation affects the migration and genetic diversity of common and widespread freshwater fishes is limited. *Etheostoma caeruleum* and *Chrosomus erythrogaster* are widespread, abundant, and have overlapping distributions with comparable patterns of naturally disjunct populations on their range margins. Both species have potentially isolated populations in tributaries on Crowley's Ridge, Arkansas and the Bluff Hills, Mississippi. These regions are recent geological formations that would have been colonized by these species within the last 10,000 years making these species excellent subjects for studying the impacts of recent, natural genetic isolation. In this study, we analyze microsatellite DNA loci from both species to evaluate genetic diversity and connectivity among populations on Crowley's Ridge, the Bluff Hills, and larger core populations. Using DNA sequence data, we also test hypotheses about the pattern and timing of colonization of Crowley's Ridge and the Bluff Hills. The results of this study will provide useful information about the biogeographic history and conservation status of these potentially disjunct populations of *E. caeruleum* and *C. erythrogaster*.

Keywords: Mississippi River Discontinuity, Tombigbee River Discontinuity, Microsatellites
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56. THE EFFECT OF POPULATION LOSS ON GENETIC DIVERSITY IN THE KENTUCKY ARROW DARTER, *ETHEOSTOMA SPILOTUM*

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The federally threatened Kentucky Arrow Darter (KAD) is restricted to 47 streams of the Kentucky River system in Kentucky. Recent and drastic population loss attributed to anthropogenic activities has been documented across its range. The impact of these losses on population connectivity and genetic diversity is not known. We evaluated contemporary and historic levels of genetic diversity and structure among 12 populations of KAD using eleven microsatellite loci and the mitochondrial ND2 gene, respectively. Several broadly shared ND2 haplotypes and low divergence among haplotypes, suggest absence of long-standing isolation among populations within or among river systems. However, contemporary patterns of genetic diversity and estimates of K (STRUCTURE) suggest little to no recent gene flow among localities examined. Only individuals from sites within 3 km of each other were recovered as a single cluster, while all other sample localities were recovered as distinct populations with little to no admixture. Although there was a significant isolation-by-distance effect, several sites had higher than expected pairwise F_{ST} values, suggesting genetic isolation is not driven exclusively by distance between populations. Moreover, effective genetic population estimates were low, particularly compared to census size estimates, and three populations showed signs of a recent bottleneck. Results suggest recent loss of gene flow, a high degree of population structure at the within-river system scale, and evidence of reduced population sizes. Thus, contemporary population losses throughout the range have had measurable and negative effects on genetic connectivity and diversity within the species.

Keywords: conservation; habitat fragmentation; benthic fish
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57. PHYLOGENOMICS OF *NOTROPIS* AND RELATED SHINERS (CYPRINIFORMES: LEUCISCIDAE)

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North American shiners represent one of the most taxonomically turbid clades of freshwater fishes due to the large number of taxa coupled with conserved morphologies. Species were moved between genera and subgenera until the community decided to lump all of the taxa into one genus, *Notropis*, which at one time held at least 213 described species. Despite advances that began to separate *Notropis* into other genera, such as *Cyprinella*, *Luxilus*, *Lythrurus*, and *Pimephales*, *Notropis* remained as a taxonomic repository for many shiners of uncertain placement. Recent advances in sequencing technologies have provided the opportunity to re-examine the shiner clade using phylogenomic markers. Using a fish probe kit from the NSF-funded FishLife project, we sequenced 89 species representing 15 shiner genera, which resulted in a dataset with 1004 loci and 286,445 base pairs. Despite the large dataset, only 32,466 bp (11.33% were phylogenetically informative). In our maximum likelihood tree, 78% of nodes are 100% bootstrap supported. Unsurprisingly, *Notropis* is recovered as nonmonophyletic. Other nonmonophyletic genera include *Hudsonius*, *Pteronotropis*, *Luxilus*, and *Alburnops*. *Cyprinella* is monophyletic only if *Cyprinella callistia* is excluded. Taxonomic revisions we propose are: elevation of *Hydrophlox*, expansion of species included in *Miniellus*, movement of *Hudsonius cummingsae* to *Pteronotropis*, resurrection of the genera *Coccotis*, *Paranotropis*, and *Chriope*, movement of *Notropis dorsalis* to *Ericymba*, and a new genus description for *Notropis scepticus*.

Keywords: Phylogeny, minnows, systematics, taxonomy
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Poster Presentations:

1. GROWTH, REPRODUCTION, AND MICROHABITAT OF THE BIGEYE SHINER, NOTROPIS BOOPS

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The Bigeye Shiner (*Notropis boops*), occupies clear, rocky streams in much of the Midwest, but has declined in many areas. Despite its recognition as a sensitive species, little data have been published, which are needed to make conservation management decisions. We studied growth, reproduction, and microhabitat of the Bigeye Shiner for eight months in Triplett Creek in northeast Kentucky. Length frequency analysis showed Bigeye Shiners averaged 38.2 mm SL at 12 months and 52.2 SL at 24 months. Examination of gonad development from monthly samples taken March through October showed sexually mature individuals were 46.7-55.1 mm SL. These mature Bigeye Shiners were in the 1+ and 2+ age classes, according to age assignments based on length frequency analysis. The majority of age 1+ Bigeye Shiners ready to spawn were males. The number of age 2+ Bigeye Shiners rapidly declined during the summer months, suggesting few individuals live past 2 years. Females have 120-392 (mean=231) advanced mature to ripe ova per ovum. Analysis of gonadosomatic indices suggests spawning occurs in June, and possibly in July and August. Principal component analysis of microhabitats indicates Bigeye Shiners occupy calm or slow-moving water immediately adjacent to faster current, over heterogeneous substrates of sand and gravel, often with *Justicia* or woody cover. We suspect this location allows them to capture drifting terrestrial insects while reducing swimming costs. Diet is being examined to determine if they feed on terrestrial insects, primarily in the upper water column. Sampling throughout late summer and early fall has yielded few young-of-the-year (YOY) Bigeye Shiners; these YOY occupied shallow water over dense leaf packs and dense *Justicia* cover.

Keywords: Notropis boops; Bigeye Shiner; Growth; Microhabitat; Reproduction
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2. CHANGE IN HISTORIC VS CONTEMPORARY FISH ASSEMBLAGES OF THE STRAWBERRY RIVER WATERSHED

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The southeastern United States has the largest diversity of fishes. Arkansas has 233 fish species, and within Arkansas, the Strawberry River is the most diverse with 107 documented species. The Strawberry River is a tributary to the Black River, located in the Salem Plateau of the Ozark Highland and Mississippi Alluvial Plain. Beef and dairy cattle, poultry, and swine operations are growing in this region; however, the poultry industry has experienced the most rapid growth in north Arkansas, including the Strawberry River watershed. Approximately 60% of this watershed is forest and 29% pasture. This watershed is of big concern to the state of Arkansas due to the increasing poultry business and the potential for impact that poultry could have on the diversity of fishes in the watershed. Historical fish assemblage data from 8 sites was compared to contemporary data (2017) to determine if land use change is affecting the fish communities of the Strawberry River. A total of 8,161 individuals representing 68 species were collected across the 8 sites both contemporary and historical. 62 were collected in 2017 and 47 were collected historically. Species relative abundance was compared between the contemporary and historical sites with a nonmetric multidimensional scaling (NMDS), 2-dimensional. There was no significant difference between historic and contemporary fish assemblages (MRPP $p=0.6908$) based on Bray-Curtis. Jaccard's similarity index was used to compare site similarity between the two-time periods and ranged from 0.28-0.62. Other results and habitat analysis will also be examined.

