

0732 ASIH: ASIH at 100 Symposium, Salon D, Saturday 9 July 2016

Mark Sabaj

The Academy of Natural Sciences of Drexel University, Philadelphia, PA, USA

Phenomenological Monsters

According to Big Bang theory, the universe originated approximately 13.8 billion years ago during the Planck Epoch, an acutely brief period of time that stretched from zero to 10^{-43} seconds. Coincidentally, some molecular clock estimates date the origin of the Percomorpha towards the end of the Planck Epoch. The ASIH Epoch began 100 years BP. Alternative molecular clock estimates date the origin of percomorphs significantly closer to the founding of the society by three organismal biologists: John Treadwell Nichols, Henry Weed Fowler and Dwight Franklin. The true origin of the Percomorpha lies somewhere between those two subjective estimates. Such truths can be hypothesized, tested and falsified, but only arrogantly treated as unassailable. Our society is bound in large part by a dogged pursuit of elusive truths via multiple lines of research that iteratively build on historical evidence, and the application of our findings to real world issues concerning the classification and conservation of fishes, amphibians and reptiles.

0217 Herp Conservation, Galerie 2, Sunday 10 July 2016

Allison Sacerdote-Velat, Charles Calafiore, Lisa Raimondi

Lincoln Park Zoo, Chicago, Illinois, USA

Nest survival of Smooth Greensnakes, *Opheodrys vernalis*, in Illinois Grasslands

Smooth Greensnakes, *Opheodrys vernalis*, are declining range-wide and are designated as State Endangered or Species in Greatest Conservation Need in many states. As part of an ongoing conservation assessment, wild nests were monitored to determine survival rates in several Illinois counties. Only five nests with 29 eggs were encountered in 2014, with 58% hatching success. 194 eggs from 24 nests were monitored in 2015, and we confirmed fates of 141 eggs. The remaining 53 eggs were in various states of decay at the final check, making it challenging to ascertain whether or not hatching occurred. Of the eggs with known fates, 19% hatched and 81% failed. Had the 53 eggs with uncertain fates been successful, hatching success would reach 41%. Had the 53 eggs failed, hatching success would decrease to 14%. We documented several incidences of nest failure attributable to invertebrates, including predation by ants and ground beetles, and burying by crayfish. Nest failure also resulted from a plant germinating through a clutch, eggs becoming moldy in poorly drained nest sites, or eggs desiccating as the substrate dried in August. For *Opheodrys vernalis*, reproductive output is limited compared to the viviparous snakes of the region with similar body size. From sensitivity analyses, we determined that survival from egg to one year old has the greatest effect on the population growth rate as compared to other life stages. Through *ex situ* incubation,

we are increasing hatching success as part of a headstarting program, expected to improve population growth.

0501 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Allison Sacerdote-Velat, Mary Beth Manjerovic, Rachel Santymire, Lisa Raimondi
Lincoln Park Zoo, Chicago, IL, USA

Understanding the relationship among *Batrachochytrium dendrobatidis*, stress physiology and land use in amphibians in the Chicago, IL region

We examined variation in incidence of *Batrachochytrium dendrobatidis* (*Bd*) and stress physiology in amphibians in 40 sites, spanning 10 watersheds within the Chicago, IL region. Sampling sites were forest preserves classified as urban, suburban, industrial, or rural. We used a novel, non-invasive technique to sample cortisol via dermal swabs while collecting *Bd* samples. Our *Bd* sampling focused on American bullfrogs, green frogs, and northern leopard frogs. However, additional species were opportunistically sampled, including red-spotted newts, spotted, tiger, and blue-spotted salamanders, American toads, western chorus frogs, spring peepers, and wood frogs. Positive *Bd* swabs were collected from 13 of 40 sites (32.5%), with positive sites in all land use categories. Of 466 samples, 7.2% tested positive for *Bd* but few were symptomatic for chytridiomycosis. We validated our non-invasive glucocorticoid sampling technique with wild and zoo-housed amphibians which will allow us to examine variation in cortisol in relation to *Bd* status, species, and land use category in the future.

0874 ASIH STOYE AWARD CONSERVATION, SALON E, Thursday 7 July 2016

Heather Saco, Ginny Adams, Reid Adams
University of Central Arkansas, Conway, Arkansas, USA

Changes in Land Use and Fish Assemblages in Four Ozark Highland Streams over Four Decades

Long-term studies evaluating land use and fish assemblage structure are often lacking but necessary to further understanding of anthropogenic influence on local fish assemblages. Land use is known to influence aquatic ecosystems and the aquatic biota. Sylamore, Piney, Jane's and Big creeks are in the White River drainage in north central Arkansas. During summers 2014 and 2015, we sampled fishes at 39 sites across the four drainages. Sites, dates, and sampling methodology were consistent with previous data collected during the 1970's. We used the NWALT dataset to determine historic (1974) and current (2012) land use for all systems. Fish assemblage persistence and stability were calculated for each site sampled and analyzed in relation to catchment land use. Persistence was highly correlated with percent land use across all systems (forest

rho=0.46, pasture -0.45, urban -0.52). In addition, stability was significantly correlated with percent forest (0.43) and pasture (-0.41) across all systems. Seven species showed significant range expansions across all four systems, and one range reduction was detected in *Micropterus dolomieu* (reduced from 20 to four sites). At sites where *Micropterus dolomieu* was missing in the current collection, we observed colonization of *Micropterus punctulatus* and *M. salmoides*. An apparent downstream shift of headwaters species, *Semotilus atromaculatus* and *Chrosomus erythrogaster*, was detected in two of the systems and suggests a change in upstream hydrology. In-stream habitat reflected changes in land use and may provide proximate factors that explain the correlation between assemblage shifts and land use.

1063 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Cyrus Sadeghian, Chad Hargrave

Sam Houston State University, Huntsville, TX, USA

Comparative Effects of High & Low Quality Allochthonous Input on Stream Food Webs

The study of conservation biology has primarily focused on the rapid decline of biodiversity over the past few centuries. Invasive species seem to be the most impactful on species at the community level. Native to eastern Asia, the Chinese tallow tree (*Triadica sebifera* or *Sapium sebifera*) has negatively affected local organisms since its large-scale introduction in the early 1900s for wax-based products and herbal medicine. Previous studies regarding tallow leaves in freshwater bodies of water have typically focused on ephemeral ponds where leached tannins are essentially recycled and the contents are maintained. We intend to focus on a stream ecosystem where the movement of water allows us to maximize leaching and truly test the quality of tallow leaves as a food source. We will expose flowing mesocosms to Chinese tallow leaves versus the leaves of a native tree: the American Sycamore tree (*Platanus occidentalis*). We would expect microbial respiration, fish growth, and invertebrate density to be hindered by the presence of a poor food quality. However, with the temporal variable associated with leaf decomposition, we would likely observe overall production to be more complex. The response variable data can be combined and scaled to represent total stream production and compared to time. Sycamore leaves will decompose much slower than tallow leaves. Therefore, the response from the tallow treatments will likely be catalyzed and peak much faster than the sycamore treatments.

1033 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

David Saenz, Kirk Winemiller

Texas A&M University, College Station, Texas, USA

Electric fishes of the Amazon: preliminary field work on signaling adaptations

Gymnotiform fishes are a diverse and widely distributed order of Neotropical fish frequently studied for their ability to generate and detect electric fields. These nocturnal fish use electrolocation as a means of navigating and foraging in dark turbid waters. The waveforms and frequencies of their electric organ discharges (EODs) are species specific, allowing them to use electrocommunication for identifying and signaling conspecifics during social interactions. A number of studies suggest that the efficiency of the EODs varies significantly with the habitat's water chemistry. In fact, it has been well characterized that species using different types of EODs (pulse vs. wave) are for the most part found in different habitats. This preliminary study focuses on the evolution of signaling adaptations and how they might be related to the ecology of these fish. Specifically, we investigated the evolution of a mechanism regulated by adrenocorticotrophic hormone (ACTH) through which some species are able to increase the amplitude of their EOD. Preliminary results suggest that not all gymnotiforms are able to increase the amplitude of their EOD and that ACTH might play different roles between families.

0465 General Herpetology, Balconies L & M, Sunday 10 July 2016

Veronica Saenz¹, Jamie Voyles², Bree Rosenblum³, Corinne Zawacki¹

¹University of Pittsburgh, Pittsburgh, PA, USA, ²University of Nevada, Reno, NV, USA, ³UC Berkeley, Berkeley, CA, USA

How Does *Batrachochytrium dendrobatidis* Pathogenicity Change After An Epidemic?

Batrachochytrium dendrobatidis (Bd), a fungus pathogenic to amphibians, is an ideal system in which to study the potential for changes in pathogen virulence over time. Survey work conducted in western Panama since 2012 suggests that while mortality rates are still high and many amphibian species have disappeared, some populations of susceptible hosts are persisting many years after in this area. For example, harlequin frogs (*Atelopus varius*) and common rocket frogs (*Colostethus panamensis*) experienced severe declines due to Bd outbreaks in 2004 - 2006 and were thought to be locally extinct. However, surviving populations of both species have been recently found in the same areas. One possible explanation for this would be a decrease in the pathogenicity of Bd with time since the outbreak. To test for this, we compared pathogenicity between historic (during epidemic) and contemporary (8-10 years post-epidemic) Bd isolates using a combination of *in vitro* phenotypic assays and *in vivo* inoculation experiments. While we did observe variation in the timing of sporangium maturity and zoospore production among fungal isolates, we did not find evidence to clearly support the

hypothesis that Bd has decreased in pathogenicity since the Panamanian epidemic. Additional studies are needed to address the potential for changes in host defenses to explain the apparent recovery of susceptible hosts in western Panama.

0956 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Kathleen Sagarin, Christopher Sheil

John Carroll University, University Heights, OH, USA

Heterochrony of Cranial Bones in Amniota and the Phylogenetic Placement of Turtles

This study presents a meta-analysis of ossification sequence data for the skull of amniotes to address heterochrony of temporal bones. Parsimonov-based Genetic Inference was used to reconstruct ancestral sequences of ossification and to infer instances of heterochrony on a constraint phylogenetic tree. Multiple analyses were run to evaluate implications of heterochrony when: 1) turtles are placed at each of three different locations on the amniote tree (i.e., sister to all other reptiles, as members of Lepidosauromorpha, and as members of Archosauromorpha); and 2) when different datasets were analyzed (i.e., a larger set of data with a large number of taxa but with some missing data, and a smaller number of taxa with no missing data). All permutations of these analyses were explored, as were the performance of different classes of bones (endochondral vs dermal) in each analysis. Endochondral bones were not found to shift more often than dermal bones. Results of the analyses of the smaller dataset do not support any particular placement of turtles over another based on the number of evolutionary shifts in bone position. Results of the analyses of the larger dataset differed dramatically when turtles were considered archosauromorphs, rather than sister to all reptiles or as lepidosauromorphs. This later result would require that turtles experienced rapid modification of the diapsid skull to become functionally anapsid.

1055 Lightning Talks, Galerie 2, Saturday 9 July 2016

Norma Salcedo

Francis Marion University, Florence, SC, USA

Fleshy Excrescence Explorations: the Skin from the Supraoccipital Region of two *Chaetostoma* species (Siluriformes: Loricariidae)

A longitudinal outgrowth of skin (fleshy excrescence) on the posterior border of the supraoccipital bone has been reported to be present, and particularly conspicuous, on several species of the genus *Chaetostoma*. The nature of this structure was explored by means of scanning electron microscopy (SEM) and light microscopy (LM). SEM revealed abundant goblet cells and Type II taste buds on the skin of specimens that exhibit a

fleshy excrescence, while specimens that lack the fleshy excrescence exhibit a reduced number of goblet cells and Type III taste buds. LM revealed differences in the thickness of the epidermis, whereas the specimens with the fleshy excrescence have an epithelium with four to five layers, with two layers of low columnar cells on the basement membrane, polygonal to rounded cells in the middle, and flattened cells on the surface; while the specimens that lack the fleshy excrescence have an epithelium with three to four layers of all polygonal to rounded cells. These morphological differences indicate possible behavioral differences associated to detection of chemical cues by fish species within *Chaetostoma*.

1086 Herp Conservation & Ecology, Galerie 2, Sunday 10 July 2016

Steven Salinas, Alfonso Trujillo, Justin Saiz, Lisa McBride, S□n Tr□n, Jesús Rivas
New Mexico Highlands University, Las Vegas, New Mexico, USA

Is the American Bullfrog (*Lithobates catesbeianus*) as successful and invader as it seems, or does it receive help from other invasives?

Invasive species can negatively affect the diversity of native species by disturbing native trophic interactions. Often times invaders work in synergy with other invaders so the role of each invasive difficult to tear apart. Analyzing the diet of a population of American Bullfrogs we found a large proportion (over 80%) of Northern Crayfish (*Orconectes virilis*), another invasive. Given the high proportion of Crayfish on the diet, we surmised that Bullfrogs may be playing a role of top-down control on the Crayfish. In this study we explore the importance of top-down control on Crayfish population by Bullfrogs, and predatory introduced trout Rainbow Trout (*Oncorhynchus mykiss*). We studied and Crayfish density at a) a site with Bullfrogs Trout predation, b) a site with Bullfrogs but no trout, and c) a site where only Crayfish occur. Early results show that in areas without trout but with Bullfrogs predation, Crayfish populations are 4.4 times higher than in areas with both predators; and when both predators are missing Crayfish population is 12 times higher. Our data strongly suggest that these two predators exert important top down control on Crayfish. Management programs to control these species must include a comprehensive control of all species involved to avoid the mesopredators to irrupt.

0198 Fish Ecology I, Salon E, Friday 8 July 2016

Jessica Sanchez, Joel Trexler

Florida International University, Miami, FL, USA

Testing a hypothesis for the evolution of herbivory using the Sailfin Molly (*Poecilia latipinna*) in the Florida Everglades

Herbivorous diets are of poor quality relative to those containing animal items, limiting the available energy to sustain life processes such as maintenance, growth and reproduction. But, herbivory evolved and has been maintained throughout many lineages alongside animal-containing diets, so it is adaptive in certain circumstances. Here, we test the “heterotrophic facilitation” hypothesis, which states that herbivory is adaptive because herbivores supplement their diets by indirectly consuming heterotrophs associated with primary producers. In lab and field studies, we manipulated the autotrophic: heterotrophic (A:H) composition of algae (using shading and Phosphorus) and examined the effects of this varying food quality on lipid assimilation, growth and survival of the sailfin molly (*Poecilia latipinna*) in the Everglades. Fish showed no differences in the A:H ratios of their tissues ($F=0.893$; $df=2$; $p=0.478$), suggesting that they assimilate algal and bacterial-derived lipids at the same rate, regardless of their dietary abundance. Interestingly, fish fed algae grown in Light only, Shade only and Light + P conditions grew better than those fed Shade + P algae or a carnivore (control) diet ($F=3.924$; $df=4$; $p=0.02$). However, those fed Light only and Shade only algae also experienced high survival ($F=3.78$; $df=4$; $p=0.026$). Based on this evidence, diets comprised of intermediate levels of both autotrophs and heterotrophs (e.g. Shade only and Light only treatments) promote increased growth and survival more than diets with higher or lower A:H ratios. Therefore, our results support the “heterotrophic facilitation” hypothesis as a potential explanation for the adaptive evolution of herbivory in freshwater systems.

1072 Fish Systematics II, Salon F-H, Saturday 9 July 2016

Michael Sandel

The University of West Alabama, Livingston, Alabama, USA

Deep, Cold, Dark and Old: Accounting for Non-neutral DNA Sequence Variation Reconciles the Perciformes Mitochondrial Phylogeny

History has shown that the limits and interrelationships of Perciformes are not resolved by phylogenetic analysis of morphology or mitochondrial DNA alone. Conversely, analyses of multi-locus nuclear data revealed concordant and well-supported Acanthomorph subgroups, including Perciformes. The origins of phylogenetic discordance in mtDNA gene trees remain largely unexplained, despite a relatively robust literature on the general function and evolution of the vertebrate mitochondrial genome. Here, I investigate the role of homoplasy and functional diversification on the

inference of mtDNA phylogeny, with a focus on the limits and interrelationships of Perciformes. I use published and novel mitochondrial genomes to account for four putative sources of incongruence (character sampling, taxon sampling, nucleotide saturation, and natural selection). Specific attention is paid to members of Cottioidei and Scorpaenoidei which exhibit extraordinary physiological adaptations likely to involve mtDNA. Nine new mitochondrial genomes are presented, representing the most long-lived bony fish, the deepest-swimming freshwater fish, a troglomorph, and their close relatives. Results suggest that natural selection introduces systematic error in phylogenetic datasets that is not detected by traditional selection scans, and that statistical correction of this error reconciles the mtDNA gene tree with strongly supported patterns observed in multi-locus nuclear studies. Results do not discount the utility of mtDNA as a phylogenetic marker, but highlight the need for more sophisticated approaches to integrating mtDNA and nuclear datasets. An integrated understanding of mtDNA function and evolution highlights the importance of historical studies, which are likely to serve as valuable resources for the study of character evolution.

0243 HL GRADUATE RESEARCH AWARD, Galerie 2, Friday 8 July 2016

Mark Sandfoss¹, Coleman Sheehy III², Harvey Lillywhite¹

¹*Department of Biology, University of Florida, Gainesville, Florida, USA,* ²*Seahorse Key Marine Laboratory, University of Florida, Gainesville, Florida, USA*

Collapse of a Unique Bird-Snake Mutualism on Seahorse Key, Florida

Seahorse Key (SHK) supports a large population of Florida cottonmouth snakes, *Agkistrodon conanti*, which have a unique mutualistic and trophic association with colonially nesting water birds. Each spring >10,000 birds nest on SHK and provide an influx of food in the form of dropped or regurgitated fish that these snakes scavenge on the ground. Because of this allochthonous input of trophic resources, the cottonmouth population on SHK has become relatively dense and many snakes are large (≥ 1 m) compared to snakes on adjacent islands without large bird rookeries. Suddenly and unexpectedly, the birds abandoned their nests during April, 2015, and did not return. Given the significant trophic dependence on fish carrion provided by nesting birds, we expected to observe an eventual decline in body condition and numbers of cottonmouth snakes on SHK. We examined historical data collected from 1999 to 2016 on the abundance and body size of snakes to quantify how the removal of food resources has affected the SHK population. Preliminary data suggest reductions have occurred in the abundance and body condition of cottonmouths between pre- and post-bird abandonment periods. We are continuing to monitor the population to quantify how the change in availability of fish carrion is affecting the snakes on SHK. Loss of the bird rookery as a source of energy suggests that the snake population on SHK will continue to decline. In contrast, numbers of cottonmouths are expected to increase on other islands adjacent to SHK where avian nesting is increasing.

**0054 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; STORER AWARD
ICHTHYOLOGY**

Andrew Savage, Bruce Felgenhauer

University of Louisiana at Lafayette, Lafayette, Louisiana, USA

**Associations between the pink wormfish, *Microdesmus longipinnis*
(Weymouth), and the ghost shrimp, *Lepidophthalmus louisianensis* (Schmitt),
in artificial burrows**

Microdesmus longipinnis (Weymouth) is a small estuarine teleost fish that is known to feed on the eggs of the axiid shrimp, *Lepidophthalmus louisianensis* (Schmitt). In the course of collecting *M. longipinnis* for physiological studies we noticed that there seemed to be a higher preference towards burrows of non-gravid and male shrimp than one would expect if the driving force behind this relationship was exclusively predatory towards eggs. Laboratory experiments were used to expand upon the understanding of the relationship between these two animals and attempt to determine if *M. longipinnis* shows a higher preference towards burrows containing male shrimp as compared to those burrows with no shrimp. The expectation that being that a non-random rate of association towards the male shrimp will suggest that the fish are not seeking out burrows based solely on food availability and supports the need for more research into this relationship. *M. longipinnis* was found to positively associate with male *L. louisianensis* when compared to empty burrows supporting the idea of a more complex relationship that has previously been reported in the literature.

0652 Herp Morphology & Genetics, Galerie 3, Sunday 10 July 2016

Anna Savage¹, Brian Gratwicke², Katherine Hope², Ed Bronikowski², Robert Fleischer²

¹*University of Central Florida, Orlando, FL, USA*, ²*Smithsonian Institution, Washington, DC, USA*

Acquired immunity causes susceptibility in frogs infected with a deadly fungus

The fungal disease chytridiomycosis has devastated amphibian populations worldwide. Functional genomic contributions to host susceptibility and pathogen virulence remain enigmatic, particularly the role of immune function, immunogenetic variation, and fungal genomic variation in contributing to variable infection outcomes. We conducted experimental infections in an amphibian host with intraspecific and intrapopulation variation in chytridiomycosis susceptibility to assess the functional genomic response to infection in two important immune tissues: the skin, where infection occurs, and the spleen, where amphibian immune responses are generated. We find significant differences in acquired, inflammatory, and innate immune gene expression profiles

among surviving versus susceptible individuals, highlighting the importance of immune responses in determining susceptibility. Surprisingly, survivors show significantly reduced immune gene expression compared to susceptible frogs, particularly among acquired immune genes, suggesting that mounting acquired immune responses is counterproductive for surviving chytridiomycosis.

0676 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: ECOLOGY, NATURAL HISTORY, DISTRIBUTION, & BEHAVIOR

David Savage, Jacob Fetterman, Justin Elchynski, Jennifer Deitloff

Lock Haven University, Lock Haven, PA, USA

Aggression in *Plethodon cinereus* in four Populations from Pennsylvania

Across the range of many species, species characteristics can vary with geographic location. Some characteristics that may differ depending on location include morphological features, habitat and prey selection, and behavior. *Plethodon cinereus* has a broad geographic range and is known to display territorial aggression in some locations, such as where they occur in Virginia. However, at other locations, the extent of aggression is reduced from what is observed in Virginia, with some populations not showing territoriality. In this study, we examined the territorial interactions of *Plethodon cinereus* from four populations across Pennsylvania. We tested the hypotheses that (1) populations differed in territorial behaviors and (2) males exhibited greater aggression than females (non-gravid and gravid females examined as separate groups) at these locations. Our results suggest that there is no difference in the behavior between these Pennsylvanian populations or among sexes (male, gravid female, non-gravid female).

0469 Lightning Talks, Galerie 2, Saturday 9 July 2016

Julie Savidge, Martin Kastner, Thomas Seibert

Colorado State University, Fort Collins, CO, USA,

A Novel Climbing Behavior Displayed by the Brown Treesnake (*Boiga irregularis*)

Because of the devastating effect on Guam's native forest birds by non-native Brown Treesnakes (*Boiga irregularis*), we have been studying means for excluding them from avian nesting structures. Published laboratory experiments on climbing behavior of this largely arboreal species suggest that it employs lateral undulation and concertina movements. Additionally, researchers report that with increased slope and diameter of cylinders lacking surface irregularities, Brown Treesnakes are unable to make forward (upward) progress. During our research we noted what we believe to be a previously undescribed mode of locomotion in snakes. When confronted with a vertical, slick, metal

cylinder, some Brown Treesnakes formed their body into a ring around the cylinder using their tail as a “slip knot” that could adjust from mid-body to the back of the head. This apparently provides greater grip and allows the snake to gradually wiggle their body up the cylinder. In this flash talk, we show short videos of the behavior, discuss characteristics of snakes employing this method, and discuss its significance.

0593 ASIH: ASIH at 100 Symposium, Salon D, Saturday 9 July 2016

Alan H. Savitzky

Utah State University, Logan, UT, USA

ASIH and the Prospects for Taxon-focused Professional Organizations

During its first hundred years, ASIH has been influenced by historical shifts in the focus of biological research, as well as broader trends in global science, publication, and shifting patterns of membership in professional societies. As a member of the society for about half its history, I have observed those shifts as they have affected the ASIH. The transition from print to electronic journal publication has often been identified as a major driver of membership decline. However, changing membership patterns in professional organizations are not limited to scientific societies, nor to organizations that publish periodicals. The causes of shifting membership patterns are more complex, and may include changes in the number of societies individual are willing to join. Furthermore, although many taxon-focused societies are losing members, some process-focused societies are thriving. Membership patterns are further complicated by competition for members among organizations with similar missions. Meanwhile, organismal journals are being challenged by mandates for open access and by the rise of publication metrics, both of which appear to drive stronger manuscripts away from such journals.

0227 AES GRUBER AWARD, Balconies J & K, Thursday 7 July 2016

Jillian Sawyna, Weston Spivia, Kelly Radecki, Deborah Fraser, Christopher Lowe
California State University, Long Beach, Long Beach, CA, USA

Examination of the Potential Association Between Chronic Organochlorine Exposure and Immunotoxicity in the Round Stingray (*Urobatis halleri*)

Chronic organochlorine (OC) exposure has been shown to cause immune impairment in numerous vertebrate species. To determine if local elasmobranchs exhibited a similar effect due to high OC contamination found along the coastal southern California mainland, innate immune function was compared in round stingrays (*U. halleri*) collected from the mainland and Santa Catalina Island, a reference site. Microscopy and flow cytometry were used to assess proliferation and phagocytosis in splenic and peripheral blood leukocytes. Percent phagocytosis, and mean fluorescence index (MFI)

were evaluated by quantifying % leukocytes positive for, and relative amounts of ingested fluorescent *E. coli* BioParticles. Total cell proliferation differed between sites, with mainland rays having a higher concentration of cells in whole blood. Splenic mean (\pm SE) % phagocytosis (24.7 ± 4.98 %) was significantly higher in mainland rays compared to Catalina (9.96 ± 1.18 %). MFI was also greater among the mainland population (2681.74 ± 410.06 and 1197.1 ± 146.97). In blood, mainland rays had a significantly higher % phagocytosis (23.44 ± 2.887 %) compared to Catalina (12.98 ± 1.58 %), yet no difference was found in MFI. Σ PCB and Σ pesticide loads were the most influential factors describing increasing splenic % phagocytosis and MFI, while Σ PCB load alone explained increasing % phagocytosis in blood. Data suggests OC-correlated immunostimulation; however, other site-specific environmental variables may be contributing to the observed effects.

0086 Fish Genetics, Salon D, Sunday 10 July 2016

Jake Schaefer, Brian Kreiser, Stephen Flanagan

University of Southern Mississippi, Hattiesburg, MS, USA

Population genomics of *Fundulus grandis* following the Deepwater Horizon oil spill

The April 2010 Deepwater Horizon incident resulted in the release of a large amount of oil and dispersants into northern Gulf of Mexico ecosystems. Based on impact studies from earlier oil spills, DWH impacts were predicted to be immense, driven by immediate direct mortality or longer term deleterious effects from chronic exposure. Traditional toxicology research on resident species has focused on a variety of responses (e.g. changes in gene expression, growth, development or survivorship) in model organisms, including the Gulf Killifish (*Fundulus grandis*). Studies at the population and assemblage level have not detected a decrease in post-DWH fish populations, including *F. grandis*. There is, therefore, a disconnect in the scientific literature between published toxicology (predicting dramatic declines) and the assemblage level data (showing no declines). We used next generation sequencing and population genomic tools to test hypotheses about *F. grandis* responses to DWH. We sampled 30-35 individuals from four coastal Mississippi populations: two barrier islands with high oil exposure and two coastal bays with lower exposure. Analysis of >25,000 SNPs will estimate effective populations size and migration rates among the four sites. We specifically test the hypothesis that any of the 4 populations are consistent with a recent population bottleneck or large scale movement in response to oil contamination.

0314 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: ECOLOGY, NATURAL HISTORY, DISTRIBUTION, & BEHAVIOR

Christopher Schalk¹, Michael Cove²

¹*Southern Research Station, US Forest Service, Nacogdoches, TX, USA*, ²*North Carolina State University, Raleigh, NC, USA*

Emergent patterns between squamate prey and their predators

Globally, squamates (snakes and lizards) are diverse and abundant organisms across various ecosystems. Understanding the relationships between squamates and their predators can provide important insights to evolution of defenses, foraging ecology, and their functional role within their ecosystems. We sought to explore the relationships between the taxonomy and body size between predators and their squamate prey. To gather data on squamate predators, we reviewed the past volumes of *Herpetological Review* (1967 - 2015) and *Herpetology Notes* (2008 - 2015), and outside sources when they provided significant contributions (e.g., unreported family of predator). Our database includes over 1,400 squamate predation events represented by 27 lizard families and 10 snake families. Both lizards and snakes were observed being preyed upon more frequently by vertebrates than invertebrates. Taxonomically, lizards had a greater diversity of predators represented by 22 vertebrate orders and 10 invertebrate orders, whereas snake predators were comprised of 19 vertebrate orders and four invertebrate orders. Snakes, lizards, and birds were documented as the most frequent predators of squamates. The predator-prey ratio increased across all predators with increasing body size for all predators, though the slopes differed across predator taxa. The patterns quantified in this study provide a baseline to explore the evolution of defensive strategies across these diverse taxa of both predators and their prey.

0313 SSAR SEIBERT AWARD CONSERVATION, Galerie 3, Friday 8 July 2016

Christopher Schalk, Daniel Saenz

Southern Research Station, US Forest Service, Nacogdoches, TX, USA

Dynamics in anuran calling phenology: implications for surveys and monitoring programs

Amphibians exhibit large natural fluctuations in their population dynamics at both the larval and post-metamorphic life stages. Compared to other taxa, amphibians exhibit the strongest to climate change and often exhibit shifts in their breeding phenology. However, many of these studies have focused on few sites or utilize a coarse-grain survey design. We sought to quantify the long-term inter-annual and intra-annual variation in calling phenology in two species of anurans (*Pseudacris crucifer* and *Lithobates clamitans*) using a fine-grained (i.e., daily) survey design. From 2000-2014, we deployed automated recording devices (Song Meters) at eight ponds to monitor nocturnally vocalizing anurans in the piney woods ecoregion of East Texas. Inter-annual

comparisons revealed that, on average, there was not a significant difference in date of first call or calling window for each species. However, there was large intra-annual variation in calling metrics across survey sites, which can likely be attributed to the variation in environmental gradients across the breeding ponds. These results suggest that monitoring programs that focus on one or few sites, especially those that share similarities in environmental gradients, will fail to capture the complete picture in calling activity. This is especially important for species that utilize breeding sites that span a number of environmental gradients (e.g., temporary and permanent ponds). Future long-term studies need to design monitoring programs to effectively capture the high intra-annual variability in calling activity and to gain a more accurate understanding on the magnitude of response in changes of calling activity over time.

0363 AES Sawfishes Symposium, Salon E, Sunday 10 July 2016

Rachel Scharer¹, Philip Stevens², Gregg Poulakis¹

¹*Fish and Wildlife Research Institute, Florida Fish and Wildlife Conservation Commission, Charlotte Harbor Field Laboratory, Port Charlotte, FL, USA,* ²*Fish and Wildlife Research Institute, Florida Fish and Wildlife Conservation Commission, St. Petersburg, FL, USA*

Not All Nurseries are Created Equal: Differences in Large-scale Habitat Use Patterns between Two Smalltooth Sawfish, *Pristis pectinata*, Nursery Areas

Endangered Smalltooth Sawfish (*Pristis pectinata*) are known to use multiple southwest Florida estuaries during their first 2-3 years of life and understanding region-specific habitat use patterns has become important for effective management. Our research in the Charlotte Harbor estuarine system, was initially focused in the Caloosahatchee River, a highly human-altered river system, and we have now expanded sampling into a more natural area, the Peace River. A total of 238 juveniles ranging from 708 to 2,640 mm stretch total length were captured, tagged, and released between 2010 and 2015. Electivity analyses showed that sawfish in both rivers had affinities for water <1 m deep, water >24°C, moderate to high dissolved oxygen levels (>4 mg l⁻¹), and salinities between 12 and 27. Movements were monitored in main-stem river habitats and non-main-stem habitats (i.e., natural mangrove-lined creeks, semi-natural creeks, seawall-lined canals) using acoustic listening stations. Sawfish used all of the habitats available to them in both rivers, but tended to reside in specific regions of the nurseries. In the Caloosahatchee River, sawfish were usually associated with five hotspots along a 25 river kilometer (rkm) stretch of the river. They moved upriver during dry, low freshwater inflow conditions and downriver during wet, high inflow conditions. In contrast sawfish tended to remain in only a six rkm portion of the Peace River during all freshwater inflow conditions. Possible reasons for these observations relate to differences in geomorphology and freshwater inflow regimes between the rivers.

0603 AES Ecology & Behavior II, Balconies J & K, Saturday 9 July 2016

Vera Schluessel

Institute of Zoology, University of Bonn, Bonn, Germany

Sharks don't just have Sharp Teeth but are also Sharp Thinkers - Cognition in Elasmobranchs

While there has been an upsurge in behavioural studies on fish and even shark cognition in recent years, comparatively few studies have tried to uncover the relevant neuronal substrates involved. Here, learning and memory functions were assessed in bamboo sharks (*Chiloscyllium griseum*) and freshwater stingrays (*Potamotrygon motoro*) on a behavioural and neuronal level. Most behavioural studies were performed as two-alternative forced choice experiments, in which the positive stimulus was reinforced by a food reward. Selected spatial and visual discrimination experiments in sharks were complemented by lesion experiments or immediate-early gene expression studies using *egr-1* and *c-fos* to determine involvement of selected brain structures. Sharks and rays successfully mastered selected object recognition and categorization tasks and showed visual perception of illusionary contours, symmetry, and movement, as well as spatial orientation and memory retention capabilities. Both lesion and gene expression studies in sharks indicate that even in the absence of a neocortex, selected cognitive functions are processed in the telencephalon, with some pallial regions matching potentially homologous areas in other vertebrates where similar functions are being processed. Results of these studies indicate that the here assessed cognitive abilities in bamboo sharks and freshwater stingrays are as well developed as in many other vertebrates, aiding them in activities such as food retrieval, predator avoidance, mate choice and habitat selection.

1118 HL, ASIH, SSAR: Eco-Evolutionary Dynamics Symposium, Salon D, Friday 8 July 2016

Thomas Schoener¹, Jason Kolbe², Manuel Leal³, Jonathan Losos², Sebastian Schreiber¹, David Spiller¹

¹University of California Davis, Davis, CA, USA, ²Harvard University, Cambridge, MA, USA, ³Duke University, Durham, NC, USA

Eco-evolutionary Aspects of the Lizard *Anolis sagrei* in an Island Metapopulation

No abstract submitted.

