

**2023 SD AFS Poster Presentations**  
**(<sup>†</sup> Best Student Poster Candidate)**  
**(\*Presenter)**

**Distribution of *Procambarus pearsei* and *Procambarus braswelli* in North Carolina and the effects of *P. clarkii* invasion**

Robert Adams\* (Appalachian State University), S.J. Busch, E.J.Thompson, R.P Creed, and M.M Gangloff (Appalachian State University)

*Procambarus pearsei* and *P. braswelli* are currently considered species of concern by the NCWRC. Both crayfish species are endemic to the lower Cape Fear, Pee Dee and Waccamaw river systems in North Carolina and South Carolina. These drainages have been extensively colonized by *Procambarus clarkii*, an invasive species that escaped from aquaculture facilities, raising concerns that this cosmopolitan and large crayfish may displace smaller and more niche-limited native crayfish species. Indeed, prior to our surveys, *P. pearsei* had not been detected in North Carolina since October of 2015. Our goal is to examine whether the distribution and abundance of *P. pearsei* and *P. braswelli* are being affected by *P. clarkii* invasions. To date, we have conducted surveys at 27 historical sites and 35 new sites across the ranges of *P. pearsei* and *P. braswelli*. We detected *P. braswelli* at 4 of 12 historically occupied sites and *P. pearsei* at 2 of 15 historically-occupied sites. Future surveys will involve sampling year-round to assess the degree to which the distributions of these species have changed over time and determine how seasonality affects the detectability of native and invasive crayfishes. We will also obtain detailed demographic and reproductive-status information to assess whether life history traits may explain some of the potential for competition between native and invasive species. These data will help guide management of both native and invasive crayfishes and hopefully highlight the potential impacts of *P. clarkii* and other invasive crayfishes in this region's unique but vulnerable freshwater ecosystems.

**<sup>†</sup>Assessing Biota and Environmental Characteristics Above and Below a Low-head Dam**

Trevor Alexander\* (Western Carolina University), Keith Gibbs (WCU) & Tom Martin (WCU)

Dams are a form of anthropogenic alteration to aquatic ecosystems that can affect natural conditions and influence aquatic fauna assemblages. The size and type of a dam can have different effects on the aquatic environment, such as altered flow rate, water temperatures, sediment transport, and can serve as barriers that limit fish migration or distribution of fishes, macroinvertebrates, and aquatic plant species. The focal point of this study is a low-head dam located on the Tuckasegee River in Jackson County, NC. Fish and macroinvertebrates were sampled at multiple sites above and below the dam to compare species assemblages. Macroinvertebrates were sampled with a kick net in shallow riffles and a D-frame net for timed multihabitat sampling. Backpack electrofishers were used to sample fish in available wadeable habitats. We used multivariate statistical analyses to determine the similarity of fish and macroinvertebrate assemblages among sites. Our results indicate the dam has minimal effect on aquatic habitat and aquatic macroinvertebrates. However, we found greater fish diversity below the impoundment. A one-way SIMPER shows that the Wounded darter and Banded darter were not detected above the dam but were present below the dam. Conversely, the Greenfin shiner, Brook trout,

and Rosyside dace were not detected below the dam but were found above the dam. Restored connectivity to this system may improve fish diversity above the dam. However, removing the dam may cause a temporary decrease in sensitive macroinvertebrates since the dam is withholding sediment. Substrate composition may change temporarily below the dam until the finer substrate is transported downstream. Overall, this study provides several years of baseline that can be referenced if the dam is removed.

### **Investigating centennial genetic changes at an epicenter of marine biodiversity through short-read genome assemblies**

Jemelyn Grace Baldesimo\* (Old Dominion University), Eric Garcia (Old Dominion University), Abner Bucol (Silliman University), Rene Clark (Rutgers University), Brendan Reid (Rutgers University), Roy Roberts (Texas A&M University-Corpus Christi), John Whalen (Old Dominion University), Chris Bird (Texas A&M University-Corpus Christi)

The Philippines is an epicenter of marine biodiversity, having more species per unit area than anywhere else in the world. However, it is also known to be heavily impacted by anthropogenic stressors. The NSF-funded Philippines PIRE Project aims to uncover changes in genetic diversity of marine fish populations due to habitat degradation, overfishing, and other anthropogenic activities. Since we have access to specimens collected in the Philippines from 1907 to 1910 by the USS Albatross through the Smithsonian National Museum, we can study temporal changes in genetic diversity for over 100 years. Appropriate extraction methods, DNA repair protocols, library variations, and sequencing methods were tested to develop a pipeline to genotype a few species with up to 40,000 loci across historical and contemporary samples. In this study, we focus on comparing the performance by four commonly used tools (ABYSS, HipMer, SOAPdenovo, and SPAdes) for assembling short reads from six species that had historical and contemporary samples. Results showed that the four assemblers produce high quality assemblies, but SPAdes consistently yielded high quality metrics, produced more contigs and assembled larger contigs. Successful genome assembly from short reads represents a new paradigm for studying non-model fisheries and organisms. Our findings can aid molecular biologists studying non-model organism with limited computational resources, which can help drastically increase genetic knowledge on systems they study.

### **Alligator Gar Research in Pensacola Bay**

Calvin Beech\* (Florida Fish and Wildlife Conservation Commission), Amanda Mattair (Florida Fish and Wildlife Conservation Commission), Mathew Wegener (Florida Fish and Wildlife Conservation Commission)

Alligator Gar *Atractosteus spatula* are large riverine fish that can grow to around 150kg and range across the southeastern U.S. In Florida, Alligator Gar are only found within Gulf Coastal rivers west of the Apalachicola River and are considered rare. Alligator Gar populations throughout their range have historically been declining or absent since the mid 1900's. Recognizing this decline and the need for conservation, Florida Fish and Wildlife (FWC) closed harvest of Alligator Gar in Florida waters in 2006 to anyone without a special permit. Abundance estimates are needed to determine if the harvest closure is necessary. A population estimate conducted on the Escambia River in 2014-2015, indicated additional research was needed throughout the range of Alligator Gar in Florida. To determine if harvest closures are necessary, additional abundance estimates are needed. While few individuals have been caught in

the Pensacola Bay system since 2016 (N<10), recent genetic and telemetry data suggest that the Escambia River could be the source population for all of Pensacola Bay. The objectives of this study were to (1) use telemetry to determine movement of tagged fish in Pensacola Bay and (2) locate when and where Alligator Gar aggregate in Escambia Bay for future population estimates. Research from this study will help inform managers better understand Alligator Gar population dynamics across their Florida range.

#### **†Fishing Preferences of Urban Anglers in the Metro-area of Richmond, Virginia**

Sophie Bels\* (Christopher Newport University), Rene X. Valdez (Virginia Department of Wildlife Resources), Mallory G. White (Virginia Department of Wildlife Resources), Clint Morgeson (Virginia Department of Wildlife Resources)

The Virginia Department of Wildlife Resources is interested in recruiting and retaining diverse anglers across the state. Urban areas in Virginia have both high numbers of current and potential anglers. To better understand current urban anglers and expand strategies for engaging this group, we developed an in-person survey to measure angler preferences for urban fishing sites, fishing satisfaction, and fishing experience. Using a roving-roving creel design, we surveyed 9 fishing sites in Henrico County and the City of Richmond in June and July 2022. We conducted 152 in-person surveys over seven weeks. Results indicate that fishing effort and catch was higher on weekdays compared to weekends, urban anglers may be less experienced than average, and are more likely to fish without a target species. Our results also show that urban sites selected by anglers are perceived as relaxing and convenient to travel to. We compare results of this project to results of a recent statewide angler survey to highlight the unique aspects of urban anglers in the Richmond area. We also present management recommendations for improving survey efforts of urban anglers and communication and outreach efforts to engage with urban anglers.