Keywords: Strawberry, Communities, NMDS, MRPP
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3. COMPARATIVE POPULATION GENETICS OF THE RELICT DARTER AND GUARDIAN DARTER IN WESTERN KENTUCKY

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The Relict Darter, *Etheostoma chienense*, is endemic to the Bayou du Chien drainage of western Kentucky. It is listed as a federally endangered species due to its limited distribution, and lack of suitable spawning habitat, as well as habitat fragmentation and historically poor land-use practices. A previous five year status review suggested that information on the levels of genetic exchange among populations within the basin was needed. Therefore, this study was undertaken to gather this relevant information. We obtained tissue samples from multiple populations of the Relict Darter from the Bayou du Chien drainage, as well as samples from another closely related congener, the Guardian Darter (*Etheostoma oophylax*) from the Clarks River. Examining genetic variation in a comparative context will give us insight on how to properly manage and protect this species. We amplified a fragment of control region of the mitochondrial genome and developed haplotype networks to compare genetic diversity within each species. Preliminary results suggest that there are similar levels of genetic variation within the populations of both species. The conservation implications of these results will be discussed.

Keywords: Percidae; mtDNA; *Etheostoma*
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4. WATER DEPTH AND SUBSTRATE USE OF *NOTURUS ELEUTHERUS* IN THE CLINCH RIVER, TENNESSEE

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The Mountain Madtom *Noturus eleutherus* is a small, benthic catfish occurring in several drainages in the eastern United States. Additional ecological data are needed for this species. We specifically examined water column depth and substrate preferences of the Mountain Madtom in the Clinch River, Tennessee, during summer 2016. Knowledge gained from this project may provide insight for understanding microhabitat preferences of the endangered Pygmy Madtom *Noturus stanauli* because it has been associated with the Mountain Madtom in past collections. Fish were collected at 51 microhabitat locations by kick-seining 4-m² plots. Water depth was measured in the kick-seined area and sediment was collected using the shovel method. Mountain Madtoms were found at water depths ranging from 20 to 57 cm deep, with a mean depth of 37 cm, and over a dominant substrate of medium-to-coarse gravel and subdominant substrate of fine gravel to coarse sand. However, there were no statistically significant preferences among depth categories ($P = 0.11$) or substrate categories ($P = 0.92$) where madtoms were present vs. absent. These results provide a better quantitative understanding of microhabitats used by the Mountain Madtom during the summer.

Keywords: *Noturus*; madtom; microhabitat; substrate; Clinch River
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5. EFFECTS OF BLACK-SPOT DISEASE ON THE BODY CONDITION OF BLEEDING SHINERS, *LUXILUS ZONATUS*

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Black-spot disease is common in freshwater fishes and results from encystment of digenetic trematodes into the fins and flesh of the fish. The fish serves as an intermediate host in the life cycle of the trematode, and deposits melanin around the cyst as an immune response, producing the black spots for which the disease is named. Several studies have documented the occurrence of black-spot disease on game fishes, but little is known about how the trematode infestations affect the health or body condition of small stream fishes. The objective of this study was to evaluate the prevalence of black-spot infection in the Bleeding Shiner (*Luxilus zonatus*) throughout Myatt Creek, a tributary to the Spring River in northeastern Arkansas. Specimens collected in the 1970s were obtained from the Arkansas State University Museum of Zoology (ASUMZ) and examined for abundance and location of black-spot infection. Infection rates were compared to the coefficient of condition ($K = W \times 10^5/L^3$), where W = mass in grams and L = standard length in millimeters. Preliminary results revealed an infection rate of approx. 80%, with a mean of 16.5 encystments per individual. Coefficient of condition ranged from 1.3–2.1, and there was a general trend of decreasing number of encystments with increasing body condition; those with $K > 1.7$ had no more than one encystment. Future work will incorporate more individuals from 1970s collections of Myatt Creek. These data will be compared to data from freshly collected specimens from Myatt Creek to evaluate 40 year change in infection rate.

Keywords: Trematodes, Cyprinidae, museum specimens
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6. HISTORICAL OCCUPANCY MODELING OF NON-GAME FISHES IN THE CLINCH RIVER WATERSHED

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The Clinch River watershed has a highly diverse fish fauna, with over 100 species occurring in the entire drainage. Many of these species are in decline and are federally listed as threatened or endangered. Historical abundance estimates for these species are highly variable. A new study was needed to estimate the historical status of these species. This new study was designed based on occupancy modeling of historical catch data collected from the Tennessee Wildlife Resource Agency, U.S. Geological Survey, Tennessee Valley Authority, and Virginia Department of Game and Inland Fisheries. These data covered a 40-year period (1976-2016). Presence-absence data for 32 species of conservation concern were analyzed using the software Presence, which estimates occupancy rate (Ψ) and probability of detection (p) for each species. Estimates of occupancy and detection were highly variable for each species due to the variability in sampling methods and the rarity of some species used in these analyses. For example, the mean \pm SE historical occupancy (i.e., probability of species occupying a certain habitat type in all sampling events) and detection (i.e., probability of a species being captured on any given sample, if the species is present at a site) of the Bluespar Darter *Etheostoma mediae* was 0.85 ± 0.14 and 0.52 ± 0.09 , and for the Stonecat *Noturus flavus*, it was 0.47 ± 0.30 and 0.62 ± 0.33 . These historical estimates suggest the need for continued monitoring efforts of these species, in order to observe changes in species status. Continued monitoring efforts would provide evidence to determine if management decisions need to be made to preserve the highly diverse fish fauna in the Clinch River watershed.