0375 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Tiffany Schriever

Western Michigan University, Kalamazoo, MI, USA

Interspecific overlap in trophic niche of larval amphibians in temporary ponds

Foraging strategy is an important life history trait that determines trophic niche width. Niche variation can occur among individuals of a population, between species, and change throughout development. It is important to understand the significant roles of amphibian larvae in wetland structure and function. In this study, I quantified the isotopic niche and overlap among several species of amphibian larvae throughout their larval development from nine woodland ponds using carbon and nitrogen stable isotopes. I calculated standard Bayesian ellipses from $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values and produced standard ellipse area and ellipse overlap using Stable Isotope Bayesian Ellipse in R (SIBER) functions. I hypothesized that gape-limited active foraging salamander larvae would have narrow isotopic niche widths and low niche overlap and that generalist feeding anuran larvae would have broad niches and high niche overlap. I also hypothesized that niche overlap would be highest during anuran tadpole stages and lowest during metamorphic stages when individuals switch to feeding on invertebrates. I examined the relationship between species richness and isotopic niche widths. Isotopic niches varied in size and overlapped considerably among the anuran species, but less so in salamander larvae. I found some support for the hypothesis that isotopic niches are larger in less species rich ponds. This study took a community approach to quantify the relationship between isotopic niche width and overlap for multiple species from different trophic levels and foraging strategies. Ponds sustain multiple functionally redundant amphibian species that may assist in ecosystem resilience to changing environmental conditions.

0390 Poster Session I, Acadia/Bissonet, Friday 8 July 2016

Katherine E. Schweiss¹, Jill M. Hendon², Nicole M. Phillips¹

¹*The University of Southern Mississippi, Hattiesburg, Mississippi, USA*, ²*The University of Southern Mississippi Gulf Coast Research Lab, Ocean Springs, Mississippi, USA*

A simplified approach to genetically sexing elasmobranchs using qualitative PCR

Determining a sex for elasmobranchs is typically done visually, by looking for the presence or absence of male claspers. While this method is easy and reliable, many current research endeavors are based on samples that are not associated with a source animal (*i.e.*, dried fins, sawfish saws), making visual assessments impossible. Having a method to determine or verify sex data for such samples would be a useful tool for increasing the value of the sample and enhancing the resultant assessments. Male heterogamety predominates in elasmobranchs; therefore, males are typically XY and

females are XX. The aim of the current study was to develop a multiplex polymerase chain reaction (PCR) to amplify a portion of each of the X and Y chromosome in elasmobranchs. Primers were developed and tested for representative shark and ray species using a qualitative PCR (qPCR) approach. Resultant dissociation peaks are produced during qPCR, where males produce two peaks (corresponding to amplicons for both the X and Y chromosomes) and females produce one peak (corresponding to an amplicon for the X chromosome). Application of qPCR for genetically sexing elasmobranchs is faster and more accurate than the conventional PCR and gel electrophoresis methods commonly employed in sexing other organisms. In addition, this method is more likely to be successful for samples with low quantity or quality DNA.

0818 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; AES CARRIER AWARD

Gail Schwieterman¹, Karissa Lear¹, Heather Marshall¹, Jack Morris¹, Connor White², Robert Hueter¹, Gregory Skomal³, Nicholas Whitney¹

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Post-Release Mortality of Coastal Sharks in a Commercial Longline Fishery

Estimating post-release mortality rates is essential to understanding the impact of fishing and properly informing management measures. However, logistical difficulties have resulted in relatively few post-release studies, typically with small sample sizes. Here, we quantify post-release mortality of large coastal sharks in the Florida commercial longline fishery using acceleration data loggers (ADLs) to infer mortality. We recorded hook times, capture measures (e.g. animal condition), took blood samples, and applied ADLs to longline-caught sharks. Between December 2013 and January 2016 we tagged 229 sharks with ADLs with a 90.8% tag recovery rate. Shark species tagged included blacktip (*C. limbatus*), sandbar (*C. plumbeus*), tiger (*Galeocerdo cuvier*), spinner (*C. brevipinna*), bull (*C. leucas*), blacknose (*C. acronotus*), great hammerhead (*Sphyrna mokarran*), scalloped hammerhead (*S. lewini*), and dusky sharks (*C. obscurus*). Species-specific post-release mortality rates ranged from 2.04% (*G. cuvier*) to 75% (*C. brevipinna*). Surviving sharks were monitored for an average of 24.9 ± 22.3 h (mean \pm SD), and up to 204.5 h post-release. Mixed modeling of blood stress indicators and capture metrics show several variables significantly correlate with post-release outcome.

**0882 SSAR SEIBERT SYSTEMATICS & EVOLUTION AWARD, Salon A-C,
Friday 8 July 2016**

Peter Scott¹, Travis Glenn², Leslie Rissler³

¹University of Alabama, Tuscaloosa, AL, USA, ²University of Georgia, Athens, GA, USA, ³National Science Foundation, Arlington, VA, USA

Species Delimitation and Systematics of Musk Turtles (Genus *Sternotherus*)

Despite being relatively well known, musk turtles (Genus *Sternotherus*) have suffered from a turbulent taxonomic and systematic history, which has resulted in currently unstable species limits, taxonomic designations of populations, and a poorly resolved understanding of interspecific relationships for the genus (particularly in the *S. minor* complex). Here, dense geographic sampling and ddRADseq methods are combined to sequence ~200 individual turtles at 4000+ genome wide loci to be used for species delimitation and systematic inference within *Sternotherus*. Multiple coalescent-based methods (BFD* in SNAPP and SVDquartets) and concatenation all strongly support an identical taxonomy including the recognition of currently nominate and novel species within *Sternotherus*. However, all methods infer conflicting and differentially supported relationships within the genus. To attempt to resolve systematic relationships, the likelihoods of alternative speciation events and demographic histories within *Sternotherus* are compared using observed and simulated site frequency spectra (SFS). The most likely demographic scenario for speciation in *Sternotherus* infers a nearly-simultaneous speciation event for four of six species, followed by low levels of more recent introgression; both events are concordant with previous geologic hypotheses for diversification within the genus. This work greatly clarifies species limits and relationships within *Sternotherus* and provides a framework by which relatively computationally inexpensive simulations of SFS can resolve systematic relationships for some of the most difficult phylogenetic nodes that may be plagued by rapid diversification, introgression, or both.

0963 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Robyn Screen¹, Max Lambert⁵, Jennifer McKenzie⁴, Greg Pauly³, Amber Wright¹, H. Bradley Shaffer²

¹University of Hawaii at Manoa, Honolulu, HI, USA, ²University of California, Los Angeles, Los Angeles, CA, USA, ³Natural History Museum of Los Angeles County, Los Angeles, CA, USA, ⁴University of Kentucky, Lexington, KY, USA, ⁵Yale, New Haven, CT, USA

Experimental Reduction of an Invasive Slider Turtle Population Affects the Basking Distribution of a Native Turtle

Red-eared Sliders (*Trachemys scripta elegans*) are one of the world's 100 worst invasive species according to the IUCN, have been released on every continent except Antarctica, and are thought to be competitively dominant to many native turtle species. The

Western Pond Turtle (*Emys marmorata*) is California's only species of native turtle and is declining throughout its range. Urban waterways can be valuable habitat for Western Pond Turtles but these habitats are also hotspots for slider introductions. The Arboretum at the University of California, Davis has served as an important study site for understanding the impacts of exotic sliders on native pond turtles. Prior work in this system has shown that these two turtles use basking sites with different features and that the two species are concentrated in different regions of the waterway. Here, we conducted an in situ field experiment where we dramatically reduced the slider population size and monitored turtle basking behavior. In total, we removed 180 sliders, representing over 100 kg of turtle biomass. Our results show that pond turtles no longer basked in one concentrated region of the Arboretum but rather basked relatively evenly throughout the waterway. The remnant slider population became sparser in some regions of the Arboretum but remained concentrated at one end of the waterway. Our removal experiment reveals that manipulating invasive slider populations may have effects on native turtle habitat use. These results may be useful for conservation efforts targeted at native turtle habitat management or invasive slider removal.

0011 Fish Morphology & Biogeography, Salon A-C, Sunday 10 July 2016

Greg Seegert

EA Engineering, Science and Technology, Deerfield, IL, USA

Evaluation of the Wabash River Fish Community After a Power Plant Shutdown

The Wabash River fish community was sampled by electrofishing and seining in 2011, 2012, and 2013 to determine if it had changed following the shutdown of a nearby power plant. Sampling yielded 87 species including a new species for Illinois. The data collected during 2011-2013 were compared to data collected from the same area in the 1970s and 1980s. ANOVA comparisons found either few changes over time or, if changes were evident, they occurred throughout the study area, not just downstream of the former power plant site. A variety of ordination and graphical techniques were used to look for changes in overall community structure. These analyses showed that the fish community has changed over time. However, like the ANOVA comparisons, these additional techniques also showed that the changes occurred throughout the study area suggesting that the shutdown of the power plant had little effect on the nearby fish community.

1099 Fish Ecology II, Salon A-C, Saturday 9 July 2016

Fredys F. Segura-Guevara, Ángel L. Martínez-González, Charles W. Olaya-Nieto
Fishery Biology Research Laboratory-FBRL, Department of Aquatic Sciences, University of Cordoba, Loricá, Cordoba, Colombia

Feeding Habits of Moncholo *Hoplias malabaricus* in the Ciénaga de Ayapel, Sinu River System

To study the feeding habits of Moncholo *Hoplias malabaricus* in the Ciénaga de Ayapel, Sinu River System, we analyzed 349 stomachs of individuals collected between August 2009 and July 2010, with sizes between 25.5 and 40.3 cm total length (TL) and total weight (WT) among 132.0 and 734.0 g. The stomach content was analyzed using the Proportion of empty stomachs, Grade of digestion, Frequency of occurrence, numerical Frequency, Gravimetry and relative importance Index. The Proportion of empty stomachs was high and most of the foods were half digested, identifying five food groups: Fishes, vegetable Rests, Insects, Detritus and Others. Different methods of evaluation of stomach content shows that Fishes were conformed by species like *Andinoacara pulcher*, *Cyphocharax magdalenae*, *Sternopygus* sp., *Plagioscion magdalenae*, *Caquetaia kraussii* and *Oreochromis* sp. and were the most common group (94.6%), the most abundant group (86.2%) and the greatest group composition in weight (97.9%). The relative importance Index indicates that Fishes is a food group of high relative importance and the main food in the Moncholo's diet, while other food groups are classified as occasional with low relative importance. The results suggest that Moncholo is a carnivorous fish with a piscivorous trend that keeps its feeding habits as they grow in the Ciénaga de Ayapel.

0986 Poster Session I, Acadia/Bissonet, Friday 8 July 2016

Fredys F. Segura-Guevara, William Pérez-Doria, Charles W. Olaya-Nieto
Fishery Biology Research Laboratory-FBRL, Department of Aquatic Sciences, University of Cordoba, Loricá, Cordoba, Colombia

Reproductive biology of Mojarra amarilla *Caquetaia kraussii* in the Ciénaga de Ayapel, Sinu River System

The reproductive biology of Mojarra amarilla *Caquetaia kraussii* in the Ciénaga de Ayapel, Sinu River System between August 2009 and July 2010 was studied. 425 individuals with total length (TL) ranged between 14.0 and 30.0 cm and total weight (TW) ranged between 48.0 and 510 g were collected. The gonads were placed in Gilson solution, the Vazzoler scale was applied and sexual proportion, sexual maturity index, spawning season, the length at first maturity, oocytes's diameter and fecundity were estimated. 244 females, 115 males and 66 undifferentiated were found, with sexual proportion female: male of 2.1:1 and sexual dimorphism in size, since males reach larger sizes than females. Sexual maturity index indicate that there spawns in October, December, April and July. The length at first maturity was estimated in 19.1, 20.4 and

20.0 cm TL for females, males and combined sexes, respectively, oocytes's average diameter was 1210 μ m and average fecundity estimated was 3215 oocytes. The results achieved in this study suggest that Mojarra amarilla in the Ciénaga de Ayapel, is a non rheophilous fish whose spawning season extends during the year with partial spawning not associated with the rains, large oocytes and high fecundity.

1105 Poster Session I, Acadia/Bissonet, Friday 8 July 2016

Fredys F. Segura-Guevara, William Pérez-Doria, Charles W. Olaya-Nieto

Fishery Biology Research Laboratory-FBRL, Department of Aquatic Sciences, University of Cordoba, Loricá, Cordoba, Colombia

Reproductive Ecology of Moncholo *Hoplias malabaricus* in the Ciénaga de Ayapel, Colombia

To study the reproductive ecology of Moncholo *Hoplias malabaricus* in the Ciénaga de Ayapel, Colombia, 349 individuals were collected between August 2009 and July 2010, with lengths ranging 25.5-40.3 cm of total length (TL) and 132.0-734.0 g of total weight (TW). The gonads were placed in Gilson solution, the Vazzoler scale was applied and sexual proportion, sexual maturity index, spawning season, the length at first maturity, oocytes's diameter and fecundity were estimated. 274 females, 64 males and 11 individuals undifferentiated were studied, with sexual proportion female: male of 4.3:1. The length at first maturity was estimated in 30.8, 32.3 y 30.8 cm TL for females, males and combined sexes; oocytes's average diameter was 1453 μ m and fecundity was estimated in 9107 oocytes by spawning batch. Sexual maturity index shows that the spawning season extends throughout the year. The results achieved in this study suggest that Moncholo in the Ciénaga de Ayapel is a fish that has large oocytes, partial spawning, high fecundity with prolonged spawning season that extends over study period.

0289 Herp Conservation, Galerie 3, Saturday 9 July 2016

Richard Seigel¹, William Saffell¹, Brian Durkin¹, Matt Gutt¹, Anna Savage²

¹Towson University, Towson, Maryland, USA, ²University of Central Florida, Orlando, Florida, USA

Do Constructed Wetlands Have Higher Rates of *Ranavirus* Infection of Amphibians Compared with Non-constructed sites?

Reports of large-scale die offs of amphibians associated with the emerging pathogen *Ranavirus* have become increasingly common in North America and elsewhere over the past decade. Understanding the distribution and habitat correlates of *Ranavirus*-associated die offs of amphibians is critical for understanding the spread and impact of this pathogen on native amphibians. In this study, we posed a question especially

germane to state and federal programs that utilize wetlands restoration as part of mitigation programs; specifically, we wanted to know whether constructed wetlands had a higher rate of *Ranavirus*-associated die offs than seen in non-constructed wetlands. Using a database of over 60 wetlands constructed or modified by the Maryland State Highway Administration, we selected 16-22 of these sites for surveillance of die offs and sampled sites for the presence of *Ranavirus* by DNA assays in both 2014 and 2015. We found that the rate of die offs at our sites was very similar among years (36.4-37.5%), which was similar to the 25-50% rate of die offs seen in non-SHA wetlands in the mid-Atlantic region. DNA testing is still in progress, and will be used to construct a model testing for associations between *Ranavirus* infection and habitat variables that will be of use for land managers.

0580 AES Sawfishes Symposium, Salon E, Sunday 10 July 2016

Jason C. Seitz¹, Jan Jeffrey Hoover²

¹ANAMAR Environmental Consulting, Inc., Gainesville, FL, USA, ²US Army Engineer Research and Development Center, Vicksburg, MS, USA

Taxonomic Resolution of Sawfish Rostra from a Private Collection

Management and recovery of endangered sawfishes worldwide is challenged by unreliability of species determination. Often, dried rostra (saws) are the only vouchered material available to represent an historical occurrence, yet traditional methods of species identification of rostra (rostral tooth counts) are fallible. We evaluated the utility of rostral morphometric characters on classification of specimens from a private collection of 25 old rostra. All rostra available from collectors and donated by fishers were obtained by a single individual (logistics permitting) so we believe the collection is representative of sawfishes globally. Rostrum data consisted of: overall length (used to standardize data), standard length, standard width, distal width, gap between right proximal teeth, gap between right distal teeth, number of teeth on each side (used for species assignments). Principal component analysis (PCA) of morphometric characters was informative. PC1 (x-axis) accounted for 74% variance and was associated with 4 variables (loadings = |0.36-0.43|), PC2 (y-axis) amounted for 14% variance and was associated with a single variable (loading = |0.70|). Point clusters were consistent with putative identifications. On PC1, *Anoxypristis cuspidata* (Knifetooth Sawfish) plotted low, *Pristis pectinata* and *P. zijsron* (smalltooth complex) at intermediate values, and *P. microdon* and *P. perotteti* (largetooth complex) at high values. *P. pectinata* and *P. zijsron* were separated from each other along PC2, as were *P. microdon* and *P. perotteti*. Results demonstrate utility of analyzing smaller collections (N < 40) and suggest that pooled data from private collections can characterize phenotypic variation in sawfish interspecifically and intraspecifically.

0136 AES Sawfishes Symposium, Salon E, Sunday 10 July 2016

Jason Seitz¹, John Waters²

¹ANAMAR Environmental Consulting, Inc., Gainesville, Florida, USA, ²Aquatic Research & Conservation Society, Inc., Little Canada, Minnesota, USA

Should Florida really be considered part of the historic range for the endangered Largetooth Sawfish (*Pristis pristis*)?

The U.S. population of the endangered Largetooth Sawfish, *Pristis pristis*, is among those populations with the highest probability of extinction. Identifying areas with valid historical records of this species is therefore critical as these areas may be important to the eventual recovery of the species. The eastern extent of the U.S. range of *P. pristis* is reported to include Florida based on only four historical records purported to be from the state: one from southern Florida based on a dried rostrum held at the American Museum of Natural History (AMNH), one from near Clearwater based on a dried whole specimen seen on display, one each from Salerno and Key West based on dried rostra. Three of these records only presume a local capture location, as the capture or landing of each specimen was not observed by the researcher. The AMNH specimen was only presumed to have been collected during the spring 1910 Tecla expedition to southern Florida but evidence indicates to the contrary. This paper discusses more likely scenarios for the appearance of these dried specimens in Florida and the most plausible scenarios as to the source of the AMNH specimen. Given the dubious nature of the four *P. pristis* accounts purported to be from Florida and the lack of verified vouchered specimens or catches in the state, Florida should be omitted from the range of this species. Texas, or possibly Louisiana, should be considered the eastern-most extent of the species in the United States.

0685 Lightning Talks, Galerie 2, Saturday 9 July 2016

Emily Seubert, Marcus Drymon

University of South Alabama, Mobile, AL, USA

Species and functional biodiversity of apex and mesopredators in the northern Gulf of Mexico

High biodiversity can enhance the resiliency of an ecosystem and hasten the recovery of collapsed populations. Apex and mesopredators often overlap trophic niches, and thus can facilitate the ability of an ecosystem to rebound from a disturbance. To investigate the species and functional diversity of apex and mesopredators across the northern Gulf of Mexico, we plan to analyze catch data from two years of bottom longline surveys conducted in both inshore and offshore waters. Species diversity will be calculated from catch data using standard diversity indices while functional biodiversity will be determined through stable isotope analysis of carbon, nitrogen, and sulfur sampled from two distinct tissue types, white muscle and blood plasma. During the first year of sampling in 2015, 24 bottom longline sets were conducted and 314 individuals from 17

different species were landed. Preliminary results show that overall, offshore sites in Louisiana have the highest diversity while offshore sites in Mississippi contain the lowest diversity. Inshore sites in Alabama had the highest number of species whereas offshore Alabama sites contained the fewest number of species per region. The addition of data collected in 2016 will elucidate the trends from Year 1. Early evidence of high predator diversity across a small spatial scale indicates that the ecosystem may be resilient in the face of environmental disturbances, which are not uncommon in the northern Gulf of Mexico. Investigating the potential for this system to recover from environmental disasters is critical for both preemptive management and post-disaster mitigation strategies.

0146 ASIH STOYE ECOLOGY & ETHOLOGY AWARD, Salon E, Friday 8 July 2016

Thomas Sevick, Jake Schaefer

The University of Southern Mississippi, Hattiesburg, MS, USA

Effect of fragmentation and habitat type on the abundance and diversity of nekton in coastal Mississippi

Coastal wetlands are extremely productive ecosystems that support an abundance of organisms at higher trophic levels. Coastal wetlands also act as important buffers from storms and help protect major cornerstones of coastal economies, such as tourism and fisheries. Despite the clear need for the protection of these habitats, anthropogenic use of coastal wetlands has increased in frequency and intensity, resulting in the fragmentation of once continuous habitats. A central challenge to assessing the impact of marsh fragmentation is the lack of quantitative distribution and abundance data from specific habitat types. This is especially true for species that are not commercially or recreationally harvested and are, therefore, not regularly monitored by state and federal resource management agencies. This study makes use of quantitative abundance, habitat use, and distribution data for non-harvested marsh nekton collected in oligohaline marshes (salinity 0.5-5ppt) of coastal Mississippi. To assess how nekton assemblages varied by habitat, patch geometry and position in patch (core vs. edge), four sites along coastal Mississippi were sampled in the summers of 2014 and 2015. Nekton were sampled in adjacent patches of submerged aquatic vegetation and emergent vegetation using a 1-m² throw trap. Marsh patch geometry was quantified, using aerial pictures taken with a GoPro camera secured to the end of a 20ft telescoping pole. Points around the patch were digitized in TPS software and analyzed using R. The results of this study indicate that diversity and abundance of nekton in the Mississippi marshes varies significantly based on habitat type and fragmentation.

0990 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Katherine Sgouros, Robert Jadin, Sarah Orlofske

Northeastern Illinois University, Chicago, Illinois, USA

A Revised Molecular Phylogeny Reveals Polyphyly in *Schistura* (Teleostei: Cypriniformes: Nemacheilidae)

With more than 215 presently known species, the genus *Schistura* dominates over the loaches with a vast range of distinct morphologies. Loaches comprise a large portion of the order Cypriniformes with an estimated 1200 species. However, the evolutionary relationships of the majority of loaches remain unresolved. Most species descriptions are based exclusively on morphological data and a limited number of loaches have sequences and placement in molecular phylogenies. This has led to inconsistencies between their taxonomy and evolutionary relationships, as many species have similar environments, life histories, and markings. Because of the great diversity in species and morphology, this research provides a broader understanding of loach taxonomy and phylogenetics while testing the validity of morphological data to infer phylogenetic relationships. A current phylogeny of *Schistura* loaches compiled by the Cypriniformes Tree of Life project indicates this group is polyphyletic. Therefore, it is paramount to include additional species, especially those recently described, into a phylogenetic analysis to obtain a stable taxonomy at the generic level. For this study, we examined the evolutionary relationships of nine members of the genus *Schistura* via mitochondrial gene fragments. Additionally, this research includes several novel species contributing knowledge about the evolutionary history of Asian freshwater fishes. The results of this study confirm polyphyly between *Schistura* and other closely related genera in two large, distinct clades. One clade has a wide Eurasian distribution while the other is limited to Southeast Asia. Lastly, this study opens up new avenues for continued research in nemacheilid evolution.

1096 ASIH: ASIH at 100 Symposium, Salon D, Saturday 9 July 2016

Brad Shaffer

UCLA, Los Angeles, CA, USA

ASIH in the Genomics Era

The first pioneering use of modern molecular genetics in evolutionary biology was published in 1966 by Lewontin and Hubby in *Genetics*. The same year, Cei and Erspamer published the first biochemical analysis in the pages of *Copeia*. Ever since, our society and our journal have championed the use of increasingly sophisticated molecular genetic analyses to unravel the phylogeny, population biology, and natural history of amphibians, reptiles, and fishes. Unlike many societies, our molecular geneticists have remained true to the idea that we use molecules to better understand our study organisms, rather than molecular biology in its own right. As we look to the next decade of work, I see an increasingly important role for the expertise in organismal biology that

characterizes members of ASIH in applying the tools of genomics research in key research areas ranging from conservation biology to assembling the vertebrate tree of life. We can now assemble a reasonable genome of most vertebrate species for a few thousands of dollars, and the world of comparative, conservation, and landscape genomics is thus a reality. Given our tremendous expertise in the vast majority of vertebrate clades on earth, the members of ASIH are well positioned to take a leadership role in the use of genomics in organismal biology, just as we have for earlier genetic techniques.

0775 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Ashley Shaw¹, Bryan Frazier¹, Amanda Barker², David Portnoy², Doug Adams³

¹South Carolina Department of Natural Resources, Marine Resources Research Institute, Charleston, SC, USA, ²Marine Genomics Laboratory, Department of Life Sciences, Harte Research Institute, Texas A&M University-Corpus Christi, Corpus Christi, TX, USA, ³Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Research Institute, Melbourne, FL, USA

Diet analysis of two cryptic Hammerhead species off the Southeastern United States

Two sympatric species, *Sphyrna lewini*, Scalloped Hammerhead and the recently described *Sphyrna gilberti*, Carolina Hammerhead, inhabit nursery areas as young-of-year along the southeastern United States. As part of ongoing research to determine spatial and temporal distribution of the two species, trophic ecology will also be examined. The diet of Hammerhead species, particularly young-of-year sharks, has not been examined in the waters off of the southeastern United States. This study examines stomach contents as well as stable isotope analyses to determine the dietary habits of the Scalloped and Carolina Hammerheads. Comparisons will be made among and between Hammerheads from two distinct habitats, Bulls Bay, an estuarine nursery in SC, and Cape Canaveral, a neritic nursery in FL.

0231 ASIH STOYE AWARD PHYSIOLOGY & PHYSIOLOGICAL ECOLOGY, SALON A-C, Thursday 7 July 2016

Tanner Shea, Mason DuBois, Natalie Claunch, Nicolette Murphey, Kiley Rucker, Robert Brewster, Emily Taylor

California Polytechnic State University, San Luis Obispo, California, USA

Testing the oxygen limitation hypothesis for the thermal tolerance of an air-breathing vertebrate

The physiological mechanisms responsible for thermal tolerance, including the critical thermal maximum (CT_{max}), in air-breathing organisms remain uncertain despite

decades of research on CT_{max}. We tested the oxygen limitation hypothesis, which states that animals reach their CT_{max} when the metabolic demand for oxygen at high temperatures exceeds the circulatory system's ability to supply it. Lizards exposed to hypoxic air (6% O₂) gaped, panted, and lost their righting response (reached CT_{max}) at far lower temperatures than lizards exposed to normoxic (21% O₂) or hyperoxic (35% O₂) air. A greater proportion of lizards in the hyperoxic treatment were able to withstand body temperatures above 44°C than in the normoxic treatment. These data suggest that oxygen limitation plays a mechanistic role in the CT_{max} of lizards. In addition, oxygen limitation may interact with other effects of high temperatures to stimulate gaping and panting and to interfere with coordinated locomotor ability.

0458 General Herpetology, Salon D, Thursday 7 July 2016

Alexander Shepack, Alessandro Catenazzi

Southern Illinois University, Carbondale, IL, USA

Prevalence of *Batrachochytrium dendrobatidis* in rebounding and remnant amphibian populations

The global decline of amphibians has captivated scientists and the general public. Although the causes behind the declines are diverse, the amphibian chytrid fungus *Batrachochytrium dendrobatidis* has been implicated in many declines and disappearances in the Americas and Australia. While many species were initially feared extinct, in recent years numerous populations of many species have been discovered. While these populations provide hope for the future of amphibian populations worldwide, the mechanisms behind their survival are still unknown. This study seeks to investigate how these populations have been able to survive or return. Current results indicate that in all studied populations Bd continues to exist in the environment. We have identified Bd in rebounding and remnant populations as well as other members of the amphibian community; with prevalence varying from 0.3-0.5. Unexpectedly, rebounding populations across sites, while apparently still increasing or maintaining size, have the same Bd prevalence as the rest of the community. These preliminary results suggest that these populations are still facing Bd in the environment and may have evolved resistance to Bd, or coping mechanisms to reduce fatal infections. In the future we will be coupling these results with examinations of the population genetics and intrinsic susceptibility of individuals to understand rapid changes in the host-pathogen system and the possibilities for conservation measures of at risk populations elsewhere.

0009 Lightning Talks, Galerie 2, Saturday 9 July 2016

C. Samantha Sherman¹, Andrew Chin¹, Michelle R. Heupel², Colin A. Simpfendorfer¹

¹James Cook University, Townsville, Queensland, Australia, ²Australian Institute of Marine Science, Townsville, Queensland, Australia

Encountering batoids on coral reefs in Malaysian Borneo

Batoids are emerging as a conservation concern, especially in locations such as South East Asia where fishing pressure is high. In this region, batoids are caught for their meat and skin. Although there is a high diversity of batoids in the region, little is known about their abundances in coral reef ecosystems. The Global FinPrint Project is the first global-scale survey of elasmobranchs in coral reef ecosystems. The project uses baited remote underwater video systems (BRUVS) to determine relative diversity and abundance of coral reef sharks and rays. These data form an important baseline for future studies, and provide data about diversity, abundance and distribution patterns that can inform fisheries and marine park management. In 2015, over 300 BRUVS were set at three sites in Malaysian Borneo in the Tunku Abdul Rahman Park near Kota Kinabalu and in the islands off of Semporna. Preliminary analyses from these Malaysian locations will be presented. Two species were seen most often: the bluespotted maskray (*Neotrygon kuhlii*) and the blue-spotted ribbontailed ray (*Taeniura lymma*). Other species were rarely observed, showing that while there is high diversity, many of those species may be quite rare, or perhaps difficult to sample using BRUVS. A cursory inspection of fish markets and of wholesale websites suggests that the bluespotted maskray and blue-spotted ribbontailed ray are amongst the most common batoid species in local markets.

0252 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; STORER AWARD ICHTHYOLOGY

Chelsey Sherwood, Ginny Adams, Reid Adams

University of Central Arkansas, Conway, AR, USA

Analysis of Historical Theses to Assess Changes in Abundance and Distribution of Cypriniformes in the Saline River, Arkansas

Long-term data sets are important in assessing changes in fish assemblages and population trends of threatened species. The Saline River has not been thoroughly surveyed in 34 years and is a diverse river with 112 known species of fishes, including several species of conservation concern. We compared collections from two historical theses (Reynolds, 1971 and Stackhouse, 1982) to assess changes in abundance and distribution of Cypriniformes over this 11-year period in the Saline River across 20 common sites. In 1982, species richness of Cypriniformes increased to 32 species with the addition of *Macrhybopsis aestivalis*, *Notropis buchanani*, *Moxostoma carinatum*, and *Moxostoma duquesnei* compared to 28 species in 1971. *Campostoma pullum* and *Notropis*

boops were the most widely distributed species in 1971 occurring at 70% of the sites; however, in 1982 *Cyprinella whipplei* (65%) and *N. boops* (70%) had the highest frequency of occurrence. For both collections, *N. boops* (1971=27%, 1982=33%) and *C. whipplei* (18%, 12%) were the most abundant species across sites with the addition of *Notemigonus crysoleucas* (12%) in 1982. Over the 11 years, there was an increase in frequency of occurrence of some low-gradient, tolerant species: *Lythrurus fumeus* (1971=20%, 1982=60%), *N. crysoleucas* (5%, 30%), and *Opsopoeodus emiliae* (15%, 45%). This trend was most pronounced in uppermost sites of the Saline suggesting fine sediments and/or sluggish flows have increased in these reaches. Beginning spring (2016), sites from historical theses will be sampled using similar techniques to assess changes in fish assemblages relative to changes in land use and in-stream habitat.

0485 Poster Session I, Acadia/Bissonet, Friday 8 July 2016

Chelsea Shields, James Gelsleichter

University of North Florida, Jacksonville, Florida, USA

Potential Associations between Gonadotropins and Reproduction in Female Stingrays

Follicle Stimulating hormone (FSH) and luteinizing hormone (LH) are glycoproteins that are responsible for regulating gametogenesis and gamete maturation in all vertebrates. However, although these hormones have been detected in some elasmobranchs, no studies have examined temporal associations with reproduction in these fishes. The goal of this study was to examine temporal changes in circulating FSH and LH concentrations in relation to the reproductive cycle of the Atlantic stingray (*Dasyatis sabina*), an elasmobranch species with a well characterized breeding cycle. Plasma samples were collected from mature female *D. sabina* from all reproductive stages. FSH- and LH-like immunoreactivity was examined using Western Blot. Dot blot analysis was used to obtain semi-quantitative data on hormone concentrations. FSH-like immunoreactivity was observed in female stingrays from all reproductive stages except late pregnancy, when females nourish developing embryos with uterine histotroph. Changes in FSH-like immunoreactivity was determined during other reproductive stages. LH-immunoreactivity was detected in plasma from female stingrays, but results were poor and did not provide a clear understanding of temporal changes in this hormone. Potential associations between gonadotropins and reproduction in female stingrays will be discussed along with preliminary observations on levels of these hormones in male stingrays.

0026 Fish Ecology I, Salon A-C, Saturday 9 July 2016

Robert Shields, Mark Pyron, Mario Minder

Ball State University, Muncie, IN 47304, USA

Effects of Silver Carp on the Wabash River Ecosystem

Invasive Silver Carp (*Hypophthalmichthys molitrix*) have been abundant in many US rivers for over 20 years. Effects of this invasion include alteration of phytoplankton communities, competition with native fishes, and a potential shift in functional feeding group dominance among large river fishes. The increased dominance of benthic invertivore fishes in the Wabash River after the invasion of Asian carps may be an indication that benthic invertebrate consumers utilize carp feces. We examined long-term Wabash River fish assemblage data to identify relationships among Silver Carp and other fish species. We tested for effects of Asian carp fecal matter on growth and survival of bluntnose minnows (*Pimephales notatus*) and freshwater snails (*Pleurocera* spp) in mesocosm experiments. Ten minnows and 20 snails were added to each of 12 experimental stream mesocosms. Half of the mesocosms received chironomid larvae (*Chironomidae*) as food sources, while the other half received the same mass of Silver Carp fecal matter. Our results provide a more complete understanding of Asian carps in invaded ecosystems.

0030 AES GRUBER AWARD, Balconies J & K, Thursday 7 July 2016

David Shiffman, Neil Hammerschlag

University of Miami, Miami, FL, USA

Intraspecific Variation in the Relative Diet Breadth and Overlap of Coastal Sharks Revealed Through Stable Isotope Analysis

Determination of the diet and ecosystem role of sharks is a research priority that is important for understanding the potential consequences of population declines. Interactions between shark species can vary widely, with documented cases of both resource partitioning and significant diet overlap. We used stable isotope analysis to assess the relative diet breadth and overlap between eleven mesopredatory and apex predatory species of sharks in three distinct South Florida coastal habitats, testing whether the ecological interactions between species remained constant. The relative diet breadth and overlap between shark species was not constant between habitats. The diet of some species pairs overlapped almost 100% in one habitat, but didn't overlap at all in other habitats. The species with the widest relative diet breadth varied from one habitat to another, as did the species with the highest trophic level. This intraspecific variation between the diet breadth and diet overlap of shark species suggests that the ecosystem role of a marine predator in one environment cannot be reliably inferred from studies in a different environment, and that habitat-specific studies are required.