#### **†Reproduction and diet of the Harlequin Darter in the Neches River basin of Texas**

Daisy Blake\* (Texas State University), Dr. Timothy Bonner (Texas State University)

Harlequin Darter *Etheostoma histrio* is widely distributed within the Mississippi River basin and gulf slope drainages of central and southeastern USA. Previous studies in more northern extents of their range report a short reproductive season (two months, February and March), life span of four or more years, and food items consisting of benthic invertebrates. The purpose of this study is to quantify monthly reproduction and diets of the Harlequin Darters taken from lower latitudes (lower Neches River of Texas) with the expectation of a longer spawning season. Harlequin Darters were taken starting in February 2022 and will be taken through February 2023. Reproduction (e.g., gonadosomatic index, ovarian stage, oocyte counts), diets, growth, and age will be described and then compared to previous reports for the purpose of exploring how life histories might change at different latitudes.

#### **Spatial and temporal variation in food affects habitat choice in competing brook trout**

Eliza Brooks\* (Randolph-Macon College), Charles Gowan (Randolph-Macon College)

Brook trout (*Salvelinus fontinalis*) search for optimal foraging locations in streams while competing in local dominance hierarchies, with higher-ranking individuals gaining access to locations with more food. This process occurs within a single pool, but field observations show that fish

periodically move among pools over the summer. We hypothesized that the cause of these movements is temporal variability in food abundance, with fish deciding to move when food availability within a pool declines relative to that in other pools. We used an artificial stream with three fish to represent a natural habitat in which food levels vary among pools and change over time. Our prediction was that fish would distribute themselves in the stream according to food level and position in the dominance hierarchy and that fish would change pools when food levels in each pool were manipulated. The data showed that dominant fish did spend most time in the best pool and would switch pools when food levels were changed. However, subordinate fish did not distribute themselves as predicted and all fish frequently moved among pools regardless of food level. These results indicate that fish do not distribute themselves strictly according to food level and position in the dominance hierarchy, and that all fish periodically search among pools, perhaps to update their knowledge of conditions throughout the stream. Understanding drivers of fish movement is important in conservation because decisions made by individual fish about where to forage ultimately determine total fish abundance in the stream.

#### **†Developing a joint species, spatially dependent physiologically guided abundance model to improve predictions under future climate change scenarios**

Christopher A Custer\* (Pennsylvania Cooperative Fish and Wildlife Research Unit, Intercollege Graduate Degree Program in Ecology, Pennsylvania State University), Erin M. Schliep (Department of Statistics, North Carolina State University), Joshua S. North (Earth and Environmental Sciences, Lawrence Berkeley National Laboratory), Gretchen J.A. Hansen (Department of Fisheries, Wildlife, and Conservation Biology, University of Minnesota), Holly Kundel (Department of Fisheries, Wildlife, and Conservation Biology, University of Minnesota), Jenna K.R. Nelson (Department of Fisheries, Wildlife, and Conservation Biology, University of Minnesota), Tyler Wagner (U.S. Geological Survey, Pennsylvania Cooperative Fish and Wildlife Research Unit, The Pennsylvania State University)

Climate change is a significant global threat to poikilotherms, with increases in temperature having the potential to alter the abundance and distributions of species across the biosphere. Predicting the response of poikilotherms to increases in temperatures, therefore, is a global conservation priority and one that often relies upon the use of correlative niche models. However, the use of these models to extrapolate abundance/distributions under future temperature conditions assumes that observed temperature-abundance relationships are valid under future temperatures - temperatures that often exceed the range of observed temperature data. We recently developed a novel physiologically guided abundance (PGA) model that relaxes this assumption by integrating data on a species' thermal preference and tolerance (e.g., thermal optimum and critical thermal maximum) into a single species correlative niche model. The fusion of lab-derived thermal performance curves effectively constrains predictions under future climates based on species-specific physiology and has been shown to produce more realistic predictions under increasing temperature scenarios. Here, we expand upon this model to account for species and spatial dependencies. We first show the validity of our newly developed joint species, spatial PGA model (jsPGA) through a simulation study. Finally, we present a case study that uses fish community data from >1,000 freshwater lakes across Minnesota. We show the utility of using the jsPGA to predict the abundance and distribution of six different species of fish that vary in their thermal tolerance under future climate change scenarios.

## **Examining home range trends of reef fish on North Carolina artificial reefs**

Reese Dorroh\* (North Carolina State University), Jeffrey Buckel, Ryan Tharp (North Carolina State University)

Artificial reefs are man-made structures that can be used to supplement or enhance natural habitats. Despite their increasing use, little work has been done examining how different species use different artificial structures or the area surrounding them. A better understanding of how fishes utilize the area around artificial structures can help managers make more informed decisions in the future. During the summer of 2021, we tagged five recreationally important species on two different artificial reef complexes off the coast of North Carolina: black sea bass (*Centropristis striata*), gag grouper (*Mycteroperca microlepis*), almaco jack (*Seriola rivoliana*), red snapper (*Lutjanus campechanus*), and greater amberjack (*Seriola dumerili*). Fishes were measured and tagged, and their fine-scale movements were tracked using a VEMCO Positioning System (VPS) for ~100 days. The results were used to calculate home ranges, with which two gamma generalized linear models were run using the log link function with total length (TL) and species as the predictors and home range (HR) as the response. Model results indicated a significant positive relationship between species and home range size, while controlling for the effects of total length. When examining total length alone, there was a marginally significant positive relationship with home range size. Black sea bass had the smallest home ranges, gag and red snapper had moderate home ranges, and jacks had the largest home ranges. Larger fish tended to have larger home ranges. Our results suggest that home range size does vary by species and total length.

## **Development of the Blue Ridge Snorkel Trail in North Carolina**

Luke Etchison\* (NC Wildlife Resources Commission), Andrea Leslie (NC Wildlife Resources Commission)

The Blue Ridge Snorkel Trail (BRST) is an innovative education project that will link together a set of publicly accessible river sites where people can safely snorkel to experience the underwater world of streams and rivers of western North Carolina. Phase I of the snorkel trail involves establishing a set of ten pilot sites, in ten different counties. Each site would be identified with an educational sign, which provides safety information, a description of notable species at the site, and a map of the snorkel trail which will note the location of all snorkel sites across western NC. Additional information on the fishes that can be found at each site will be provided in a link to the North Carolina Fishes website. The BRST is set to break ground in Spring 2023.

## **Making sausage with countless cooks; combining genetic and acoustic telemetry data from many collaborators to understand coastwide migration patterns of Atlantic Sturgeon**

Dewayne Fox\* (Delaware State University), Matthew Breece (University of Delaware), David Kazzyak (USGS), Matthew Balazik (USACE), Hal Brundage (Environmental Research and Consulting Inc.), Keith Dunton (Monmouth University), Adam Fox (University of Georgia), Mike Frisk (Stony Brook University), Christian Hager (Chesapeake Scientific), Danielle Haulsee (Hubbs Seaworld Research Institute), Amanda Higgs (Cornell University), Eric Hilton (Virginia Institute of Marine Sciences), Joe Iafrates (US Navy), Robin Johnson (USGS), Jason Kahn (NMFS), Micah Kieffer (USGS), Michael Loeffler (North Carolina Division of Marine Fisheries), Barbara Lubinski (USGS), Pat McGrath (Virginia Institute of Marine Sciences), Mike O'Brien (University of Maryland), Ian Park (Delaware Division of Fish and Wildlife), Bill Post (South Carolina Department of Natural Resources), Eric Reyier (NASA), Tom Savoy (Department of Energy and

Environmental Protection), Dave Secor (University of Maryland), James Sulikowski (Arizona State University), Carter Watterson (US Navy), Shannon White (USGS), Gayle Zydlewski (University of Maine)