Keywords: Modeling; conservation; river; diversity
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7. HABITAT AND COMMUNITY DIFFERENCES IN THE HISTORIC AND CURRENT RANGE OF THE BUCK DARTER (*ETHEOSTOMA NEBRA*)

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The Buck Darter (*Etheostoma nebra*) is a recently described species of darter, native to the Buck Creek system in southeastern Kentucky, that is critically imperiled. Past collection records from 1955-1981 show that the buck darter was once found throughout the Buck Creek system, whereas now it is limited to only two small tributaries: Big Spring Branch and Stewart Branch. It has not been determined whether the loss of habitat was random, or if there are conditions in Big Spring Branch and Stewart Branch that have allowed the species to remain. The objective of this study was to compare and contrast the habitat, fish communities, and land use at historical locations, as well as the locations where the species is currently found. Six historical headwater streams in the Buck Creek system were studied along with the two streams where the Buck Darter is currently found. All streams were compared using hierarchic clusters to determine how similar the sites were to one another, and variables from the habitat and land use were used to determine which variables were correlated with Buck Darter abundance. Big Spring Branch and Stewart Branch were more similar to each other than they were to any other stream, indicating that something about these streams allows the species to persist, and that the range has not randomly decayed. Environmental fitting was performed on the community data to see which habitat variables had a significant association (p -value < 0.1) with the fish species that were found. Conductivity of the water, number of springs in the watershed, and percent land cover in the watershed that was evergreen were found to be associated with the Buck Darter. These variables may be good candidates for further research to determine what conditions the Buck Darter needs to survive.

Keywords: Buck Darter; *Etheostoma nebra*; *Etheostoma*; imperiled species; habitat
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8. CONTRASTING TAXONOMIC AND FUNCTIONAL β -DIVERSITY OF FISH COMMUNITIES IN A RIVERINE NETWORK ACROSS AN ENVIRONMENTAL TRANSITION ZONE

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Riverine networks constrain metacommunity structure, yet it is still poorly understood how diversity patterns differ at intermediate spatial scales across strong environmental transition zones (i.e. ecoregions). We used fish community data (2016-2017) from the Saline River basin (Ouachita Mountains and Coastal Plains ecoregions), Arkansas to examine patterns of taxonomic and functional β -diversity at three spatial scales: entire river network, mainstem, and tributaries. Specifically, Sorensen pairwise dissimilarity (β_{sor}) was calculated and decomposed into pure spatial turnover (β_{sim}) and nestedness (β_{nes}) to test for distance decay relationships (DDR). Additionally, environmental dissimilarity was calculated between pairs of sites. Environmental dissimilarity was positively correlated with watercourse distance (rkm) at the largest extent and in the mainstem, but not in the tributaries. However, environmental heterogeneity was significantly greater in the tributaries as indicated by tests for homogeneity of multivariate dispersions (PERMDISP). Taxonomic β_{sim} was positively correlated with watercourse distance at all spatial scales, but β_{sim} was stronger in the tributaries. Functional β_{sim} was positively correlated with watercourse distance at the largest spatial extent and in the tributaries. In contrast, functional β_{nes} was positively correlated with watercourse distance in the mainstem. Partial mantel tests revealed environmental heterogeneity was an important driver of taxonomic and functional β -diversity at the largest spatial extent and in the tributaries, but not in the mainstem. Tributary fish communities were structured by local forces and showed dispersal limitation, whereas mainstem fish communities were structured by both local and regional (i.e. dispersal-driven dynamics) processes. Furthermore, DDRs were non-existent at the tributary scale when compared within ecoregions, suggesting the geologic Fall Line influences regional diversity patterns. Our findings support that riverine networks influence metacommunity structure, and highlight the importance of incorporating functional β -diversity to fully understand diversity patterns.

Keywords: dendritic networks; dispersal; distance decay relationships; metacommunities; environmental selection
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9. GENETIC DIVERSITY AT NEUTRAL AND ADAPTIVE LOCI IN THE BARRENS TOPMINNOW

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Preservation of adaptive genetic variation is a fundamental consideration for establishing and prioritizing management units below the species level. Patterns of genetic diversity at genes of the Major Histocompatibility Complex (MHC) suggest that this gene complex is particularly important for adaptive fitness of vertebrate populations. Here we surveyed genetic variation at an MHC class II gene in the four extant natural populations and one recently extirpated population of the Barrens Topminnow (*Fundulus julisia*). The Barrens Topminnow is considered to be one of most critically endangered fishes of the Southeastern United States and is currently under status review for federal listing under the Endangered Species Act. Genetic variation within and between populations at the MHC was compared to patterns observed at 14 microsatellite loci and at the mitochondrial control region. Patterns of sequence variation were consistent with an evolutionary history of balancing selection. Expected heterozygosity estimates at the MHC were high across all five natural populations despite an absence of mitochondrial sequence diversity. Estimates of population divergence (pairwise F_{ST} values) were highly correlated for microsatellite and MHC markers suggesting that drift has played an important role in diversification of MHC among populations. Combined results from mitochondrial haplotypes, microsatellite genotypes, and MHC alleles were used to identify evolutionary significant units (ESUs) and management units (MUs) that warrant consideration in future management efforts.

Keywords: Population structure; MHC; Microsatellites; Barrens Topminnow
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10. THE EFFECTS OF CUMULATIVE DRAINAGE AREA ON SPECIES VARIABILITY

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Species variability in freshwater streams is characterized by the river continuum concept. In theory, as drainage areas increase, species variability will also increase. This is due to both abiotic and biological factors. Abiotically, susceptibility to disturbances, such as heavy rain, will alter the nature of smaller headwater streams drastically more than larger main streams. Headwater streams are more variable in flow, water temperature, pH, and other abiotic conditions. This variability only allows for specialized species to inhabit these smaller streams. Main streams should be less variable in their abiotic patterns, allowing for a greater diversity of species to inhabit their waters. The consistency in abiotic factors in main streams shifts the influence of community diversity to competition interactions between species. In this study, we tested for the relationship between stream size and difference in assemblage structure and species composition. By comparing data collected between 2008-2017, conclusion can be drawn on the changes in community assemblage due to abiotic and biotic conditions. The results of this study can be also used to assess whether there has been a change in community composition over time, ensuring that the streams and rivers are maintaining a healthy ecosystem.

Keywords: Community structure; Species composition; Cumulative drainage area; Freshwater ecology
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11. IMPACT OF WATER FLUCTUATIONS AND INTERMITTENCY ON STREAM FISH COMMUNITY STRUCTURE

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Flow intermittency in streams produce episodic hydrologic disconnection causing disruptions in stream biota community structure. The objective of this study was to determine stream fish community structure at three seasons as a means of assessing effects of hydrologic disruption on an intermittent stream. Little Creek (LC) is a second-order stream characterized by a longitudinal gradient with continuous flow upstream and seasonal drying downstream. LC was divided into three reaches based on flow during dry conditions- upstream (flowing), intermediate (separated pools), and downstream (completely dry) with six sample sites within each reach. During three seasons- immediately post-reconnection, four months post reconnection, and pre-disconnection of hydrology at all sites, fish community abundance data was collected. Significant variation in community structure due to reach location was found immediately post-reconnection. Community structure from other seasons are in the process of being analyzed. These data will allow us to predict changes in stream fish community structure due to hydrologic disturbances, especially those caused by increased water consumption.