0058 Amphibian Ecology & General Herpetology, Salon F-H, Sunday 10 July 2016

Richard Shine, Michael Crossland, Jayna DeVore, Simon Ducatez, Greg Clarke
University of Sydney, NSW, Australia

Malevolent Tadpoles and Their Rapidly Evolving Weaponry

Many invasive species exploit disturbed habitats where native taxa are scarce, and the invader's greatest competitors are members of its own species. In response to that pressure, cane toad (*Rhinella marina*) tadpoles eliminate future competitors by producing chemicals with devastating effects on younger conspecifics (eggs and hatchlings). Remarkably, the intensity of this intraspecific competitive mechanism varies dramatically among different populations of cane toads. Production of the suppressor chemical, and sensitivity of the targeted eggs, is highest at the invasion front in Western Australia, intermediate in long-colonised sites in eastern Australia, and minimal in Hawai'i. That diversity plausibly reflects environmental factors that influence the costs and benefits of a chemical "arms race" between successive larval generations. The 80-year invasion of tropical Australia has prompted the rapid evolution of a powerful new mechanism of intraspecific suppression, so far unreported in any other anuran species.

0581 HL GRADUATE RESEARCH AWARD, Galerie 2, Thursday 7 July 2016

Jamie Shinskie, Amber Pitt, Tina Delahunty
Bloomsburg University, Bloomsburg, PA, USA

Influence of Land Cover Change on Eastern Hellbender Occurrence within the Susquehanna River Drainage of Pennsylvania

Habitat degradation and loss continue to be primary drivers of wildlife population declines and biodiversity loss. Anthropogenic land use along streams alters both terrestrial and aquatic habitats and detrimentally impacts aquatic species. We examined the influence of reach-scale land cover change on Eastern Hellbender (*Cryptobranchus alleganiensis alleganiensis*) population persistence and extirpation. We used environmental DNA (eDNA) sampling techniques to reassess previously documented hellbender sites (n=25) within the Susquehanna River drainage in Pennsylvania in order to determine population persistence or extirpation. We assessed land use/land cover change by comparing historical and recent aerial imagery for the study sites. Our results indicated that hellbenders were still present in only 9 of the 25 historical location sites. Extirpations of hellbender populations within the Susquehanna River drainage of Pennsylvania have resulted in range constriction, and extirpations corresponded with land use/land cover change. The results of our study can be used to inform hellbender conservation and reintroduction programs.

0260 AES Ecology & Behavior I, Balconies L & M, Thursday 7 July 2016

Oliver Shipley¹, Emily Tolentino², Lucy Howey-Jordan², Lance Jordan², Edward Brooks¹

¹*Shark Research and Conservation Program, The Cape Eleuthera Institute, Eleuthera, Bahamas,* ²*Microwave Telemetry Inc, Columbia, Maryland, USA*

Pop-up satellite archival tags reveal the extent of post-release survivorship and vertical habitat use in a data-deficient, deep-water chondrichthyan, the Cuban dogfish (*Squalus cubensis*)

Pop-up satellite archival tags have proven a valuable method to quantify behavioral modification and the extent of post-release survivorship in large fishes, which are ubiquitously caught in commercial fisheries worldwide. The need to assess these parameters is required within deep-water species, where the effects of fisheries exploitation are exacerbated by extreme *K*-selected life-history traits. We deployed 7 High Rate pop-up satellite archival tags (PSATs) on the data-deficient (IUCN), medium-bodied, deep-sea shark, the Cuban dogfish (*Squalus cubensis*), to investigate how experimental capture may affect susceptibility to post-release mortality. We examined: post-release recovery behavior, subsequent vertical movement, and incidents of predation. Data were retrieved from 6 individuals with deployment durations ranging from 5 to 14 days. Recovery periods (defined by <5m vertical movement between consecutive depth records, once individuals had returned to depth) ranged from 0 to 1.5 days among individuals, suggesting some animals required re-acclimatization before becoming active. Half of the tagged animals were consumed by predators within 24 hours of release during the active phase and after the initial recovery period. The three surviving individuals exhibited clear diel-vertical behavior (ca. 24 hour cycle) such that shallower depths were occupied during the night. Animals occupied depths between 903.8 m and 324.1 m and experienced temperatures between 5.83 to 18.26 °C. PSAT data suggest Cuban dogfish may be highly susceptible to post-release mortality, primarily through predation, after being released from longlines. Depth data also suggest this species may be highly susceptible to commercial fisheries capture, through movement across a broad depth range.

0439 General Herpetology, Galerie 2, Thursday 7 July 2016

Spencer Siddons, Jeff Wesner, Jacob Kerby

University of South Dakota, Vermillion, SD, USA

Increased species richness reduces pathogen infection risk in amphibians: a meta-analysis

In amphibian communities, the presence of pathogens such as *Batrachochytrium dendrobatidis* (Bd) and trematodes can reduce amphibian biodiversity and negatively alter aquatic ecosystems. Maintaining biodiversity is vital as it can reduce infection risk via the dilution effect. Herein, we report a meta-analysis in which we analyzed the

relationship between amphibian richness and infection risk to test the hypothesis that increased amphibian richness reduces the risk of infection by Bd and trematode pathogens. We found that treatments with >1 species reduced risk of infection by 48% on average relative to treatments with 1 species. There was no additional reduction in infection risk among treatments with 2-4 additional species. This suggests that the dilution effect saturates rapidly at relatively low species richness. Our results provide ecologically relevant insight into the dilution effect in amphibian communities, single host-pathogen studies, and the possibility of a positive feedback in which disease-related amphibian declines could make communities more at risk of infection and lead to further declines. We speculate that community composition or species interactions may be the mechanisms behind our results but further studies are needed to fully understand this relationship. These are important findings in light of ongoing amphibian declines as pathogens continue to play a major role.

0773 Fish Systematics II, Salon F-H, Saturday 9 July 2016

Brian Sidlauskas¹, Michael Alfaro², Michael Burns¹, Casey Dillman³, Brant Faircloth⁴, Kendra Hoekzema¹, Bruno Melo⁵, Mark Sabaj Perez⁶, Claudio Oliveira⁵, Richard Vari³

¹Oregon State University, Corvallis, OR, USA, ²University of California, Los Angeles, CA, USA, ³Smithsonian Institution, Washington, DC, USA, ⁴Louisiana State University, Baton Rouge, LA, USA, ⁵Universidade Estadual Paulista, Botucatu, SP, Brazil, ⁶Academy of Natural Sciences of Drexel University, Philadelphia, PA, USA

Morphological and Macroevolutionary Implications of a Densely Sampled Molecular Phylogeny for Anostomoidea (Characiformes)

Using Sanger sequencing and ultraconserved elements, we reconstruct the phylogeny for 70% of the ecomorphologically diverse characiform fishes in superfamily Anostomoidea. Comparison with a prior, equally rich morphological reconstruction reveals much congruence, but also significant disagreement on the placement of the headstanders in family Chilodontidae, the position of the morphologically divergent genus *Ichthyoelephas* within Prochilodontidae, and the placement of the superior-mouthed Anostominae within Anostomidae. These novel molecular placements suggest substantial oral jaw shape convergence within Anostomidae, and reinterpret features of the pharyngeal jaws and other systems as homoplastic or plesiomorphic for the superfamily rather than synapomorphic for Anostomidae and Chilodontidae. Several characters proposed originally as homoplasies optimize as synapomorphies on the molecular topology, such as the unique hypertrophy of the fourth upper pharyngeal toothplate shared by *Prochilodus* and *Semaprochilodus*. The phylogeny resolves longstanding polytomies resulting from scant or conflicting osteological variation the species-rich genera *Leporinus*, *Cyphocharax* and *Prochilodus*, thereby providing a framework for taxonomic revision and comparative phylogenetic analysis. Phylomorphospace analysis of head and gill arch shape variation reveals initial radiation of all four families into distinct morphospaces regions. Subsequent

diversification varies among families, with the ecomorphologically diverse Anostomidae demonstrating particularly high rates of change in oral and pharyngeal jaw shape, and the detritivorous Curimatidae diversifying substantially internally, but not externally. Evolutionary dynamics in Prochilodontidae differ and indicate early fixation of a highly specialized bauplan that apparently allows them to achieve huge body and population sizes but affords little opportunity for subsequent morphological diversification.

0006 Lightning Talks, Galerie 2, Saturday 9 July 2016

Dustin Siegel¹, Yousif Al-Baghdadi¹, Michael Frangelo¹, Madison Herrboldt¹, Sam Alvino¹, Stanley Trauth², David Sever²

¹*Southeast Missouri State University, Cape Girardeau, MO, USA*, ²*Arkansas State University, State University, AR, USA*, ³*Southeastern Louisiana University, Hammond, LA, USA*

“sexual Tears” in a salamander?

Historical observations detail the possibility of orbital gland involvement in reproduction of spelerpine salamander, particularly *Eurycea*. Orbital glands in *E. longicauda* were assessed for sexual dimorphism and a distinct seasonal secretory cycle that mirrored the reproductive cycle. Orbital glands were found not to be sexually dimorphic in *E. longicauda* and possessed constant secretory activity in males and females throughout the year. Known secondary sexual glands (mental glands, caudal courtship glands, and cloacal glands) were sexually dimorphic between males and females and possessed a secretory cycle that could be correlated with events of the reproductive cycle; i.e., hypertrophy of glands during the mating season. Thus, no evidence was found for orbital gland involvement in reproduction in *E. longicauda*. To this date, only one taxon of salamander, *E. bislineata*, was reported to have orbital glands involved in reproduction through rudimentary gross examination of the head of males and females. Orbital glands of both male and female *E. longicauda* produce copious lipoproteins throughout the year and these secretions are undoubtedly involved in the prevention of fluid evaporation from the eye and maintenance of a smooth corneal surface as described for lipoprotein secretions in other terrestrial vertebrate lineages.

0975 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Priscilla Silva, Maria Malabarba, Luiz Malabarba

UFRGS, Porto Alegre, RS, Brazil

Historical DNA solving taxonomic puzzles: examples in the family Characidae (Teleostei, Characiformes)

Historical DNA is the DNA isolated from ancient samples as subfossil bones, mummies, or museum specimens, which have not been preserved for later DNA analyses. The use

of this tool for biodiversity and evolutionary studies has increased due to the development of new techniques in molecular biology, like New Generation Sequencing. The high level of degradation of the DNA obtained from this kind of samples conversely turns traditional sequencing methodologies, like Sanger, less often in use. The use of historical DNA can help to solve taxonomical problems when name-bearing types have no more diagnostic morphological features that allow an accurate identification of the species involved. We were allowed to extract DNA from 53 type specimens stored in collections around the world, which were processed in the molecular biology facilities of the NMNH (Smithsonian Institution). The DNA extraction was conducted in a special clean room, free from any previous fish DNA handling, using commercial kits; whilst PCRs were carried out in an isolated chapel of a different laboratory. From the 53 samples, so far we amplified nine and obtained sequences for COI (Sanger sequencing) from five samples. We got a mean of 120 ng/ul of DNA in the extractions and no correlation between amount of DNA and age of the sample (collecting year) was observed. The sequences indicated taxonomically significant results for the proper recognition of the species *Deuterodon pedri* Eigenmann 1908, *Astyanax rutilus jequitinhonhae* (two syntypes) Steindachner 1877 and *Astyanax eigenmaniorum* Cope 1894.

0512 Poster Session I, Acadia/Bissonet, Friday 8 July 2016

Diana Lorena Silva-Garay¹, Ximena Vélez-Zuazo¹, John G. Ramírez², Aldo S. Pacheco³

¹Center for Conservation and Sustainability, Smithsonian Conservation Biology Institute, National Zoological Park, Washington, D.C., USA, ²Instituto de Ciencias del Mar de Barcelona CSIC-ICM, Barcelona, Spain, ³CENSOR Laboratory, Instituto de Ciencias Naturales Alexander von Humboldt, Universidad de Antofagasta, Antofagasta, Chile

Feeding Partitioning in an Assemblage of Demersal-Neritic Elasmobranchs in the Southeastern Pacific

Elasmobranchs play a regulatory role over prey populations; however, this is less understood for demersal-neritic species, which are facing numerous threats in coastal ecosystems. Dietary studies are a useful tool for understanding species role and their trophic interactions. To this purpose, we investigated the diet from stomach contents of four stingrays (*Dasyatis dipterura*, *Myliobatis peruvianus*, *M. chilensis*, *Urotrygon chilensis*), a guitarfish (*Rhinobatos planiceps*), a shark (*Mustelus mento*), and a chimaera (*Callorhynchus callorhynchus*) collected around an artificial reef along the central coast of Peru from 2012 to 2014. We investigated (1) their diet composition, trophic interactions, trophic level (TL) and niche breadth, and (2) the likely influence of the artificial reef in their feeding dynamics. We used the index of relative importance (IRI%) and PERMANOVA-test to this analysis. All species exhibited a high feeding specialization (Levin<0.3) and dietary separation (p<0.05). While stingrays preferred soft bottom polychaetes and pelagic teleost fish (p>0.09), the shark and guitarfish fed on crabs (p>0.06) and the chimaera

consumed mostly mollusks. The species which diet included bivalve mollusks were more associated with the artificial reef, an important hard-bottom food supply for species that feed on hard bottom prey items. The results highlight the relevance of the assemblage predatory activity (mean TL=2.85 ± 0.47) on a broad group of prey taxa and their predation over pelagic and benthic fauna gives insights of their feeding dynamic in this rich upwelling coastal ecosystem.

0129 AES Sawfishes Symposium, Salon E, Sunday 10 July 2016

Colin Simpfendorfer¹, Peter Kyne², Tansyn Noble¹, Julie Goldsbury¹, Rose Basiita¹, Rob Lindsay³, Amos Shields³, Camillus Perry⁴, Dean Jerry¹

¹James Cook University, Townsville, Queensland, Australia, ²Charles Darwin University, Darwin, Northern Territory, Australia, ³Malak Malak Ranger Group, Darwin, Northern Territory, Australia, ⁴Wudikupildiyerr Ranger Group, Darwin, Northern Territory, Australia

Environmental DNA detects Critically Endangered largetooth sawfish in the wild

Environmental DNA (eDNA) is a relatively new tool for the detection of rare, threatened and invasive species in water bodies. In this study we investigated the utility of an eDNA approach in detecting the Critically Endangered largetooth sawfish, *Pristis pristis*, in freshwater habitats in northern Australia. Water samples were collected from a large aquaria mesocosm containing sawfish and other aquatic species, and floodplain waterholes and the main river channel of the Daly River, Northern Territory. Water samples were filtered using a 20 µm nylon filter. DNA was extracted from filters and analysed with PCR using species -specific mitochondrial cytochrome oxidase subunit 1 (COI) primers designed to amplify only largetooth sawfish DNA. PCR products were cleaned and the COI gene sequenced to confirm the species identity. Testing this method using three aquaria, one containing a largetooth sawfish, positively identified sawfish only in the correct aquarium. In the field water samples, seven of eight floodplain waterholes produced a sawfish eDNA PCR product, while eDNA was not detected in the main river channel. Based on gillnet sampling and traditional ecological knowledge, sawfish were known to occur at half of the waterhole and floodplain sites that tested positive for sawfish eDNA. These results demonstrated that an eDNA approach to detecting largetooth sawfish can produce reliable results and can be used as a survey tool to help with conservation efforts for this and other threatened elasmobranchs.

0100 ASIH STOYE GENERAL ICHTHYOLOGY AWARD, Galerie 2, Friday 8 July 2016

Randy Singer, Lawrence Page

Florida Museum of Natural History/iDigBio, Gainesville, FL, USA

Jar Wars: The (data) Source Awakens: Exploring New Ichthyological Frontiers in Specimen-based Research, Education and Outreach

A long long time ago on a natural history collection shelf far far away, a jar of fish is placed on a shelf next to similar species with a label containing precious and irreplaceable data. These specimens collected over hundreds of years and ultimately encased within millions of jars, tanks and boxes in various states of curation await the careful examination by a researcher. In both the past and present these specimens and the data, tissues and photos have been utilized in numerous studies of taxonomy, phylogenetics, biogeography and ecology. In the advent of better media technology and in an age of rapid digitization of specimens and their data through digitization initiatives like iDigBio, we have only begun to scratch the surface of the usefulness of museum specimens like those housed in ichthyology collections. One specimen can answer dozens of research questions across many disciplines of biology. Some novel and underutilized research questions using fish specimens will be discussed. In addition to research uses of collections, outreach using collections has been largely limited to collection tours, specimen observations and the occasional outreach event hosted by the collection's home institution. In a similar light, creative education and outreach initiatives have begun to surface that require minimal effort for large amounts of impact. As we begin to enter a largely digital era, collections have begun to offer an unmatched service to the scientific community, and we have but to ask in order to unlock its potential.

0500 HL GRADUATE RESEARCH AWARD, Galerie 2, Friday 8 July 2016

Shashwat Sirsi¹, Shailendra Singh², Shawn F. McCracken¹, Michael R.J. Forstner¹

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Variation in Reproductive Output of two Endangered Freshwater Turtles (*Batagur* spp.) in North India

The largest known wild population of the endangered Three-striped Roofed Turtle (*Batagur dhongoka*) and last known wild population of the critically endangered Red-crowned Roofed Turtle (*Batagur kachuga*) occur in the Chambal River of North India. Both species are threatened by habitat loss, offtake and accidental drowning in gill nets. Three years of field work (2007, 2008 and 2010) from ongoing population supplementation projects were used to examine annual differences in reproductive output among and within species. Nests were located each year using boat-based surveys and foot patrols. Clutch sizes were enumerated for each nest and egg volumes

were calculated for a subset of nests. Generalized linear models were used to determine annual differences in number of nests while ANOVAs were used to test for annual differences in fecundity and egg volume. The number of nests differed significantly for both species - with the greatest number of nests occurring in 2007 and mid-season (nesting season: February to April; peak season: late February through March) across all years. Fecundity also showed a significant annual decline. Available habitat and resource acquisition patterns may affect these differences. Additionally, *B. kachuga* was found to lay significantly larger and fewer eggs than *B. dhongoka*, but within year trends for clutch size imply that two nesting events annually occur in the latter. These data shed some light on these poorly documented species in need of better conservation coverage.

1088 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Garrett Sisson, Willem Roosenburg, Shawn Kuchta

Ohio University, Athens, Ohio, USA

When the Rocks are Hotter on the other side of the Fence: Use of Roadside Habitats by Reptiles and Consequences for Mitigation Structures

Roads threaten wildlife populations by destroying and fragmenting habitats, isolating populations, and increasing mortality, among other impacts. Barrier fencing and ecopassages are used to reduce mortality and promote population connectivity, but their effectiveness for reptiles and other small vertebrates remains understudied. We evaluated the effectiveness of barrier fencing and ecopassages for reptiles occurring along a four-lane divided highway in southeastern Ohio. Radio telemetry and capture-mark-recapture on multiple species revealed that snakes trespass the fencing to access habitats located within the right-of-way (ROW). Edge habitat and artificial rocky structures along the roadside may attract snakes because they provide habitat where snakes can thermoregulate and avoid predators. Use of roadside habitat may be intensified if basking habitat in the surrounding landscape is rare or of poor quality. However, if using roadside habitats results in additive mortality from vehicle collisions, higher predation rates, or collection, then these features are ecological traps. Determining whether roadside habitats can have compensatory benefits or function as ecological traps is needed to manage these areas, and inform the design and placement of functional barrier fencing. In 2016 we will compare habitat use and mortality between ROW and forest habitats, and quantify the thermal environment to determine if snakes are using ROW habitats for thermal opportunities unavailable elsewhere within their home ranges.

0473 ASIH STOYE AWARD GENERAL HERPETOLOGY, Salon F-H, Friday 8 July 2016

Phillip Skipwith¹, Paul Oliver²

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Phylogeography of the marbled velvet gecko (*Oedura marmorata*) species complex in the Australian Monsoonal Tropics

The monsoonal tropics of northern Australia has been found to harbor high species diversity as well as numerous short-range endemic lineages. Many of these lineages are tied to important biogeographic barriers including numerous river drainages, limestone escarpments, and tropical regions isolated by extensions of the arid zone. Here, we investigate the phylogeographic patterns of the diplodactylid gecko *Oedura marmorata*. An extensive mtDNA dataset strongly indicates that there are at least seven distinct lineages, including what has been referred to as *O. gemmata*, though inter-clade relationships are poorly resolved. These mitochondrial clades correspond somewhat to the Daly River drainage, Carpentarian Gap, and Arnhem Plateau. However, preliminary data based on 4,000 ultraconserved elements suggests a different pattern of relationships, though this tree has very limited sampling. Several lineages appear to be closely tied to limestone formations while others seem generalized on karst and vegetation. Morphological diversity is high in this species complex and rupicolous lineages are noted in having longer limbs and flatter heads. However, phenotypic convergence analyses fail to find shared morphological regimes between any *O. marmorata* lineage and other distantly related but ecologically similar dipodactylids based on external ecomorphology. This species complex illustrates the high genetic and morphologic diversity maintained in the geologically old monsoonal tropics of northern Australia.

0407 AES Ecology & Behavior I, Balconies L & M, Thursday 7 July 2016

Rachel Skubel, Neil Hammerschlag

University of Miami, Miami, FL, USA

Estimates of apex predatory sharks' energetic scope from long-term multi-sensor tags, and applications to climate change

All animals' performance is inherently limited by temperature. Quantifying a species' optimal thermal environment, particularly for ectothermic fish whose body temperature is dictated by that of the surrounding water, is necessary in order to project their behaviors with respect to climate change. Here, we demonstrate a novel application of estimation of pop-up satellite archival tag (PSAT) acceleration data to estimate temperature preferences of apex predatory sharks in the wild, including the longest accelerometry record for any organism to date (378 days). For three tiger sharks (*Galeocerdo cuvier*) and two great hammerhead sharks (*Sphyrna mokarran*), vectorial

dynamic body acceleration (a proxy for oxygen consumption) was calculated from acceleration along three axes, and then related to ambient water temperature to approximate scope for oxygen consumption over a temperature range. Tiger sharks, tracked for 31, 22, and 378 days had greatest oxygen consumption in cooler waters (~10-20°C). Great hammerhead sharks, tracked for 8 and 10 days, consistently exploited warm shallow waters. Tiger sharks' scope for oxygen consumption declined sharply between 30 and 31°C, while great hammerhead sharks appeared not to reach waters warm enough to result in a significant decline. These results (a) suggest that tiger sharks spend most of their time in waters warmer than optimal for oxygen consumption, as a possible tradeoff for foraging and reproduction opportunities, and (b) demonstrate the feasibility of using long-term accelerometry records to obtain physiologically relevant estimates of thermal preferences.

0890 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Veronica Slobodian¹, Gleidson Figueiredo², Janice Muriel-Cunha²

¹MZUSP- Museu de Zoologia da Universidade de São Paulo, São Paulo, SP, Brazil,

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Taxonomy of cave and epigeal *Pimelodella* species (Siluriformes: Heptapteridae) from Southeastern Brazil

Cavefishes and related surface fishes have been used as models in studies of convergent evolution and phylogeography. However, in order to make solid studies in these matters, the taxonomy decisions must be carefully taken, and the exclusive use of troglomorphic autapomorphies itself has been shown as questionable to delimit species. Concerning the cavefish *Pimelodella kronei* and its related epigeal species, *Pimelodella transitoria*, we conducted a morphological study, aiming to determine the validity and delimitation of both species, using external morphology, meristics, osteology, myology and sensory canals information. We found that populations of *P. kronei* of distinct cave sets from the same karstic area (Iporanga, Upper Ribeira de Iguape basin), which are isolated, bear no significant morphological differences. Populations of *P. transitoria* near those caves also bear no consistent morphological differences, but these populations near cave entrances are different from populations found along rivers from Ribeira de Iguape basin. The populations of *Pimelodella* found far from cave entrances and usually identified as *P. transitoria* are, in their turn, indistinguishable from *Pimelodella lateristriga*, that inhabits rivers along the Southeastern Atlantic basins. The differences found between *P. kronei* and *P. transitoria* near cave entrances populations constitute mostly of troglomorphisms. We discuss the possibility of *P. transitoria* being a junior-synonym of *P. kronei*.

0495 Herp Conservation, Galerie 3, Saturday 9 July 2016

Peter Smiley Jr.¹, Mark Jordan², Abel Castaneda², Robert Gillespie², Douglas Smith³, Kevin King¹

¹USDA-ARS, Columbus, Ohio, USA, ²Indiana University-Purdue University, Fort Wayne, Indiana, USA, ³USDA-ARS, West Lafayette, Indiana, USA

Conservation Implications of Amphibian Habitat Relationships within Channelized Agricultural Headwater Streams in the Midwestern United States

The widespread use of stream channelization and subsurface tile drainage for removing water from agricultural fields has led to the development of numerous channelized agricultural headwater streams within agricultural watersheds of the Midwestern United States. Channelized agricultural headwater streams have been documented to serve as habitat for amphibians, but information on amphibian habitat relationships within these streams is lacking and needed for developing effective conservation strategies. We quantified instream habitat, water chemistry, and sampled amphibians from seven sites in three channelized streams in Cedar Creek, Indiana in 2008 and 2009 and five sites in five channelized streams in Upper Big Walnut Creek, Ohio in 2009. We conducted an indirect gradient analysis involving the use of Principal Component Analysis and Generalized Linear Mixed Effect Model Analysis to determine which variables had the greatest influence on amphibian community and population structure. Overall, amphibian community and population structure was most strongly correlated with water chemistry rather than instream habitat within channelized agricultural headwater streams in Indiana and Ohio. Ten of 12 amphibian response variables were most strongly correlated with either a water chemistry gradient of nitrate+nitrite and acetochlor or a gradient of total nitrogen and ammonia. Only two amphibian response variables were most strongly correlated with an instream habitat gradient of dissolved oxygen and water depth. Our results suggest that conservation strategies that target reductions of nutrients and herbicides will provide the greatest benefits for amphibians within channelized agricultural headwater streams in the Midwestern United States.

0872 HL GRADUATE RESEARCH AWARD, Galerie 2, Friday 8 July 2016

Sarah A. Smiley-Walters¹, Terence M. Farrell², H. Lisle Gibbs¹

¹The Ohio State University, Columbus, Ohio, USA, ²Stetson University, DeLand, Florida, USA

Venoms of Pigmy Rattlesnakes (*Sistrurus miliarius*) Show Significant Functional Differences on Prey Mortality

Snake venom composition varies between species, populations, and individuals, yet the functional significance of this variation is poorly understood, especially at the level of individual snakes. Our previous work has shown that pooled venoms from different populations of pigmy rattlesnakes have a slightly different functional response in treefrog prey. In this study, we examined whether venom collected from 32 individual

pigmy rattlesnakes (*Sistrurus miliarius*) from 7 different populations differed in its toxicity to a prey species – the brown anole (*Anolis sagrei*). We conducted toxicity tests in which lizards were injected with weight-adjusted dosages (close to the expected LD50) of venom from randomly chosen individual snakes or saline controls. A total of 384 venom-injected lizards and 37 saline-injected controls were used in this study. Lizards were monitored out to 48 hours post-injection. Of the 384 venom-injected lizards, 135 were dead by 48 hours, resulting in a mortality rate of 35.2%. Lizard mortalities were not equally distributed among snakes. The number of kills per snake was bi-modal with some snake venoms being very lethal to lizards while others induced no mortality. Using a logistic regression, lizard mortality was significantly explained by venom concentration (Chi-squared = 81.3, $p < 0.001$), population of snake origin (Chi-squared = 41.9, $p < 0.001$), and individual snake nested within population (Chi-squared = 113.2, $p < 0.001$). This work provides evidence that previously well-documented differences in venom composition between individuals and populations likely have functional consequences for the ability of snakes to capture prey.

0530 General Ichthyology II, Balconies J & K, Sunday 10 July 2016

Amelia Smith¹, James Sulikowski¹, John Mandelman², David Rudders³

¹University of New England, Biddeford, Maine, USA, ²New England Aquarium, Boston, Massachusetts, USA, ³Virginia Institute of Marine Science, Gloucester Point, Virginia, USA

Stress and discard mortality of *Lophius americanus* in the scallop dredge fishery

Post-release mortality (PRM) studies are considered a primary research priority, particularly for species and fisheries where discard rates are high, and/or for overfished stocks and species of concern. *Lophius americanus*, the most lucrative finfish in New England, constitutes the second highest bycatch species within the scallop dredge fishery. Despite its commercial importance, no data exists on the mortality rates of monkfish for any gear type. Given these shortcomings, our goals were to evaluate the stress and PRM of monkfish captured in scallop dredge gear. This was accomplished by assessing various physical and physiological conditions. To quantify stress levels, blood samples were taken to measure cortisol, lactate, hemoglobin, and hematocrit concentrations. In addition, a series of reflex responses were tested and injury codes, ranging from 1 (uninjured) to 4 (dead), were assigned to each monkfish in order to develop vitality indices. To correlate the aforementioned parameters to discard mortality, monkfish were held in onboard flow-through seawater tanks and all stress indicators were reassessed after a 72-hour holding period. Preliminary results suggest that average cortisol levels increased as assigned injury code (injury 1 = 4.8 ng/ml; injury 3 = 15.7 ng/ml) increased while lactate (injury 1 = 0.9 mmol/L; injury 3 = 0.5 mmol/L), hemoglobin (injury 1 = 2.2 g/dl; injury 3 = 1.4 g/dl) and hematocrit (injury 1 = 12.7%; injury 3 = 10.9%) concentrations were unexpectedly decreased. Analysis of the

tank study indicates that 80% of monkfish placed in holding tanks died after 72 hours, regardless of initial vitality index.

0540 Herp Ecology, Salon F-H, Sunday 10 July 2016

Brian J. Smith¹, Christina M. Romagosa², Frank J. Mazzotti¹, Mathieu Basille¹, Kristen M. Hart³

¹University of Florida - FLREC, Davie, FL, USA, ²University of Florida, Gainesville, FL, USA, ³US Geological Survey - WARC, Davie, FL, USA

Does GPS Technology Help Refine Our Understanding of Invasive Burmese Python Spatial Ecology?

In the last two decades, invasive Burmese pythons (*Python bivittatus*) have spread throughout the Greater Everglades and have severely affected native wildlife. Monitoring and managing their population has proven extremely challenging, and a better understanding of python spatial ecology in the Everglades would improve our ability to remove pythons and mitigate their effects on the ecosystem. GPS technology could allow for detailed analysis of spatial behavior at a fine temporal resolution, but the application of GPS telemetry in snakes is largely untested. We GPS-tagged 12 wild Burmese pythons in Everglades National Park between July and December 2015, with the tags programmed to attempt a GPS fix every 90-minutes. While preliminary analysis of GPS data showed that 81% of attempted fixes failed (n=4394), we were still able to identify patterns. All pythons exhibited a movement bout every 3-5 weeks, and analysis of selection ratios suggested that pythons positively selected only dry prairie overall, with no difference in habitat selection between daytime and nighttime locations. However, published analyses of VHF data showed that pythons tend to select habitats with dense vegetation, suggesting a potential habitat-driven bias in GPS fix success. Although GPS telemetry has the potential to reveal important patterns of python spatial behavior, such as movement patterns and rates, the potential for habitat-driven bias in GPS relocations must be considered.

0496 ASIH: ASIH at 100 Symposium, Salon D, Saturday 9 July 2016

David Smith

Smithsonian Institution, Washington, DC, USA

Ichthyology, herpetology, and the world in 1916

The ASIH was organized in 1916 and held its first meeting in New York at the American Museum of Natural History. What was the world like in those days? If you were a herpetologist or ichthyologist in 1916, what did you know? What did you not know? How did you communicate? How did you get around? Where did you publish your work? In this presentation, I will talk about that first meeting and about the world that

those ichthyologists and herpetologists worked and lived in, a very different place from our world today.

0462 AES Conservation & Management II, Balconies L & M, Saturday 9 July 2016

Kelcee Smith¹, Sabrina Taylor¹, William Kelso¹, Michael Kaller¹, John Carlson², Dana Bethea²

¹Louisiana State University, Baton Rouge, LA, USA, ²NOAA Fisheries Service - Southeast Fisheries Science Center, Panama City, FL, USA

Estimating Abundance of Smalltooth Sawfish (*Pristis pectinata*) with Capture-Mark-Recapture Data

In the United States, the Smalltooth Sawfish (*Pristis pectinata*) is an endangered elasmobranch currently comprising a single population restricted to southwestern Florida. The population has been drastically reduced and fragmented during the 20th century due to overfishing and habitat loss and was listed federally as endangered in 2003. Although habitat use and migration, age and growth, and other life history characteristics have been studied, current abundance remains unknown. Capture-mark-recapture data collected in southwestern Florida from 2009-2015 was used to determine a contemporary census size of juvenile *P. pectinata*. Data were separated into two cohorts (spring/summer & fall/winter) based on length-frequency distribution in order to minimize zeroes in the dataset. Program MARK was used to estimate recapture probabilities and apparent survival from individual capture histories, assuming a closed population. Models with time dependent capture probability and constant recapture probability estimated 181 and 79 individuals in the spring/summer and fall/winter cohorts, respectively. Estimates of population size largely determine risk of extinction in population viability analysis; therefore, historic population estimates will be compared to contemporary estimates of abundance to assess the extent of the population decline and extinction risk, allowing for more direct and effective management, conservation, and recovery efforts for the species.