Following decades of intensive conservation efforts, many US Atlantic Sturgeon distinct population segments remain critically imperiled. Still experiencing the negative impacts brought on by historic overharvest and habitat loss, Atlantic Sturgeon are also being exposed to threats including marine construction, vessel strikes, and fisheries bycatch. Due to species' long lifespan and the tendency for adults and sub-adults to engage in coast-wide migrations, these threats are often realized over vast temporal and spatial scales that are difficult to monitor and even more difficult to mitigate. Moreover, interpopulation variation in spawning phenology likely results in substantial variation in the timing and magnitude of migration, which inhibits the transferability of individual studies across the species' range. Although many private, academic, state, and federal institutions have been independently conducting regional studies of Atlantic Sturgeon migration, integration of these efforts is needed to gain a more comprehensive understanding of continental scale habitat use. Working collaboratively with 14 institutions, we have compiled telemetry data (n= 32 million detections) and genotypes for 2650 telemetered Atlantic Sturgeon. We are using this dataset to characterize the migrations and habitat use of Atlantic Sturgeon across broad spatial scales. Genetic assignment tests will provide insight into when and where specific population segments occur, and in turn where they are exposed to threats, thereby improving our ability to mitigate potential damage. Results from this study will be used to identify important critical habitat areas and improve our ability to protect Atlantic Sturgeon during vulnerable life stages.

### **Effectiveness of Reduced Representation Sequencing on Century-Old Ethanol-Preserved Museum Fishes**

Eric Garcia\* (Old Dominion University), Martin French (Texas A&M University-Corpus Christi), Chris Bird (Texas A&M University-Corpus Christi)

Museum specimens have a largely underutilized potential to allow biologists to study rare, ancient, or extinct organisms using genomic methods. However, museum samples often have degraded and fragmented DNA making it more difficult to sequence. Reduced representation sequencing has proven to be affordable and effective for population genomic applications but is sensitive to the degradation inherent with museum samples. Here, sequence quality and error rates were compared between reduced representation libraries constructed from century-old, ethanol-preserved museum and contemporary samples for two fishes (*Atherinomorus duodecimalis* and *Siganus spinus*). Museum specimens had a larger proportion of reads filtered due to low base call quality and adapter sequences, while having a lower proportion of targeted reads. Museum specimens exhibited equal or higher error rates in the synthetic adapter sections of reads, suggesting that contaminants retained in museum DNA extracts altered DNA polymerase specificity or nucleotides directly. Museum specimens exhibited substantially elevated error rates in the first two natural nucleotides (last two positions of the SbfI restriction site, 7 & 8), and a model assuming an error at position 7 results in a random nucleotide in 8 fit the data well. The base call error patterns were consistent with chemical contaminants in museum samples reducing restriction enzyme specificity. Overall, sequencing of degraded museum specimens is possible, but all else being equal, it can result in more errors and lower depth of coverage per locus than for contemporary samples. Consequently, more DNA per museum library needs to be processed to achieve reliable results.

## **†Taxonomic Standing and Genetic Surveillance of *Cambarus jezerinaci* in Kentucky**

Cassidy Gebhardt\* (West Liberty University), Nicole Garrison and Zachary Loughman (West Liberty University)

*Cambarus jezerinaci*, is a small, cold stream-dwelling crayfish found in Southeastern Kentucky which may or may not be a member of a species complex. Previous research completed in 2008 compared the Cytochrome Oxidase I (COI) gene between *C. jezerinaci* and a closely related species, *Cambarus parvoculus*. This work identified a third genetically distinct lineage most similar to *C. jezerinaci* that occurred in both the Cumberland and Kentucky River watersheds in Kentucky. In 2022, surveys were completed throughout the proposed range of *C. jezerinaci* in Kentucky, with a special emphasis focused on surveying the Kentucky River watershed. Initial morphology identifications indicated that specimens collected are of the unique lineage, not of nominate *C. jezerinaci*. Determination of the taxonomic standing of *C. (cf.) jezerinaci* in the Kentucky River is important for the conservation of these animals and helps broaden our understanding of what it means to be a species. Continuing to perform research to genetically identify cryptic species allows for a better understanding of biodiversity on our planet and the process of speciation itself. Given the rapidly changing climate, it is imperative to catalog the true diversity of our freshwater streams and develop conservation action plans for endemic species such as *C. jezerinaci*.

## **Hatchery capacity needed to support Atlantic surfclam fishery enhancement**

Caela Gilsinan\* (William and Mary - Virginia Institute of Marine Science), Dr's. Andrew Scheld and Sarah Borsetti (William and Mary - Virginia Institute of Marine Science), Dr. Daphne Munroe (Rutgers the State University of New Jersey, Haskin Shellfish Research Laboratory)

High demand for renewable energy has stimulated offshore wind farms' development along the east coast of the United States, with over two million acres currently leased for development. It is expected that access to important Atlantic surfclam fishing grounds will be limited or lost due to the overlap with wind lease areas. This study explores the economic viability of large-scale hatchery production to offset additional costs, reduced revenues, and potential job losses associated with the displacement of the fishing fleet. Reports and primary literature were used to understand growth and survival of Atlantic surfclams in hatchery and nursery settings. This information was used to calculate the scale of hatchery efforts needed to support one million bushels of fishery-sized clams (>120mm). Data on labor, energy, construction, and material inputs and costs for hatchery and nursery production were gathered by analyzing literature and meeting with hatchery managers, researchers, and others knowledgeable about shellfish hatchery production. A techno-economic cost model and Monte Carlo analyses were employed to explore average costs and their variability. This study suggests that 374 million to 2.1 billion Atlantic surfclams are needed at the end of the hatchery stage to produce one million bushels of market-sized product. Total production costs range from \$3.7M to \$15.1M, including \$2.9M - \$13.3M in hatchery costs and \$800K-\$1.9M in nursery costs. Under current market conditions, where Atlantic surfclams regularly sell for \$14-\$17/bushel, this analysis suggests that hatchery production could be a viable fishery enhancement method for offsetting losses associated with offshore wind development.

## **Spatial distribution and habitat associations of mussel and fish communities in the upper Guadalupe River basin (TX) during extreme drought**

Zachary Hutchens\* (Department of Biology, Texas State University), Timothy Bonner (Department of Biology, Texas State University)

Surface waters in upper reaches of Edwards Plateau (TX) streams are supported primarily by springs from karst aquifers. Availability of groundwater is sufficient to keep surface water flowing, in at least part of the upper reaches, during periods of drought, thereby providing refuge for numerous Edwards Plateau endemic fauna. Purposes of this study were to identify surface water availability and the existing mussel and fish communities within the upper Guadalupe River basin (TX) during a period of extreme drought in 2022. Study objectives were to quantify mussel and fish communities and their habitat associations in a river network from multiple headwater streams to their convergence in a single channel downstream. Most headwater streams maintained flowing waters during the extreme drought, whereas lower reaches of the mainstem only contained pool habitats or completely dry. Correspondingly, species richness and abundances of endemic spring-associated fishes were greatest within the headwater streams with flowing waters and become reduced or absent in pooled water in the mainstem. Other species not necessarily associated with springs systems, such as several mussel species, also were more abundant in headwater streams with flowing waters. Our findings offer insights into why mussel and fish communities are not homogeneously distributed within the upper reach of the Guadalupe River basin during wet periods (e.g., source and sink dynamics) but also identify areas as drought refugia, which might be targeted for conservation action during wet and dry periods.