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12. MICROHABITAT ANALYSIS OF THREE CO-OCCURRING SCULPIN SPECIES (COTTIDAE)

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Generally, species occurrences are influenced by the presence and availability of required resources across broad spatial scales. However, in cases where species with similar ecological needs co-occur in local scale communities, resource partitioning may further refine breadth of habitat use. Thus, a finer spatial focus is needed to properly examine differences in habitat use among co-occurring species. In the Gasconade drainage (Missouri, U.S.), three species of sculpin (*Cottus carolinae*, *C. bairdi*, and *C. hypselurus*) co-occur, often dwelling in cold water riffle areas. Due to their general similarities in habitat use, we examined whether or not co-occurring sculpin species partition habitat to avoid (or as a result of) interspecific competition at fine scales. Microhabitat measures included stream flow velocity, depth, substrate size, and spatial location within riffle segments. We compared microhabitat use between sculpin species collected at stream sites, and tested for differential habitat use. Results suggest the existence of some differentiation among species based on microhabitat measures. The influence of interspecific competition on sculpin microhabitat use differences, and the implications of these results on future conservation efforts will be discussed.

Keywords: habitat partitioning; interspecific competition; *Cottus*
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13. IMPACTS OF ANTHROPOGENIC LAND USE ALTERATION ON THE MORPHOLOGY OF STREAM FISHES IN ARKANSAS

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Habitat alteration, most notably stream impoundment, has been shown to cause variation in the morphology of fishes. The impact of in-stream habitat alteration on morphology due to land use changes within a stream catchment area, is still a novel concept. Changes in land use have been shown to alter in-stream habitat characteristics, such as pool depth and substrate through sediment deposition. These factors also influence the flow regime of a stream, which can directly impact the biota within. Determining how habitat alteration drives morphological variation can provide insight into the ecology of fishes, as well as lead to a better understanding of how organisms cope with anthropogenic driven impacts through adaptation. The Big Creek system in north central Arkansas has been subject to substantial land use alteration from forested to mostly pasture land use. Species representing three major habitat types (i.e. riffle, run, pool) were compared from the Big Creek system to three other reference systems with lower percent pasture land use: Sylamore Creek, Piney Creek, and Jane's Creek. Morphological variation was quantified through use of geometric morphometrics, using DIGTPS2 software. Landmarks were placed on digitized images of the specimens and then realigned to account for effects of scale, translation, and rotation. Data will be compared within species across the two land use treatments, as well as across species to determine if any general morphologic response to habitat alteration is present. We hypothesize that some morphological variation should be present in response to habitat alteration across all species; species within specific habitat types (e.g. riffle) should display similar responses to habitat alteration; and that some species-specific morphological variation might be present across land use effects.

Keywords: habitat alteration; morphology; morphometrics
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14. ASSESSING THE MITOCHONDRIAL GENETIC DIVERSITY OF THE SMALLSCALE DARTER, *NOTHONOTUS MICROLEPIDUS*

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The Smallscale Darter, *Nothonotus microlepidus*, is a species of conservation concern, known from less than 40 localities in four tributary systems (Stones, Harpeth, Red, and Little rivers) of the Cumberland River in Tennessee and Kentucky. Within these systems, it occurs in fast-flowing riffles that are patchily distributed. Furthermore, each tributary system is separated by long reaches of the Cumberland River mainstem that may limit or reduce movements of individuals among systems. We sequenced the mitochondrial ND2 gene for 120 individuals from 8 localities (2 from each tributary system) to examine phylogeographic structure in the Smallscale Darter and assess whether the Cumberland River has been a long-standing barrier or filter to its dispersal and gene flow. We recovered 22 unique ND2 haplotypes. Divergence among haplotypes was low, with haplotypes differing by only one to six mutations. Although several haplotypes were unique to a given system, they were typically shared between sites within a system, suggesting no long-standing structure among habitat patches. One haplotype was shared among all sites and systems and three others were shared between two systems. The pattern of broadly shared haplotypes among the four tributary systems and low divergence among all haplotypes implies the Cumberland River has not served as long-standing barrier to dispersal for these fishes. Understanding the underlying phylogeographic structure for this species has relevance in conservation and management decisions and will be compared to results from a microsatellite data set to elucidate the impact of anthropogenic habitat alteration on the genetic diversity and population connectivity of this imperiled species.

Keywords: genetics; mtDNA; darter; Nothonotus; conservation
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15. ASSESSMENT OF BLACK (*MOXOSTOMA DUQUESNEI*), GOLDEN (*M. ERYTHRURUM*), AND SICKLEFIN (*M. SP.*) REDHORSE POPULATIONS IN THE UPPER OCONALUFTEE RIVER, QUALLA BOUNDARY, WESTERN NORTH CAROLINA

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Impoundments in river systems can act as barriers to population connectivity and produce alterations in species assemblage between upstream and downstream reaches. The Bryson Dam impounds the Oconaluftee River near its confluence with the Tuckasegee River. Population health of Golden and Black Redhorse that persist in the isolated upper Oconaluftee River is unknown. Sicklefin Redhorse, endemic to western North Carolina and northern Georgia, is thought to have been extirpated from much of its historical habitat due to hydroelectric dams. In an effort to establish a new population above Bryson Dam, 12,045 fingerlings have been introduced. From April to September 2017, multiple Redhorse age classes were sampled from the upper Oconaluftee River to assess the health of Black and Golden Redhorse populations as well as look for indications of an established Sicklefin Redhorse population. Mark-recapture electrofishing was used to provide data on demographics and population size of juvenile and adult redhorse, while drift net and light trap sampling were used to provide occurrence and drift density information for larval Redhorse. Larval samples and pectoral fin rays collected for aging are currently being processed. Five electrofishing samples over the six months of the study produced 628 Black Redhorse, 139 Golden Redhorse, and 4 unidentified Redhorse. Of these, 465 Black Redhorse, 94 Golden Redhorse, and 1 unidentified Redhorse were PIT tagged. There was a recapture percentage of 14.97% for Black Redhorse and 4.48% for Golden Redhorse. The preliminary population estimates for reaches sampled produced through the Schumacher-Eschmeyer method are N= 2106 with a range of 1544 – 3312 for Black and N= 1049 with a range of 478 – 5341 for Golden at the 95% confidence interval. No Sicklefin Redhorse were captured, indicating that restoration attempts have yet to establish a persistent Sicklefin Redhorse population.

Keywords: Redhorse; *Moxostoma*; Dams; Population; Little Tennessee
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16. PRELIMINARY ANALYSIS OF AGE-CLASS STRUCTURE AND LONGEVITY FOR THE ENDANGERED PYGMY MADTOM, *NOTURUS STANAULI*

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The Pygmy Madtom (*Noturus stanauli*) is federally listed as endangered and only occurs in a few reaches of the Clinch and Duck rivers in Tennessee. Scant ecological and life history information exists for this species. In this project, we assembled a list of standard (SL) and total (TL) lengths for 29 individuals from our field observations, museum records, and agency reports. Results using TL indicate two age classes (young-of-the-year and adult) throughout the year, a spawning period in June and July, and maximum longevity of approximately 1.5 years. In our collections, lengths ranged from 14-42 mm TL, with a mean of 29.3 mm TL. Future collections should include measurement of SL and TL at moment of capture to expand this baseline information into a more comprehensive understanding of this aspect of pygmy madtom life history.