0983 ASIH STOYE ECOLOGY & ETHOLOGY AWARD, Salon E, Friday 8 July 2016

Thomas Smith

University of Hawaii at Manoa, Honolulu, HI, USA

I Come From the Land Down Under: Ecological Niche Modeling of Hierarchical Spatial Scales to Predict the Range of an Invasive Skink in Hawaii

The delicate skink, *Lampropholis delicata*, represents an example of a successful invasive reptile with a single introduction, from a single source population with limited genetic diversity. All individuals across the main Hawaiian Islands share one haplotype with their introduction source in suburban Brisbane, Australia. The extent of the native range of the species, however spans the entire eastern coast of Australia, and includes 120 haplotypes. The source of the introduction represents a small geographic area with a narrow range of environmental conditions relative to its introduced range in the Hawaiian Islands. Nineteen environmental variables were obtained from BioClim and occurrence records were collected from VertNet for both the native and introduced ranges, and ecological niche models (ENMSs) were constructed using Maxent. Therefore, the objectives of this study were to use population, clade, and entire native distribution environmental data to 1) model whether conditions present at the source population accurately predict the niche of introduced populations and 2) use this prediction to evaluate potential range expansions. This study has implications for the long-term invasion assessment and management strategy of *L. delicata* across the Pacific Basin as well as implications for invasive systems of similar taxa where limited native geographic ranges or single introductions obscure the potential invasibility in a novel environment.

0585 Fish Systematics I, Salon F-H, Saturday 9 July 2016

W. Leo Smith¹, Jennifer Stern¹, Matthew Girard¹, Matthew Davis²

¹*University of Kansas, Lawrence, Kansas, USA*, ²*Saint Cloud State University, Saint Cloud, Minnesota, USA*

Phylogenetic and Anatomical Diversity of Venomous Cartilaginous and Ray-Finned Fishes

Venoms and their associated delivery structures have been explored in a diversity of cartilaginous and ray-finned fish clades. Building off new and previously published anatomical studies, we will show the results of a molecular phylogenetic analysis across cartilaginous and ray-finned fishes that hypothesizes at least 18 independent evolutions of this specialization. Likelihood ancestral-states reconstructions of venomous structures indicate that they have evolved four times in extant cartilaginous fishes, once in eels (Anguilliformes), once in catfishes (Siluriformes), and 12 times in spiny-rayed fishes (Acanthomorpha). From our anatomical studies and phylogenetic reconstruction, we

show that dorsal spines are the most common envenomed structures (~95% of venomous fish species and 15 independent evolutions). In addition to envenomed spines, fishes have also evolved venomous fangs (2% of venomous fish species, two independent evolutions), cleithral spines (2% of venomous fish species, one independent evolution), and opercular or subopercular spines (1% of venomous fish species, three independent evolutions). The diversity, anatomy, and biology of each venomous clade will be discussed.

1028 General Herpetology, Galerie 2, Thursday 7 July 2016

Itzue Caviedes Solis, Adam Leache

University of Washington, Seattle, Washington, USA

Leap frogging the Mexican Highlands: diversification of the *Plectrohyla bistincta* species complex (Anura: Hylidae)

The geological history of the Mexican highlands has influenced the diversification of the genus *Plectrohyla*. Most of the species are microendemic; however, some widespread species still enclose cryptic diversity with unique levels of gene flow. The present study aims to understand the biogeographical events that influenced the diversification of the *Plectrohyla bistincta* complex across the Mexican highlands. The complex includes the widespread species *P. bistincta*, which is paraphyletic to *P. pentheter* and *P. calthula*. We collected ddRADseq data for 51 individuals from 42 localities along eight mountain systems to identify the number of genetically distinct populations and cryptic species. The ddRADseq data matrix contained 3,113 loci and 1,484 SNPs. We implemented a k-means clustering algorithm of unlinked SNPs to determine the number of populations, which supported six clusters: four groups within *P. bistincta*, *P. calthula*, and *P. pentheter*. A species tree estimated using SNAPP, a multispecies coalescent model method that uses unlinked bi-allelic markers, does not support the monophyly of *P. bistincta*. For *P. bistincta* Transvolcanic Belt and Sierra Madre Occidental enclose a distinctive population, and Sierra Mixteca represents a barrier between lineages from Sierra Madre del Sur of Oaxaca and Guerrero. *P. calthula* and *P. pentheter* are restricted to Sierra Mixte and Sierra madre del Sur, respectively. Speciation and population structure in the complex has been determined by geological events, landscape modifications, and climate changes during the Pleistocene. Despite their similarities in morphology and natural history, the Mexican highlands played an important role in lineage diversification in *Plectrohyla*.

0232 Lightning Talks, Galerie 2, Saturday 9 July 2016

Ann Somers, Aerin Benavides, Catherine Matthews

University of North Carolina at Greensboro, Greensboro, N.C., USA

Lassoing Lizards, Trapping Turtles, and Snatching Snakes

The HERP Project (Herpetology Education in Rural Places & Spaces) developed six curricula for herpetology education in informal science education settings. These curricula, designed for our summer programs called Herpetological Research Experiences (HRE), were developed over a five year period to engage youth from a variety of backgrounds with snakes, lizards, stream amphibians, ephemeral pools, box turtles, and semi-aquatic turtles. Instead of listening to talks, participants in our programs engage in hands-on activities facilitated by scientists and environmental educators to learn how to safely capture wild reptiles and amphibians. Students collect and report morphometric and habitat data and then release the animals safely at the point of capture. Instead of just holding pet-store snakes, as is the tradition in many nature centers, participants learn how to catch wild snakes that might bite. They trap and mark aquatic turtles, lassoed lizards, check cover boards, and track box turtles. The program has been effective in engaging youth with nature and with STEM. Additionally, many of our participants have had limited experience and little affinity with the natural world prior to the HRE. After the HREs, youth's stories overwhelmingly had to do with the novel experience of collecting data on animals in the wild, laced with descriptions of excitement and overcoming fear. The curricula are available for free download.

0364 ASIH STOYE AWARD CONSERVATION, SALON E, Thursday 7 July 2016

Julia Sonn, Cori Richards-Zawacki

Tulane University, New Orleans, LA, USA

The Influence of Temperature on Chytridiomycosis In Vivo

Identifying which environmental features are most influential in the spread and virulence of emerging pathogens can be critical to the prevention of diseases. For example, high temperatures appear to negatively impact the fungal pathogen *Batrachochytrium dendrobatidis* (Bd) and may inhibit the persistence of amphibian chytridiomycosis in certain habitats. We investigated the effects of small differences in host body temperature on pathogenicity of Bd and the outcome of infection in Northern cricket frogs (*Acris crepitans*), a species that is reported to be declining in the northern part of its range. We chose six temperature treatments (11, 14, 17, 20, 23, and 26°C) based on the thermal range of the fungus and analyzed how these treatments affected the course of infection with Bd. Our results will provide insight into the influence of host body temperature on Bd infection, which can be used to model the pathogenicity of chytrid fungus within living amphibian hosts. In addition, to better understand the

effects of season and latitude on Bd, we took temperature data from wild cricket frogs and tested them for Bd. We tested the hypotheses that 1) hosts exhibit behavioral thermoregulation and that infected individuals choose warmer microclimates than uninfected individuals and 2) that infection intensity differs with latitude and season. Our results will help predict times and locations during which hosts are unable to reach body temperatures needed to avoid or combat Bd, leaving them susceptible to declines and extinctions.

0590 AES Ecology & Behavior II, Balconies J & K, Saturday 9 July 2016

Conrad Speed¹, Mark Meekan¹, Mike Cappel²

¹*Australian Institute of Marine Science, Perth, Western Australia, Australia,*

²*Australian Institute of Marine Science, Townsville, Queensland, Australia*

Evidence of recovery of shark and ray populations at a remote Marine Reserve in north Western Australia

There is an ongoing debate about the efficacy of Marine Reserves to protect large and highly mobile organisms. Using Baited Underwater Video Stations (BRUVS) as part of the Global FinPrint Project, we assessed whether elasmobranch abundance and diversity has changed with Marine Reserve enforcement at Ashmore Reef, Western Australia. Ashmore Reef is an emergent continental shelf-edge reef in the Indian Ocean, located 800 km west of Darwin and 140 km south of Indonesia. A Commonwealth Marine Reserve was established in 1983, although historically this area was fished by traditional Indonesian fishers. Illegal fishing has since been observed at Ashmore; however Australian Customs have had an ongoing permanent presence at the reef since 2000. We compare archival data from a 2004 BRUVS survey with a recent survey in 2016. We deployed over 100 BRUVS during 2016 around the shallow (0-40 m) reef slope and backreef habitats within the Marine Reserve. The shark assemblage was dominated by *Carcharhinus amblyrhynchos* in the current and previous surveys. The current survey showed numerous species that were not observed in 2004, such as: *Galeocerdo cuvier*, *Nebrius ferrugineus*, *Stegostoma fasciatum*, and *Himantura granulata*. Members of the Rhynchobatidae family were also observed more frequently in the current survey. Our results might have been due to a greater extent of spatial sampling in 2016, or seasonal differences in species distribution between the two surveys. We assess how species distribution and abundance varies across habitats, depth, and through time and discuss whether changes to border enforcement have affected elasmobranch populations.

**0319 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; STORER AWARD
HERPETOLOGY**

McKayla Spencer, C.M. Gienger

Austin Peay State University, Clarksville, TN, USA

**Metabolic and Thermal Responses to Feeding: Comparing a Semi-aquatic and
a Terrestrial *Agkistrodon* Species**

Investigating patterns of energy use by different species gives insight into survivorship and general ecology. Commonly used measures such as Standard Metabolic Rate (SMR) and Specific Dynamic Action (SDA) are especially informative for comparing patterns of energy use among species and in comparing sources of variation in energy use. Cottonmouths (*Agkistrodon piscivorus*) and Copperheads (*Agkistrodon contortrix*) offer a unique situation for comparison of patterns of energy use because of their differing ecologies and diets. Cottonmouths are a semi-aquatic species foraging opportunistically on a variety of prey, while Copperheads are terrestrial and primarily prey on rodents. Data was collected using an open-system respirometer to measure metabolism and a laboratory thermal gradient to measure post-prandial body temperature selection by digesting snakes. We measured standard and post-prandial metabolism of the two species at different temperatures and at different levels of feeding (meal sizes). Analysis is ongoing to compare energy use as a function of physiological and behavioral responses to feeding between two *Agkistrodon* species.

**0591 ASIH STOYE AWARD CONSERVATION, SALON E, Thursday 7 July
2016**

Brenton Spies¹, David Jacobs¹, Camm Swift², Ryan Ellingson¹

¹*University of California, Los Angeles, Los Angeles, CA, USA*, ²*Natural History
Museum of Los Angeles, Los Angeles, CA, USA*

Evolution, Speciation, and Endangerment of the Tidewater Gobies

The endangered closed-estuary specialist goby genus *Eucyclogobius*, the tidewater gobies, is the most locally differentiated vertebrate taxon on the Pacific coast. It is subdivided into regional clades, which are further subdivided into long isolated entities. Clades and subclades exhibit regionally distinct metapopulation processes. In addition, the southernmost clade is deeply divergent with a lineage separation occurring in excess of a million years ago. It is reciprocally monophyletic in nuclear and mitochondrial markers and morphologically distinct in counted lateral line attributes, fin rays, and measured characters as determined by discriminant function analysis as well as rate of development. This distinctive southern entity is currently under review as a new species. The southern tidewater goby is critically endangered, having been reduced to three small lagoonal populations on Camp Pendleton, Northern San Diego County. Captive refuge populations derived from the three remaining populations have recently been established to reduce the risk of extinction associated with the vulnerability to

drought and flood. Due to their metapopulation process and subdivision, the Tidewater Gobies are of exceptional scientific interest. We will outline the events that led to range reduction and endangerment of the southern species, current status and management goals, as well as the steps being taken to increase their likelihood of persistence.

1007 General Herpetology, Galerie 3, Thursday 7 July 2016

Kari Spivey, Brian Greene

Missouri State University, Springfield, MO, USA

Variation in venom expenditure in cottonmouths (*Agkistrodon piscivorus*) across prey sizes, prey types, and snake body temperatures

Pit vipers possess a sophisticated venom delivery system enabling them to efficiently disable prey. To avoid retaliatory countermeasures, snakes typically release envenomated prey which are then trailed and consumed after succumbing to venom effects. Successful retrieval of released prey should vary with venom resistance and trail ability of prey types. Rattlesnakes have been suggested to adaptively modify envenomation strategies to compensate for variation in prey susceptibility: adjusting venom expenditure and holding, rather than releasing, prey. Variation in envenomation strategies has been evaluated in a limited number of snake species. We examined the effects of prey size and prey type (mice, lizards, and frogs) on foraging behavior and venom expenditure in a cohort of juvenile cottonmouths. In the prey size experiment snakes injected significantly larger amounts of venom into small mice than in larger size classes. Venom expenditure did not vary significantly among prey types. However, lizard prey were held significantly more often, and survived significantly longer, than mice. We also evaluated the effect of snake body temperature on foraging response variables across a range of ecologically relevant temperatures (18°C-30°C). Cottonmouths were equally willing to forage across the entire range of body temperature treatments but injected significantly less venom, and held prey significantly more often, at 18°C than at 25 or 30°C. These results are consistent with a thermal constraint on envenomation performance at lower operant temperatures. Overall, our results suggest that cottonmouths modify foraging behavior to compensate for both venom resistance in ectothermic prey and decreased performance at lower temperatures.

**0962 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; STORER AWARD
ICHTHYOLOGY**

Geoffry Spooner¹, Reid Adams¹, Lindsey Lewis²

¹University of Central Arkansas, Conway, AR, USA, ²US Fish and Wildlife Service, Conway, AR, USA

Upriver Population Characteristics of the Ohio shrimp, *Macrobrachium ohione*, in Arkansas

The Ohio shrimp (*Macrobrachium ohione*) is amphidromous, where marine habitats are required for early juvenile development, but other life stages are able to be completed in freshwater. In the Mississippi River system, upriver adult habitat historically included the Ohio River and Upper Mississippi River, but abundance has reportedly declined, particularly upriver of Louisiana. Migration has been hypothesized to be impacted by dams and channel flow alterations. Current range, abundance, and life history of Ohio shrimp are relatively unknown upriver of Louisiana. During May-October of 2015, 48 Ohio shrimp were trapped in the lower Arkansas River, eight in the White River, two in the St. Francis River system, and 43 in the Arkansas reach of the Mississippi River. These are the first collections indicating tributaries to the Mississippi River in Arkansas are upriver habitat for Ohio Shrimp. Young-of-year females were more abundant than males, but Age-1 females were rarely caught compared to Age-1 males. Our overall upriver sex ratio was 60% male and 40% female, whereas coastal populations tend to be female skewed. Additionally, four Age-1 females were caught in the White River during late June/early July 2015 that had eggs visible between the swimmerets suggesting downriver reproductive migrations by adult females. Ohio shrimp occur in Arkansas habitats greater than 600 river kilometers from the Gulf of Mexico and show patterns suggestive of downriver female migration to complete the amphidromous life cycle.

0721 Herp Conservation & Ecology, Galerie 2, Sunday 10 July 2016

James Spotila¹, Pilar Santidrián Tomillo², Gabriela Blanco³, Nathan Robinson⁴, Rotney Piedra⁵, Bryan Wallace⁶, Vincent Saba⁷, Tera Dornfeld⁸, Julianne Koval⁴, Jennifer Swiggs⁴, Pamela Plotkin⁹, Richard Reina¹⁰, Anthony Steyermark¹¹, Frank Paladino⁴

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27 Years and Counting: Leatherback Turtles, *Dermochelys coriacea*, at Parque Marino Nacional Las Baulas in Costa Rica- Down but not Out!

We have been measuring the size of the leatherback turtle population at Parque Marino Nacional Las Baulas in Costa Rica since 1988. During that time we have marked 1993 nesting females and produced about 1,132,000 hatchlings from the beach and a hatchery. In 1988 the population was 1504 nesting females. In 2015-2016 the population was 25. That decline was predicted in a population model that we published in 2000. At that time we predicted that there would be about 25 turtles nesting in 2015 even with beach protection, an end to egg poaching and a hatchery. While the park has been partially consolidated and construction of homes and hotels stopped, the population has still declined. The decline still appears to be due to mortality at sea due to fishing activities such as gill nets and longlines along the South American coast. Mortality rates remain about 22% per year on nesting females and are probably the same on subadult animals. Unless these activities change the population will not survive. The adult population nesting at Las Baulas and Northwest Costa Rica is about 120 nesting females and the East Pacific nesting leatherback population is about 300. While these numbers are very disappointing from a conservation perspective, it is important to note that the population can still recover. Protection of nesting turtles and their beaches provides a continuing supply of hatchlings to the population. If protection can be improved at sea the population can rebound.

1092 Fish Ecology I, Salon A-C, Saturday 9 July 2016

Griffin Srednick, Mark Steele

California State University, Northridge, Northridge, California, USA

Influence of the Structure of an Invasive Alga on the Distribution of Fishes

In temperate marine environments, the physical structure of algae (e.g. giant kelp) can provide important shelter from predation for juvenile fishes and increased access to

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food. Recent variation in local sea surface temperature has led to decreases in giant kelp and increases in the invasive alga *Sargassum horneri* along the southern California coast. The structure provided by *S. horneri* is far different than that of giant kelp (especially the height), as well as many of the native algae. These changes are expected to alter the distribution of fishes throughout the water column. To investigate the effects of these changes, we conducted underwater visual surveys of the fish and algal assemblage at seven sites along the leeward coast of Santa Catalina Island. Transect surveys were performed at three strata: upper-water column, mid-water column, and benthic, to quantify differences in the fish assemblage due to variation in algal structure. The results indicate that the fish assemblage differs among different depth strata and that this difference depends on the type and density of algae present. There were seasonal differences in the fish assemblage among sites due to differences in algal composition and density among seasons. The results of this study indicate that the fish assemblage is influenced by changes in algal structure, and suggests the importance of considering algal identity, structure, and density when attempting to predict fish distribution in a changing marine environment.

0567 Poster Session I, Acadia/Bissonet, Friday 8 July 2016

Katherine St. Clair, Tasha Metz, David Wells

Texas A&M University - Galveston Campus, Galveston, TX, USA

Stable isotope variability in cownose rays (*Rhinoptera bonasus*) within the northwestern Gulf of Mexico

The trophic ecology of cownose rays (*Rhinoptera bonasus*) has been studied extensively along the Atlantic coast and eastern Gulf of Mexico, but is not well described in the northwestern Gulf of Mexico. Therefore, this study examined spatial and temporal trends in carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) stable isotopes along the Texas coast, as well as the influence of size and sex of individuals on stable isotopes by quantifying isotopic niches via Bayesian ellipses created within the R package 'Stable Isotope Bayesian Ellipses in R' (Jackson et al. 2011). Epidermal samples, from the trailing edge of the pectoral fin, were collected for isotopic analysis during in-water entanglement netting surveys conducted along the Texas coast from 2009 - 2012. Isotopic niche size was comparable across Texas bay systems in 2012, with only the lower Laguna Madre (spring) significantly different. However, mean $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ signatures varied spatially across bay systems. Isotopic niche size varied seasonally within the lower Laguna Madre, with summer 2012 significantly different than all other sampling periods. Additionally, female mean $\delta^{13}\text{C}$ signatures were significantly enriched compared to those of males, indicating female rays are foraging over longer periods of time within inshore habitats. There was also evidence of differential foraging between life history stages, with mean $\delta^{13}\text{C}$ signatures of subadults differing significantly from adult rays in Aransas Bay. Future studies should utilize a multi-tissue approach to enable

comparisons of trophic ecology over both short- and long-term timescales, as well as incorporate stomach content analysis to identify prey species consumed.

0897 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Daniel Stadtmauer¹, Mark Sabaj²

¹*Yale University, New Haven, CT, USA*, ²*The Academy of Natural Sciences of Drexel University, Philadelphia, PA, USA*

Taxonomic Overview of Mongolian Stone Loaches (Cypriniformes: Nemacheilidae)

Kottelat (2006) reported five nominal valid species of Nemacheilidae (stone loaches) in Mongolia: *Barbatula compressirostris*, *B. dgebuadzei*, *B. toni*, *Lefua costata*, and *Triplophysa gundriseri*. He also noted two unnamed species of *Barbatula* from the Selenge Basin, one of which was subsequently described as *B. sawadai* from the Tuul/Yeruu subbasin (Prokofiev 2007). The second unnamed *Barbatula* was from the Eg River, the sole outflow of Lake Hovsgol. Kottelat also noted an unnamed species of *Triplophysa* in the Tuul River (Selenge Dr.). Prokofiev (2007) recognized four *Barbatula* in Mongolia: *B. barbatula toni*, *B. dgebuadzei*, *B. sawadai*, and *B. golubtsovi* and the lattermost was treated as a questionable synonym of *B. compressirostris* by Kottelat (2006). Over the course of three expeditions to Mongolia in 2006, 2011 and 2012, large series of nemacheilid loaches were collected throughout Mongolia except for its westernmost limits. From those samples, analyses of internal and external morphology have identified three distinct lineages: *Barbatula toni* group, “*Barbatula*” *sawadai* group, and *Triplophysa* group. Morphotypes within the *Barbatula toni* group are relatively uniform and appear to be conspecific (i.e., *B. dgebuadzei* is a junior synonym of *B. toni*). “*Barbatula*” *sawadai* is restricted to the Selenge Basin, morphologically uniform, and unlikely related to true *Barbatula*. At least two nominal valid species of *Triplophysa* occur in Mongolia: *T. arnoldii* and *T. gundriseri*. Three potentially undescribed species of *Triplophysa* occur in the rivers draining the Hangay Plateau south into the Gobi desert, west into the Central Depression, and north into the Selenge Basin.

0737 Lightning Talks, Galerie 2, Saturday 9 July 2016

Bruce Stallsmith, Tiffany Bell

University of Alabama in Huntsville, Huntsville, AL, USA

Unusual Female-Biased Sex Ratios in Syntopic Populations of Two Species of *Ulocentra* Darters, *Etheostoma simoterum* and *E. duryi*, in the Flint River of Alabama

Etheostoma simoterum (Tennessee Snubnose Darter) and *E. duryi* (Blackside Darter) are similar species in the subgenus *Ulocentra* often found syntopically in stream systems

tributary to the Tennessee River in north Alabama. We made 12 monthly collections of these species from September, 2014, through August, 2015, at a site on the Flint River in Madison County, Alabama. Fish were collected with a four meter long seine along a 300 meter stretch of river characterized by alternating runs and riffles over a substrate that is variously gravel, cobble and boulder. For almost all of these months we have 16 or more adults of both species, typically 30–40 and sometimes as many as 100. Our primary interest was to examine reproductive schedules of the two species to see if there are any significant differences in timing, gonadal maturation, and oocyte number and size. Our initial assumption was that we would find roughly equal numbers of males and females in collections of both species. We found instead that in 11 of 12 monthly collections of *E. simoterum* there was a female skew of as much as 6:1, while *E. duryi* collections were less female skewed with seven months showing a female skew, three months a male skew, and two months with equal numbers. We have not seen or heard of other darter collections with consistent sex ratio skews. We are curious if anyone has seen such sex ratios in any species of darter, and hopefully why this might be.

1021 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Nathanael Stanek, Evon Hekkala

Fordham University, New York, NY, USA

Phylogeography of the Forest Hinged Tortoise, *Kinixys erosa*

We examined the phylogeographic differentiation of forest hinged tortoises, *Kinixys erosa*, using sequence fragments from three regions of mitochondrial DNA: 12S rRNA, ND4, and *cyt-b* from archived specimens representing much of the known geographic distribution of the species. Maximum parsimony, maximum likelihood, and haplotype network analysis congruently defined three distinct mitochondrial lineages corresponding to major geographic regions of African rainforest. Most notably, our preliminary results have identified a highly-divergent Congo Basin group. Since the archival tissues available for this study do not represent the full extent of *K. erosa* populations, there is potential for uncovering additional cryptic lineages in other biogeographic regions. To rule out competing explanations for the phylogeography and evolutionary history of *K. erosa*, additional sampling should be directed towards these data gaps. We are optimistic that the conservation of *K. erosa* will be advanced by this and future work that seeks to define significant management units.

0792 General Herpetology, Balconies L & M, Sunday 10 July 2016

Edward Stanley

Florida Museum of Natural History, Gainesville, Florida, USA

Phylogenetic and ecological diversity within the widespread melanistic species *Hemicordylus capensis*

The Cape Fold Mountains (CFM) are a topologically and ecologically diverse range of shale and sandstone formations that run the length and breadth of South Africa's Western Cape Province. Melanism has evolved multiple times in ectotherms of the CFM, invariably as an adaptation to cold environments. *Hemicordylus capensis* is unique among melanistic lizards from the Western Cape in having a broad distribution, occurring across the entire range, and is seemingly able to tolerate a large range of climatic conditions. In the warm northern extremes of its range, for example, *H. capensis* utilizes specific habitats that allow the lizards to thermoregulate more effectively. Despite receiving attention from ecologists and conservation biologists, the evolutionary history of *Hemicordylus* is poorly known and a phylogenetic assessment of the group is overdue. This study utilizes sequence data from *H. capensis* collected from across the full extent of its range and combines multi-locus molecular phylogenetic analyses with CT-based morphological analysis and ecological niche modeling to identify the extent of populations' genetic, phenotypic and ecological divergence within *H. capensis*. Five major clades were recovered from the phylogenetic analysis, corresponding to four major mountain ranges in the CFM. CT scans of representatives from each clade revealed that the "heat-tolerant" northern forms were morphologically distinct from all the other clades, being much more gracile and poorly armored. Significant breaks in suitable habitat exists between four of the five populations and significant ecological divergence is seen between all populations, suggesting that the group may contain significant amounts of unrecognized species diversity.

0224 Herp Morphology & Genetics, Galerie 3, Sunday 10 July 2016

C. Tristan Stayton

Bucknell University, Lewisburg, PA, USA

What Proportion of Turtle Shell Shape Evolution Can Be Explained by Functional Performance?

The turtle shell is a unique morphological structure that performs a number of functional roles. Most obviously the turtle shell serves as armor to resist forces imposed on the shell by predators. In addition, the shell is a hydrodynamic element that generates drag during swimming, an obstacle to righting when the turtle is overturned, and a structure which exchanges heat with the environment. The shape of a turtle's shell can affect its performance in all of these roles. This study addresses two questions: first, is it possible to integrate performance measures among all these functions to determine optimal shell shapes, or ranges of shell shapes, for various ecological categories of

turtles? Second, what proportion of the variation in shell shape can be explained by reference to performance in these functions? Using engineering optimization principals (including reference to Pareto optimization) and newly-developed comparative techniques, the actual distribution of turtles in shell shape space is compared with predicted optimal ranges. Although the optimal shapes for certain ecological groups generally conform to the observed shell shapes for those groups, there are many exceptions. Surprisingly little variation - only ~30% - is explained by functional performance. Together, these findings point towards the presence of additional and highly influential functional factors affecting shell shape evolution, or towards the action of non-adaptive processes (such as developmental constraints) in the evolution of turtle shell shape. In either case, the results suggest a number of fruitful avenues for future research in understanding the diversification of this fascinating structure.

1060 Fish Conservation, Galerie 3, Sunday 10 July 2016

Clare Steele¹, Vanessa van Heerden¹, Mark Steele², Sean Anderson¹

¹*California State University, Channel Islands, Camarillo, CA, USA*, ²*California State University, Northridge, Northridge, CA, USA*

Evidence for Human Impacts on Reef Fish Communities on an isolated Oceanic Island

Remote oceanic islands offer an opportunity to study the interaction of human and natural systems in relative isolation. Aitutaki Island (Cook Islands) offers a unique location to observe the coupled dynamics between human systems and coral reefs. Aitutaki is an almost-atoll in the South Pacific that is subject to a variety of synergistic threats, including poor water quality, overfishing, ciguatera, marine debris and climate change. The coral reefs surrounding Aitutaki present a gradient of human influence, with reefs around the inhabited main island suffering the effects of increased turbidity and elevated nutrients from freshwater runoff. We evaluated how reef fish communities differed between reefs near the main island versus those more distant from human influence. Along transects at twelve shallow reef sites, we assessed reef fish abundance and diversity, and evaluated the habitat. Reefs closer to human populations had lower species richness of reef fishes, less coral, and higher densities of macroalgae. Reefs further from the inhabited island had a significantly greater diversity of fishes, as well as higher densities of coral-dependent species, and harvested species such as Lethrinids and Serranids. Coral reefs are a vital marine resource for Cook Islanders, yielding a variety of foods, supporting sustainable tourism and providing coastal protection. Understanding the influence of anthropogenic impacts is an important step in restoring and maintaining the health of these systems.

1071 Fish Reproduction, Physiology, & Conservation, Balconies J & K, Sunday 10 July 2016

Mark Steele, Mia Adreani

California State University Northridge, CA, USA

Effects of temperature on interannual variation in reproduction of three batch-spawning kelp forest fishes

The extent to which reproductive success of fishes varies from year to year is seldom known, even for ecologically and economically important species. We studied the reproductive ecology of three key species in kelp forests in southern California: kelp bass (*Paralabrax clathratus*), California sheephead (*Semicossyphus pulcher*), and señorita (*Oxyjulis californica*) over 7 years that varied widely in temperature regime and included one of the largest El Niño events ever recorded. We tested the general hypothesis that interannual variation in reproductive parameters could be predicted from water temperature. Spawning season duration, spawning frequency, batch fecundity, and total annual reproductive output were measured at 3 large reefs (>70 hectares each). Specifically we tested the hypotheses that in warmer years (1) the onset of reproduction would occur earlier, (2) the reproductive season duration would be longer, (3) total annual reproduction would be higher, but (4) batch fecundity would be unrelated to temperature. Reproduction started earlier in warm years for one species, but not the other two. Contrary to our expectation, the duration of the reproductive season was unrelated to water temperature, and it tended to end earlier in warm years in all three species. Batch fecundity and total reproductive output varied markedly (2-4 fold) among years, but were not related to water temperature. Thus, for this suite of temperate reef species from families with tropical affinities, our expectation that warm years would be better for reproduction was not generally upheld.

0070 NIA BEST STUDENT PAPER, Salon A-C, Friday 8 July 2016

Sarah E. Steele¹, Hernán López-Fernández²

¹*University of Toronto, Toronto, Canada*, ²*Royal Ontario Museum, Toronto, Canada*

Examining the Role of Ontogeny and Body Size Evolution in the Diversification of Neotropical Cichlid Fishes

The association between body size diversity and species, morphological and ecological diversity has been explored in fishes yet the role, if any, of body size in fish macroevolutionary divergence is still poorly understood. Changes in body size and shape are ultimately driven by changes in the timing of developmental events. Perturbations of growth rate and duration during ontogenetic development lead to the natural variation in populations that natural selection acts upon and directly determines the variation in traits that we study in adults. Trajectories of species growth (i.e. morphological shape change over age or size) have commonly been studied in vertebrates, yet the macroevolution of ontogenetic information and how ontogenetic

development influences adult variation have rarely been studied. Using geometric morphometrics, we studied the ontogenetic allometry of Neotropical cichlids to determine when the morphological and ecological diversity seen in adult fishes is produced and to describe the patterns of ontogenetic changes over the phylogeny of Neotropical cichlids. Divergence in morphology among species occurs early in ontogeny, with species developing into an adult-like form at early ontogenetic stages followed by relative stasis of morphology and proportional growth. Functionally specialized groups are also highly divergent even in their early ontogenetic stages, suggesting ontogenetic shifts occur rapidly in early development. Understanding the growth of organisms and the variation among individuals across population can aid in understanding the divergence of adult morphology and ecology across species that is so commonly studied in macroevolution.

0354 Amphibian Ecology & General Herpetology, Salon F-H, Sunday 10 July 2016

John Steffen, Stephen Drozda, Jessica Hultberg

Penn State Erie, The Behrend College, Erie, PA, USA

The effects of carotenoid and food supplementation on Blood Plasma Reactive Oxygen Species levels in Painted Turtles

Animals use a variety of pigments to color their integument, including pigments known as carotenoids. Carotenoids are photosynthetic pigments in plants that animals must acquire from their diet and play diverse and important roles in photo-protection and free-radical scavenging. As a result, carotenoid-based skin colors are hypothesized to function as honesty-reinforcing mechanisms that underlie the use of colorful ornamental traits in sexual selection. The Painted Turtle (*Chrysemys picta*) has red and yellow patches and stripes on the skin and carapace which are colored by two carotenoids: an apocarotenoid (which generates yellow colors) and astaxanthin (which generates red colors). We performed a two factor lab experiment to investigate the effect of carotenoid access and food amount (i.e., food quantities to facilitate weight maintenance vs weight gain) on Reactive Oxygen Species (ROS) level in blood plasma. ROS levels are known to increase dramatically during times of environmental stress (e.g., UV or heat exposure) and promote tumor development. We found no evidence that male Painted Turtles mediate ROS levels by using carotenoids as free-radical scavengers in the blood. However, we found that weight maintained turtles had significantly higher ROS levels than weight gained individuals suggesting that a) turtles that eat only enough to maintain weight are stressed, or b) turtles that gain weight are gaining anti-oxidant benefits.

0491 Lightning Talks, Galerie 2, Saturday 9 July 2016

Ehlana Stell², Glen Parsons¹, Jan Hoover²

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Estimating Burst Swim Speeds and Jumping Characteristics of Silver Carp (*Hypophthalmichthys molitrix*) Using Video Analyses and Projectile Physics

Invasive fish species management has long been an issue for consideration in all wildlife and fishery industries. Without management control, invasive species such as the Asian silver carp (*Hypophthalmichthys molitrix*) will continue to exploit already vulnerable habitats disrupting native fisheries and inflicting unknown ecological damage. In this study we used on-line videography to estimate burst swim speeds, horizontal and vertical distance traveled, and angle of exit of silver carp during leaps. Additionally, we tested the hypothesis that carp exit the water at an angle that maximizes distance traveled. Our data show that silver carp reach speeds near 10 body lengths per second which is much higher than previously believed. Carp reach mean heights of 1.93 body lengths and travel a mean distance of 4.76 per leap. Maximum height and distance traveled were 4.58 and 11.5 body lengths, respectively. Our results, while preliminary, suggest the leaping abilities of silver carp may be greater than previously documented. These data may be valuable in the development of control methods to halt or slow the spread of Asian carp. Further investigation is needed particularly regarding the effects of environment on leaping characteristics in this fish.