## **Artificial illumination of trawl gear components to reduce Pacific halibut bycatch in the US West Coast bottom trawl fishery**

Derek Jackson\* (Virginia Institute of Marine Science)

In the last decade there has been a concentrated interest in the use of artificial light serving as a bycatch reduction device for a number of different fisheries around the world. In the US west coast groundfish fishery, previous studies found success reducing Pacific halibut, *Hippoglossus stenolepis*, bycatch caught in low-rise, cutback trawls. However, since those studies were conducted, regulations have changed to allow for less species and size selective high-rise trawls in areas that were once highly restricted. The goal of this study was to investigate the efficacy of green LEDs at reducing Pacific halibut bycatch for this trawl configuration. Catch comparison analysis found that illuminated trawls caught significantly less halibut than the non-illuminated trawls albeit with reductions in the target catch as well. The results from this study further explore the potential of a low-cost device, serving as a potential BRD for the fishery.

## **<sup>1</sup>Feeding Habits of *Carcharhinus plumbeus*, Off of the Southeast U.S Coast From 2006-2022**

Emma Jackson\* (NOAA Hollings Scholar; University of South Carolina), John Carlson (National Marine Fisheries Service)

Sandbar sharks, *Carcharhinus plumbeus*, are apex predators that may structure marine communities through predation. This study describes the diet, highlighting changes in feeding habits,



determining ontogenetic shifts, and comparing this contemporary study with historical studies. From North Carolina to the Gulf of Mexico (GOM), 705 shark stomachs were obtained through the NOAA Fisheries Observer Program between 2006 and 2022. Of the 705, 258 were used for diet analysis, excluding empty and those with only bait as contents. In the two regions, there were 173 females and 85 males caught with similar numbers of juvenile and mature adults but females being more prevalent in both. Diet was assessed by life-stage and quantified using five indices: percent by number, percent by weight, frequency of occurrence, the index of relative importance (IRI), and IRI expressed as a percent (%IRI) for prey categories and lower taxonomic classifications. The largest consumed prey item between age class, sex, and region were teleost followed by cephalopods according to their indices of relative importance (IRI). The survey of prey items ranks cephalopods of higher importance than previous studies. Ontogenetic shifts were not likely due to large juveniles and a lack of neonates within the region.

#### **<sup>†</sup>Comparison of Redfin Darter (*Etheostoma whipplei*) Diets from Two Spatially-Distinct Streams in the Arkansas River Valley.**

Ben Johnson\* (Arkansas Tech University, Department of Biological Sciences), Ethan Dodson (Arkansas Tech University, Department of Biological Sciences), Kyler Hecke (Arkansas Tech University, Department of Biological Sciences)

Diet-data collection is increasingly difficult for darters, as most methods require the dissection of each specimen and the removal of the digestive tract, which is fatal. In result, the diets of many darter species have been relatively understudied. The Redfin Darters (*Etheostoma whipplei*) is one species where there is very little information on its diet. We wanted to use a non-lethal diet extraction method to see how the diet of this species varied between two spatially-distinct streams, Bakers Creek and Shoal Creek, tributaries of Lake Dardanelle (Arkansas River) in Arkansas. We employed two sampling gears (kick-nets and seines) to collect this species. Small-scale gastric lavage was used to extract diet data from all individuals at two different streams. All prey items were preserved and identified to the genus level (if possible). Bray-Curtis dissimilarity was used to assess the composition of prey item in fish from the two streams. A total of 176 different prey items from 17 fish (37-69 mm), covering 10 orders were extracted from Redfin Darters sampled in Bakers Creek. Diptera was the most abundant (59.1%) order for diets from Bakers Creek. Dipterans from the family Chironomidae and sub-family Tanypodinae comprised (47.2%) majority of diet items from Bakers Creek. In Shoal Creek, a total of 187 different prey items from 18 fish (32-67 mm), covering 10 orders were extracted from Redfin Darters sampled. Diptera was the most abundant (63.6%) order for diets from Shoal Creek. Dipterans from the family Chironomidae and sub-family Tanypodinae comprised (47.6%) majority of diet items from Bakers Creek. The composition of prey items from the two streams were relatively similar (Bray-Curtis distance = 0.125). Diets from both streams were comprised mostly of chironomids, suggesting that this prey item is an important part of Redfin Darter diets. This research is will aid in the understanding of darter diets. Future research will assess the seasonality of diets in Redfin Darters.

#### **<sup>†</sup>Longitudinal Assessment of Fish Communities of Moro Creek, Arkansas.**

Andrew Julian\* (Arkansas Tech University), Dr. Kyler Hecke (ATU)

Longitudinal differences in fish communities are due various factors that shape the functional diversity for an aquatic system. However, these longitudinal relationships are seldom assessed in freshwater

streams. Moro Creek, a tributary of the Ouachita River in Arkansas, is one system that has been understudied in the last ~50 years. New research is needed on this system to fully understand the variation in species occurrences throughout this watershed. We assessed the spatial relationships of fish communities on longitudinal scale in Moro Creek. Eleven sites were sampled on a longitudinal scale (4 upper reach, 4 middle reach, 3 lower reach) in the watershed. A depletion sampling approach was employed to increase detection of species. Species abundance was estimated at each of the sites. We used non-metric multidimensional scaling models (NMDS) to assess how species compositions varied across a longitudinal gradient. The three most abundant species at upper reach sites were Western Mosquitofish (250), Banded Pygmy Sunfish (87), and Flier (51). At middle reach sites, the three most abundant species were Western Mosquitofish (92), Blackspotted Topminnow (55), and Ribbon Shiner (42). At lower reach sites, the three most abundant species were Ribbon Shiner (114), Western Mosquitofish (61), and Bluegill (34). NMDS suggests that fish communities exhibit similarities relative to their position within a watershed and could be related to associated environmental and habitat parameters. This research is important for the management of fish communities in south-central plain streams. Future research should consider longitudinal relationship of fish communities on a temporal scale.

### **U.S. inland creel programs: a review and management recommendations**

Anna L. Kaz\* (Louisiana State University), Stephen R. Midway (Louisiana State University)

In United States inland waters recreational anglers, rather than commercial fishers, account for the primary fishing pressure. As such, the recreational sector can be a substantial driver of fish mortality, making well-informed management imperative for the sustained viability of fish populations and the fisheries they support. Creel surveys are often the only system in place for monitoring fish mortality in inland waters, because population and stock assessments are not routinely done. Thus, creel surveys are vital for informing fishery management decisions with necessary ecological and human dimension data. Here, we use the novel CreelCat dataset, comprised of state creel surveys from over 45 participating states and territories, to characterize U.S. recreational angling at the national level. Specifically, we 1) provide a summary and scope of U.S. inland creel programs in CreelCat, 2) compare current and recommended creel programs and protocols, and 3) highlight successful creel programs and offer management suggestions along a tiered approach of input resources and output data quality. In reviewing creel data from 45 states, access and roving type surveys were the most used creel designs, and lentic habitats were the most common waterbodies creeled. Most surveys recorded catch and effort metrics, with fewer surveys recording demographic and biological information. We found regional differences in spatiotemporal data coverage, with the Midwest being particularly data-rich across time and space.