Keywords: Pygmy Madtom; Clinch River; Duck River
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17. CEPHALIC AND BODY TUBERCULATION OF THE SHOAL CHUB *MACRHYBOPSIS HYOSTOMA* (TELEOSTEI: CYPRINIDAE)

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Cyprinidae, the largest family of fishes, currently contains 3000+ species of freshwater fishes that exhibit remarkable diversity in morphology, ecology and habitat. Most species of cyprinid possess tubercles (aggregations of keratinized cells) on the surface of the epidermis of the head, body, and fins. These structures have been hypothesized to primarily play a role in reproduction, including (but not restricted to) aiding close bodily contact between male and female individuals during spawning, aiding nest building, or the defense of a territory. In many species of cyprinid tubercles are conical, with many cell layers contributing to the formation of a single pointed structure, and are sexually dimorphic in size and position. Despite the potential importance of tubercles to the life history of cyprinids, these structures have yet to be studied in detail for the majority of species, including most members of the relatively well-studied radiation of North American cyprinids. In order to further our understanding of the diversity, distribution and potential function of tubercles across the radiation of North American cyprinids, we provide a detailed description of the gross morphology and distribution of tubercles located on the head and body of *Macrhybopsis hyostoma* using a combination of light microscopy, scanning electron microscopy and histology. The tubercles of *M. hyostoma* depart from the typical conical shape ubiquitous in minnows and instead consist of low, oval plates of keratinized cells, each with a single microprojection arising from the surface. These tubercles do not appear to be sexually dimorphic and we propose a hydrodynamic (vs. reproductive) function for the tubercles located on the surface of the head and body of *M. hyostoma*.

Keywords: Tubercles; cyprinidae; morphology; histology; sem
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18. OBSERVATIONS ON THE REPRODUCTIVE BIOLOGY OF THE DARTER FISH *ETHEOSTOMA KENNICOTTI* IN RESPONSE TO GILL PARASITE INFECTIONS

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Parasitic infections can affect host reproductive capacity through nutrient theft which may result in a reduced reproductive output, or cessation of reproduction altogether. Some fishes have developed mechanisms in which they are able to lessen the effects of these parasites. Amongst these fishes infected females produced larger clutch sizes of smaller eggs than uninfected females, reflecting a trade-off between egg size and egg number. This mechanism is known as fecundity compensation, and has been partially observed in the Fantail darter (*Etheostoma flabellare*). The purpose of this study is to determine to what extent the fecundity compensation hypothesis applies to infection by a monogenoidean *Aethycteron* species gill parasite in a population of Stripetail darters, a close relative of the Fantail darter. The Stripetail darter, *Etheostoma kennicott*, is found in streams in Tennessee, Ohio, Kentucky, Illinois, Alabama, Georgia, and Mississippi. The population of *E. kennicott* studied was collected monthly in Estill Fork in Jackson County, Alabama from August 2016 to June 2017. Peak reproduction was observed between the months of March and May. Average female host gonadosomatic index (GSI) began to rise in March at 4.75, peaked in April at 12.88, and declined to 8.26 in May before falling off in June to below 3, a post-spawning value. Parasite load was found to be higher during this period, peaking in March with an average of 4.75 parasites per female, and 8.17 per male. Consistent with the fecundity compensation hypothesis, female Stripetails bearing a larger parasite load were found to have been carrying larger clutches of smaller oocytes than females infected with fewer parasites. Similar trends were found in the mean intensity of parasitism. There was a negative correlation between mean intensity and clutch size as clutch size increased into the cessation of spawning in May.

Keywords: Fecundity; Compensation; *Etheostoma kennicott*
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19. TESTING DIEL FISH MIGRATIONS BETWEEN RIFFLE-POOL HABITATS

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Diel turnover in assemblage composition is reported from a number of aquatic species, including stream fishes. However, there is a paucity of work addressing diel fluctuations by small-bodied stream fishes. We tested for fish migrations between riffle and pool habitats across transitional diel periods (i.e., sunrise and sunset) in Little Creek, Putnam County, TN using directional weir traps placed between four riffles and the adjacent upstream and downstream pools. We hypothesized that small-bodied fishes use pools during diurnal hours, migrate into riffles during the transition to night (i.e., sunset), and then move back into pools during the transition to day (i.e., sunrise). We compared the number of fishes captured in weirs blocking movement out of pools and into riffles with fish captured moving out of riffles and into pools for both transitional periods and in upstream and downstream directions. We found that fish movement (i.e., weir capture) during sunset was higher than sunrise, and the largest amount of movement was into riffles at sunset. There was no apparent difference between movements into riffles from upstream or downstream directions. We then set bidirectional weir traps in the center of riffles and assessed capture rates every four hours for 72 consecutive hours and found capture rates were greatest during nocturnal hours. Our results suggest fish movement into and activity within riffles is greatest during nocturnal hours, and that small-bodied stream fishes exhibit diel migrations between riffle and pool habitats.

Keywords: migration; stream; fish; riffle; diel
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20. LINKING INTER-RIVER MOVEMENTS OF SAVANNAH RIVER STRIPED BASS, *MORONE SAXATILIS* WITH SPAWNING ACTIVITY IN THE NEARBY OGEECHEE RIVER.

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The Savannah River population of striped bass (*Morone saxatilis*) collapsed in the late-1980s, due in part to dredging activity within their estuarine spawning habitat which altered flow regimes and increased salinity to levels lethal to eggs and larvae. The population is now supported through a stocking program by the Georgia Department of Natural Resources, and there is little indication of natural recruitment within the system. Previous mark-recapture surveys suggest that some adult striped bass may be moving between the Savannah and nearby Ogeechee Rivers via coastal waterways, and we hypothesize these movements correspond to spawning activity in the less physically altered Ogeechee River. Our study involves telemetering of adult striped bass captured in each river coupled with an ichthyoplankton survey in the Ogeechee River to estimate striped bass temporal spawning effort. To date, we have surgically implanted coded acoustic transmitting tags in 18 adult striped bass (>6 lb.) in the Savannah River Estuary and two adult striped bass (>12 lb.) in the Ogeechee River Estuary. An existing array of receivers allows us to gather spatiotemporal movement data within and between each river. To identify spawning activity in the Ogeechee River, we annually sample striped bass ichthyoplankton through a boat-mounted plankton tow from February to May. Of the twenty fish tagged, two have relocated from the Savannah River to the Ogeechee River. These short-term residencies (2014-2016) corresponded to our detected spawning window in the Ogeechee River (2017).