0814 SSAR SEIBERT AWARD CONSERVATION, Galerie 3, Friday 8 July 2016

Anne Stengle¹, Paul Sievert¹, Tom Tynning², Alan Richmond¹

¹University of Massachusetts, Amherst, MA, USA, ²Berkshire Community College, Pittsfield, MA, USA

Conserving Snake Species of Greatest Conservation Need Threatened by an Emerging Fungal Skin Disease

Within the past several years, there appears to be an increase of observations of snake species exhibiting facial lesions, leading to many studies as to the cause. Recent work has correlated these facial lesions to fungal species *Ophidiomyces ophiodiicola*, also known as snake fungal disease (SFD). These lesions often involve the orbit, pit-organ, or labial region, causing concern for the individuals' survivorship. Following protocols of the New England Timber Rattlesnake (*Crotalus horridus*) research of SFD by Roger Williams Park Zoo (Providence, RI), we currently have a 9 state SWG grant (2014-2015) to investigate effects of SFD on populations. With this study we assess the presence of SFD in all snake species in nine states by submitting biopsies to the National Wildlife Health Center. We're also assessing treatment strategies for severely infected individuals. In addition, the one MA population of Timber Rattlesnakes with the highest report of SFD is currently being radio tracked to assess if there are any

differences between infected and non-infected regarding overwintering, movements, and habitat use. We are currently assessing management strategies of headstarting and captive breeding for populations not only suffering from SFD, but isolation, inbreeding, and increased mortality from road kill, poaching, and intentional killings. Our future project includes introducing a new population in a protected area within the Quabbin Reservoir, in Massachusetts.

0452 Lightning Talks, Galerie 2, Saturday 9 July 2016

Sean Sterrett¹, Todd Dubreuil², Evan Grant²

¹*Penn State University, University Park, PA, USA*, ²*U.S. Geological Survey, Turners Falls, MA, USA*

Development of a novel passive integrated transponder (PIT) vertical telemetry system for studying hypogean movements of woodland salamanders (*Plethodon*)

Woodland salamanders (genus *Plethodon*) are the most abundant vertebrate group in Eastern temperate forests, have their center of diversity in the U.S., and have unique roles in ecosystem function. Widespread declines have been recently suggested based on re-visits to historically occupied sites. However, we know that up to 80% of a salamander population is belowground, which means that perceptions of population declines may result from most individuals simply hiding underground with greater frequency in contemporary surveys compared to historic visits. This difficulty in detecting surface-active individuals, combined with their known sensitivity to temperature and moisture, has implications for their conservation. Woodland salamanders are known to make daily and seasonal vertical movements in the forest floor, although no technology exists to quantify these fine scale movements. Here, we report on the development and testing of an antenna and experimental mesocosm system for tracking salamander movements in an environment aimed to mimic forest floor conditions. We monitored the vertical movements of twelve PIT-tagged red-backed salamanders (*P. cinereus*), using this new technique over three months in a laboratory environment. The development of these methods will guide our understanding and broaden our ability to test hypotheses related to salamander microhabitat ecology, which is critical for setting management goals for resource management agencies and predicting true population declines under changing environmental conditions. Based on this successful testing, we are developing field-deployed arrays to observe and map below-ground movements in response to real environmental conditions and at real population densities.

0781 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Duane Stevenson, Gerald Hoff, James Orr, Ingrid Spies, Chris Rooper

NOAA/National Marine Fisheries Service, Alaska Fisheries Science Center, Seattle, WA, USA

Fishery Interactions with Skate Nursery Areas in the Eastern Bering Sea

Since early 2015, fishery observers in the North Pacific Groundfish and Halibut Observer Program have been receiving training in the identification and sampling of skate egg cases. The goal of this training has been to support an NPRB project examining the unique properties of skate nursery sites in the eastern Bering Sea and the interactions of fisheries with skate egg cases. During the 2015 training year, over 230 observers received training in egg case identification and sampling, and recorded data on over 1000 skate egg cases. A total of 11 skate taxa were identified from egg cases, and over half (58%) of the egg cases were identified as Alaska skate (*Bathyraja parmifera*). Observers scored each egg case as either “viable”, meaning it contained an intact egg or embryo in some stage of development, or “non-viable”, meaning it was either empty or full of mud.

Approximately 33% of the egg cases sampled by observers were classified as viable. Program wide, over 10,000 skate egg cases were encountered by observers. The majority of those egg cases (87%) were encountered on longliners targeting Pacific cod in the Bering Sea. Egg case encounters were concentrated on the outer shelf of the eastern Bering Sea, and over half of all egg cases reported were encountered in the area of Bering Canyon. Data collection for this project will continue through 2017, by which time we hope to have a comprehensive overview of fishery interactions with skate nursery areas in the eastern Bering Sea.

1006 NIA II, Galerie 3, Sunday 10 July 2016

Donald Stewart

SUNY Coll. Envir. Sci. & For., Syracuse, NY, USA

Taxonomic and Conservation Status of *Arapaima mapae*: Data Deficient Fishes in Limited Habitat

Conservation status of all five nominal species of *Arapaima* remain uncertain; these fishes should be considered ‘data deficient’ based on IUCN criteria. *Arapaima mapae* was described from a 2-m long, dried/stuffed mount. It was collected in 1837 from Lago do Amapá, a coastal lagoon in Brazil north of the Amazon delta. *Arapaima mapae* is distinguished from all other *Arapaima* by a distinctive, horizontally-elongate first lateral-line scale (versus such scales transversely ovate in other *Arapaima*); *A. mapae* is further distinguished from *A. arapaima* by its slender body form, and from *A. arapaima*, *A. gigas* and *A. leptosoma* by its slender caudal peduncle (~4% SL vs. ~6% SL in latter three taxa); it is readily distinguished from *A. agassizii* by its relatively larger eye, longer anal-fin base and other characters. Lago do Amapá is one of a series of lagoons along the Brazilian coast between the Amazon mouth and French Guiana (or Guyane) from which

not a single specimen of *Arapaima* has been collected since 1837. A 1949 report from Guyane indicated that *Arapaima* occurred in most of the larger rivers of that country, but recent studies by French biologists failed to find any. Much farther south in the Brazilian state of Bahia, a single *Arapaima* specimen was collected about 1851, but there are no records from that area since then. Implications are that coastal drainages may have limited habitat for *Arapaima*, and such populations may be vulnerable to extirpation. Assessment of conservation status of *A. mapae* is urgently needed.

0379 Fish Systematics I, Salon F-H, Saturday 9 July 2016

Melanie Stiassny¹, Prosanta Chakrabarty², Fernando Alda²

¹American Museum of Natural History, New York, NY, USA, ²Louisiana State University, Museum of Natural Science, Baton Rouge, LA, USA, ³Louisiana State University, Museum of Natural Science, Baton Rouge, LA, USA

Out of Tanganyika or into Tanganyika? Genome-wide UCE data elucidate the relationships and biogeographic history of the enigmatic lamprologines of the Lower Congo River

The large cichlid tribe Lamprologini numerically dominates inshore fish communities in Lake Tanganyika (LT) and due, in large part, to their ecological, behavioral, and reproductive diversity lamprologines have been subject to extensive field and lab-based study. Unlike the other LT cichlid lineages, lamprologines are represented not just in the lake but also throughout the Congo basin, with a noteworthy concentration of species diversity centered along the lower reaches of the Congo River (LCR). While monophyly of the tribe is strongly supported by both morphological and molecular data, no consensus has yet been reached regarding lamprologine intrarelationships, and in particular the placement of the riverine taxa remains unresolved. Most previous studies have focused on LT species and relied primarily on mtDNA data to resolve their intrarelationships; a strategy driven principally by a noteworthy lack of ncDNA variation in commonly sampled markers. Of the few mtDNA studies that have included one or more riverine taxon, all have them as nested within the lacustrine radiation. A single study utilizing ncDNA (RAG1) suggests an alternative placement with riverine species resolved as sister to the LT radiation. In the present study we investigate the utility of genome-wide UCE data to resolve lamprologine phylogenetics at multiple scales; from the placement of riverine taxa in relation to the lamprologine radiation as a whole, as well as for elucidating species-level relationships and population structuring within and between LCR and upstream Congo River species.

1000 General Ichthyology I, Balconies J & K, Sunday 10 July 2016

Warren Stiles, Carol Johnston

Auburn University, Auburn, AL, USA

Hydrologic Change as a Driver in Fish Assemblage Shifts in Alabama, USA

Past studies within single watersheds in the Southeast have found that unnatural changes in stream hydrology affect the fish assemblage negatively. With increases in land development and water withdrawals, significant declines in discharge and increases in flashiness have been seen in some Southeastern streams over the past 50 years. In this study, contemporary fish assemblage data collected in the summers of 2013 and 2014 were compared to historic collections in 6 unregulated watersheds across the physiographic regions of Alabama. Using redundancy analysis (RDA) relationships between land cover, hydrologic variation, and stream fish assemblages were investigated. Hydrology was found to have a significant effect on the fish assemblages in 4 of the watersheds. Where hydrologic regimes were found to have been altered, the assemblages were dominated by generalist species and were variable through time. In a watershed on the Talladega National Forest, the fish assemblage was found to be more stable over time than those in more developed watersheds. In another watershed that drains to the Tennessee River, it was found that flashiness had decreased over the past 30 years and this was coincided with stable assemblages that were dominated by a mix of generalists and specialist. Many of the hydrologic changes seen in this study were related to changes in land cover that in some instances led to an increase in flashiness and sometimes a decrease in average discharge. These changes are important to keep in mind for the conservation of the diverse and distinct fish fauna of Alabama.

0207 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Andrew Stites¹, Joshua Sherwood¹, Jeremy Tiemann¹, Michael Dreslik¹

¹*Illinois Natural History Survey, Champaign, IL, USA*, ²*University of Illinois Urbana-Champaign, Champaign, IL, USA*

Reassessment of Iowa Darter Habitat in Illinois

The Iowa Darter (*Etheostoma exile*) is a state-threatened fish species inhabiting a limited range in northern Illinois. Historical surveys (from 1901-1995) found Iowa Darters at only 40 sites, with 19 sites being from glacial lakes near the Wisconsin border leading to the conclusion they primarily inhabited glacial lakes. Recent surveys (since 1995) have found *E. exile* at 37 sites, with only 13 of those sites being from glacial lakes. Many of the recent surveys have focused on headwater streams that have had limited to no previous records of fish sampling. The combined findings illustrate the need to evaluate whether populations of Iowa Darters routinely inhabit the headwater streams of northern Illinois. Using the recent collection locations, species distribution models were created to guide future sampling in streams potentially having *E. exile* populations. Models indicated many of the potential locations for *E. exile* are headwater streams with no previous

history fish community sampling. This might be because small streams having predications for occurrence are not routinely sampled by natural resource agencies. With the information we have provided, targeted surveys in areas of high predicted probability will afford assessing the frequency which *E. exile* occupy headwater streams in northern Illinois and determining their local habitat needs.

0739 AES GRUBER AWARD, Balconies J & K, Thursday 7 July 2016

Ashley Stoehr¹, Jeanine Donley², Scott Aalbers³, Doug Syme⁴, Chugey Sepulveda³, Diego Bernal¹

¹University of Massachusetts Dartmouth, Dartmouth, MA, USA, ²MiraCosta College, Oceanside, CA, USA, ³Pfleger Institute of Environmental Research, Oceanside, CA, USA, ⁴University of Calgary, Calgary, Alberta, Canada

Thermal sensitivity of red muscle function in a deep-diving shark

Amongst pelagic elasmobranchs, bigeye thresher sharks (*Alopias superciliosus*) exhibit robust vertical mobility, undertaking routine long-duration dives from the surface (18-20°C) to beneath the thermocline (5-10°C). Unlike pelagic fishes capable of regional endothermy (e.g., common thresher sharks, swordfish), the subcutaneous red muscle (RM) morphology of bigeye threshers precludes heat retention and results in large RM temperature fluctuations during prolonged dives. This study used the work loop technique to determine if bigeye thresher RM was impaired at cool temperatures or functioned across naturally-occurring temperatures (8, 16, 24°C). Bigeye thresher RM did not produce positive power above a presumed tail beat frequency of 0.5 Hz, even when warmed to 24°C. However, RM produced positive power at 8-24°C and 0.25-0.5 Hz. The lower thermal sensitivity of bigeye thresher RM suggests that fishes lacking RM endothermy exhibit greater thermal independence. This thermal strategy may provide a cost-effective mechanism to facilitate sustained swimming in disparate thermal environments, but may compromise swimming speeds during prolonged cold exposure.

0542 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; STORER AWARD HERPETOLOGY

Jason Strickland¹, Miguel Borja², Andrew Mason¹, Darin Rokyta³, Christopher Parkinson¹

¹University of Central Florida, Orlando, Florida, USA, ²Universidad Juárez del Estado de Durango, Gómez Palacio, Durango, Mexico, ³Florida State University, Tallahassee, Florida, USA

Convergence within a Species? Venom Evolution in Mojave Rattlesnakes

Convergent phenotypes typically arise through independent mechanisms in highly divergent taxa due to similar selection pressures. However, recent research indicates

convergence may be common in closely related species when a phenotypic trait, such as venom, is highly adaptive. Rattlesnake venom can be broadly characterized as either hemorrhagic (found in most species) or neurotoxic. Interestingly, in Mojave Rattlesnakes, *Crotalus scutulatus*, the majority have neurotoxic venom which is hypothesized to be ancestral. The exceptions are two populations, one in Arizona and one in Mexico, that are hemorrhagic suggesting convergence. To test this hypothesis, we collected venom and tissue from 120 *C. scutulatus* from throughout their range. We identified individuals of each phenotype as well as eight individuals with a hybrid phenotype and found higher proteomic variation among individuals than previously documented. Neurotoxic and hemotoxic individuals were not phylogenetically distinct indicating gene flow between phenotypes and we determined the two hemorrhagic populations are not closely related but have similar venom. Species distribution models of both phenotypes and of the two populations did not indicate significant differences in range suitability, suggesting environmental variables are not entirely responsible for the venom phenotypes. Based on these data, the venom polymorphism is being maintained in spite of gene flow and without an obvious environmental difference and the two hemorrhagic populations could be a result of convergent changes. Future work will compare venom gland transcriptomes among phenotypes and populations to determine if changes in expression are facilitating the convergence in phenotype.

0553 ASIH STOYE AWARD GENERAL HERPETOLOGY, Salon F-H, Friday 8 July 2016

Brock Struecker, Joseph Milanovich

Loyola University Chicago, Chicago, IL, USA

Can Pond-Breeding Salamanders Alter Invertebrate Assemblages in Forested Wetlands? A Case Study in Northern Illinois

A critical factor in the widespread decline of amphibians is habitat loss, fragmentation, and degradation. This is especially true for wetlands, and furthermore ephemeral wetlands, in which little conservation efforts are directed. However, these temporary wetlands provide a great deal of habitat for a diversity of taxa and are often critical breeding locations for amphibians. Although abiotic metrics for wetlands have been extensively tested for effects on amphibians, we do not have a good indication of how ephemeral wetland biological characteristics shape amphibian populations, or how amphibian populations shape invertebrate diversity in ephemeral wetlands. We sampled five wetlands in Lake County, Illinois from May 15th to October 1st, 2015 for larval pond-breeding salamanders (*Ambystoma laterale* and *Ambystoma tigrinum*) and water-column invertebrates to assess wetland community interactions between larval salamanders and available prey. We sampled biweekly with mesh minnow traps in each wetland and collected a subset of captured larval salamanders once per month for gut-content analysis. Additionally, we sampled water-column invertebrates (available prey) coinciding larval salamander captures. We found several environmental variables influenced both salamander and invertebrate communities, but the impact of

salamanders on invertebrates was not measurable. This was further supported by showing larval salamander diets varied across wetlands and between species. These data show abiotic and biotic factors help shape wetland communities and should be incorporated into management decisions regarding ephemeral wetlands.

1019 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Tyler Stuck, Shaojie Zhang, Yier Jin, Anna Savage

University of Central Florida, Orlando, Florida, USA

SmartPhrog: A Long-Term, Active Bioacoustic Monitoring Solution Using Raspberry Pi For Frog Population Monitoring

This project aims to develop a bioacoustic monitoring device using a computer system called Raspberry Pi. Raspberry Pi is a low cost, credit-card sized computer that is designed for programming education and ease of use. As a consequence of these design goals, it can be easily modified to fit many different applications. Population demographics can be challenging to assess for cryptic species such as amphibians, but accurate data on population size and activity are critical to determine overall population health. Long term monitoring using acoustics is a viable solution, but often requires sorting through many hours of data manually. The Raspberry Pi's processing capabilities enhance its potential functionality beyond the recording capabilities of current bioacoustic devices and also cost a fraction of the price. Specifically, our "SmartPhrog" will be programmed to change behavior based on what it records. With proper instruction it will be able to determine optimal recording times to save power, take pictures when a frog is within range, and potentially recognize and respond to certain calls. Based on current data sampled with the SmartPhrog prototype that has been transformed using a frequency based principal component analysis, an untrained observer is able to separate and identify frog calls visually. This is the first step towards automatic classification of frog calls. The low cost of this system in applications for monitoring vocalizing animals make SmartPhrog a strong contender in bioacoustics as a tool for biologists in the future.

0898 Fish Conservation & Morphology, Galerie 2, Sunday 10 July 2016

Kristine Stump¹, Craig Dahlgren², Krista Sherman³, Charles Knapp¹

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Discovery of an Unknown Grouper Spawning Aggregation in The Bahamas Through the Use of Acoustic Telemetry

Globally, many fish species migrate to fish spawning aggregations (FSAs). Temporal and spatial predictability of these migrations and FSA locations make species vulnerable

to overfishing, since the majority of a region's adult population may be harvested quickly with minimized effort. Historically, the Nassau Grouper (*Epinephelus striatus*) was an important fishery throughout the Caribbean, but due to FSA overfishing, it is now rare in many reef ecosystems. In The Bahamas, stocks continue to decline despite the implementation of FSA protections. While more Nassau Grouper FSAs have been reported in The Bahamas than any other country, very few have been validated, and the dynamics of migrations to and from these sites is even less understood. We used acoustic telemetry to describe, for the first time, Nassau Grouper migrations along Andros Island, Bahamas, which is bordered by one of the longest barrier reefs in the world. We report the likely extirpation of a historically important FSA and suggest Nassau Grouper are migrating to an unreported spawning location. Synchronous with winter full moons, fish migrated in groups along the barrier reef shelf edge at an average speed of 1.67 km/hr and traveled roundtrip distances of 71.5 km to 260.3 km ($x = 164.5 \pm 65.7$ km, $n = 10$). These results are critical to assessing the efficacy of current management strategies in The Bahamas. Thus far, all known FSAs have been reported to the scientific community by fishermen. Our study represents the first time an FSA has been identified using telemetry.

0294 Snake Ecology, Galerie 3, Sunday 10 July 2016

Eric Suarez¹, Christina Romagosa¹, Carla Dove², Bryan Falk³, Robert Reed³

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Prey species composition and dietary shifts of the Burmese python (*Python molurus bivittatus*) in southern Florida

The impact of invasive species has emerged as a high-priority issue in planning the restoration and conservation of the Greater Everglades Ecosystem. Resource managers in Florida are particularly interested in one of the most direct impacts of the invasive Burmese python population: what are they eating, and has it changed over time? We identified prey species from the digestive tract contents of 350 pythons collected from 2010 to 2016 using a morphological approach (i.e., using hair, feather, and scale morphology). Digestive tract contents were derived from the southern Everglades, north to Water Conservation Area 3A, and west to Collier County. We found that shifts are occurring over time in diet composition for pythons collected from within Everglades National Park (ENP) boundaries, with birds becoming more prevalent in the diet as compared to data collected before 2008. The percentage of birds found in the python diet north and west of ENP remained near previously reported numbers (~25%). The mammalian component of the diet for pythons collected within the ENP boundaries consisted of primarily rodents (85%). The mammalian component north and west of ENP was more diverse, and rodents were only 45% of the diet. These results suggest spatial and temporal shifts in prey species composition for pythons throughout their range, which supports previous studies showing declining trends for some mammal

species throughout the ENP. Dietary shifts in this common invasive species may have implications for ecosystem stability, as well as Everglades restoration.

0747 AES Morphology & Reproduction, Balconies L & M, Friday 8 July 2016

James Sulikowski¹, Carolyn Wheeler¹, Bianca Prohaska², Neil Hammerschlag³

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Stick it where the sun don't shine: Advances in the non lethal study of elasmobranch reproductive biology for conservation management

Data on maturity state, gestation period, and fecundity are essential for proper conservation and management of elasmobranchs. Historically, this information has been collected by lethal sampling, an approach that is problematic for threatened and endangered species. Recent studies have demonstrated that non-lethal approaches can be as effective as lethal ones for assessment of the reproductive status of elasmobranchs. Using examples from various species and reproductive modes, this study summarizes our current knowledge of several techniques: 1) analysis of circulating plasma hormones; 2) concentrations of steroid hormones from skeletal muscle tissue; and 3) the use of ultrasonography to discern pregnancy and follicular development and their use as reliable indicators of reproductive status in elasmobranchs.

0159 Fish Morphology & Biogeography, Salon A-C, Sunday 10 July 2016

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Scan All the Fishes - Open Source CT data

Computed tomography scanning with x-rays is an effective technique for visualizing radiodense skeletal tissues. With the addition of contrast techniques, iodine or phosphotungstic acid for example, it is also capable of revealing soft tissue anatomy. CT scanning has been expensive and the reconstructions of specimens a time consuming process that required expensive software. I will report on simple techniques for scanning large numbers of specimens at the same time. The data are then digitally dissected into single specimen scans. An important question to consider when bulk scanning is resolution – it will certainly be less than can be achieved scanning a single specimen. I propose a policy of scanning fishes at a resolution that allows morphometric measurements at higher resolution than traditional 2-d techniques (i.e. calipers, ocular micrometers). The throughput that is possible with a single CT scanner and a single person doing reconstructions is demonstrated at 32 species per day. We expect it is possible for a single person to scan 50 species a day of similarly sized fishes. We are

engaged in scanning a specimen of every species of fish. Each species will be scanned at a resolution sufficient for many purposes. Slice data, STL files, PLY files and JPGs of volume and surface renderings are being made available immediately through an open access model. Our first groups of interest are the Cottoids, Gobeisocids, and Blennies. Uploading the data to the web remains a bottleneck. The processes we have developed for rapidly scanning, tracking and returning specimens are also available open access as living documents.

**0401 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; STORER AWARD
HERPETOLOGY**

Jenny Sutherland^{1,3}, Amber Stedman¹, David Mifsud², Maegan Stapleton²,
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USA

**Use of Landcover Data and eDNA to Determine Occupancy of the Mudpuppy
(*Necturus maculosus maculosus*) in the St. Clair-Detroit River System**

The Mudpuppy (*Necturus maculosus maculosus*) is a fully aquatic salamander with a range that spans the Great Lakes region. Although this species was once abundant throughout its range, evidence suggests that there have been widespread declines as a result of habitat modification, pollution, and over collection. Land use practices in the St. Clair-Detroit River System (SCDRS) have altered habitat, reducing shelter and breeding sites for mudpuppies, but information on their current status is lacking. We used trapping records and Geographic Information Systems (GIS) analysis to determine if landcover predicts the presence of mudpuppies along the project area. Additionally, we are investigating the utility of environmental DNA (eDNA) to aid future monitoring efforts. A number of sites along the St. Clair River have recently been restored, providing cover objects suitable for use as mudpuppy nesting habitat. We use eDNA sampling and quantitative PCR (qPCR) to compare mudpuppy presence in restored versus unrestored locations. These data will help prioritize management on a local and range-wide scale, resulting in more successful conservation of this ecologically important species.

0780 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Tracey Sutton¹, April Cook¹, Kevin Boswell², Heather Bracken-Grissom², Sergio deRada³, Ron Eytan⁵, Dante Fenolio⁶, Tamara Frank¹, Chuamin Hu⁴, Matthew Johnston¹, Heather Judkins⁷, Jose Lopez¹, Jon Moore⁸, Brad Penta³, Isabel Romero⁴, Mahmood Shivji¹, Michael Vecchione⁴, Jay Rooker⁵, David Wells⁵, Marsh Youngbluth¹⁰

¹Guy Harvey Oceanographic Center, Nova Southeastern University, Dania Beach, FL, USA, ²Florida International University, North Miami, FL, USA, ³Naval Research Laboratory at Stennis Space Center, Bay St. Louis, MS, USA, ⁴University of South Florida College of Marine Science, St. Petersburg, FL, USA, ⁵Texas A&M University Galveston, Galveston, TX, USA, ⁶San Antonio Zoo, San Antonio, TX, USA, ⁷University of South Florida St. Petersburg, St. Petersburg, FL, USA, ⁸Wilkes Honors College, Florida Atlantic University, Jupiter, FL, USA, ⁹NOAA NMFS National Systematics Lab, Washington, DC, USA, ¹⁰Harbor Branch Oceanographic Institute at Florida Atlantic University, Ft. Pierce, FL, USA

Deep-Pelagic Research in the Gulf of Mexico: the DEEPEND Consortium

The *Deepwater Horizon* oil spill (DWHOS) was unique not only for its volume, but also for its depth of influence (0-1500 m). Variable amounts of hydrocarbons reached the ocean surface and/or seafloor, whereas 100% occurred within the water column. Understanding this pelagic habitat is important because about half of all fish species that occur in the Gulf of Mexico (GoM) spend all or part of their lives in the open ocean. Many mesopelagic and bathypelagic fishes vertically migrate each night to feed in the upper water column and return to deep water during the day. This behavior promotes rapid cycling of natural and anthropogenic material in the water column. Deep-pelagic fishes are prey for gamefishes, seabirds, and marine mammals. Given the steady growth of oil exploration and operations, the likelihood of future spills emphasizes the need to document acute and chronic effects on the pelagic fauna. The GoMRI-funded DEEPEND (Deep-Pelagic Nekton Dynamics) consortium was created for that purpose. DEEPEND is beginning the second of a 3-year program that builds on two intensive NOAA-supported surveys during 2010-11. DEEPEND will focus on short-term and long-term timescales to appraise the dynamic nature of communities using a suite of integrated approaches. These investigations include: 1) a direct assessment of GoM deep-pelagic community structure including the physical and biological drivers of this structure; 2) a time-series analysis/comparison of biophysical data; 3) a time-series examination of differences in genetic diversity among key species; and 4) a biogeochemical analysis of the effect of DWHOS on pelagic biota.

0305 Fish Ecology II, Salon A-C, Saturday 9 July 2016

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Active Linkage of Large Vertebrates and the Deep-Pelagic Fauna of the Oceanic Gulf of Mexico after *Deepwater Horizon*: Vertical Dynamics of the Epipelagic, Mesopelagic and Bathypelagic Ichthyofauna

Large predatory fishes, toothed whales, and smaller cetaceans rely on deep-pelagic nekton as primary or secondary prey. This trophic interaction is mediated by downward and upward vertical migration (e.g., sperm whales and mesopelagic lanternfishes, respectively). This interaction also links particulate-feeding lower trophic levels with top predators in a manner that spans the gamut of depth domains. This is particularly important with respect to a whole-water column disturbance such as the *Deepwater Horizon* oil spill. Here we present highly resolved vertical distribution and migration data collected during a large-scale, NOAA-supported, deep-pelagic (0-1500 m) survey in 2011, along with data collected during ongoing GoMRI-supported DEEPEND consortium surveys. The deep-pelagic nekton community of the Gulf of Mexico is a complex mixture of migrating, non-migrating, and partially migrating assemblages that connect surface waters with depths well in excess of 1000 m. Major patterns of the vertical distribution of 151 species of fishes are summarized and quantified with the goal of highlighting potential vectors of anthropogenic contamination transfer in the deep-pelagic, the Gulf's largest ecosystem. Among the key findings: 1) the epipelagic is truly two ecosystems, depending on time of day; 2) the largest active flux is that of the synchronous migrators, but a large biomass component of the epipelagic at night is contributed by deep-to-very-deep asynchronous migrators; and 3) vertical migration by the bathypelagic fauna is readily apparent. In summary, the deep-pelagic nekton provide an essential intermediate service with respect to ecosystem functioning, efficiently linking lower and higher trophic levels through movement and consumption.

0671 Herp Conservation, Galerie 3, Saturday 9 July 2016

William Sutton¹, Kyle Barrett², Cynthia Loftin³, Phillip deMaynadier⁴, Priya Nanjappa⁵, Allison Moody⁶

¹*Tennessee State University, Nashville, TN, USA*, ²*Clemson University, Clemson, SC, USA*, ³*Maine Cooperative Fish and Wildlife Research Unit, Orono, ME, USA*, ⁴*Maine Department of Inland Fisheries and Wildlife, Bangor, ME, USA*, ⁵*Association of Fish and Wildlife Agencies, Washington, DC, USA*, ⁶*University of Maine, Orono, ME, USA*

Determining Vulnerability of Priority Amphibian and Reptile Conservation Areas to Climate Change and Urbanization in the Northeastern United States

Climate change represents one of the most complex and globally important ecological stressors. As virtually all ecosystems will face impacts from climate change, it is essential

to develop strategies that include pro-active conservation planning measures. The effort to establish Priority Amphibian and Reptile Conservation Areas (PARCAs) was initiated to identify valuable habitat for priority herpetofauna throughout the United States. Implicit in the identification of these habitats includes understanding long-term persistence to ecological stressors. We developed a framework for assessing the long-term vulnerability of proposed PARCAs in the North Atlantic Landscape Conservation Cooperative region to climate change. Our framework determines vulnerability by incorporating exposure (i.e., extent of climate change experienced by a species or locale), sensitivity (i.e., degree to which survival, persistence, or fitness may be impacted), and adaptive capacity (i.e., capacity of a species or locale to cope with climate change). We used a variety of spatially-explicit metrics that included projected temperature change, projected precipitation change, projected landuse change, priority amphibian and reptile species sensitivity, geographic context, and topographic relief to assess vulnerability. We found that projected temperature increases, landscape urbanization, and climatic niche loss of priority herpetofaunal species led to higher landscape vulnerability. Collectively, our efforts provide a science-based structure to assess the long-term vulnerability of these habitats to climate change, which will aid in the allocation of conservation efforts to priority landscapes based on projected climate resiliency.

0655 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

William Sutton¹, Michael Osborne², Jeff Bailey³, Thomas Pauley⁴

¹Tennessee State University, Nashville, TN, USA, ²Appalachian State University, Boone, NC, USA, ³West Virginia Department of Environmental Protection, Charleston, WV, USA, ⁴Marshall University, Huntington, WV, USA

Landuse Impacts on Stream Salamanders in West Virginia: An Ecoregion-Wide Analysis

Globally, amphibians represent one of the most endangered vertebrate taxa. A variety of stressors, including landscape destruction and landuse change, emerging pathogens, aquatic pollution, and global climate threaten amphibian populations. Salamanders in the family Plethodontidae represent the only amphibian family where species lack lungs and rely completely on cutaneous respiration. These adaptations increase the vulnerability of these organisms to ecological disturbance, which makes them keen indicators of ecological condition. We evaluated the impacts of landscape disturbance on streamside salamanders at 45 streams in West Virginia over a three-year period. We used a combination of transect and quadrat surveys to survey and capture salamanders. We used both ordination and occupancy modeling approaches to evaluate potential impacts of stream disturbances. We captured over 2500 total adult and larval salamanders representing 9 species throughout the study period. The most commonly captured species included the Northern and Southern Two-lined Salamander (*Eurycea bislineata* and *E. cirrigera*), which tended to be common at most sites. We detected an effect of landscape disturbance on salamander populations and found that both richness and abundance of adult and larval salamanders were significantly lower in degraded

streams versus streams of intermediate and reference conditions. A variety of landscape disturbances, including both agricultural and mining operations appear to be the greatest threat to salamanders in streams throughout West Virginia. Collectively, our study defines the greatest threats to stream salamanders throughout the state and also provides an additional evaluation of using salamanders as indicators of aquatic biological condition.

0219 General Herpetology, Balconies L & M, Sunday 10 July 2016

Jennifer Swanson¹, Clay Pierce², Erin Muths³, Kelly Smalling⁴, Mark Vandever³

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Habitat Use and Pesticide Exposure in Northern Leopard Frogs in Conservation Reserve Enhancement Program Wetlands

Amphibian populations are declining, with habitat alteration due to land use change consistently identified as one of the biggest contributing factors. In agricultural landscapes, habitat loss may interact with other stressors such as environmental contaminants to exacerbate declines. Much of the landscape in northern Iowa has been transformed from a mosaic of seasonal wetlands and grasslands to row crops. In 2001, the Conservation Reserve Enhancement Program (CREP) was created to improve water quality through construction of wetlands positioned on the landscape to catch runoff from tile drainage systems and reduce nutrient effluent. However, these CREP wetlands may provide additional benefits, particularly as wildlife habitat. Our objective was to radio track northern leopard frogs (*Lithobates pipiens*) to record their movement at CREP wetlands and assess the pesticides in which they may come in contact. Although these sites are surrounded by vegetative buffers, they are often located in close proximity to agricultural fields where pesticides and fertilizers are applied. During the summer of 2015 we captured and radio tracked frogs (n=38) at two CREP wetlands in Iowa. Passive pesticide samplers (PPSs) were placed in locations frequented by frogs to test for presence and concentration of contaminants to which frogs were exposed. Presence and concentrations of pesticides on PPSs were compared to corresponding values found in a subset of frogs that were euthanized after they had been tracked. Frogs moved from their original capture points to a variety of habitats at each site and traveled up to 1,000m during the tracking period.

**0924 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; STORER AWARD
HERPETOLOGY**

Meredith Swartwout¹, Philip Vogrinc¹, Joseph Alex Baecher², Chelsea Kross¹,
John Willson¹

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**Growth and Phenotypic Plasticity of *Nerodia sipedon* in Response to Feeding
Frequency and Prey Size**

Because snakes are gape-limited predators, plasticity in trophic morphology may allow them to modify the sizes of prey that they are able to consume. Evidence suggests that some snakes can alter their head morphology in response to larger prey, but it is unknown whether this effect is mediated by growth rate. To test how prey size and feeding frequency influences head morphology and growth of a common water snake, we randomly assigned 33 lab-born neonate *Nerodia sipedon* to feeding treatments representing a factorial combination of two prey sizes and two feeding frequencies: Big-High (BH), Big-Low (BL), Small-High (SH), Small-Low (SL). Snakes in the BH treatment were offered one sunfish (*Lepomis* sp.) weekly that was 30% of their body mass; BL were offered one sunfish that was 30% of their body mass every other week; SH were offered two sunfish that were each 15% of their body mass weekly; and SL were offered one sunfish that was 15% of their body mass every other week. We photographed snakes at the beginning of the experiment and when they reached 400 mm snout-vent length (SVL) and analyzed images to compare head morphometrics among treatment groups. Snakes in the High treatments (SH and BH) had higher growth rates, while snakes in the Low treatments (BL and SL) had low growth rates. However, due to high variability in head morphology among individuals, we found limited evidence for plastic responses of trophic morphology to prey size or growth rate.