### **Assessing the ecological impacts of remnant hydrological modifications on the integrity of barrier island freshwater habitats**

Raymond P. Kidder II\* (Georgia Southern University), Dr. J. Checo Colon-Gaud (Georgia Southern Biology Department), Dr. Rachel Guy (Sapelo Island National Estuarine Research Reserve)

Estuaries and their barrier islands are crucial nursery habitats for a variety of coastal fisheries including gamefish, oysters, and shrimp. These habitats are currently at risk due to the compounding effects of climate change, sea level rise, and hydrological modification. Sapelo Island, Georgia, like most

southeastern barrier islands, has a lengthy history of human habitation. Plantation-based agriculture and associated industry led to the construction of a network of ditches and canals on Sapelo in the early 1800's. Though most of the island has been left to return to its natural state, questions remain regarding the impacts of these historical hydrological modifications on the ecological integrity of the island's interior freshwater aquatic habitats. To better understand the effects of these modifications on the hydrology of Sapelo Island, we have deployed a network of four water parameter monitoring stations along Oakdale Creek, the island's longest artificial channel. This network will allow us to quantify the magnitude and frequency of intrusion events that reach the island's interior. We are assessing the impacts of these intrusion events on biotic integrity by quantifying detrital decomposition, a fundamental ecological function, using a standard leaf pack methodology. Preliminary findings showed the presence of a strong salinity gradient in the study reach with salinities ranging from 0.25 to 30 ppt. Additionally, salinity was positively related to both macroinvertebrate biomass and detrital processing rates. Updated findings will be presented including hydrological data and updated values for detrital processing rates and macroinvertebrate community descriptions.

### **The Distribution of Per- and Polyfluoroalkyl Substances in Northern Snakehead of the Potomac River: Implications for Potential Consumption Limits**

Tabitha King\* (George Mason University), T. Reid Nelson (George Mason University), Tom Huff (George Mason University)

With the US Environmental Protection Agency's recent reduction of PFAS lifetime health advisory limits to humans, it is increasingly important to understand potential PFAS exposure pathways. As of 2022, only one Potomac River tributary has been evaluated for PFAS consumption advisories in surface water and game fishes. Swimming and species-specific consumption advisories were created for the tributary. A popular game fish excluded from the study was Northern Snakehead (*Channa argus*). The present study's objective is to gather preliminary data on five Virginia Potomac River tributaries' PFAS concentrations in surface water and Northern Snakehead. Out of the 26 PFAS assessed, 18 were detected in surface water using triple quadrupole liquid chromatograph mass spectrometry. Surface water from Powells, Neabsco, Dogue, Little Hunting, and Pohick Creeks each had total PFAS concentrations of at least 54.3 parts per trillion. The concentrations of PFOA and PFOS in surface water from all five tributaries exceeded the USEPA's lifetime health advisory limits. The bioaccumulation potential and tissue distribution of PFAS in Northern Snakehead will be determined next. The bioaccumulative nature of PFAS, combined with the substantial biomass consumed by Northern Snakehead, has led to the expectation that fish consumption advisories will be needed.

### **Benthic tray sampling and electrofishing capture different changes in nekton assemblages as restored reef complexity changes**

Sean Kinney\* (Louisiana Department of Wildlife and Fisheries), Melanie Bates (School of Renewable Natural Resources, Louisiana State University Agricultural Center), Steve Midway (Department of Oceanography and Coastal Sciences, Louisiana State University), Megan La Peyre (U.S. Geological Survey, Louisiana Fish and Wildlife Cooperative Research Unit, School of Renewable Natural Resources, Louisiana State University Agricultural Center)

Different sampling gears have different selectivity that may result in varying metrics of species abundances, assemblages and diversity. Benthic habitat tray sampling and electrofishing are both

commonly used to sample nekton communities in shallow water environments but have not typically been compared due to historic limitations of electrofishing in saline conditions. Oyster reefs provide hard to sample, complex habitat supporting both reef resident and reef-associated nekton, providing an opportunity to investigate selectivity of two different gear types. Using a Calcasieu Lake, Louisiana reef restoration project built over a five-year period, density of recruiting organisms was quantified as a proxy for habitat complexity, while nekton were sampled using benthic habitat trays and electrofishing. The varying ages of the reef sections provide the opportunity for a space-for-time study to examine how nekton use correlates to reef development. We hypothesized that as reefs age, they become more structurally complex, and support increasing diversity and abundance of nekton. Annual winter sampling of encrusting organisms from 2017 to 2022 indicate that older reefs support greater density of encrusting organisms, resulting in a more complex habitat structure. Spring and summer 2022 nekton sampling by tray and electrofishing resulted in similar species richness, but species assemblages differed by reef age and sample gear. Understanding how reef complexity influences nekton assemblages and how sampling gear might affect species assemblage and diversity data informs managers interested in designing better restoration projects. In addition, this project will provide information on how gear choice may impact restoration monitoring outcome data.

### **Application of the Microrefugia Concept to explain disjunct and peripheral mussel and fish populations near endemic-rich Edwards Plateau (central Texas)**

Elibardo Leal\*, Joshua D. Tivin, Timothy H. Bonner (Texas State University)

Aquatic organisms generally inhabit geographic ranges that encompass favorable environmental conditions (e.g., water quality, habitat preferences) that support their life history. However, shifts in range and habitats can occur over glacial-interglacial timescales, thereby isolating a population in environments very different than most of the population. Often referred to as disjunct or peripheral populations, conservation value of disjunct or peripheral populations is debated and persisting disjunct or peripheral populations can confuse habitats needs, especially for imperiled species. In this study, we quantified contemporary mussel and fish communities of a prairie stream system (Elm Creek drainage in north-central Texas with turbid and saline surface waters) with a population of a mussel species found elsewhere only in the adjacent Edwards Plateau with clear and fresh surface waters, described the likely historical climate and hydrogeology of the prairie stream system, and argue that the mussel species persistence in the prairie stream system is consistent with the Microrefugia Concept rather than a more recent dispersion event. The intent of this case study is not to conclusively identify origin of the one mussel in a prairie stream system but to establish that the Microrefugia Concept is a viable explanation for understanding disjunct and peripheral populations of several rare and imperiled species within the Edwards Plateau, an area with high amounts of endemic aquatic organisms.

### **Removal of Northern Snakehead from Conowingo Dam Fish Lifts in Upper Chesapeake Bay**

Joseph Love\* (Maryland Department of Natural Resources)

Aquatic invasive species present diverse challenges as fishery managers seek to prevent expansion of established populations and mitigate negative impacts. Unfortunately, invasive Northern Snakehead (*Channa argus*) increased its range between 2010 and 2020 and established populations from the lower to the upper Chesapeake Bay watershed. Expansion slowed at the head of Chesapeake Bay because of Conowingo Dam in Susquehanna River, which drains New York, Pennsylvania, and

Maryland. Fish lifts of the dam operate between April and June to facilitate upstream passage of anadromous fishes; in 2017, they also began passing Northern Snakehead. To reduce upstream spread of snakeheads and enable passage of anadromous fishes, a partnership was established among Exelon Corporation, J.J. McDonnell and Company, U.S. Fish and Wildlife Service, and Maryland Department of Natural Resources to remove snakeheads from the fish lifts. Since 2020, 1,827 Northern Snakeheads (466 mm - 771 mm Total Length) were removed and were either dissected (N = 158) or processed by J.J. McDonnell for food pantries. The majority of dissected snakeheads were females (59%) with between 26,397 ova and 213,180 ova, depending on female size. Work is on-going to measure ova diameters and determine if multiple sizes of ova exist within a single ovary. Few of these individuals had discernable gut contents, though six had eaten American Eel (*Anguilla rostrata*). Removing female snakeheads during their upstream spawning migration focuses control efforts during a period of heightened vulnerability and helps reduce spawning stock in the fight to prevent expansion and negative impacts.