Keywords: species declines, telemetry, fisheries management, sport fish restoration
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21. ANALYSIS OF BODY SHAPE VARIATION AMONG RESTRICTED AND WIDESPREAD POPULATIONS OF THE SOUTHERN REDBELLY DACE, *CHROSOMUS ERYTHROGASTER*

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The Southern Redbelly Dace *Chrosomus erythrogaster* has a widespread distribution throughout most of the eastern United States, with several disjunct populations in midwestern states and in the lower Mississippi River drainage. Of particular interest are potentially isolated populations on Crowley's Ridge in Arkansas and the Bluff Hills in Mississippi. Currently, it is unclear whether these populations share connections with larger core populations in the nearby Ozark and Eastern highlands, or represent isolated populations on these "upland islands" within the Gulf Coastal Plain. This study used geometric morphometric techniques to evaluate body shape differences among *C. erythrogaster* from loess habitats of Crowley's Ridge and the Bluff Hills of Mississippi. In order to determine variation in body shape, focal populations were compared to populations from the Ozark and Eastern highlands. Principal Component and Canonical Variance Analyses revealed variation in body shape across the geographic range, and the populations of interest seem to be showing patterns of intermediate body depth compared to other populations. In conjunction with an ongoing population genetic study, results from this study will provide valuable information about the distinctiveness of potentially isolated populations in Arkansas and Mississippi.

Keywords: Southern Redbelly Dace; Morphometrics; Arkansas
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22. RESPONSE OF RIFFLE FISH COMMUNITIES TO MORPHOLOGY CHANGES RESULTING FROM STREAM DEGRADATION

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The streams of the Arkansas Ozarks have experienced extensive erosion and gravel intrusion due to changing land use. As a result, modifications to instream habitat have resulted in an increase in transverse and diagonal gravel bars along with associated shallow, low flow riffles. This study was conducted to determine if variation in riffle habitat (depth, velocity, substrate size) affects the riffle fish community. Understanding how fishes are using different riffle habitats is crucial to ensuring restoration efforts provide the necessary habitats for fishes throughout their various life history stages. For this study 22 riffles were sampled in the King's River, Arkansas using seines and kick set methods. Fishes were preserved in 10% formalin and identified in lab; standard lengths of benthic fishes were taken. Habitat data were taken at each riffle including velocity, pebble count, depth, and water quality. The King's River exhibited a gradient in available riffle habitat with two extremes being shallower, slower, wider riffles with smaller substrate (unstable riffles) and deeper, faster, narrower riffles with larger substrate (stable riffles). Results of community and species level analyses in relation to habitat will be discussed.

Keywords: King's River; Ozarks; Riffles; Gravel
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23. BODY SHAPE VARIATION WITHIN AND AMONG LINEAGES OF THE RAINBOW DARTER, *ETHEOSTOMA CAERULEUM*

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The Rainbow Darter (*Etheostoma caeruleum*) is distributed widely throughout the eastern United States, with several disjunct populations in the lower Mississippi River drainage. An unpublished morphological study of *E. caeruleum* suggested potentially distinct species in the White River drainage and in tributaries of the lower Mississippi River drainage. However, morphologically distinct groups do not necessarily correspond to published mtDNA based phylogeographic studies and a recent microsatellite DNA based study of *E. caeruleum*. This study used geometric morphometrics to evaluate body shape differences of *E. caeruleum*, with particular emphasis on disjunct populations in the lower Mississippi River basin. Specifically, we asked whether differences in body shape corresponded to: (1) unpublished "species" based on meristic data; (2) previously identified mtDNA lineages; or (3) recently identified microsatellite DNA based clusters. Results from this study showed that body shape corresponds with some aspects of meristic, mtDNA, and microsatellite DNA data, but it is still unclear whether body shape is more aligned one data type. Despite the broad variation of body shape within *E. caeruleum*, both CVA and PCA analyses of body shape suggest high levels of distinction for White River populations. Results of this study provide additional information about diversity within *E. caeruleum* and highlight the distinctiveness of White River populations, which warrant further taxonomic examination.

Keywords: Geometric morphometrics, Crowleys Ridge, polytypic species
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24. PHYLOGEOGRAPHIC ANALYSES SUGGEST CRYPTIC DIVERSITY WITHIN THE BLUNTNOSE DARTER, *ETHEOSTOMA CHLOROSOMA*

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Previous morphological studies of the Bluntnose Darter (*Etheostoma chlorosoma*) revealed little variation among populations across the Gulf Coastal Plain. While some western populations (e.g. Colorado River, Texas) showed significant divergence from other populations, there was little support for taxonomic recognition of these populations. As a part of a larger study to evaluate phylogeographic patterns of Gulf Coastal Plain fishes, we sequenced mtDNA and multiple nuclear loci for *E. chlorosoma* to evaluate the Mississippi and Tombigbee river discontinuity hypotheses. Preliminary analyses reveal a deep phylogeographic break (TMRCA approx. 8 mya) among members east and west of the Mississippi River for *E. chlorosoma*. The deep divergence among eastern and western clades of *E. chlorosoma* suggests previously unrecognized cryptic diversity within the species. However, individuals from the Sabine River fall within the eastern clade. Ongoing work with additional nuclear DNA markers and increased sampling will be incorporated into this framework, shedding light on this unique phylogeographic pattern in the Gulf Coastal Plain.

Keywords: Species delimitation, cryptic species

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25. WESTERN BLACKNOSE DACE IN THE BLACK WARRIOR RIVER DRAINAGE, ALABAMA

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The Western Blacknose Dace, *Rhinichthys obtusus*, has populations reaching as far south as Alabama, where it is found in the Tennessee, Coosa, and Black Warrior River basins. Although populations appear well-established in the Tennessee and Coosa River basins, the Black Warrior drainage has limited occurrences. In the Sipsey Fork drainage of the Black Warrior, only small samples (n=1-4) of Western Blacknose Dace are reported. During the course of survey fieldwork in the fall of 2015, the authors found a large population of dace in the Brushy Creek System (Sipsey Fork, Black Warrior River). The authors returned to the site during high flow in spring 2016 to quantify population density. The findings suggest that populations of Western Blacknose Dace may be more prevalent within the headwaters of this system than previously believed.

Keywords: dace; new report; headwaters; Alabama

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26. WHO IS SPAWNING HERE? DEVELOPMENT OF AN RFLP LIBRARY FOR MINNOWS IN THE RED RIVER SYSTEM (CUMBERLAND RIVER DRAINAGE)

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Identification of fish eggs, particularly those belonging to the minnow family, is difficult when based on morphology alone. This is particularly challenging when trying to determine successful egg deposition of species which engage in spawning aggregations (e. g. nest associations). Genetic tools, such as bar coding, can be used to identify morphologically similar eggs. We have created a diagnostic RFLP (restriction fragment length polymorphism) library using the mtDNA cytochrome b gene and the restriction enzyme Rsa I for six minnow species in the Red River system of the Cumberland River Drainage. All six minnow species either engage in nest building or nest association. Moreover, a subset of these species appear to be facultative nest associates, so identifying successful egg deposition in nest vs. non-nest sites will help to further elucidate the reproductive strategy these species employ.