0824 Lightning Talks, Galerie 2, Saturday 9 July 2016

John Swenson, Karen Crow

San Francisco State University, San Francisco, CA, USA

**How the Devil Ray Got Its Horns: The Evolution and Development of
Cephalic Lobes**

Devil rays and their relatives (Family: Myliobatidae) are derived and highly divergent batoids, with some taxa considered the only living vertebrates with three functional paired appendages. The third set of appendages, termed "cephalic lobes", are modifications of the anterior pectoral fin that evolved to assist with feeding as the myliobatids transitioned from a benthic to a more pelagic lifestyle. To investigate the genetic underpinnings of these unique appendages, we collected embryos from the cownose ray (*Rhinoptera bonasus*) and will sequence the transcriptome of developing cephalic lobes for comparison with pectoral fin. Preliminary data indicate previously

underappreciated genetic pathways may be responsible for modifying multiple regions of the body in this taxon.

**0807 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; STORER AWARD
HERPETOLOGY**

Shantel Swierc¹, Kim Withers¹, J. Derek Hogan¹, Michael R.J. Fostner²

¹Texas A&M University- Corpus Christi, Corpus Christi, Texas, USA, ²Texas State University, San Marcos, Texas, USA

Demographics, distribution, and genetic variation in the Texas diamondback terrapin (*Malaclemys terrapin littoralis*) within the Corpus Christi and Aransas bay systems

The goals of this research are to determine the population genetics and population dynamics of the Texas diamondback terrapin (*Malaclemys terrapin littoralis*) within the Nueces/Corpus Christi Bay and Aransas Bay estuaries on the central Texas coast. The genetic data produced by this study can be integrated with previous DNA analyses on Nueces Bay populations and provide needed information for development of management strategies. It will also provide the first genetic data on populations located within Oso Bay (Nueces/Corpus Christi Bay estuary) and Aransas Bay. An understanding of the population genetics from these terrapins will help answer various questions for conservation management in an underrepresented region from bays that are relatively isolated from one another. Terrapins were captured between April 2015 and December 2015. Sex was determined based on morphological characteristics and females were checked for gravidity. Photographs, standard measurements, body condition score, age estimates, physical abnormalities, scute notches and PIT tags were all performed and applied for each individual. Blood samples were drawn from all captured individuals to genetically compare individuals within, and across, these bay systems using microsatellite DNA analysis. Preliminary captures, sex ratios, and standard measurement data for individual males and females are currently being analyzed, providing insight on the demographics of Texas diamondback terrapins in the study sites. DNA analysis will be performed on a ABI 3730xl DNA Analyzer, utilizing a multiplex PCR strategy involving M13 fluorescent labeled forward primers and the same 12 SSR primers that multiple previous studies have used for this species.

0201 Poster Session I, Acadia/Bissonet, Friday 8 July 2016

Dominic Swift, David Portnoy

Texas A&M University-Corpus Christi, Corpus Christi, TX, USA

High-throughput Sequencing for Genetic Monitoring and Stock Structure Assessment of Blacktip Sharks (*Carcharhinus limbatus*)

Blacktip sharks (*Carcharhinus limbatus*) are one of the dominant large coastal species landed by commercial and recreational fisheries in the U.S. Atlantic and Gulf of Mexico. Blacktips give birth in nursery areas which are vital for juvenile survival and are considered essential fish habitat. In blacktips and other large coastal sharks, females may show philopatry to these nurseries and this may result in substructure, making these sharks more vulnerable to localized overfishing. Further, nurseries along the U.S. Atlantic and Gulf of Mexico coasts differ in environmental conditions which may lead to localized adaptation, important for population viability when the environment is heterogeneous in space and time. We will sample 500-600 young-of-the-year and mature blacktip sharks across the U.S. Atlantic and Gulf of Mexico. We will use double digest restriction-site associated DNA (ddRAD) sequencing to (i) establish baseline genetic monitoring data for blacktips, (ii) provide high-resolution genetic data for blacktip stock assessment, (iii) develop replicable methods for genetic monitoring and stock structure assessment of other shark species. Genomic monitoring will involve estimating the effective number of breeders (N_b) and the minimum number of female breeders (N_{mf}) at each nursery area, as well as characterizing baseline genetic diversity of the breeding stock. We also will investigate the potential for localized adaptation associated with nurseries and develop fine-scale genetic tags to be used in future mark-and-recapture studies.

0864 Fish Behavior & Development, Salon A-C, Sunday 10 July 2016

Stephen Szedlmayer, Megan McKinzie

Auburn University, Auburn, Alabama, USA

Gray Triggerfish, *Balistes capriscus*, Movement Patterns, Residency, and Mortality on Artificial Reefs in the Northern Gulf of Mexico

Gray triggerfish, *Balistes capriscus*, are ecologically and economically important in the northern Gulf of Mexico, yet little is known on their movement patterns, habitat use and residency to artificial reef structures. In the present study we successfully tagged and acoustically tracked gray triggerfish ($N = 22$) using the Vemco VR2W Positioning System (VPS). Individual fish were remotely tracked for 8 to 622 d from Oct 2012 through Jul 2015. Gray triggerfish showed diel and seasonal movement patterns, high site fidelity and long term residency to reef sites. Mean \pm SD home range (95% KDE) = 3238 ± 3687 m² and core areas (50% KDE) = 278 ± 331 m², and were larger during the day than night time periods. Fall home range (mean \pm sd = 4966 ± 4713 m²) was significantly greater than spring home range (1950 ± 1587 m²). Tracked individuals remained close to

reef structures (mean distance from reef = 46.3 ± 1.3 m) and residency was estimated at 163 d. Several individuals (N = 8) made large-scale directed movements to other nearby reef sites. Three fish returned to their release site after emigration periods of 8 to 200 d. Due to high residency and close proximity to reef structures, gray triggerfish may be highly susceptible to increased fishing mortality.

0927 Fish Conservation & Morphology, Galerie 2, Sunday 10 July 2016

Stephen Szedlmayer, Peter Mudrak

Auburn University, Auburn, Alabama, USA

A Comparison between Conventional and Transmitter Tagged Red Snapper, *Lutjanus campechanus*, to estimate Fishing Mortality in the Northern Gulf of Mexico

Estimates of fishing mortality (F) are critical for valid management of red snapper, *Lutjanus campechanus*, in the Gulf of Mexico. To reduce difficulties of fisher non-reporting, unknown tag shedding and tagging artifact mortality with conventional tagging, telemetry methods have been developed. One difficulty with telemetry methods are low sample sizes compared to conventional tagging. The present study applied both conventional tagging (to increase sample size) and telemetry methods (to reduce error inherent with conventional tagging). For telemetry, we used the Vemco VR2W Positioning System to estimate red snapper F on artificial reefs in 2015. We released 63 transmitter tagged red snapper on 4 artificial reefs with Vemco VPS receiver arrays. Telemetry methods are unique in that they are entirely independent of fisher reported recaptures. For conventional tagging we release 364 Floy tagged red snapper on 38 artificial reefs at close to 10 tagged fish per reef. Conventional tagging methods are dependent on fisher returns, but we increased the probability of fisher returns by offering \$150 rewards for returned tagged fish. In 2015, telemetry tagged fish showed a high $F = 0.33$ based on fisher reported recaptures. Conventional tagging also showed the same high $F = 0.33$. After applying non-reporting rate (35 %) based on telemetry, estimates increased to $F = 0.46$. Thus telemetry based estimates were validated by conventional tagging methods and indicate that even with low sample sizes they provided accurate estimates, but at the same time can provide critical information that is not attainable with conventional tagging.

0190 AES Ecology & Behavior I, Balconies L & M, Thursday 7 July 2016

Elena Tamburin¹, Mauricio Hoyos Padilla Hoyos Padilla², Felipe Galván Magaña¹, Sora Kim³, Alberto Sánchez González¹, Agustín Hernández Herrera¹, José Leonardo Castillo-Geniz⁴

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Trophic habitat of mako and white shark in a nursery area

Juveniles of white sharks (*Carcharodon carcharias*) and mako sharks (*Isurus oxyrinchus*) are captured in the artisanal fishery on the western coast of Baja California (B.C.): white sharks as by-catch with bottom gillnets and mako sharks as a target species with gillnets and pelagic longlines. The aim of this research is to study the habitat use of both species using stable isotopes analysis of C and N in muscle tissue, which reflected the diet integrated in a large time scale. Sebastian Vizcaino Bay represents a nursery area in B.C. for both species and Isla Cedros likely represents a new pupping area for white sharks, based on observations and tissue collection (n=2). During 2015, 45 muscle samples were collected in Laguna Manuela (n=30), Bahía Tortugas (n=13) and Isla Cedros (n=2). We observed mako sharks between 67- 196 cm total length (TL) and white sharks between 97-240 cm TL, which represent young of the year and juvenile sharks. The mean isotopic values in muscle were $\delta^{13}\text{C} = -17.3\text{‰} \pm 0.3$ and $\delta^{15}\text{N} = 18.4\text{‰} \pm 0.9$ for mako sharks and $\delta^{13}\text{C} = -15.7 \pm 0.4$ and $\delta^{15}\text{N} = 17.3 \pm 0.9$ for white sharks. In addition, smaller individuals have greater nitrogen isotope values, which could be due to maternal contributions or foraging in ^{15}N -enriched environments. The isotopic niche for white and mako sharks do not overlap suggesting that sharks are not sharing feeding resources. Mako sharks of different age and sex classes showed a similar habitat use ($\delta^{13}\text{C}$) and segregation between neonates and juveniles.

0664 ASIH STOYE AWARD GENETICS, DEVELOPMENT, & MORPHOLOGY, Salon F-H, Friday 8 July 2016

Milton Tan, Jonathan Armbruster

Auburn University, Auburn, AL, USA

Transcriptome Evolution of Paedomorphic Cyprinidae

The relationship between functional genomic evolution and evolution of extreme phenotypes is of major interest in evolutionary biology. Cypriniformes includes multiple genera of paedomorphic taxa, such as *Paedocypris*, *Sundadanio*, and *Danionella*, representing some of the world's smallest vertebrates. Previous phylogenomic investigation demonstrated these taxa do not form a clade, and thus there have been multiple, independent transitions to paedomorphism. To study the relationship of phenotypic convergence in paedomorphic taxa and functional genomic evolution, we

sequenced transcriptomes of *Paedocypris*, *Sundadanio*, and *Danionella* and compared their transcriptome sequences to publically available cypriniform transcriptomes. We first inferred the phylogeny of Cypriniformes using transcriptomic data. We then explored the relationship of transcriptomic sequence evolution with the evolution of paedomorphism, and tested for shifts in the level of selection specific to paedomorphic taxa relative to other cypriniforms in functional genes across the transcriptome.

0547 Fish Systematics I, Salon F-H, Saturday 9 July 2016

Kevin Tang

University of Michigan–Flint, Flint, MI, USA

Systematics of Damselishes

The family Pomacentridae is a widespread and species-rich group, forming a major component of the world's reef communities. Over 250 damselfish species, representing all 29 pomacentrid genera, were examined for this study. Over 100 acanthomorph species were also included for analysis. Sequence data from mitochondrial (12S, 16S, ATPase 8/6, cytochrome b, cytochrome c oxidase I) and nuclear (histone 3, recombination activating gene 1, and tmo-4c4) genes were used for the phylogenetic analyses. The results of these analyses found support for the monophyly of the family as well as the monophyly of many previously recognized groups, corroborating other recent molecular phylogenies of this family. These relationships, particularly their implications for the classification and taxonomy of Pomacentridae, will be discussed.

0728 Fish Morphology & Biogeography, Salon A-C, Sunday 10 July 2016

Juliette Tariel², Gary Longo¹, Giacomo Bernardi¹

¹*UC Santa Cruz, Santa Cruz, CA, USA*, ²*Ecole Normale Supérieure de Lyon, Lyon, France*

Tempo and Mode of Speciation in *Holacanthus* Angelfishes Based on RADseq Markers

In this study we estimated the timing of speciation events in a group of angelfishes using 1186 RADseq markers corresponding to 94,880 base pairs. The genus *Holacanthus* comprises seven species, including two clades of Panama trans-Isthmian geminates, which diverged approximately 3-3.5 Mya. These clades diversified within the tropical Eastern Pacific (TEP, three species) and tropical Western Atlantic (TWA, two species), which our data suggest to have occurred within the past 1.5 My in both ocean basins, but may have proceeded via different mechanisms. In the TEP, speciation is likely to have followed a peripatric pathway, while in the TWA, sister species are currently partially sympatric, thus raising the possibility of sympatric speciation. This study

highlights the use of RADseq markers for estimating both divergence times and modes of speciation at a 1-3 My timescale.

0466 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Christopher Taylor

University of Texas Rio Grande Valley, Edinburg, TX, USA

The spatial scale of similarity and patterns of homogenization and differentiation in Chihuahuan Desert riverine fish assemblages

Desert aquatic ecosystems around the world are declining in water quantity, quality and native species diversity. Fish assemblages in these ecosystems are increasingly becoming homogenized, although the degree of homogenization is dependent on the magnitude and direction of change following extirpation and colonization events and the spatial scale of observation. The frequency of species loss and gain, the identity of those species, and the regional extent of these changes interact with historical patterns of species diversity and environmental change, and determine resulting patterns. We examined the spatial scale of similarity for fish assemblages in the highly modified Rio Grande basin in the Chihuahuan desert of West Texas using a well-documented historical data set and recent collections that provided a paired analytical design across 29 localities spanning approximately 30 years of time. Results indicated that homogenization and differentiation occurred, but these patterns depended on the spatial resolution of comparison. The greatest changes were found between stream reaches within a sub-basin. The Rio Grande sub-basin showed strong convergence between upstream and downstream reaches that corresponded to declining water quality and quantity from the Rio Conchos in Mexico. The Pecos River sub-basin showed strong differentiation between upstream and downstream reaches that was associated with a strong shift in geomorphology. Assemblage similarities within specific river reaches of each sub-basin were variable in their degree of historical change, which was largely dependent on anthropogenic modification to the flow regime change and variability in the success of invasive species.

0946 Lightning Talks, Galerie 2, Saturday 9 July 2016

Emily Taylor

California Polytechnic State University, San Luis Obispo, CA, USA

What's behind the critical thermal maximum?

The critical thermal maximum (CT_{max}) is a commonly used measure of thermal tolerance in ectotherms. It is defined as the temperature at which they lose coordinated locomotor function. The physiological mechanism responsible for the CT_{max} is largely unknown in air-breathing ectotherms. Recent studies in my lab have tested the oxygen

limitation hypothesis, which suggests that the CT_{max} is reached when metabolic demand for oxygen exceeds the cardiovascular system's ability to supply it. I will briefly discuss the results of these studies and describe current studies underway to further test the hypothesis, which so far is being strongly supported in our studies on *Sceloporus* lizards.

0238 AES Physiology, Paleontology, & Collections, Balconies L & M, Friday 8 July 2016

Jordan Taylor, Gavin Naylor

College of Charleston, Charleston, SC, USA

A Morphometric approach for assessing the Elasmobranch Fishes from the Late Eocene of South Carolina

Isolated chondrichthyan teeth are the most abundant vertebrate fossils represented in the fossil record, and are widely distributed along the southeastern United States. The coastal plain in South Carolina contains an abundance of chondrichthyan remains from the Eocene epoch. It is distinguishable from other epochs by the presence of distinct, calcareous nannofossil assemblages and levels of dissolved carbon. The Eocene lasted from 55.8 to 33.9 million years ago and is characterized by accelerated global cooling, changes in ocean circulation, and a drop in global temperature of about 2°C. The effects of this climatic transition on fauna diversity have been observed in the calcareous nannofossil assemblage, but have yet to be observed in vertebrate macrofauna, specifically elasmobranchs. The present study aims to identify the diversity and distribution of the elasmobranch fauna using isolated teeth found in the Parkers Ferry formation (33.239068° N, -80.425665°W), which represents a period of cooling in South Carolina. Many extant sharks can be identified on the basis of tooth morphology, which has been typically qualitative in nature. This sorting "technique" has led to taxonomic problems in the fossil record, because there are several patterns of heterodonty that influence tooth shape. In this study, a geometric morphometric technique will be applied to extant and fossil teeth as a quantitative approach to identify the elasmobranch taxa from the late Eocene. The results of the present study will provide a reliable and unbiased method to identifying sharks' teeth.

0388 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: ECOLOGY, NATURAL HISTORY, DISTRIBUTION, & BEHAVIOR

Julie Taylor, Matthew Lattanzio

Christopher Newport University, Newport News, Virginia, USA

Blue Gets the Boulder, but Yellow is Bolder: Territorial Dynamics of a Color Polymorphic Lizard

Social dynamics in territorial species reflect the outcome of interactions between multiple traits, including dominance and boldness, yet these traits are often treated independently. For example, in ornate tree lizards (*Urosaurus ornatus*), males differing in dewlap color diverge in social dominance: whereas blue males are aggressive and always territorial, yellow males usually exhibit a less-aggressive satellite behavioral tactic. However, in habitats with fewer available microhabitats, yellow males defend territories and increase in relative abundance, despite still losing to blue males in controlled dominance experiments. These observations suggest that consideration of social dominance alone may be insufficient to explain *U. ornatus*' territorial dynamics in the wild. In this study we tested how both dominance and boldness contribute to the outcome of territorial disputes in tree lizards. We recorded the territory-use behavior of blue and yellow male tree lizards (entered in pairs) in the lab. At the end of each trial, we approached each male and recorded whether it fled (shy) or not (bold) in response to our approach. Our results support previous findings for *U. ornatus*; namely, dominant blue males occupied the higher-quality territory more often than yellow males. However, when approached by a simulated predator, blue males were more likely to flee than yellow males. Thus, while blue males are more dominant, yellow males may be bolder. In conclusion, although social dominance may drive initial territory acquisition patterns among competing males, asymmetries in their boldness behavior may perturb the nature of these patterns across environments.

0392 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: ECOLOGY, NATURAL HISTORY, DISTRIBUTION, & BEHAVIOR

William Ternes, Matthew Lattanzio

Christopher Newport University, Newport News, Virginia, USA

Trophic Niche Variation in a Widespread Lizard

A growing body of evidence supports that dietary differentiation among populations may contribute to the ecological success of widespread taxa. However, the degree that populations vary in foraging tactics (i.e., generalist versus specialist with respect to resource availability) and prey selection (i.e., variation in trophic level) remains poorly understood. Here we will evaluate the degree of dietary divergence among 17 populations of the ornate tree lizard (*Urosaurus ornatus*), and characterize the

mechanism(s) contributing to observed inter-population differences in diet. At each population we captured 10 lizards with a noose-pole, recorded their body size, and collected a tissue sample for stable isotope analysis of their carbon and nitrogen content. At each site of capture, we also estimated the percent vegetation cover. We will use our stable isotope data to describe each population's diet and test whether populations diverge in foraging tactics (carbon), prey selection (nitrogen), or both. Preliminary analyses from a subset of our populations support that *U. ornatus* populations vary in diet selection ($P < 0.05$), and do not generalize on available resources ($P > 0.05$). Currently, we are in the process of analyzing our remaining data. If populations occupy distinct ecological roles in terms of their diet, then this would suggest ecological heterogeneity among populations plays a role in the ability of widespread species to occupy diverse microhabitats. In this manner, we will provide key insights into the factors contributing to and the nature of diet variation in a widespread taxon.

1073 Herp Conservation, Galerie 2, Sunday 10 July 2016

Kimberly Terrell¹, Daniel Breaux², Shelley Stiaes²

¹Memphis Zoo, Memphis, TN, USA, ²Southeast Louisiana Refuge Complex, US Fish and Wildlife Service, Lacombe, LA

High Incidence of Snake Mortality at Bayou Sauvage National Wildlife Refuge (New Orleans, LA)

Bayou Sauvage National Wildlife Refuge (NWR) is located entirely within the city limits of New Orleans and is considered the nation's largest urban wildlife refuge. It encompasses ~24,000 acres of intermediate and brackish marsh, as well as ~200 acres of forested lands on low ridges. The refuge is highly impacted by anthropogenic development. It is located in an area of high industrial/petrochemical activity and is intersected by a major interstate. In early 2006, wetlands along the eastern edge of the refuge were developed into a landfill to accept 2.6 million tons of residential debris from Hurricane Katrina. We conducted a herpetological inventory of Bayou Sauvage NWR from Jan - Dec 2015, funded by the US Fish and Wildlife Service. We detected 27 amphibian and reptile species, including 10 snake species. Dead or moribund snakes were encountered throughout the year, including *Agkistrodon piscivorus*, *Coluber constrictor*, *Farancia abacura*, *Lampropeltis nigra*, *Liodytes rigida*, *Nerodia cyclopion*, and *Thamnophis proximus*. In many cases, no gross abnormalities were observed. Freshly-dead carcasses of three species were submitted to the National Wildlife Health Center for necropsy. Severe internal infections were identified in *T. proximus* and *F. abacura*, but the cause of death was undetermined in six necropsied *L. rigida*. Chemical or thermal skin burns were observed in the *T. proximus* carcass and in a live *C. constrictor* (not collected). Additional tests for environmental contaminants are ongoing. There is an urgent need to identify and mitigate the causes of mortality, disease susceptibility, and skin abnormalities in this population.

The findings and conclusions in this abstract are those of the author(s) and do not necessarily represent the views of the U.S. Fish and Wildlife Service.

0053 Herp Ecology, Salon F-H, Sunday 10 July 2016

Christopher Thawley, Tracy Langkilde

Penn State University, University Park, PA, USA

Invasive Fire Ant (*Solenopsis invicta*) Predation of Eastern Fence Lizard (*Sceloporus undulatus*) Eggs

Invasive species are a threat to biodiversity, and understanding their impacts on native ecosystems is a research priority. Red imported fire ants (*Solenopsis invicta*) are invasive in the southeastern United States and have multiple effects on a variety of native species. In some species, particular life stages, including juveniles and eggs, may be especially vulnerable to fire ants, but research on these impacts has been limited. Fire ants occupy microhabitats used for nesting by Eastern Fence Lizards (*Sceloporus undulatus*) across much of their range. We examined the extent of fire ant predation on fence lizard eggs by constructing artificial nests at a fire ant-invaded location and monitoring them for predation for up to 20 days. During this period, 24% of nests were predated by fire ants, and survival curves suggest 61% of nests may be vulnerable to fire ant predation over the entire incubation period. Distance of nests to the nearest fire ant mound and canopy cover above nests were not significant predictors of predation, indicating that nest site choice by fence lizards may not be able to avert fire ant predation. Invasive fire ants likely represent a novel level of predation pressure on many species, and these effects should be accounted for in management and conservation strategies.

0923 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; STORER AWARD ICHTHYOLOGY

Cheryl Theile, Terry Grande

Loyola University Chicago, Chicago, IL, USA

Developmental Changes in Lower Jaw Functional Morphology of North American Esocids

Northern Pike (*Esox lucius*) and Muskellunge (*Esox masquinongy*) are two closely related fishes within the order Esociformes. Their geographical distributions overlap in North America and they are known to compete for resources in many localities. While both are voracious ambush predators later in life, Muskellunge appears to transition to a piscivorous diet sooner than Northern Pike. The development of Northern Pike and Muskellunge was examined to study how changes in the functional morphology of the lower jaw might be correlated to the timing of their diet shifts. The theoretical mechanical advantage (MA) for jaw opening and closing was calculated using

ontological measurements of cleared and stained hatchery specimens (330.25 to 1,577.5 hours post fertilization). In addition, the effective mechanical advantage (EMA) was for stained and dissected specimens (960.75 to 2131.25 hours post fertilization) for two subsections of the abductor mandibulae muscle, A2 and A3. Preliminary data for Northern Pike and Muskellunge suggest shifting MA for jaw opening and closing is correlated to age and size. Both species display a decrease in MA for jaw opening. However, MA for jaw closing increased with age for both species. The timing of these changes in MA are similar in both species and occur once the yolk sac is fully consumed but before their ontogenetic diet shifts. In addition, EMA was lower than MA for each muscle subsection, while both MA and EMA was lower for A3 than for A2. EMA did not change significantly over the time period studied for either muscle section.

0265 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: ECOLOGY, NATURAL HISTORY, DISTRIBUTION, & BEHAVIOR

Alex A Thomas, Peter A Zani

University of Wisconsin - Stevens Point, Stevens Point, WI, USA

Experimental Test of Overwinter Site Selection by Ectotherms Based on Thermal and Spatial Cues: Side-blotched Lizards Prefer Smaller Crevices over Warmer Sites

Winter site selection by ectotherms is often complex and the factors influencing this process are not yet fully understood. In many reptilian species microhabitat temperature appears to influence overwintering site selection, but the importance of spatial cues cannot be ruled out. To clarify the role of thermal and spatial cues, we independently tested how temperature and crevice size affects overwintering site selection of side-blotched lizards in the lab. Winter-acclimated lizards were allowed crevice selection in an artificial hibernaculum (winter habitat) in which heat and space were altered separately. This allowed us to test gradients of heat (~5–15 °C), or space (6, 13, or 19 mm-tall crevices), or both. Experiments were preformed i) with a heat gradient, but without a space gradient, ii) without a heat gradient, but with a space gradient, and iii) with both heat and space gradients. The results of this experiment show that thermal or spatial cues by themselves may influence site selection, but when both heat and space gradients are available, lizards prefer smaller crevices over warmer sites. These results indicate that for overwintering ectotherms, crevice size may be more influential than temperature for site selection.

0534 Lightning Talks, Galerie 2, Saturday 9 July 2016

Meagan Thomas, Alanna Horton, Michael Dorcas

Davidson College, Davidson, North Carolina, USA

Predicting Total Body Length of Incomplete Rattlesnake Skeletons Through X-ray Technology and Vertebral Measurements

The Eastern diamondback rattlesnake (*Crotalus adamanteus*) is the largest species of rattlesnake in the world, with adults typically reaching lengths of 1.2-1.5 m (4-5 ft). Although there are reports of individuals up to 2.4 m (7.8 ft), physical evidence (e.g. museum specimens, skins, scalable photographs) is limited for individuals over 2.1 m (7 ft). In this study we used museum specimens (skeletal and preserved) to develop a model that would allow determination of body length from skeletal remains of *C. adamanteus*. We X-rayed 15 preserved known-length specimens of varying size and measured the pre- and post-zygapophyseal articular facets of the largest vertebra for each specimen. We used these data to develop body length estimates for three partially complete *C. adamanteus* skeletons with highly variable vertebral size (largest vertebra of each specimen measured 14.16, 16.60, 27.04 mm long). We discuss our findings and how they relate to what is currently known about *C. adamanteus* body size and natural history. Studies such as this are important for developing new techniques which can further our understanding of the natural history of extinct, rare, or understudied organisms that are difficult to acquire in nature, but are available through museums or other similar collections.

0690 ASIH STOYE AWARD GENERAL ICHTHYOLOGY, SALON F-H, Thursday 7 July 2016

Andréa T. Thomaz¹, Mark R. Christie², L. Lacey Knowles¹

¹*University of Michigan, Ann Arbor, MI, USA*, ²*Purdue University, West Lafayette, IN, USA*

Riverscape genetics: modeling genomic expectations to test hypotheses about river network architecture as drivers of evolutionary dynamics in aquatic populations

It is widely recognized that physical landscapes can shape genetic variation within and between populations. However, it is not well understood how riverscapes, with their complex architectures, affect patterns of neutral genetic diversity. Using a spatially explicit agent-based modeling (ABM), we evaluate the genetic consequences of dendritic river shapes on local population structure. We disentangle the relative contribution of specific river properties to observed patterns of genetic variation by evaluating how different branching architectures and downstream flow regimes affect the genetic structure of populations within rivers. Irrespective of the river length, our results illustrate that the extent of river branching, confluence position, and asymmetric downstream migration dictate patterns of genetic variation in riverine populations.

Comparisons between simple and highly branched rivers show a 20-fold increase in the overall genetic diversity and a 7-fold increase in the genetic differentiation between local populations. Given that most rivers have complex architectures, our findings highlight the importance of incorporating riverscape information into evolutionary models of aquatic species to disentangle neutral divergence caused by river architecture from adaptive processes. Also, the high genetic differentiation observed in complex architectures could help explain why riverine fishes represent a disproportionately large amount of global vertebrate diversity. In addition to exploring the genetic consequences of the riverscape theoretically, the framework is also useful for addressing how different aspects of river architecture might impact observed patterns of genetic variation in empirical systems; in this case, tests of hypotheses about genomic variation in the tetra *Mimagoniates microlepis* (Characidae) from southern Brazil.

0427 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Andrew Thompson¹, Andrew Furness², Guillermo Orti¹

¹The George Washington University, Washington D.C., USA, ²University of California, Irvine, Irvine, California, USA

Phylo-transcriptomics of Annual Killifishes

Annualism or seasonality is hypothesized to have evolved multiple times in Aplocheiloid killifishes (Cyprinodontiformes). These are fishes that live in ephemeral bodies of water subject to seasonal desiccation. When the pools dry up, adults bury their eggs in the soil, and embryos enter diapause stages and tolerate desiccation until the rains return. Once the rains return, they are then able to hatch. The phylogeny of this group has never been inferred with “big data” and many interrelationships in this clade are undetermined. Here, the phylogeny is inferred with orthologous genes of nearly 30 transcriptomes of aplocheiloid killifishes from most annual and non-annual lineages. This phylogeny is the foundation for future comparative work on the evolution of annualism in this group of organisms.

0423 Fish Genetics, Salon D, Sunday 10 July 2016

Andrew Thompson¹, Jason Podrabsky², Guillermo Orti¹

¹The George Washington University, Washington, D.C., USA, ²Portland State University, Portland, Oregon, USA

The Transcriptomics of Delayed Hatching and Desiccation Tolerance in the Non-Annual Killifish *Aplocheilus lineatus*

Annual killifish (Cyprinodontiformes: Aplocheiloidei) are known for their seasonality and their ability to inhabit temporary or ephemeral environments, which are subject to desiccation. Embryos undergo a diapause stage in the pre-hatching stage and they can

also tolerate desiccation. This is a convergent trait that has evolved multiple times in this suborder of fishes. However, all related non-annual species also have embryos that possess the ability to tolerate desiccation and delay their hatching in a way that is similar to annual species. To explore the evolution of annualism and investigate the intermediate phenotype of non-annual fishes, replicated transcriptomes were sequenced for water-incubated pre-hatching and air-incubated delayed hatching embryos of the non-annual fish *Aplocheilichthys lineatus*. Hundreds of candidate genes involved in delayed hatching and desiccation tolerance have been identified. Results are compared to other transcriptomic studies of diapause and desiccation tolerance in cyprinodontiform fishes.

0490 General Ichthyology II, Balconies J & K, Sunday 10 July 2016

Kenneth Thompson

Lock Haven University of Pennsylvania, Lock Haven, Pennsylvania, USA

Karyotypes of Two Species of Sculpin (*Cottus*) and their Hybrid in Central Pennsylvania with a Discussion of Chromosomal Evolution in the Cottidae

Specimens of *Cottus cognatus*, *C. bairdi* and their hybrids were collected from the West Branch of the Susquehanna River in Lycoming and Clinton Counties in Central Pennsylvania. Air dried, C-metaphase chromosome preparations were produced from gill epithelium. Diploid counts (2N) of 48 were determined for all three of these. Diploid counts for 19 specimens of *C. cognatus*, (nine males and nine females), eight specimens of *C. bairdi* (three males and five females) and seven hybrids (two males and five females) were determined. A total of 372 spreads were counted, 237 (63.7%) were determined to have 2N counts of 48 chromosomes. Metaphase spreads with 2N=48 were considered to be complete diploid sets and these were measured and classified by type (metacentric, submetacentric or subtelocentric/telocentric). It was found that there were eight bi-armed (msm) and 40 uni-armed (stt) chromosomes. The chromosome formulae (2N/NF) for all three were thus determined to be 48/56. Karyotypes for 34 species in 16 genera are known for the family Cottidae. Twenty-four (70.6%) have 2N values of 46 - 48. Ten (14.5%) of the 69 species in the genus *Cottus* have been karyotyped and nine of these (90.0%) have 2N=48. Eight of these (80.0%) have NF values of 56 - 58 indicating the conservative nature of chromosomal evolution within this genus.

0209 ASIH STOYE AWARD CONSERVATION, SALON E, Thursday 7 July 2016

Michelle E. Thompson, Maureen A. Donnelly

Florida International University, Miami, FL, USA

Recovery of Amphibian Communities in Regenerating Forest: Two Case Studies in Riparian and Upland Habitats of Secondary Forest, Costa Rica

The extensive degradation of natural systems caused by anthropogenic activities is a pressing global conservation concern. There is hope that some of the negative impacts caused by forest loss such as reduction of ecosystem services and loss of biodiversity may be offset by the regeneration of altered landscapes to secondary forests. However, the value of secondary forests to fauna is poorly understood. In our study, we examined the differences in species richness among riparian and upland habitats in a chronosequence of secondary forest in two tropical lowland wet forest regions of Costa Rica. We found that riparian habitats maintain high species diversity in modified habitats and early successional stages of forests. In harsh landscapes, such as those generated as a result of land-use change, riparian zones may be especially crucial to maintaining amphibian populations by serving as a refuge for a variety of species.

0592 ASIH: ASIH at 100 Symposium, Salon D, Saturday 9 July 2016

Mike Thompson

University of Sydney, Sydney, NSW, Australia

Eggs and Live Birth: A Retrospective and Prospective Look at the Evolution of Viviparity in Reptiles

The 100th anniversary of ASIH is a terrific milestone and it is timely to reflect on the next 100 years. The evolution of viviparity has been the major focus of my research career. From the seminal paper by Packard, Tracy and Roth in 1977, the field developed in a number of ways, from understanding the selective pressure leading to the evolution of live birth to the morphology and ontogeny of placental development, with squamate reptiles playing a major role in those studies. In last 40 years, methodological advances have pushed our studies further than we ever imagined. First, major advances in imaging technology and rapid development of sophisticated molecular techniques now allow us to address many new questions. We now combine the morphology of placental development, especially in skinks, and next generation sequencing to understand both the function and the evolution of gestational structures. The hunt for "the" gene for viviparity proved naïve and we now know that all of the same genes present in oviparous species are also present in viviparous species, but their timing and level of expression varies. The evolution of viviparity from oviparity seemingly involves 100s of genes, making it extremely complex. Many fields of biology, viviparity included, had firm roots in studies of reptiles, but they are now developing as broader evolutionary questions where reptiles act as a model. Consequently, many of us now use multiple

models to address our questions (for me that includes marsupials and fishes), although our passions remain with reptiles.