### **"Home is where you make it" Exploring genetic variation in populations of the red claw crayfish (*Cherax quadricarinatus*) introduced to the island of Puerto Rico**

Nicholas A. Macias\* (Georgia Southern University), Dr. Checo Colon-Gaud (Georgia Southern University), Dr. J. Scott Harrison (Georgia Southern University)

Crayfish introductions have been widely recognized as a threat to native diversity and ecosystem function. Introduction events involve a few founding individuals which could limit genetic diversity and establishment potential. We present here a case study which documents genetic variation of *Cherax quadricarinatus* (Red Claw) introduced to the island of Puerto Rico. Red Claw were sampled from six reservoirs (Loiza, Cidra, Carite, Guajataca, El Guineo, Dos Bocas) throughout the island, as well as an aquaculture facility (Caribe Fisheries) located in the Southwest. Seven microsatellite loci were used to assess genetic variation between populations. Allelic diversity was observed to be highest in Caribe and lowest in Cidra. AMOVA supported significant variation within total individuals (50%;  $p < 0.001$ ). Pairwise  $F_{st}$  was lowest between Cidra and Guajataca ( $F_{st} = 0.007$ ), and the number of migrants per generation ( $N_m$ ) was highest between these two populations ( $N_m = 36.167$ ). The approaches presented here can be utilized to assess introduction success of Red Claw populations recently documented in southeastern states of the US.

### **Seasonal movements of a native species, Bowfin (*Amia calva*), and an invasive species, the Northern Snakehead (*Channa argus*) in the Piankatank River, Virginia.**

Patrick McGrath\* (Virginia Institute of Marine Science), Eric Hilton

Bowfin, *Amia calva*, are a native, carnivorous fish inhabiting freshwater systems throughout eastern North America. Although Bowfin are one of the top predators in these systems, little research has been conducted on its seasonal movements. Northern Snakehead, *Channa argus*, are native to eastern Asia but have been introduced throughout the world, and was first documented in the Piankatank River, Virginia, in 2013. The Northern Snakehead is also a top predator, overlapping the ecological niche of Bowfin. In this study, 14 Bowfin and 8 Northern Snakeheads were acoustically tagged to compare their spatial overlap and seasonal movements. In the winter, both species inhabited the same deep (3-4 m) portion of the river. In March, almost every bowfin moved upstream 9.5-25.8 km, presumably to spawn. The movement upstream correlated with a rain event that significantly increased water levels allowing access above beaver dams and other obstructions. Northern Snakeheads during

this time did not have a directed upstream movement, instead moved rapidly upstream and downstream 0-6.5 km. During April and May, 7 tagged bowfin returned to the original tagging area. The other half remained upstream during the summer, likely confined in sections of the river due to low water levels restricting movements. This past fall an additional 4 Northern Snakeheads and 1 Bowfin were tagged, as well as 5 more receivers put in service to increase coverage of upstream habitat. The results of this study will contribute to the understanding of how native and invasive species that occupy similar niches interact spatially.

#### **<sup>†</sup>Rare and Endangered Species Habitat Modeling in the Upper Little Tennessee River Basin**

James Miles\* (Western Carolina University), Keith Gibbs (WCU), and Tom Martin (WCU)

The Southeastern United States is known for rich levels of aquatic diversity, especially within its fish and mussel species. Decreases in diversity have been associated with the degradation and fragmentation of aquatic habitats essential to these diverse communities of aquatic organisms. Quantification and characterization of habitat use of imperiled fish and mussels are vital to fully understanding these species, with the hopes of preserving and possibly reintroducing them into their historic range where suitable habitat possibly still exists. Throughout this study, we identified, assessed, and compiled habitat availability in sites across the Little Tennessee River Basin upstream of Fontana Reservoir. We used geospatial and multivariate statistical analyses to develop habitat models for species of greatest conservation need to identify potential reintroduction sites. These models have been developed for several fish species such as Stonecat (*Noturus flavus*), Spotfin Chub (*Erimonax monachus*), and the undescribed Sicklefin Redhorse (*Moxostoma* sp.). Mussels of interest include the Tennessee Clubshell (*Pleurobema oviforme*), Appalachian Elktoe (*Alasmidonta raveneliana*), and Slippershell (*Alasmidonta viridis*). Analysis of Similarity resulted in significant differences between mainstem sites above and below impoundments and tributary sites. The SIMPER function identified sand, silt, and woody debris percentages as being influential to differences among sites. These characteristics could prove to be limiting habitat factors for translocating some species. This information can be used by management organizations to further support the conservation needs of these species.

#### **<sup>†</sup>Conservation and taxonomic assessment of an undescribed crayfish species complex in coastal Virginia.**

Alyssa Oppedisano\* (West Liberty University), Dr. Zachary Loughman (West Liberty University, Department of Organismal Biology, Ecology, & Zoo Sciences), Dr. Sujan Henkanaththegedara (Longwood University, Department of Biological & Environmental Sciences), Dr. Paul Cabe (Washington and Lee University, Department of Biology)

*Creaserinus fodiens* (Cottle 1863), commonly known as the digger crayfish, is a primary burrowing species that inhabits complex burrows in wetlands, seasonal pools, wooded floodplains, and roadside ditches. Historically, *C. fodiens* has been found from Ontario, Canada following the United States down to Texas and across four Atlantic slope states including Virginia, Maryland, North Carolina, and South Carolina. The Atlantic slope clades are geographically isolated from other *C. fodiens* populations by the continental shelf on the East coast, the Blue Ridge Mountains, and the Appalachian mountain range. Despite having a large geographical range, little research has been done on the Atlantic slope clades of *Creaserinus* spp. Recent genetic sequencing from the mitochondrial COI, 12s, and nuclear 28s genes have suggested that the Virginia population of *C. fodiens* could be described as multiple

different species, suggesting a species complex. Additional morphological and genetic data from gill samples will lead to a better understanding of where the separation in classification lies among the Virginia population. A conservation and taxonomic assessment will contribute to our understanding of global crayfish biodiversity and provide important biological insight to the management and conservation of these species.

### **A New Open Textbook for Nonmajors: Fish, Fishing, and Conservation**

Donald J. Orth\* (Department of Fish and Wildlife Conservation, Virginia Polytechnic Institute and State University), Anita R. Walz and Kindred Grey (Virginia Polytechnic Institute and State University, University Libraries)

Few opportunities exist for college students who are not fisheries majors to learn about fish, and issues surrounding fishing and conservation. *Fish, Fishing, and Conservation* (forthcoming 2023) was written for a broad audience of undergraduate students. All fifteen chapters were developed after consultation and review by experts and students to ensure that material is current and presented in ways that are compatible with student learning preferences. This book will be released in multiple formats with a Creative Commons (CC BY) copyright license that permits no-cost access, re-use, repurposing, adaptation, and redistribution by others. Consequently, this information is readily accessible to teach undergraduate students and flexible for use by other instructors.

The book places substantial attention on overfishing and loss of biodiversity as pressing problems facing society. The book examines solutions implemented in for a variety of cases. People, places, and approaches to fishing are as varied as the diverse fish fauna that exists on the planet. Therefore, responsible fisheries practices should recognize the rights of all people to decide how to manage and conserve fish, their habitats, and how they are utilized. Incorporating findings from studies of fish conservation and management along with approaches to ethical reasoning aids students who will play key roles in resolving future issues of fish conservation and welfare. The book examines the roles of gender, conservation organizations, recreational fishing, and fisheries governance and highlights modern principles of conservation and management as they play out in fish controversies around the globe.

The project was funded in part by VIVA (Virginia's academic library consortium). It is developed in collaboration with the University Libraries at Virginia Tech's Open Education Initiative, and Virginia Tech Publishing.