Keywords: egg identification, reproduction, Cyprinidae
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27. MICROHABITAT OF THE CHAINBACK DARTER, *PERCINA NEVISENSE* (ACTINOPTERYGII: PERCIDAE) IN THE ROANOKE RIVER IN SALEM, VA

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Microhabitat for *Percina nevisense*, Chainback Darter (Actinopterygii: Percidae) was quantified from April 2016 to September 2017 using snorkeling observations and measurements of depth, current velocity approximately five cm above the substrate, and substrate size at the point of first observation for each specimen (n = 267). Mean depth of observation was 58.8 cm with a standard deviation (SD) of 16.7. Mean current velocity at observation points was 0.17 meters per second (m/s) with SD = 0.11. Mean substrate size was 8.2 cm (SD = 11.5). To test if the mean depth, current velocity, and substrate size at observation points differed from available habitat, these parameters were measured from 30 evenly spaced spots within the study site during October 2016. A t-test (alpha = 0.05) was used to test for a difference in the means of observation points during October 2016 and available habitat data from the same month. None of the means for measured parameters of occupied points were significantly different from available habitat (depth p = 0.22, velocity p = 0.11, substrate size p = 0.54). However, using Bonett's test for difference in variance, occupied and available habitat for October 2016 was different for depth (p = 0.002) and velocity (p = 0.044), but was not different for substrate size (p = 0.063). A one-way ANOVA was used to detect differences among occupied habitat parameters among months. All three measured variables were not uniform among months (depth p < 0.001, velocity p = 0.001, substrate size p = 0.011). These analyses suggest that *Percina nevisense* occupy specific habitats and that those habitats do change from month to month.

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28. ALLOPATRIC SPECIATION OF *LEPOMIS MEGALOTIS* IN THE HILL COUNTRY OF TEXAS

Mike Stegall

The Edwards Plateau and aquifer region comprises an area of central Texas commonly known as the Texas Hill Country. It is a land of many springs, stony hills, steep canyons and very clear creeks and rivers. The region is home to a whole host of rare plants and animals found nowhere else on earth. In the central part of the Hill Country are the Frio, West Nueces, Medina and Sabinal Rivers. A color phase of *Lepomis megalotis* inhabits these rivers. Its colors are very different from all other *L. megalotis* color types. This is a very interesting example of allopatric speciation. This color phase of *L. megalotis* is in the highest elevation of the Hill Country. It is almost completely surrounded by another color phase of *L. megalotis* which covers most of the range of *L. megalotis* in Texas. The *L. megalotis* DNA is too close to be a different species by color differences. Allopatric speciation has caused these two color types to be separated over time and become very different in color. Further study needs to be done on this interesting example of allopatric speciation.

Keywords: *Lepomis megalotis*; Hill Country; color
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29. A PRELIMINARY LOOK AT THE GREEN RIVER FISHES WITHIN MAMMOTH CAVE NATIONAL PARK FOLLOWING THE REMOVAL OF LOCK AND DAM #6

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The lower section of the Green and Nolin Rivers within Mammoth Cave National Park historically have been inundated by lock and dams #5 and #6. In the spring of 2017, lock & dam #6 was removed by the partnership of the USACOE, NPS, and USFWS. Discussions and details for the removal of lock & dam #5 are ongoing, but its removal is imminent. Kentucky State Nature Preserves Commission was contracted to document the current physical and biological conditions from the historical footprint of lock & dam #6, approximately 12 miles upstream the Green River and two miles upstream the Nolin River during summer 2017. The lower half of the study area along the Green River and all of the Nolin River were still inundated from lock & dam #5, but the upper half of the Green River was free-flowing. Fish assemblage data were collected from one site within the Nolin River and four sites within the Green River, with two sites each from the free-flowing and inundated sections. Boat electrofishing of 500 meters along each bank was conducted at each site, with supplemental seining and backpack electrofishing conducted at the free-flowing sites in shoal habitat. Preliminary results indicate distinct fish assemblages between the free-flowing sites and inundated sites, with a greater species richness and more benthic species present at the free-flowing sites. Numerous species of conservation interest were encountered, such as the western sand darter (*Ammocrypta clara*), stargazing minnow (*Phanacobius uranops*), and the popeye shiner (*Notropis ariommus*). Overall, more than 50 species of fish were encountered during the surveys.

Keywords: Green River; Mammoth Cave National Park; Dam Removal
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30. DEVELOPMENT OF A MICROSATELLITE MARKER PANEL FOR GENETIC CHARACTERIZATION OF BLUEHEAD CHUB (*NOCOMIS LEPTOCEPHALUS*) IN SOUTH CAROLINA

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The bluehead chub (*Nocomis leptoccephalus*) is a cyprinid native to freshwater rivers and streams in the Atlantic and Gulf Slope drainages of the southeastern United States. Bluehead chub is a nest-associating species that constructs gravel mounds for spawning. These spawning mounds are used by over 30 types freshwater fishes, making bluehead chub an important keystone species in these riverine systems. Although bluehead chub are not considered threatened throughout their general distribution, they may face local threats including habitat loss. To date, no molecular markers have been developed specifically for bluehead chub to assess population genetic diversity or for comparison to other nest-associating species. Our objective was to assemble a panel of microsatellite markers to characterize the genetics of bluehead chub, distinguish between bluehead chub and the nest-associating yellowfin shiner (*Notropis lutipinnis*), and answer population-level questions regarding bluehead chub in South Carolina. A total of 40 microsatellite markers developed for related cyprinid species were tested on bluehead chub and yellowfin shiner fin clips collected from Shoal Creek in Pickens County, South Carolina. Of these, 12 markers were selected based on amplification success and degree of polymorphism. These markers were amplified in three multiplexed reactions and tested for departure from Hardy-Weinberg Equilibrium, linkage disequilibrium, and the presence of null alleles. This suite of microsatellite markers provides a valuable tool to improve our understanding of genetic connectivity and population dynamics of bluehead chub and allow for informed management recommendations. Applications of this microsatellite marker panel include evaluating genetic variation (i.e. genetic diversity, allelic richness, effective population size) of bluehead chub populations, screening egg samples from nesting sites to discriminate between bluehead chub and yellowfin shiner, and investigating bluehead chub paternity on nesting mounds.

Keywords: Bluehead chub; microsatellite markers
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31. DIEL PATTERNS IN BENTHIC RIFFLE SPECIES DIVERSITY IN THE KING'S RIVER, ARKANSAS

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Understanding species demographics of benthic fishes within riffle habitats during both day and night can offer insight on the mating, spawning, movement, and feeding patterns. Little research has been conducted on diel movements in benthic species in upland rivers of the southeastern United States, partly due to the time period in which sampling of these species must be conducted. Eleven riffles in the King's River, Arkansas were sampled (9/9-10/17) during the day along the river using a 3 meter wide, 4.75mm-mesh seine net. These eleven riffles were re-visited two weeks later (9/22-23/17) with sampling beginning at 9:00 pm. Kick sets were performed along the riffle until all microhabitats were sampled and it was determined that a good representative community sample had been collected. Several species of benthic and pelagic fishes (e.g. *Noturus albater*, *Micropterus dolomieu*, and *Etheostoma euzonum*) were sampled in higher abundances during the night sampling, in comparison to daytime samples. Species patterns and variation in standard length will be examined. Differences in species composition relative to sample times within the riffles may be explained through predator evasion, prey availability, etc. Knowledge of diel movements exhibited by these benthic species can provide understanding of the effects of erosive flooding on riffle habitats, as well as future insight on conservation/restoration efforts in freshwater streams and rivers.