0951 Herp Biogeography, Phylogeography, & Systematics, Salon E, Saturday 9 July 2016

Robert Thomson¹, Phillip Spinks², Bradley Shaffer², Anthony Barley¹

¹University of Hawaii, Honolulu, Hawaii, USA, ²University of California, Los Angeles, California, USA

Phylogeny of the Map Turtles (*Graptemys*)

The emydid turtle genus *Graptemys* primarily inhabits large river systems that are drainages of the Gulf of Mexico. The species shows strong endemism, with each major system typically supporting one or two species within the genus. This radiation appears to have occurred both rapidly and recently, which has made phylogenetic resolution within the clade difficult. Here we present a well sampled molecular phylogeny comprising all species and subspecies recognized in the genus. We recover a well resolved phylogeny that is congruent with the presumed biogeographic history of the group. We also find a complicated history within the false map turtle complex, a group that contains several morphologically similar species, which may be due to incomplete lineage sorting, hybridization, or a combination of these factors. To further elucidate this history, we present preliminary results on a follow-up population genetic study comprising many thousands of SNP markers for several hundred individuals.

0677 Fish Genetics, Salon D, Sunday 10 July 2016

Jeremy Tiemann¹, Trent Thomas², John Epifanio¹, Wendy Schelsky¹

¹Illinois Natural History Survey, Champaign, IL, USA, ²Illinois Department of Natural Resources, Gibson City, IL, USA

The Redspotted Sunfish Saga: From statewide surveys to genetic analyses, captive propagation, and reintroduction efforts

The Redspotted Sunfish (*Lepomis miniatus*) occurs in clear, slow-flowing, well-vegetated streams and backwater lakes from the Illinois River basin south through the Mississippi River Valley. The range of *L. miniatus* in Illinois has been greatly reduced since the pre-1908 collections of Forbes and Richardson. Our surveys of known historical collection sites and other promising sites with favorable habitat in the mid-2000s suggested that only two populations now exist in the state - one in the Saline River basin (Ohio River drainage) and one in the Sangamon River basin (Illinois River drainage). Subsequent to our surveys, *L. miniatus* was designated as a state-endangered species in Illinois. Decimation of the species was probably the result of the drainage of swamps and bottomland lakes, loss of aquatic vegetation, and the general deterioration of water

quality. We established a Redspotted Sunfish recovery team and established goals that included propagating the fish and releasing young-of-year (YOY) into restored Illinois River backwater lakes. From 2008-2010, *L. miniatus* was collected from Fish Creek (Sangamon River basin) and stocked into nursery ponds. Approximately 8,500 YOY were released into the 72-acre Fish Preserve Lake, a protected waterbody at Emiquon Nature Preserve near the Sangamon – Illinois confluence. These individuals spawned the following summer, allowing us to expand our stocking efforts by translocating the fish to five additional suitable waters in the region. Testing of the F2 generation suggested we were able to maintain the genetic diversity of this population of *L. miniatus*.

0241 AES Ecology & Behavior II, Balconies J & K, Saturday 9 July 2016

Thomas TinHan, R.J. David Wells

Texas A&M University at Galveston, Galveston, Texas, USA

Feeding Ecology of Juvenile Bull Sharks in the Northwest Gulf of Mexico

Estuaries along the Gulf coast provide valuable nursery habitat for juveniles of several species of elasmobranchs (e.g. Bull Sharks), but questions remain as to how young sharks exploit resources along the marine-freshwater continuum. In this study, we examine spatial and temporal patterns in the feeding ecology of juvenile (<210 cm total length) Bull Sharks in estuaries along the Texas coast. Juvenile sharks (N = 142) were collected opportunistically from five estuarine complexes along the Texas coast over a two-year period. Stomach contents from all individuals were identified to the lowest possible taxon, and four metrics of dietary composition were calculated: 1) percent number, 2) percent weight, 3) percent frequency of occurrence, and 4) index of relative importance (IRI and % IRI) as an omnibus metric of dietary composition. Stomach contents were dominated by teleost prey, particularly drums/croakers (45% IRI), mullets (25% IRI), and catfishes (13% IRI), and taxonomic contributions to dietary composition were consistent across multiple metrics. Stable isotopes of carbon ($\delta^{13}\text{C}$), nitrogen ($\delta^{15}\text{N}$) and sulfur ($\delta^{34}\text{S}$) obtained from epaxial tissue of juvenile sharks were used to infer trophic position and sources of organic matter in Bull Shark diets. In addition, we examined differences in feeding ecology among sharks from distinct estuarine complexes, and the shifts in diet or trophic position occurring with respect to season or ontogeny. Here we present the results of these analyses and discuss the role Bull Sharks may play in the trophic connectivity of Texas nearshore systems.

0093 Herp Ecology, Salon F-H, Sunday 10 July 2016

Brian Todd¹, Justin Nowakowski¹, Steven Whitfield², Evan Eskew¹, Michelle Thompson³, Jonathan Rose¹, Benjamin Caraballo⁴, Jacob Kerby⁵, Maureen Donnelly³

¹UC Davis, Davis, CA, USA, ²Zoo Miami, Miami, FL, USA, ³Florida International University, Miami, FL, USA, ⁴Renaissance Charter High School for Innovation, New York, NY, USA, ⁵University of South Dakota, Vermillion, SD, USA

Variation in Host Thermal Tolerances Explains Patterns of *Batrachochytrium dendrobatidis* Infection in Amphibians

The fungal pathogen *Batrachochytrium dendrobatidis* (*Bd*) has caused the greatest known wildlife pandemic to date, infecting over 500 amphibian species. Although many species develop disease as a result of infection and suffer from consequent mortality, others persist despite infection or avoid infection altogether. Our understanding of factors shaping differences in chytridiomycosis susceptibility among amphibians remains incomplete, limiting our ability to effectively predict infection and disease risk. Here, we introduce a conceptual model that explains differential susceptibility of ectothermic hosts to a generalist pathogen. Our model predicts that, given a conducive environment, infection risk will be lower for amphibian host species whose thermal tolerances exceed that of the *Bd* pathogen. We tested this prediction with a global database of *Bd* infection prevalence records representing 11,435 assays from 53 species across five continents. We supplemented this global database with infection data we collected in Costa Rica for 16 additional species. Host species with higher thermal tolerances had lower *Bd* infection prevalence than did species with lower thermal tolerances. The relationship between host thermal tolerance and infection prevalence was generalizable across multiple amphibian families and spatial scales, and depended on environmental context, but host thermal tolerance was always the single best predictor of infection risk. Our study is the first to show how variation in thermal tolerance among host species underlies differential disease susceptibility. Given parallels in other disease systems, tolerance mismatches between host and pathogen may broadly shape disease risk among many ectotherm hosts besieged by host-generalist pathogens.

1054 ASIH STOYE AWARD CONSERVATION, Salon F-H, Friday 8 July 2016

Erin Toffemier, H. Bradley Shaffer

University of California, Los Angeles, Los Angeles, CA, USA

Metapopulation dynamics of the critically endangered Santa Barbara Distinct Population Segment of the California tiger salamander, *Ambystoma californiense*

The Santa Barbara county population of the California tiger salamander, *Ambystoma californiense*, is recognized as a Distinct Population Segment (DPS) under the Federal Endangered Species Act (2000) and is one of the most endangered salamanders in the

United States. The entire range of this lineage is contained in a 30 by 40 km region in northern Santa Barbara County, virtually all of which is in privately owned. Current recovery and management efforts focus on six geographically isolated metapopulations with the goals of maintaining and developing suitable habitat to support population growth and connectivity among breeding ponds. However, our understanding of current and historical movement patterns is extremely limited. Using both existing microsatellite data and newer genomic level target capture markers, we examined the genetic connectivity and effective population sizes of 23 breeding ponds across the metapopulations sampled from 1986 to 2001. Preliminary analyses show that there is strong genetic subdivision both among metapopulations and among breeding sites within these metapopulations, suggesting a history of restricted gene flow and local differentiation. These results indicate that metapopulations may not be interchangeable, and that local, on-site conservation methods may be called for, even in a geographically restricted species.

0649 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Samantha Tomczewski¹, Gary S. Casper², John D. Peterson¹

¹University of Wisconsin - Platteville, Platteville, Wisconsin, USA, ²University of Wisconsin - Milwaukee Field Station, Saukville, Wisconsin, USA

Comparing Survey Techniques for Monitoring Wisconsin's Endangered Cricket Frog

Manual calling surveys have historically been the method of choice for monitoring frog populations. During these surveys researchers travel to wetlands and listen for frog species following a standard protocol. These surveys can be time intensive and occur late into the evening. Additionally, incorrect detections, observer differences, logistics, and safety and environmental factors can constrain data collection in manual surveys. The development of automated recording systems and their accompanying software can offer a solution to some of the drawbacks of manual calling surveys. In our study we used a combination of manual calling surveys and automated recording systems to monitor three populations of the state Endangered Blanchard's Cricket Frog (*Acris blanchardi*) at 3 sites in Grant County Wisconsin. Results from manual calling surveys done by novice observers were compared to the audio playback of recordings from the same time. During manual calling surveys, observers made an error of omission 7% of time compared to zero commission errors in the audio playback. Current DNR management guidelines for this species involve assessing populations via manual calling surveys. Our data suggest that automated recording systems have several advantages over manual calling surveys. Our results may lead to improved guidelines for monitoring this species, especially as regards increasing sample sizes for statistical analysis, thereby improving the conservation of this imperiled species.

0735 Turtle Ecology, Salon A-C, Sunday 10 July 2016

Pilar Santidrián Tomillo¹, Meritxell Genovart¹, Frank Paladino², James Spotila³, Daniel Oro¹

¹Institut Mediterrani d' Estudis Avançats, IMEDEA (CSIC-UIB), Esporles, Spain,

²Indiana Perdue University Fort Wayne University, Fort Wayne/Indiana, USA, ³Drexel University, Philadelphia, PA, USA

Temperature-dependent sex determination (TSD) is linked to temperature-dependent embryo mortality in sea turtles

Sea turtles have temperature-dependent sex determination (TSD) and high temperatures in the nest reduce hatching success and emergence of hatchlings. We modeled the effect of increasing nest temperature on a critically endangered population of leatherback turtles (*Dermochelys coriacea*) and assessed the relationship between TSD and temperature-dependent hatchling output. Our results showed that TSD is advantageous for sea turtle populations when temperatures rise to the levels that increase their embryo mortality. Populations compensate for the increased mortality of hatchlings by increasing production of female hatchlings and therefore, future fecundity. This mechanism seems advantageous under fluctuating environments but it may become ineffective under climate change, as temperatures are projected to rise over the levels that produce 100% female hatchlings and cause death.

0248 AES Morphology & Reproduction, Balconies L & M, Friday 8 July 2016

Taketeru Tomita¹, Chip Cotton², Minoru Toda³

¹Okinawa Churashima Research Center, Motobu, Okinawa, Japan, ²Florida State

University Coastal and Marine Laboratory, St. Teresa, FL, USA, ³Okinawa Churaumi Aquarium, Motobu, Okinawa, Japan

Gas diffusion model indicates that oxygen diffusion through uterine wall is insufficient to sustain dogfish embryo

Unlike mammals or some "placental viviparous" sharks, most viviparous elasmobranchs lack connection with the mother, and thus, the embryos must acquire oxygen from the surrounding uterine fluid for a period ranging from several months to more than a year. However, the mechanisms underlying oxygen delivery and uptake in elasmobranchs remain largely unknown. Diagnostic sonography performed on a captive Japanese dogfish (*Squalus japonicus*) at the Okinawa Churaumi Aquarium demonstrated that a late-stage embryo used buccal movement to pump uterine fluid, suggesting that the embryo acquires oxygen from uterine fluid via gill ventilation. A previous study hypothesized that embryonic respiration in aplacental elasmobranchs depends on oxygen supplied by the uterine wall. To test this hypothesis, the rate of oxygen supply from the uterus was estimated by applying a "gas diffusion model" to the uterine wall of two dogfish species (*Squalus cf. mitsukurii* and *Squalus cubensis*). Our model calculations suggested that the supply of oxygen via diffusion through the uterine wall contributes

less than 15-30% of the total oxygen demand of late-stage embryos, indicating that uterine wall is not the main source of oxygen for embryonic respiration. Previously, some authors have suggested that pregnant dogfish intermittently exchange uterine fluid with external seawater during late gestation. Thus, late-stage embryos may acquire oxygen primarily from uterine seawater introduced from the external environment.

0629 HL GRADUATE RESEARCH AWARD, Galerie 2, Thursday 7 July 2016

João Tonini¹, Karen Beard², Rodrigo Ferreira³, Walter Jetz⁴, R. Alexander Pyron¹

¹*The George Washington University, Washington, DC, USA*, ²*Utah State University, Logan, UT, USA*, ³*Universidade Vila Velha, Vila Velha, ES, Brazil*, ⁴*Yale University, New Haven, CT, USA*

Fully-sampled phylogenies of squamates reveal evolutionary patterns in threat status

Macroevolutionary rates of diversification and anthropogenic extinction risk differ vastly throughout the Tree of Life. This results in a highly heterogeneous distribution of evolutionary distinctiveness (ED) and threat status among species. We examine the phylogenetic distribution of ED and threat status for squamates (amphisbaenians, lizards, and snakes) using fully-sampled phylogenies containing 9,574 species and expert-based estimates of threat status for ~4,000 species. We ask whether threatened species are more closely related than would be expected by chance and whether high-risk species represent a disproportionate amount of total evolutionary history. We found currently-assessed threat status to be phylogenetically clustered at broad level in Squamata, suggesting it is critical to assess extinction risks for close relatives of threatened lineages. Our findings show no association between threat status and ED, suggesting that future extinctions may not result in a disproportionate loss of evolutionary history. Lizards in degraded tropical regions (e.g., Madagascar, India, Australia, and the West Indies) seem to be at particular risk. A low number of threatened high-ED species in areas like the Amazon, Borneo, and Papua New Guinea may be due to a dearth of adequate risk assessments. It seems we have not yet reached a tipping point of extinction risk affecting a majority of species; 63% of the assessed species are not threatened and 56% are Least Concern. Nonetheless, our results show that immediate efforts should focus on geckos, iguanas, and chamaeleons, representing 67% of high-ED threatened species and 57% of unassessed high-ED lineages.

0633 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

João Tonini¹, Karen Beard², Rodrigo Ferreira³, Walter Jetz⁴, R. Alexander Pyron¹

¹The George Washington University, Washington, DC, USA, ²Utah State University, Logan, UT, USA, ³Universidade de Vila Velha, Vila Velha, ES, Brazil, ⁴Yale University, New Haven, CT, USA

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0921 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Luke Tornabene¹, D. Ross Robertson², James Van Tassell³, Carole Baldwin¹

¹National Museum of Natural History: Smithsonian Institution, Washington, DC, USA, ²Smithsonian Tropical Research Institute, Balboa, Panama, ³American Museum of Natural History, New York, NY, USA

A cache of new gobies (Gobiiformes: Gobiidae) from mesophotic reefs in the Caribbean discovered by manned submersibles

The Smithsonian's Deep Reef Observation Project (DROP) has reinvigorated the exploration of mesophotic and other deep-reefs in the Caribbean. Through the use of Substation Curacao's manned submersible *Curasub*, along with its tender vessel the *R/V Chapman*, DROP has discovered a cache of undescribed fish biodiversity from reefs below traditional scuba diving depths (~150-1000 ft). Many of the new species

discovered by DROP belong to the family Gobiidae (gobies), the most diverse family of marine fishes in the world. Here we present an overview of the different gobiid taxa found on deep reefs in the Caribbean, including several species and genera that have been recently described as well as many other taxa that await formal description.

0668 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Josiah Townsend¹, Kayla Weinfurther¹, Ileana Luque-Montes¹, Thomas Firreno¹, James Austin²

¹Indiana University of Pennsylvania, Indiana, Pennsylvania, USA, ²University of Florida, Gainesville, Florida, USA

Underestimated diversity in Mesoamerican true frogs (Family Ranidae)

True frogs (Family Ranidae) are a taxonomically and ecologically diverse radiation of with New World distributions reaching from Alaska to the Amazon. The taxonomy of ranids has historically been underestimated, particularly in reference to leopard frogs (*Rana pipiens* complex). In Mesoamerica, our understanding of species-level diversity in these ubiquitous frogs is poor, and lacks a well-resolved phylogenetic hypothesis to guide species delimitation. Recognized taxa include *Rana brownorum* (low and moderate elevations along Caribbean versant of northern Mesoamerica), *R. forreri* (low elevations along Pacific versant), *R. macroglossa* (western Nuclear Central American highlands), *R. maculata* (Nuclear Central American highlands), *R. taylori* (low and moderate elevations along Caribbean versant of southern Mesoamerica), and *R. warszewitschii* (humid lowlands southern Mesoamerica). We sampled for over 200 Mesoamerican ranids representing six recognized species, and used DNA sequence data from three mitochondrial (12S, 16S, and COI) and four nuclear (BDNF, RAG1, Rhodopsin, and Seventh in Absentia) gene regions to estimate a new phylogeny. Our results suggest that there are at least eight unconfirmed candidate species in Central America, in addition to the six named taxa, with multiple cryptic lineages concealed within *Rana brownorum*, *R. maculata*, and *R. warszewitschii*. The taxonomy of both *R. forreri* and *R. macroglossa* also require additional attention. These results provide the phylogenetic backbone to support further work to delimit these candidate taxa and evaluate species boundaries in areas of potential sympatry and parapatry.

0952 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Claire Tracy, Kerry Cobb, Rafe Brown

University of Kansas, Lawrence, Kansas, USA

Identification of Unknown Tadpoles from the Philippines

With amphibian declines currently plaguing biodiverse regions around the planet, there is a need to focus further research on areas like the Philippines – regions that can utilize improved biological surveys to fuel conservation efforts. The lack of recent research including information on tadpoles, and the benefit that this information can have on biological assessments, conservation efforts, and phylogenetic relationships, puts a need for further descriptions and identifications of poorly studied amphibian larvae. A paper delimiting Philippine anuran species via tadpole descriptions, and including identification of those that have yet to be described, will greatly increase our current level of knowledge on the tadpoles in the Philippines. Standard Phenol-Chloroform extraction protocol was used followed by PCR to amplify the target region of the 16S rRNA locus. The amplified product was then sequenced using Sanger Sequencing by Beckman Coulter Genomics, and homologous sequences obtained from the National Center for Biotechnology (NCBI) nucleotide database using the Basic Local Alignment Search Tool (BLAST). By sequencing unknown tadpole specimens in the Herpetology collection at the University of Kansas, I was able to correctly identify these tadpoles and allow for further descriptions that can make a substantial contribution to the literature for both basic and applied science. It is anticipated that this contribution will form both a fundamental contribution to larval biology of Philippine amphibians – and also make practical, useful contribution for species identification, which should have an applied value for management purposes.

0065 Turtle Ecology, Salon A-C, Sunday 10 July 2016

Stan Trauth¹, Dustin Siegel², Malcolm McCallum³, David Jamieson⁴, Anthony Holt⁵, Joy Trauth¹, Hilary Hicks¹, Jonathan Stanley¹, Jonathan Elston¹, John Kelly¹, Johnny Konvalina¹

¹Arkansas State University, Jonesboro, AR, USA, ²Southeast Missouri State University, Cape Girardeau, MO, USA, ³Scientific Investigator's Alliance, Holden, MO, USA, ⁴Crowder College-Cassville, Cassville, MO, USA, ⁵University of Arkansas Community College at Morrilton, Morrilton, AR, USA

Long-term Monitoring and Recovery of a Population of Alligator Snapping Turtles, *Macrochelys temminckii* (Testudines: Chelydridae), from a Northeastern Arkansas Stream

We conducted a mark and release study of the alligator snapping turtles, *Macrochelys temminckii*, on Salado Creek (Independence Co., Arkansas) during 10 trapping seasons, which spanned a 20-year period (1995 - 2015). We trapped a total of 163 alligator snapping turtles during 416 trap nights; we also recorded a total of 35 recaptures during

this study. The catch per unit effort (CPUE) averaged slightly greater than 0.24 (317 trap nights) during the first 4 years (1995-1998), showed an increase to 0.64 by 2001 (only 14 trap nights), and then dramatically increased during the final 5 years to average 0.92 (85 trap nights). The population size estimates during the early period of the study (1995-2001) ranged from 20 alligator snappers in 1995 to as many as 88 snappers in 1998, whereas the population size estimates from 2011-2015 ranged from 105 snappers in 2011 to as many as 282 snappers in 2015. The male turtles recaptured had a higher average growth rate than females. These data, however, should be used with caution as age was not known. Most of the 22 recaptured alligator snapping turtles exhibited some degree of site fidelity. Within our sample, recaptured males grew faster on average than females or juveniles in both straight carapace length and mass. Both CPUE and Jolly-Seber approaches demonstrate that this population benefitted from removal of fishing pressure, thus leading to an increase in abundance of alligator snapping turtles in the lower ~5 km of the creek.

0862 ASIH: Lessons From, and Visions For Symposium, Salon D, Sunday 10 July 2016

Joel Trexler¹, William Loftus²

¹Florida International University, North Miami, FL, USA, ²Aquatic Research & Communication, LLC, Vero Beach, FL, USA

Thirty years of bird food in the Everglades: Monitoring key links in the food web of an iconic ecosystem

We are conducting a long-term study of aquatic animals in the Everglades that was started in the late 1970's. In the early 1990's we expanded the study from three sites in Everglades National Park to 20 sites over two drainages in the Park and in state-owned lands to the north. The goals of this study have been to gather information on fish and macroinvertebrates that indicate status of ecosystem function and particularly support key apex predators, especially wading birds. By the 1990's it was concluded that wading bird nesting success had declined because of food limitation during the nesting season, leading to the hypothesis that poorly planned water management failed to support aquatic animal production and seasonal concentration that historically coincided with the bird's nesting season. The long-term data gathered have been used to assess management actions as part of the Comprehensive Everglades Restoration Plan and contribute to a biannual report for the US Congress on the status of restoration efforts. This project is currently funded by the US National Park Service, though state and other Federal agencies contributed funding for the original expansion of the work outside of the National Park. The study design uses random sampling at fixed plots, which has generated time-series data yielding adequate statistical power to detect effects of importance for management. Recent uses of the project have been to develop models for evaluation of alternative restoration plans and climate change scenarios, and to track the invasion of non-native species.

1047 Fish Behavior & Development, Salon A-C, Sunday 10 July 2016

Timothy C. Tricas, Kelly S. Boyle

University of Hawai'i at Manoa, Honolulu, HI, USA

Evolutionary Patterns of Sound Production in Coral Reef Butterflyfishes (Chaetodontidae)

Fish produce context-specific sounds during social communication, but evolutionary patterns of sound production are poorly known for most taxa. Butterflyfishes (family Chaetodontidae) are prominent members of coral reefs and use a diversity of acoustic behaviors during social communication. At least two sound production mechanisms exist in the bannerfish clade, and additional mechanisms exist in the *Chaetodon* clade which is distinguished by anterior swim bladder horns and the laterophysic connection. Some *Chaetodon* species share the head bob acoustic behavior with *Forcipiger flavissimus*, which along with other sounds in the 100–1000 Hz spectrum, are likely adequate to stimulate the ear, swim bladder or LC of a receiver fish. In contrast, only *Chaetodon* species produced the tail slap sound, which involves a 1–30 Hz infrasound pulse that can stimulate the receiver's ear or lateral line at close distances, but not the swim bladder or its horns. Reconstructions of ancestral character states appear equivocal for the head bob and divergent for the tail slap acoustic behaviors. Independent contrast analysis indicates a correlation between sound duration and stimulus intensity characters within the family. The intensities of the tail slap and body pulse sounds in *Chaetodon* and the head bob sound in *Forcipiger* are correlated with body length, thus they provide honest acoustic signals of size. Future studies on fish acoustic communication should investigate low frequency and infrasound acoustic fields to understand the integrated function of the ear and lateral line, and their evolutionary patterns in acoustic communication.

0486 Fish Systematics II, Salon F-H, Saturday 9 July 2016

Michael Tringali¹, Brandon Barthel¹, John Knight²

¹*Florida Fish and Wildlife Commission, Saint Petersburg, FL, USA*, ²*Florida Fish and Wildlife Commission, Holt, FL, USA*

An Undescribed species of *Micropterus* in Florida and Southeastern Alabama

An undescribed species of the genus *Micropterus* has been discovered in coastal plain drainages of the Florida panhandle and southeastern Alabama. Taxonomically this species occurs within the *M. punctulatus* species group, which otherwise consists of *M. punctulatus*, *M. treculii*, and *M. tennesseensis*. It is monophyletic within the genus in phylogenetic reconstructions based on mitochondrial and nuclear-inton sequences, respectively, and is diagnosable with respect to all recognized members of *Micropterus*

by multiple molecular autapomorphies. It is phylogenetically positioned such that failure to elevate it would require synonymizing other *M. punctulatus* group members. Its distinctiveness has been further corroborated by morphological-based canonical discriminant analyses, logistic regression, and, to lesser degree, recursive partitioning. Morphological and molecular analyses also elucidated another novel population of *Micropterus* inhabiting the coastal drainages in Mississippi. Specimens from this region, which are phylogenetically and morphologically distinct from the undescribed species, were thought to be intergrades of *M. punctulatus* × *M. henshalli*. However, the intergrade hypothesis is an oversimplification of its complex evolutionary dynamics and its taxonomic position within the genus remains uncertain.

0916 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Kelcie Troutman, Renata Platenberg

University of the Virgin Islands, St Thomas, U.S. Virgin Islands

Call Recognition of Virgin Islands Frogs using Bioacoustic Analysis Software

Frog populations are declining globally and there is a critical need to rapidly identify changes in population distribution, activity patterns, and community composition, and to correlate these changes with potential influences to direct management actions. Frogs in the Virgin Islands can be effectively surveyed using acoustic methods; each species has a unique call that can be recognized by trained personnel even across distances of hundreds of meters. We conducted an experimental synoptic survey using a citizen science model where community members submitted cell phone recordings collected during a specific time window, along with a screenshot of their location coordinates. We received over 300 2-minute recordings from across the US and British Virgin Islands. Using bioacoustic analysis software, the call structures for each frog species were isolated to allow automatic classification; species IDs were verified aurally. From the recordings, we identified three native (*Eleutherodactylus antillensis*, *E. cochranæ*, and *Leptodactylus albilabris*) and two non-native (*E. coqui* and *Osteopilus septentrionalis*) species, while an additional two species (*E. lentus* and *Rhinella marina*) remained undetected. The recording locations have been mapped and will be used to spatially analyze patterns in frog distributions. Although the learning curve for this effort has been steep, this combination of bioacoustics and citizen science offers a promising method for rapidly collecting data for amphibian community monitoring.

0965 ASIH STOYE AWARD GENERAL HERPETOLOGY, Salon F-H, Friday 8 July 2016

Derek B. Tucker¹, S. Blair Hedges², Guarino R. Colli³, R. Alexander Pyron⁴, Jack W. Sites, Jr.¹

¹Brigham Young University, Provo, UT, USA, ²Temple University, Philadelphia, PA, USA, ³Universidade de Brasilia, Brasilia, DF, Brazil, ⁴The George Washington University, Washington, DC, USA

A Fossil-Calibrated Time Tree of Teiid Lizards and Historical Biogeography of the West Indian *Ameiva* (Teiidae: Squamata)

The West Indian *Ameiva* (N = 21) are a radiation of teiid lizards with a distribution across the Greater Antilles, Lesser Antilles, and Bahamas, with the remaining species in the genus occupying diverse habitats in South America. We propose to test hypotheses of the historical biogeography of the group. To accomplish this goal, we use a combination of NextGen sequence data (316 nuclear loci) and the mitochondrial ND2 gene to reconstruct phylogenetic relationships, estimate divergence times, and conduct ancestral area estimations. Our results support previous studies of *Ameiva* showing a single radiation to the Caribbean islands consisting of four species groups. A fossil-calibrated time-tree estimates that West Indian *Ameiva* diverged from its sister group 27–23 MYA and diversification within the group has taken place over the last 12–10 MYA. If contemporary ocean currents are not considered in the analyses, the ancestor of Caribbean *Ameiva* likely began diversification in Cuba or the Bahamas. Animals from here also colonized Jamaica and Hispaniola with a long distance dispersal event to Puerto Rico. Subsequently, the Lesser Antilles were colonized from the Puerto Rican ancestor. If the probability of dispersal is reduced against ocean currents, the ancestor of the group likely dispersed from South America to Dominica with subsequent dispersal to Hispaniola. Both of these groups (Dominica and Hispaniola) then dispersed to nearby islands with the Dominica group colonizing Puerto Rico and the remaining Lesser Antilles while the Hispaniola group colonized the remaining Greater Antilles (except for Puerto Rico) and the Bahamas.

1037 Poster Session I, Acadia/Bissonet, Friday 8 July 2016

Cassandra Turinske¹, Michael Pauers⁰

¹UW-Waukesha, Waukesha, WI, USA, ²Milwaukee Public Museum, Milwaukee, WI, USA, ³UW-Milwaukee School of Freshwater Science, Milwaukee, WI, USA

Morphological Variation among Wisconsin Populations of the Orangespotted Sunfish (*Lepomis humilis*)

While studies of intraspecific morphological variation in centrarchid sunfishes are fairly common, these studies are often focused on a select few species of the genus *Lepomis*. Nonetheless, many species of *Lepomis* have been overlooked, including the Orangespotted Sunfish, *Lepomis humilis*. As a first attempt to explore the possibility of

intraspecific variation in *L. humilis*, examined morphological variation among nine Wisconsin populations of this species. While we found no morphometric variation among these populations, we did find one, from Lake Belle View in Dane County, which had an unusually low number of lateral line scales; these scales were also larger than those found in the other populations. To the best of our knowledge, this is the first demonstration of any kind of morphological variation among populations of *L. humilis*; a fruitful second step would be to expand the geographical range of these comparisons.

**0374 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; STORER AWARD
ICHTHYOLOGY**

A.J. Turner, William Ludt, Prosanta Chakrabarty

Louisiana State University, Baton Rouge, LA, USA

Molecular phylogeny of threadfin breams (Nemipteridae), with comments on their habitat transitions to and from coral reefs

Fishes in the family Nemipteridae, also referred to as threadfin or whiptail breams, are carnivorous fishes inhabiting shallow, continental habitats. They are widely distributed throughout tropical and subtropical waters in the Indo-West Pacific and are important for artisanal and commercial fisheries in the region. Approximately 67 species are currently described and placed within five genera, which exhibit strikingly different ecologies. Fishes in *Nemipterus* and *Parascolopsis* generally occur over sandy or muddy bottoms and consume benthic invertebrates, while species of *Pentapodus*, *Scolopsis*, and the monotypic *Scaevius* occur near coral reefs. Although they are widely distributed throughout many habitat types across their range, life history information on many species is poorly studied and phylogenetic relationships among genera remain unresolved. At present, less than ten species have been included in phylogenetic analyses. Here we present the most inclusive dataset of nemipterid fishes to date by including approximately half of the described species diversity in the family, and representatives from all genera. Using a combination of mitochondrial and nuclear loci, we demonstrate the monophyly of this group with both maximum likelihood and Bayesian approaches. Furthermore, the relationships among different genera are discussed, along with historical transitions between reef and non-reef habitats. With this dataset, Nemipteridae has the potential to become a new model system for investigating how transitions to coral reef habitat influence speciation in marine fishes.

0647 Fish Ecology I, Salon A-C, Saturday 9 July 2016

Thomas Turner

University of New Mexico, Albuquerque, New Mexico, USA

Stable Isotopes and museum specimens offer new insights into ecological processes over centuries of environmental change

Natural history collections offer vast resources and deep time series for stable isotope analysis (SIA). In turn, SIA offers insights into ecosystem processes that shape biodiversity. The highest value of museum holdings may be to establish baseline conditions to evaluate ecosystem and food web processes over the last century. This is notable because this time period is marked by unprecedented landscape transformation and climate change. Using river systems as an example, I explore several scenarios of how isotopic techniques and museum specimens can be used to evaluate effects of river flow homogenization, invasive species, and water extraction. A recently developed analytical framework places isotopic ratios into niche modeling context that opens up new possibilities for process-oriented analysis of species distribution and abundance. Constraints involve the effects of museum preservatives and temporal and spatial depth of museum sampling events. Incorporation of isotope ratios into natural history collections databases could enhance interpretation and utility immeasurably.

0193 ASIH STOYE AWARD CONSERVATION, SALON E, Thursday 7 July 2016

Annalee Tutterow¹, Shannon Pittman¹, Gabrielle Graeter², Michael Dorcas¹

¹*Davidson College, Davidson, NC, USA*, ²*North Carolina Wildlife Resources Commission, Raleigh, NC, USA*

The State of North Carolina Bog Turtle Populations: Assessing Bog Turtle Population Demography and Landscape Factors Affecting Their Persistence

Turtles are among the most vulnerable vertebrate group to declines, extirpations, and extinctions, especially those species with specific habitat requirements. The bog turtle (*Glyptemys muhlenbergii*) occupies small bogs, fens, and wet meadows in the eastern United States and is listed as federally threatened. We used a long-term mark-recapture dataset and applied a Cormack-Jolly-Seber model to calculate annual adult, sex-specific, and juvenile survival for intensively-sampled bog turtle populations in North Carolina. We found that adult survivorship remained constant over time for all populations, but was relatively low (0.869-0.942) when compared to the 0.96 adult survival estimate documented for northern bog turtle populations. We also analyzed landscape-level factors potentially affecting North Carolina bog turtle populations across multiple spatial scales (500-3000 m). We evaluated the impact of landscape conditions on turtle densities (range 4-224 turtles/ha) for the eight most intensively-sampled populations and considered the distribution of eleven bog turtle wetlands within a broader spatial context. We found that percent forest cover and wetland connectivity at the highest

spatial scale (3000 m) were the only significant predictors of bog turtle densities in North Carolina. Our studies indicate that North Carolina bog turtle populations are likely declining and that without stronger protection measures, including the mitigation of large-scale effects, local and regional extirpations of the species may occur.