### **Molecular identification of freshwater mussel glochidia from naturally parasitized fish in a small stream community**

Olivia Poelmann\* (Clemson University), Katherine Silliman (South Carolina Department of Natural Resources, Marine Resources Research Institute), Daniel Farrae (South Carolina Department of Natural Resources, Marine Resources Research Institute), Brandon Peoples (Clemson University), Catherine Michelle Bodinof Jachowski (Clemson University), Morgan Kern (South Carolina Department of Natural Resources, Freshwater Fisheries), Tanya Darden (South Carolina Department of Natural Resources, Marine Resources Research Institute)

North America hosts the largest number of freshwater mussel species globally, with the majority currently listed as endangered, threatened, or under special concern. Many mussel species utilize fish

hosts to complete juvenile metamorphosis, making them especially vulnerable to environmental perturbations like fish invasions or host declines. Host identification mostly occurs in a laboratory setting, and few studies have focused on fish host use in the wild. This seeks to investigate wild fish community host usage in a small South Carolina stream. Fish were collected bi-weekly from January through May 2022. The gills and fins from ~900 total fish of 14 species were inspected for glochidia under a microscope, and the pooled glochidia per individual fish were then subjected to DNA metabarcoding. Both the COI and ND1 genes were targeted with primers designed to amplify across Unionidae and Margaritiferidae mussel species. After high-throughput Illumina sequencing, sequence reads were filtered, clustered by similarity, and assigned taxonomy based on a database derived from NCBI GenBank. Using metabarcoding results, we will be investigating species richness, host specificity, and quantifying total host usage. Finally, we will quantify the phenology of host usage using environmental variables. Results from this study will help to understand the relative importance of various fish hosts for mussel populations in small tributaries and streams.

### **<sup>†</sup>Spatiotemporal variability in abundance and biomass of Mississippi River floodplain associated fish species**

Adam H. Quade\* (Coastal Behavioral Ecology Lab, Louisiana Universities Marine Consortium; Fish Morphology and Behavior Lab, Department of Biological Sciences, University of New Orleans), Kelly S. Boyle (Fish Morphology and Behavior Lab, Department of Biological Sciences, University of New Orleans) Guillaume Rieucou (Coastal Behavioral Ecology Lab, Louisiana Universities Marine Consortium)

Anthropogenic modifications such as levee construction and flood control structures have decoupled the floodplain from the Mississippi River and disrupted the biogeochemical cycles and trophic stability of this biologically, economically, and culturally significant habitat. Many of Louisiana's emblematic fish species rely on the timing, magnitude, and duration of the Mississippi River flood pulse to trigger key aspects of their life history. To further the conservation and management of native Louisiana fishes, a multidisciplinary and interagency approach to restoring and monitoring floodplain connectivity to the Mississippi River is underway. The Richard K. Yancey Wildlife Management Area is 70,872 acres of floodplain habitat near the confluence of the Red River and Mississippi River. 700 acres are proposed for weir and culvert repair to retain proper water depth and improve water quality for native Louisiana fish species, with particular focus upon gars (*Lepisosteidae*). Our project will capitalize on the integration of high-resolution imaging sonar technology (Adaptive Resolution Imaging Sonar, ARIS 3000) which provides a non-intrusive means of recording high-quality data of nekton abundance, size, and behavior irrespective of light level or turbidity. Since summer 2021, we conducted acoustic monitoring of floodplain fish species across seasons at four sites across a latitudinal gradient of decreasing hydrologic connectivity. Our acoustic monitoring reveals the dynamic nature of the fish community and highlights an unsuspected degree of both temporal and spatial variability in abundance, biomass, and size class distribution driven by the degree of floodplain inundation. Shifts in abundance of small-bodied fish (e.g., gizzard shad, *Dorosoma cepedianum*) through time were observed, supporting the function of an inundated floodplain as an important foraging opportunity for large piscivorous fish species. Observed fluctuations in native alligator gar (*Atractosteus spatula*), longnose gar (*Lepisosteus osseus*), shortnose gar (*L. platostomus*), and spotted gar (*L. oculatus*) abundance, biomass, and size-class distribution supports the link between inundation level and available nursery habitat. We also observed invasive carp species (*Cyprinidae*) within the system. Our ongoing acoustic monitoring effort will



continue to provide useful information on the complex interactions between floodplain associated fishes and how they utilize their habitat in relation to the inundation level and restoration effort.

### **Systematic distributional survey of endemic and invasive crayfishes in the upper Saint Francis River drainage, Missouri**

Anna Raney\* (School of Natural Resources, University of Missouri), Jacob Westhoff (U.S. Geological Survey, Missouri Cooperative Fish and Wildlife Research Unit, School of Natural Resources)

Crayfish invasions are among the top global threats to native crayfish populations. The Saint Francis River crayfish (*Faxonius quadruncus*) and Big Creek crayfish (*F. peruncus*), endemic to the upper Saint Francis River drainage in Missouri, are currently under threat of extinction due to invasion of the woodland crayfish (*F. hylas*) from nearby drainages. Sampling of selected streams in 2008 documented reduced abundances and range reductions for both native species in reaches invaded by *F. hylas*. *F. quadruncus* and *F. peruncus* are in the final stages of federal listing for protection by the USFWS. However, the entire native range of the endemic crayfishes has not been systematically sampled, and the most recent data documenting *F. hylas* invasions are over 13 years old. Management agencies need updated distributional data to create an informed recovery plan for these two threatened species. We used stratified random sampling to select 96 sites across the USFR basin for a distributional survey and sampled crayfish at 71 sites in 2022. Our analyses will incorporate presence-absence data from sites sampled in 2022 with coarse-scale GIS data into random forest, boosted regression, and spatial stream network models to create probability of presence maps for the invasive and two endemic crayfish species. In summer 2023, we will sample the 25 remaining sites to complete the distributional survey and conduct intensive targeted sampling to determine the leading edges of *F. hylas* invasions. Results from this study could be used to identify refugia for native species and locate barriers to further invasion.

### **Whole genome sequencing of century-old Philippine reef fishes**

Roy Roberts\* (Texas A&M University - Coprus Christi), Sharon Magnuson (Texas A&M University - Coprus Christi), Christopher E. Bird (Texas A&M University - Coprus Christi)

The genomes of organisms stored in museums hold a wealth of information that is challenging to access. Recent success has been reported in sequencing desiccated museum insects involved using whole genome amplification (WGA) and enzymatic repair (NEBNext FFPE Repair Mix) of DNA damage, but these techniques have not been tested on historical EtOH preserved fishes. Here, we use factorial treatment combinations to test for the effects of WGA, repair, and amount of starting DNA on whole genome sequencing of historical (1907 - 1909) and contemporary (2017) Philippine marine fishes. A total of 192 extractions were performed, 165 (76 +WGA, 89 -WGA) of which were put through each treatment combination before library prep. Contrary to expectation, WGA had a negative effect on success of libraries and repair had no consistent effect at all. A greater percentage of historical libraries treated with WGA failed than those that weren't (48% +WGA, 32% -WGA). Within the +WGA treatment group there was a much lower yield of DNA in the historical specimens compared to the contemporary. For the contemporary samples, there was a positive relationship between DNA yield and starting amount of DNA, however this was not the case in historical samples. In total we successfully sequenced 136 libraries (61 +WGA, 75 -WGA; Illumina). The success of these methods means that these museum specimens can be used to test for the effects of human activities on the evolution of fishes.

## **Conservation Assessment and Genetic Haplotype Mapping of the Greenbrier Cave Crayfish (*Cambarus nerterius*)**

Addie Shanor\* (West Liberty University), Dr. Zachary Loughman (West Liberty University), Dr. Nicole Garrison (West Liberty University)

*Cambarus (Punticambarus nerterius)*, the Greenbrier cave crayfish, is West Virginia's only troglobitic crayfish. It is endemic to the Greenbrier Karst System within the Greenbrier River drainage. At its description in 1964, Horton Hobbs recorded that it inhabited only 11 caves, all but one being in Greenbrier County, West Virginia. There have been unconfirmed reports of cave-dwelling crayfish within other caves in the karst system by both cavers and biologists, although these have not all been confirmed to be *C. nerterius* as it is difficult to diagnose. Because of the stygiobitic nature of *C. nerterius*, little is known about its ecology, and it faces a unique set of threats. Surface runoff transporting contaminants and hazardous materials, agricultural waste due to livestock's use of caves as heat refuge, commercial surface activities, and invasive species are some of the most pressing threats. The last formal survey of *C. nerterius* occurred in the summers of 1988 and 1989. Since that time, zero dedicated effort has occurred for this West Virginia endemic. In this project, we will conduct a comprehensive year long life history study, confirm the presence of *C. nerterius* in caves known to or speculated to contain *C. nerterius* in the Greenbrier Karst System, and complete a genetic study to determine the interconnectedness of populations of *C. nerterius*.