Keywords: diel movement; riffle; benthic; nocturnal; diurnal
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32. THE ECOSYSTEM ROLE OF SOUTHEASTERN STREAM FISHES: WHEN, WHERE, AND WHY DO THEY MATTER?

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Stream fishes can be important drivers of ecosystem processes, but the extent and magnitude of their effects are variable. Conceptual frameworks have been proposed to predict fish-mediated ecosystem effects in streams, but the ecosystem impact of most species remains unknown, including fishes in the Southeastern United States. We considered the role of Southeastern fishes in lotic ecosystems by first providing examples of charismatic fauna with potentially profound effects on ecosystems. Then, as an example of fish-ecosystem interactions, we used published syntheses of nutrient excretion and uptake to simulate the potential importance of nitrogen and phosphorous inputs by small-bodied shoal fishes in the Conasauga River, Georgia. Our results indicated that shoal fish excretion could meet 7.2% (median) of nitrogen demand and 7.0% (median) of phosphorus demand, with nitrogen dynamics exhibiting more variability. Our results suggested the potential importance of nutrient excretion by small-bodied, nongame shoal fishes of the Conasauga River. These findings reinforce the need to explore the places and moments in which fish effects may be especially important and may provide insight into the consequences of historical and contemporary fish biomass and biodiversity loss.

Keywords: fish effects, nutrient cycling
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33. FRESHWATER INFORMATION NETWORK (FIN): A USER-FRIENDLY WEBPAGE FOR RECORDING AND SHARING FIELD DATA

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The Mobile, Tennessee and Cumberland watersheds are hotspots for freshwater biodiversity. Unfortunately, this region is also a hotspot for imperilment. We developed an application that connects information from freshwater conservation scientist's aquatic surveys to other scientists and the rest of the conservation community. Traditionally, scientists would preserve specimens for morphological studies and store them in natural history collections. However, with the increased number of imperiled species, many scientists are looking for alternatives to catalog these data. As photo vouchers allow specimens to be released unharmed, the Freshwater Information Network (FIN) allows scientists to submit their photo vouchers to create a "Living Museum" in an interactive application. This webpage will permit the entry of ideal field information such as location, species, number of specimens, etc. Our web-based application will consolidate museum databases based on vouchered specimens with photo voucher data submitted through FIN. This aquatic natural history data will be easily accessible to other freshwater biologists, land trust managers, conservation organizations and even citizen scientists. In turn, the connection to the scientific community within these watersheds will facilitate freshwater research and conservation ideas for groups not previously connected.

Keywords: Data Collection; Museum; Maps
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34. THE SIRAJO SHUFFLE: A SYSTEMATIC STUDY TO IDENTIFY RESIDENT SPECIES OF ENIGMATIC AMPHIDROMOUS WATERFALL-CLIMBING *SICYDIUM* GOBIES IN PUERTO RICO

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“Sirajo” is a generic term used colloquially to refer to a poorly studied group of fascinating amphidromous fishes ranging throughout the Caribbean. Adults, especially when in spawning condition, exhibit strikingly brilliant electric blue-green coloration. In some areas of the Caribbean, especially Puerto Rico (a Commonwealth of the US), the larval stages of these gobies, locally known as “ceti”, have important cultural and culinary significance; an artisanal fishery supports local economies during times of postlarval immigration to rivers from the ocean or estuaries. These fishes display convergent and presumably confusing gross morphological characters that might confound identification in the field. Studies by Hildebrand (1935) and by Erdman (1961, 1986) purported to find only a single species, the widespread *Sicydium plumeri*, to be present on Puerto Rico. Watson (2000) revised the group to four distinct species that can be identified using upper jaw dentition characters. Though much of the focus was on the neighboring island of Hispaniola, considerable *Sicydium* material from several Puerto Rican streams was also included in Watson’s effort. We present data from over 500 specimens of *Sicydium* collected from 16 sites across the island of Puerto Rico in 2011. Both dentition and DNA barcoding was used to assign individuals to species. While dentition supports recognition of Watson’s 4 species, DNA only identified 3 of these as valid taxonomic assignments. We describe these findings and propose that Sirajo gobies on Puerto Rico are represented by three species with the fourth likely to represent a relatively rare hybrid of various F1 crosses of the other forms.

Keywords: Sirajo; *Sicydium*; Puerto Rico; goby; amphidromous
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35. STATUS SURVEY AND CONSERVATION GENETIC ASSESSMENT OF THE PALEBACK DARTER (*ETHEOSTOMA PALLIDIDORSUM*)

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The Paleback Darter (*Etheostoma pallididorsum*), an endemic to the Ouachita Mountain Ecoregion, is a Species of Greatest Conservation Need in Arkansas. A prior allozyme-based study found evidence of small effective population size, which is indicative of low genetic diversity for *E. pallididorsum* populations, raising conservation concern for the species. As a result, the Center for Biological Diversity petitioned *E. pallididorsum*, among 400 other southeastern U.S. aquatic species, for federal listing. Therefore, the objectives of this project were to (1) survey historic localities, (2) estimate size-distribution data and relative abundance on a seasonal basis, and (3) assess population dynamics and phylogeographic history with microsatellite DNA loci and mitochondrial cytochrome *b* DNA sequences. Average relative abundance (catch per unit effort) for all four seasonal sites was similar between winter and spring (0.36 and 0.39, respectively), with highest values in the summer (0.94). Over all seasons, relative abundance was similar between Caddo and Ouachita river drainages (0.59 and 0.54, respectively). Analyses of microsatellite DNA loci revealed low, but significant genetic structure among localities ($F_{st} = 0.17$, $P < 0.001$), with the highest levels of structure observed between river drainages. Population genetic diversity is relatively low (mean $H_e = 0.59$; mean alleles per locus = 5.06), but comparable to close relatives *Etheostoma boschungii* (mean $H_e = 0.67$; mean alleles per locus = 6.74) and *Etheostoma tuscumbia* (mean $H_e = 0.57$; mean alleles per locus = 5.53). Bayesian phylogeographic analyses resulted in the Caddo and Ouachita rivers as reciprocally monophyletic, with divergence among the drainages estimated approximately 60,000 years ago. Despite evidence for isolation among Caddo and Ouachita river populations, these results suggest that *E. pallididorsum* is relatively stable and abundant at sampled historic localities.

Keywords: population genetics, endemism, habitat fragmentation
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