## **Identification of host fish species parasitized by freshwater mussels of Florida**

Kallie Thornhill\* (Florida Fish & Wildlife Conservation Commission- FWRI), Susan Geda (FWC), and Lauren Patterson (FWC)

Nearly all freshwater mussels within the family Unionidae have a unique life cycle requiring a host fish to complete development from a larval mussel (glochidia) to a juvenile mussel. A vital component to understanding and managing mussel populations is knowledge of their host fish requirements and reproductive timing. In Florida, there are currently 61 described species, of which nine are federally endangered, seven are federally threatened, and 13 are designated by the state fisheries agency as species of greatest conservation need. Of the 61 species, host fish requirements are unknown for 26 species. We received Federal Section 6 funds to evaluate potential host fish for 10 species of freshwater mussel: one federally endangered species (*Obovaria choctawensis*, Choctaw Bean), one federally threatened species (*Elliptio chipolaensis*, Chipola Slabshell), and eight species petitioned for federal listing (*E. ahenea*, Southern Lance; *E. arctata*, Delicate Spike; *E. fraterna*, Brother Spike; *E. monroensis*, St. Johns Elephantear; *E. purpurella*, Inflated Spike; *Strophitus radiatus*, Rayed Creekshell; *S. williamsi*, Flatwoods Creekshell; *Utterbackiana heardi*, Apalachicola Floater). To achieve our goals, we spent the last three years renovating and expanding an aquaculture setup, collecting suitable host fish and mussel broodstock, inoculating the fish with viable glochidia, and subsequently monitoring to confirm any host fish species for our target mussels. This research has increased the life history knowledge of imperiled mussel species and will help make decisions on petitioned species listings and recovery plans.

**†Do electrofishing catch rates of Alabama Bass and Largemouth Bass differ between day and night?**

Isabel Tiller\* (Clemson University), Adam Smallridge (Clemson University), Madison Byars (Clemson University), Brittany Darrington (Clemson University), Andrew Peel (Clemson University), Preston Chrisman (SCDNR), William Wood (SCDNR), Deon Kerr (Clemson University), Troy Farmer (Clemson University)

Illegal introductions of Alabama Bass into reservoirs along Atlantic Slope drainages has increased in recent years. Monitoring approaches are needed to detect Alabama Bass in recently invaded reservoirs and continued monitoring in reservoirs with established populations. However, recent observations by SCDNR biologists suggest that daytime boat electrofishing failed to detect Alabama Bass for several years after initial detection in Lake Wylie by anglers. In other reservoir systems, Alabama Bass comprise the majority of black bass in creel surveys despite continued low catches in daytime boat electrofishing surveys. Our study aimed to determine if boat electrofishing catches of Alabama Bass and native Largemouth Bass differed between day and night periods on Lake Hartwell, South Carolina. We randomly selected 8 coves along the Seneca River arm of Lake Hartwell, stratified by habitat type (coves with and without installed habitats), and randomly assigned each cove to be sampled during day or night. In each cove, we conducted four 15-minute boat electrofishing transects during fall 2021 and spring 2022. We used a mixed effect generalized linear model to test for species, time of day (day or night), and season (spring or fall) effects on catches. Catches of both species were greater at night, but the effect of time of day differed seasonally, with the greatest differences between day and night occurring during fall. Size structure of Alabama Bass also increased during night. This work highlights important elements of study design to consider in monitoring Alabama Bass populations.

### **Using DNA Metabarcoding to Characterize the Rufa Red Knot's (*Calidris canutus rufa*) diet at Grand Isle and the Chandeleur Islands**

Wyatt Voelker\* (Nicholls State University), Dr. Justine Whitaker (Nicholls State University)

In January 2021 at the Chandeleur Islands in Louisiana, we observed a Rufa Red Knot (*Calidris canutus rufa*), which has been considered a molluscivore, catch and eat a fish. The Rufa Red Knot is a shorebird with one of the longest migrations in the animal kingdom and adequate prey abundance along their migration paths is necessary for success and survival. In the early 2000s, overfishing of prey species led to Rufa Red Knot population decline leading to their listing as federally threatened in the United States and endangered in Canada. The purpose of this study was to characterize the diet of the Rufa Red Knot and compare the diets between locations. Rufa Red Knot fecal samples were collected from Grand Isle and the Chandeleur Islands. DNA was extracted, amplified, and sequenced from the scat to identify invertebrate and fish prey in separate reactions. DNA was amplified with MiFish and 18S primers, and sequenced on the Illumina® platform and assigned to the phyletic group or as close to species as possible using the BLASTn database. Having a better understanding of the Rufa Red Knot's diet gives baseline data for further research and allows management decisions to be focused on conserving benthic and fish communities for Rufa Red Knots at their various stopover and winter sites, thereby allowing a higher probability of Rufa Red Knot migration success and survival.

### **Juvenile Gulf Sturgeon Dynamics in the Pensacola Bay Watershed**

Bradford Warland\* (Florida Fish and Wildlife Conservation Commission), Kirsten Humphries, John Knight

Juvenile Gulf Sturgeon (*Acipenser oxyrinchus desotoi*) movements and estuarine habitat use in the Yellow and Escambia rivers are currently being monitored in an ongoing 4-year project that commenced in 2020. Juvenile Gulf Sturgeon (Ages 1-5) were tagged with Vemco V7 or V9 acoustic transmitters during the spring, summer, and fall and monitored by acoustic receivers (n=~70) in the Pensacola Bay watershed. Coordinated outmigration, estuarine, and immigration movements were observed in both rivers correlated with several different environmental factors. Individuals age-1 to age-3 demonstrated high fidelity to river mouths while the age-4 and age-5 individuals traveled further into the marine system. Understanding habitat use of juvenile Gulf Sturgeon is crucial in aiding future conservation efforts for the recovery of the species.

#### **†Reproductive Periodicity in a Threatened Freshwater Mussel: *Pleurobema riddellii***

Alexander Zalmat\* (Texas State University), Timmothy Bonner PhD (Texas State University)

Reproductive life history data is important for understanding ecological and evolutionary dynamics, and holds implications for conservation and management strategies of imperiled species. These kinds of data are relatively lacking for freshwater mussels (Unionidae) in general, and are especially important for the management of threatened mussel species in Texas, where several threatened species are pending review for listing as endangered species. In this study, we aim to estimate the reproductive life history of two Unionid mussel species; *Pleurobema riddellii* (Louisiana pigtoe), and *Cyclonaias pustulosa* (pimpleback), in an east Texas canal system in order to address this lack of data. *P. riddellii* is an imperiled mussel species occurring in several east Texas drainages. *C. pustulosa* is a common species found throughout east Texas. Throughout the 2022 year, we collected monthly gonadal fluid samples and gill brood samples from 30 mussels of each species using a non-lethal syringe technique. Mussels were then measured for length, and then placed back in the substrate from which they were sampled. The reproductive samples were preserved in 10% formalin and then brought back to the lab for quantification and estimation of the timing of gametogenesis and brood production. Preliminary results suggest that female gametogenesis ramps up in the spring and summer months, and then declines into the fall and winter. Brooding appears to lag slightly behind female gametogenesis. The male data suggests that spermatogenesis occurs nearly year-round. The study is ongoing, and the data being produced will help to inform management and conservation decisions in these systems.