0907 SSAR SEIBERT PHYSIOLOGY & MORPHOLOGY, Galerie 3, Friday 8 July 2016

Catherine Tylan¹, Kiara Camacho¹, Sean Graham², Mark Herr¹, Jermayne Jones¹, Gail McCormick¹, Melissa O'Brien¹, Jennifer Tennesen¹, Christopher Thawley¹, Tracy Langkilde¹

¹*Department of Biology, The Pennsylvania State University, University Park, PA, USA,*

²*Department of Biology, Sul Ross State University, Alpine, TX, USA*

Collecting baseline corticosterone samples in reptiles and amphibians: is under 3 minutes good enough?

There is growing interest in the use of glucocorticoid (GC) stress-relevant hormones as a way to understand how wild animals interact with their environment. The best medium for obtaining recent information about GC levels is blood, as the earliest changes in GC concentrations occur in blood plasma. Unfortunately, it is stressful to capture, restrain, and obtain blood from wild animals. As the hypothalamic-pituitary-adrenal axis requires some time to respond to a stressor with increased GC concentrations, the prevailing assumption is that blood taken within three minutes of capture should not yet be affected by the stress of capture, and thus reflect a true baseline level of GCs. This has been tested and confirmed in numerous laboratory rodents and birds, but there has been minimal work done in wild reptiles and amphibians. Here we compiled data collected from three species of wild caught reptiles (cottonmouths, rattlesnakes, and eastern fence lizards) and one species of laboratory acclimated amphibian (wood frogs). Blood samples to measure baseline GC concentrations (corticosterone, CORT) in these animals were taken between 1 and 13 minutes after first disturbing the animal, depending on the species. We used a nonparametric change point analysis test to determine if there was a statistically significant change point in the concentrations of CORT in samples taken after longer duration of captivity stress. We will present our findings and discuss the implications of the potential similarities and differences in character between the stress physiology of endotherms and ectotherms.

**0988 HL, ASIH, SSAR: Eco-Evolutionary Dynamics Symposium, Salon D,
Friday 8 July 2016**

Mark Urban

University of Connecticut, Storrs, CT, USA

**Do Eco-evolutionary Dynamics Promote Resilience of Amphibian
Communities to Climate Change?**

Understanding the resilience of natural systems to climate change is necessary to predict and ameliorate future impacts on biodiversity and ecosystem dynamics. In particular, we cannot accurately understand climate change risks to particular species and communities without understanding the interacting contributions of ecological and evolutionary resilience. Yet, most research fails to address one or more of these fundamental forms of resilience, and these gaps currently limit our ability to predict ecological responses with accuracy. Here I evaluate evidence for both ecological and evolutionary resilience in spotted salamanders (*Ambystoma maculatum*) and wood frogs (*Rana sylvatica*) to the climate-fueled expansion of the marbled salamander (*Ambystoma opacum*), an apex predator in temporary ponds. Results demonstrate that the apex predator substantially affected community and ecosystem properties in whole-pond manipulations. Experiments show that both spotted salamanders and wood frogs have adapted to the predator at fine scales. These adaptations could increase the resilience of some but not all ecological properties of ponds. Also evolution might not occur quickly enough relative to the rate of climate change. Also, populations located outside of the current marbled salamander range are adapted to other selection regimes that could interfere with these dynamics. Understanding the full complexity of both ecological and evolutionary responses will often be necessary to predict climate change responses with accuracy.

0321 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Robin Van Meter¹, Donna Glinski², Matthew Henderson³, Tom Purucker³

¹Washington College, Chestertown, MD, USA, ²Oak Ridge Institute of Science & Education, Oak Ridge, TN, USA, ³US Environmental Protection Agency, Athens, GA, USA

**Soil organic matter content effects on dermal pesticide bioconcentration in
American toads (*Bufo americanus*)**

Pesticides have been implicated as a major factor in global amphibian declines and may pose great risk to terrestrial phase amphibians moving to and from breeding ponds on agricultural landscapes. Dermal uptake from soil is known to occur in amphibians, but predicting pesticide availability and bioconcentration across soil types is not well understood. This study was designed to compare uptake of five current-use pesticides (imidacloprid, atrazine, triadimefon, fipronil, pendimethalin) in American toads (*Bufo americanus*) from exposure on soils with significant organic matter (OM) content

differences (14.1 % = high OM and 3.1% = low OM). We placed toads on high or low OM soil after applying individual current use pesticides on the soil surface for an 8-hour exposure duration. Whole body tissue homogenates and soils were extracted and analyzed using LC-MS to determine pesticide tissue and soil concentration, as well as bioconcentration factor in toads. Tissue concentrations were greater on the low OM soil than the high OM soil across all pesticides (average \pm SE; 1.23ppm \pm 0.35 and 0.78ppm \pm 0.23, respectively), and bioconcentration was significantly higher for toads on the low OM soil (ANCOVA $p = 0.002$). Soil organic matter is known to play a significant role in mobility of pesticides and bioavailability to living organisms. The potential for pesticide accumulation in amphibians moving throughout agricultural landscapes may be greater and should be considered in conservation and policy efforts.

0806 Lightning Talks, Galerie 2, Saturday 9 July 2016

Alex Van Nynatten¹, Devin Bloom², Belinda Chang¹, Nathan Lovejoy³

¹University of Toronto, Toronto, Ontario, Canada, ²Western Michigan University, Kalamazoo, Michigan, USA, ³University of Toronto Scarborough, Scarborough, Ontario, Canada

Visual Evolution in Marine Derived Amazonian Fishes

Incursions of marine water into South America during the Miocene prompted colonization of freshwater habitats by ancestrally marine species, and present a unique opportunity to study the molecular evolution of adaptations to varying environments. Freshwater and marine environments are distinct in both spectra and average intensities of available light. Higher concentrations of organic material and suspended particulate matter red-shift the underwater visual environment of large freshwater rivers. We have identified increased rates of molecular evolution in rhodopsin, the protein component of the photosensitive pigment in the eye expressed in the dim-light sensitive rod cells, in lineages of marine derived Amazonian fishes. Using likelihood-based comparative sequence analyses, we found evidence for positive selection in the rhodopsin of freshwater inhabiting lineages at sites known to be important for aspects of rhodopsin function such as spectral tuning. Differences are also observed between marine and freshwater lineages at known red-shifting sites, shifting the sensitivity of this pigment towards wavelengths of light more predominant in freshwater rivers. Our results suggest that an increased rate of rhodopsin evolution was driven by diversification into freshwater habitats, thereby constituting a rare example of molecular evolution mirroring large-scale palaeogeographical events.

**0812 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; STORER AWARD
ICHTHYOLOGY**

Alex Van Nynatten¹, Devin Bloom², Belinda Chang¹, Nathan Lovejoy³

¹*University of Toronto, Toronto, Ontario, Canada*, ²*Western Michigan University, Kalamazoo, Michigan, USA*, ³*University of Toronto Scarborough, Scarborough, Ontario, Canada*

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0691 AES Ecology & Behavior II, Balconies J & K, Saturday 9 July 2016

Maurits van Zinnicq Bergmann¹, Tristan Guttridge¹, Mark Bond², Samuel Gruber¹, Yannis Papastamatiou²

¹*Bimini Biological Field Station, South Bimini, Bahamas*, ²*Florida International University, Miami, Florida, USA*

**Movement Networks and Habitat Preferences of a Multi-Species
Elasmobranch Assemblage in Bimini, Bahamas**

Describing the ecological role of a species is contingent upon a holistic understanding of the relationships between animal movement, physical environment, and interactions with con-/heterospecifics. Such interactions define the structure and dynamics of populations and communities. How large predators influence these processes in marine systems, however, remains poorly understood. Here, a combination of passive acoustic telemetry, baited remote underwater video system (BRUVS) and fixed environmental data loggers in an island system in Bimini, The Bahamas, to identify physical (water temperature, depth) and biological drivers (competition, prey availability) of movement,

habitat and space use, habitat specificity and spatial hotspots of lemon *Negaprion brevirostris* ($n=14$), great hammerhead *Sphyrna mokarran* ($n=20$), tiger *Galeocerdo cuvier* ($n=12$), nurse *Ginglymostoma cirratum* ($n=14$), bull *Carcharhinus leucas* ($n=7$), blacktip *C. limbatus* ($n=7$), Caribbean reef *C. perezii* sharks ($n=6$), and southern stingray *Dasyatis americana* ($n=6$). A multi-habitat acoustic array monitored localized movements and residencies, while a data share collaboration of acoustic arrays monitored long-distance movements. BRUV surveys assessed relative abundance and distribution of elasmobranch and prey species for each habitat type that were representative of the Bimini array. Preliminary results revealed singular and diverse habitat use (Caribbean reef and nurse/great hammerhead, respectively), spatial hotspots and concentrated movements (around coral reefs/deep-water drop-off), numerous (trans-national boundary) migrations (nurse, lemon, hammerhead) and long-term, seasonal site fidelity. The creation of mechanistic home range models, through quantification of elasmobranch habitat associations and movement networks, will be vital to delineate key areas for protection and predict home range size and the impacts of anthropogenic perturbations.

1078 General Herpetology, Balconies L & M, Sunday 10 July 2016

John Vanek¹, Russell Burke²

¹*Southern Illinois University, Carbondale, IL, USA*, ²*Hofstra University, Hempstead, NY, USA*

Behavioral Ecology of Dwarfed Eastern Hog-nosed Snakes (*Heterodon platirhinos*) on a Barrier Island

We studied the behavioral ecology of Eastern Hog-nosed Snakes (*Heterodon platirhinos*) on a New York barrier island (~1800 ha) that reach smaller maximum sizes than mainland populations. Snakes on the island only have access to a single prey species (*Anaxyrus fowleri*), occur in large numbers ($n > 180$ marked) with high densities (> 4 snakes/ha), and lack color polymorphism that is characteristic of the species. We used radio-telemetry ($n = 12$), visual encounter surveys, and trapping to analyze the home range, habitat selection, and activity periods of this unique population. We found that dwarfed Eastern Hog-nosed Snakes utilize small home ranges, and that males (100% MCP = $40.6 \text{ ha} \pm 8.9$) have significantly larger home ranges than females (100% MCP = $12.0 \text{ ha} \pm 9.4$) home range sizes. Dwarfed Eastern Hog-nosed Snakes utilized open habitat with low canopy cover, but unlike other studies they also exhibited high use of Common Reed (*Phragmites australis*) dominated wetlands. Visual encounter surveys were male biased and revealed bimodal seasonal activity, with peaks in the spring and fall corresponding to the breeding seasons. Trapping was female biased, and remained successful during the summer, when concurrent visual encounter surveys were of diminished utility. Our success trapping ($n = 52$ unique individuals captured) suggests that this combination of survey techniques can be used very successfully, particularly in the northeastern United States where the species is of regional concern.

0304 ASIH STOYE AWARD GENERAL HERPETOLOGY, Salon F-H, Friday 8 July 2016

Mariana Vasconcellos¹, Guarino Colli², Miguel Rodrigues³, David Cannatella¹

¹The University of Texas, Austin, Texas, USA, ²Universidade de Brasilia, Brasilia, DF, Brazil, ³Universidade de São Paulo, São Paulo, SP, Brazil

Historical Climate Change Shapes Population Structure and Genomic Divergence of Treefrogs in the Neotropical Cerrado Savanna

Although the impact of Pleistocene glacial cycles was once dismissed in tropical regions, increasing evidence suggests that tropical organisms were greatly affected by Pleistocene climatic fluctuations resulting in distributional shifts. The genetic consequences of such responses to past climate change are just now being uncovered in several regions. Using genome-wide SNPs and mitochondrial DNA combined with species distribution models across the late Quaternary until the present, we evaluate the effect of paleoclimatic shifts on the present genetic structure and population differentiation of *Hypsiboas lundii*, a treefrog endemic to the South American Cerrado savanna. Our results show a recent and strong genetic divergence across the Cerrado landscape from west to east that does not seem congruent with any current physical barrier to gene flow. Isolation by distance explains much of the population differentiation in *H. lundii*, but we also find substantial support for the role of past climatic changes when controlling for the geographic distance among populations. Areas of more stable climatic conditions allowing population persistence since the Pleistocene appear to have played a strong role establishing the present genetic structure of this treefrog. This pattern is consistent with a model of isolation by instability, highlighting the strong effects of Pleistocene climatic shifts on tropical savannas.

CANCELLED

0576 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; AES CARRIER AWARD

Victoria Elena Vásquez, David A Ebert

Moss Landing Marine Laboratories, Moss Landing, CA, USA

'IT'S HAMMERTIME!': Uncovering the Secrets of an Iconic Shark with Citizen Science

Hammerhead sharks (*Sphyrna spp.*) are distinctive, and rather iconic, among shark species, with their "hammer-shaped" head. Two species are known to occur in the Northeast Pacific off southern California; the Scalloped (*Sphyrna lewini*) and Smooth (*S. zygaena*). Of these two species, the Smooth Hammerhead is the more temperate occurring species and is not uncommon off southern California. However, the extent of its occurrence is poorly known. The Scalloped Hammerhead is less common to rare in this area, typically only observed during warm water years usually associated with El Niño events. In recent years the use of mobile devices and through social media the general public and media has captured and informally documented images of

Hammerhead Sharks, prompting interest from the public. The public's perception is that they are increasing in abundance. Therefore, in an effort to better document and identify the Hammerhead species involved, a citizen science project was initiated in 2014 called 'Hammerhead'. Information is gathered through a web-based survey designed and monitored by the Pacific Shark Research Center. Basic, or more detailed, observational information, such as date and time of sightings, can be entered through a portal. Data collected overtime will allow researchers to evaluate long-term trends. This knowledge is of particular importance for Smooth and Scalloped Hammerhead Sharks since little is known about their use of Southern California waters. A better understanding of abundance, distribution and seasonality of Hammerhead Sharks in Southern California waters will help to better inform conservation and fishery management practices.

0868 Poster Session I, Acadia/Bissonet, Friday 8 July 2016

Jeremy Vaudo¹, Bradley Wetherbee², Jessica Harvey³, Alexandra Prebble¹, Keith Bruni², Mark Corcoran¹, Matt Potenski¹, Guy Harvey¹, Mahmood Shivji¹

¹Guy Harvey Research Institute, Nova Southeastern University, Dania Beach, FL, USA, ²University of Rhode Island, Kingston, RI, USA, ³Cayman Islands Department of Environment, George Town, Grand Cayman, Cayman Islands

Characterization and monitoring of one of the world's most valuable ecotourism animals, the southern stingray, *Dasyatis americana*, at Stingray City, Grand Cayman

Marine wildlife-oriented ecotourism often involves the provisioning of animals to increase the reliability of human-animal interactions. While these practices may increase the enjoyment of tourists, the long-term effects on wildlife are often unclear. The Stingray City Sandbar (SCS), Grand Cayman, is a location where southern stingrays, *Dasyatis americana*, are provisioned for ecotourism, resulting in behavioral and physiological changes. Recently, tourist operators have claimed that the number of stingrays at SCS has decreased substantially, however, there has never been a formal survey of stingrays at SCS. We examined over 13 years of southern stingray tagging data and enacted a structured census of the SCS aggregation to provide a formal characterization of the aggregation, establish a baseline for future monitoring, and provide some basic biological information on southern stingrays. Mature females dominated the SCS aggregation across years, and confirming operator fears, the size of the SCS declined between 2008 and 2012 from >100 to ~60 stingrays. Since 2012, stingray numbers have increased and appear to have stabilized at ~90 stingrays, which is still lower than historical levels. Females tended to be recaptured over much longer periods of time than males, with ~20% of recaptured females present for 10+ years, while male recaptures typically occurred within 3 years. As a result, there was more consistency of females over time, while males turned over more quickly. Our results suggest the SCS aggregation is highly dependent on recruitment from the general population and highlight the importance of regular monitoring for successful management of ecotourism activities.

0211 ASIH STOYE GENERAL ICHTHYOLOGY AWARD, Galerie 2, Friday 8 July 2016

Diego F B Vaz, Eric J Hilton

Virginia Institute of Marine Science, College of William and Mary, Gloucester Point, Virginia, USA

The caudal-fin skeleton of Batrachoidiformes (Teleostei: Percomorphacea) and its implications for the systematics of the order

The caudal-fin skeleton is a primary data source for studies of the systematics of fishes, with characters from it being proposed as synapomorphies at many levels of organization. Batrachoidiformes is recognized as a monophyletic group, although the interrelationships among the genera and species are not entirely clear. Similarly, the relationships of this order to other percomorph fishes are not well established. The distinctive caudal skeleton of Batrachoidiformes has not been thoroughly studied and the characters from this complex are poorly represented in recent phylogenetic analyses. This analysis of the caudal-fin skeleton of Batrachoidiformes, based on cleared and stained specimens representing the diversity of the order, emphasized the detection of intraspecific variation to better recognize morphological characters of possible phylogenetic significance. There is a high level of intraspecific variation, especially in the shape of the epurals and the margin of the parhypural flange. However, the parhypural articulates with the haemal spine of PU2 in two distinct patterns: 1) tightly with the haemal spine through a straight edge (e.g., *Opsanus tau*, *Thalassophryne maculosa*, *Allenbatrachus reticulatus*), and 2) loosely through an acute stay (e.g., *Aphos porosus*, *Porichthys porosissimus*). The support for the caudal-fin rays by the epurals also has two conditions: 1) the anteriormost epural supporting one or two procurrent caudal-fin rays (e.g. *Halobatrachus didactylus*, *Batrachoides pacifici*) and 2) the anteriormost epural not supporting any caudal-fin ray (e.g. *Porichthys plectrodon*, *Daector dowi*, *Amphichthys cryptocentrus*). The implications of these and other characters on interpreting the phylogenetic relationships within Batrachoidiformes will be discussed.

1004 General Ichthyology II, Balconies J & K, Sunday 10 July 2016

Page E. Vick¹, Mark S. Peterson¹, William T. Slack², Paul O. Grammer¹

¹University of Southern Mississippi, Department of Coastal Sciences, Ocean Springs, MS, USA, ²U.S. Army Corps of Engineers Research and Development Center, Vicksburg, MS, USA

Are there differences in critical habitat use between western and eastern Gulf Sturgeon (*Acipenser oxyrinchus desotoi*) population segments on Ship Island, Mississippi Sound, north-central Gulf of Mexico?

Federally-mandated critical habitat was designated for Gulf Sturgeon (GS) in 2003 across the species range including the Mississippi barrier islands. Earlier research showed that Ship Island (SI) provides critical overwintering habitat for members of the western population segment (WPS), and our preliminary research indicates members of the eastern population segment (EPS) also use SI. We used acoustic telemetry data to generate conservative estimates of travel time, travel distance, and travel rate for individual WPS and EPS members by drainage. The SI four year acoustic array (2011-2015) detected 60 acoustically-tagged GS (89.9-195 cm FL); 26 were EPS with the majority from the Blackwater River (FL) whereas 30 were WPS, representing the Pearl (MS/LA) and Pascagoula (MS) rivers. Fish residency averaged 33 days for EPS and 37 days for WPS annually, with WPS fish arriving in late October and leaving in early March and EPS fish arriving in mid-November and leaving in early April. Although arrival and departure times differed, annual residency (~6 mo) was about the same for both population segments. Conservative travel distances to SI from EPS ranged from 185 to 276 km whereas WPS ranged from 32 to 53 km. In one case, a Blackwater fish traveled from SI to its drainage within 11 days averaging 17 km/d; however, most travel between SI and natal drainages is about 1 km/d for both EPS and WPS. Arrival and departure of WPS was earlier than EPS suggesting either faster swimming speeds or earlier departure for natal drainages.

1013 AES Genetics, Genomics, Biogeography, & Systematics, Balconies J & K, Saturday 9 July 2016

Eduardo Villalobos¹, Héctor Espinosa¹, Paulo Brito³, Jesús Alvarado²

¹Instituto de Biología, UNAM, Ciudad de México, Mexico, ²Instituto de Geología, UNAM, Ciudad de México, Mexico, ³Universidade do Estado do Rio de Janeiro, Rio de Janeiro, Brazil

Morphological analysis of the genus *Zapteryx* (Rhinobatidae: Batoidea) and its phylogenetic implications

The genus *Zapteryx* is composed of three species, which are distributed in the coasts of the American continent: in the Pacific side *Z. exasperata* and *Z. xyster* and in the Atlantic coast *Z. brevirostris*. This genus poorly studied from the phylogenetic perspective and its phylogenetic relations with other members of the family Rhinobatidae (*Aptychotrema*,

Rhinobatos and *Trygonorrhina*) are uncertain. Using a parsimony phylogenetic analysis with chondroskeleton characters, the present study seeks to determine the phylogenetic topology of the genus *Zapteryx* and its phylogenetic relations with the family Rhinobatidae. The phylogenetic analysis included several species from the guitar fishes sensu (Compagno, 1977) and five fossil species of guitar fishes from the Upper Cretaceous. The character review was made via dissections or using images from x-rays and tomographs from specimens kept in the Colección Nacional de Peces, del Instituto de Biología UNAM, the Colección Nacional de Paleontología del Instituto de Geología UNAM, the Ichthyology Collection of the University of the State of Rio de Janeiro and from bibliographical reviews. The matrix for the phylogenetic analysis was elaborated using the program WINCLADA and analyzed using the algorithms of TBR and Ratchet in the program TNT. The results of these analyses show that the genus *Zapteryx* has not immediate phylogenetic affiliations with the genus *Rhinobatos* and *Aptychotrema* and that the family Rhinobatidae could be divided in at least two taxonomic entities of the same hierarchy.

**0601 ASIH STOYE AWARD GENERAL ICHTHYOLOGY, SALON F-H,
Thursday 7 July 2016**

Kirill Vinnikov

University of Hawaii at Manoa, Honolulu, Hawai'i, USA

**Complete Phylogeny of the Righteye Flounders (Teleostei: Pleuronectidae)
Provides the New Evidence for Vicariant Speciation Event after the Bering
Strait Opening**

The family Pleuronectidae is a group of righteye flounders with 62 currently described species. Ten occur exclusively in the Northern Atlantic and the others live in the Northern Pacific, with a few polar species that can be found in both regions. A recent phylogenetic study of bony fishes provided the first molecular time estimate for the origin of Pleuronectidae at <25 mya (Betancur-R et al., 2013), which contradicts the fossil evidence for pleuronectids from the early Oligocene deposits. Moreover, those deposits have been found in several regions in Europe and in Japan, suggesting conflicting hypotheses for the geographic origin of the family. In the present study, I propose the first complete phylogeny of Pleuronectidae reconstructed from the Bayesian analysis of two mitochondrial and three nuclear genes. The phylogenetic tree was used to estimate the ancestral states of osteological characters commonly applied in pleuronectid fossil identification. Then, a set of 23 known pleuronectid fossils was thoroughly reanalyzed, discarding all the specimens with uncertain taxonomy and dating. The remained fossils were used for node calibration under the UCLN clock model and the birth-death prior in BEAST. Based on the calibrated phylogeny, the origin of Pleuronectidae is estimated to be between 38-50 mya. According to that estimate, Atlantic species had begun to diverge independently from the Pacific species starting around 5 mya, which corresponds with the time of the Bering Strait's first opening. Thus, this study provides new insights into the origin of the righteye flounders in the Northern Atlantic by vicariant speciation.

0707 AES GRUBER AWARD, Balconies J & K, Friday 8 July 2016

Elizabeth Vinyard¹, Walter Bublely², Bryan Frazier², Marcus Drymon³, Jim Gelsleichter⁴

¹The Graduate School at the University of Charleston, South Carolina, Charleston, SC, USA, ²South Carolina Department of Natural Resources, Charleston, SC, USA, ³University of South Alabama, Mobile, AL, USA, ⁴University of North Florida, Jacksonville, FL, USA

Age, growth, and maturation of the Finetooth Shark, *Carcharhinus isodon*, in coastal waters of the western North Atlantic Ocean

Age, growth, and maturity was examined for Finetooth Sharks, *Carcharhinus isodon*, in coastal waters of the western North Atlantic Ocean (WNA) from Winyah Bay, South Carolina to Cape Canaveral, Florida. Vertebrae from 190 males and 217 females were aged, and the maximum observed age for males and females was 21.9 years and 22.3 years, respectively. Sizes ranged from 376 mm to 1174 mm FL for males and 380 mm to 1282 mm FL for females. Significant differences were detected between the sexes necessitating sex-specific von Bertalanffy growth models. These models yielded the following equations: $L_t = 1141 \text{ mm FL} - (1 - e^{-0.279(t-1.857)})$ for males and $L_t = 1257 \text{ mm FL} - (1 - e^{-0.197(t-2.335)})$ for females. Median length (L_{50}) and age (A_{50}) where 50% of the population is mature were 999 mm FL for males and 1041 mm FL for females corresponding to 6.4 years and 6.9 years, respectively. Significant differences in growth were detected between the current study and previously published parameters for the WNA. The current study found greater observed maximum ages, A_{50} , t_0 , and L_0 for both sexes and greater L_{50} for females. Both sexes were found to have lower L_{∞} parameters and males displayed lower L_{50} and lower k compared to the previous study. Previously no significant differences were detected in growth models from the WNA and Gulf of Mexico (GOM); however, results from the current study as well as reproductive, tagging and genetic studies suggest separate stocks in the WNA and GOM.

0488 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; STORER AWARD ICHTHYOLOGY

Stacey Virtue-Hilborn, Mark Steele

California State University, Northridge, Northridge, CA, USA

Bay Pipefish Abundance, Distribution and Ecological Function in Southern California Eelgrass Beds

As a result of human population pressures, seagrasses have experienced rapid environmental changes and large scale losses over that last 20 years. These losses directly threaten the survival of organisms like the bay pipefish (*Syngnathus leptorhynchus*), which is highly specialized to seagrass environments and unlikely to

survive outside of them. The bay pipefish is an abundant microcarnivore and may be affecting the trophic structure of these beds but it has not been well studied. Through seasonal surveys as well as caged experiments in the field, the distribution, abundance and ecological role of the bay pipefish in the trophic system of seagrasses was assessed in order to understand how to better protect these fragile marine ecosystems and the organisms that inhabit them. Seasonal surveys were conducted to confirm that pipefish abundance and distribution stay constant throughout the year (regardless of temperature and eelgrass density changes) unlike other fish and invertebrate species that inhabit these nursery habitats temporarily. Caged experiments in the field concluded that the bay pipefish may be having an effect on the density of crustacean algal grazers in this system. Preliminary results suggest that the loss of these grazers are resulting in either immense algal growth on eelgrass blades or community structure change as other grazers, including mollusks, increase in density in these areas. Further analysis on the ecological function of the bay pipefish in these habitats could provide meaningful information needed to better understand how to protect a fish that is dependent on this fragile marine ecosystem.

0575 HL: Social Behavior in Reptiles Symposium, Salon E, Saturday 9 July 2016

Richard Vogt¹, Camila Ferrara², Virginia Bernardes¹

¹*Instituto Nacional de Pesquisas da AmazÇonia, Amazonas, Brazil*, ²*Wildlife Conservation Society-Brazil, Amazonas, Brazil*

Communication and Social Life of the Giant South American River Turtle (*Podocnemis expansa*)

Most turtles do not appear to have much of a social life apart from courting and copulating, and a few territorial disputes among males, however we have found that the Giant South American River Turtle has a much more complex social life and dynamic vocal repertoire beginning while still in the egg. Over 25 years studying a population of this species in the Brazilian Amazon in the Rio Trombetas has shown *Podocnemis expansa* to be one of the most social species of turtles in the world: 1) communication with siblings while still in the egg, in the nest, scampering across the beach, entering the river and migrating with adult females; 2) group migratory behavior of adults from the flooding forests where they feed to the nesting beaches, group basking on the nesting beach, communal nesting, aggregation of females waiting for their young to hatch, communicating with hatchlings vocally, leading their hatchlings to the flooded forests to feed. We documented that many of these activities are synchronized by vocalizations. Through the use of hydrophones and microphones in the nest, sonic, vhf, and satellite transmitters as well as Crittercams attached to the carapaces of females and 1000s of pit tagged hatchlings we have confidently described post natal maternal care and other attributes suggesting group selection. These turtles use both visual and auditory signals to communicate, although they do not wag their tails like a dog when they come to greet

you it is apparent that they also recognize individual humans besides individual conspecifics.

0529 NIA II, Galerie 3, Sunday 10 July 2016

Joseph Waddell, William Crampton

University of Central Florida, Orlando, Florida, USA

Condition-dependent Electric Signaling in a Community of the Gymnotiform Knifefish *Brachyhypopomus* from the Upper Amazon

Brachyhypopomus generate pulsed electric organ discharges (EODs), and exhibit notable interspecific and intraspecific waveform diversity. Many studies have shown that these electric signals play a significant role in both mate attraction and intrasexual competition. Here, we summarize evidence for condition dependent signaling in a community of nine species of *Brachyhypopomus* from terra firme stream and floodplain lake habitats in the Upper Amazon. To best characterize signaling status in a natural social environment, we recorded head-to-tail EOD waveforms in the field at night, during peak hours of activity, within two minutes of capture (before the onset of most melanocortin-mediated EOD modulation). We investigated the correlation between overall body condition and calibrated EOD amplitude by correcting for covariance between EOD amplitude, body length, and body mass (utilizing residuals from log-normalized regressions). Our results show considerable variation in the correlation between body condition and size-adjusted EOD amplitude among species and sexes, and also seasonally. We found that condition dependence is strongest during the breeding season and largely restricted to species with EODs consisting of one or two phases. We also found that individuals with caudal filament damage exhibit reduced EOD amplitude, and/or considerably altered EOD waveform shape: both of which may impact sexual selection. Species with one or two EOD phases exhibited higher rates of caudal filament damage (ca. 20-40% of individuals) when compared to species with more than two phases (ca. 10-25%). Across all species, we found that males exhibited higher rates of caudal filament damage than females.

0930 General Herpetology, Galerie 2, Saturday 9 July 2016

Hardin Waddle, Brad Glorioso

U.S. Geological Survey, Lafayette, LA, USA

Site Occupancy Characteristics of the Gulf Coast Waterdog (*Necturus beyeri*)

The Gulf Coast Waterdog (*Necturus beyeri*) is a neotenic salamander known primarily from sandy spring-fed streams along the Gulf Coastal Plain of Texas, Louisiana, and Mississippi. In Louisiana, the current distribution of the species is not well known. Likewise, there is little specific information on the characteristics of sites that may

explain occupancy and abundance of waterdogs. We sampled for waterdogs using minnow traps along Bayou Lacombe in southeastern Louisiana at 25 sites from the headwaters to where the stream widens and slows. Using hierarchical models of abundance from repeat count data we determined that waterdog abundance within Bayou Lacombe was positively related to lower turbidity and higher pH. In southwestern Louisiana, we conducted an occupancy study to better determine the characteristics of sites that are occupied by waterdogs. Sites were chosen at random from a database of stream crossings in the known range of the species in the region. Each site was trapped for two consecutive weeks during the active season for the species. Stream characteristics such as width, bottom substrate, pH, and turbidity were measured at the study sites. Additional characteristics about the streams including drainage area and impervious surface estimates were derived from GIS information. A hierarchical occupancy model will indicate the relative importance of these factors for occurrence of waterdogs. Similar analyses for Lesser Siren (*Siren intermedia*) and Three-toed Amphiuma (*Amphiuma tridactylum*) also caught during the study reveal the apparent habitat differences among these three aquatic salamanders in the coastal plain.

0165 ASIH: ASIH at 100 Symposium, Salon D, Saturday 9 July 2016

Marvalee H Wake

University of California, Berkeley, Berkeley, CA, USA

ASIH At Crossroads

Scientific societies are at crossroads—how can they advance their missions, increase membership, invigorate their journals, and integrate their science with 21st century techniques, questions, problems, and social concerns, given the precipitous changes in the practice of science, and the public's regard for it? The American Society of Ichthyologists and Herpetologists has a long history of achievement, but we cannot rest on our laurels. Our journal is important, and our meetings offer rich science that includes everything from passion about taxa to a broadly-based scientific repertoire that represents all of the dimensions of the hierarchy of biological organization, often integrative of several of them. But how can ASIH sustain these attributes? How can it be sure that its approach to organismal biology, which most of us believe is essential to major questions in several areas (e. g., conservation, evolutionary biology, development, behavior, ecology, etc.), has a significant place at the table where funding and policy decisions are made? We have the potential to make that happen, but we must develop an agenda that has specific goals, and that outlines the means to meet those goals. It should be part of our legacy to today's students, and those who will follow them. ASIH is poised to provide major scientific leadership!

0753 Lightning Talks, Galerie 2, Saturday 9 July 2016

Paddy Walker, Irene Kingma

Dutch Elasmobranch Society, Amsterdam, The Netherlands

Baseline Study for Underpinning of the Management of Sharks and Rays in the Dutch Caribbean

In August 2015 the *Save our Sharks* project was launched in the Netherlands and the Dutch Caribbean. This is a 3 year campaign which aims to stop the decline of sharks and rays in the Dutch Caribbean. During the project dedicated research, stakeholder involvement and participatory development of management measures should ultimately lead to better protection of the elasmobranchs around the islands. The project will focus on: education on the importance of sharks in the marine ecosystem; working with local fishermen to find solutions workable solutions to stop shark (by)catches; working with government to realise effective management and control of shark populations; and enhancing the scientific knowledge needed for conservation and management. In this talk we will present the first results of the project, including baseline studies carried out around the islands of Saba and St Maarten using Baited Remote Underwater Videos (BRUVs) and tagging studies carried out using acoustic tags. The results will be put into the context of broader conservation and management measures and the need for international collaboration.

0982 SSAR SEIBERT AWARD ECOLOGY, Galerie 3, Thursday 7 July 2016

Danielle Walkup, Wade Ryberg, Toby Hibbitts, Lee Fitzgerald

Texas A&M University, College Station, TX, USA

Survivorship of the Dunes Sagebrush Lizard (*Sceloporus arenicolus*) in disturbed and undisturbed habitat

Fragmentation and habitat disturbance are predicted to cause population declines in habitat specialists. *Sceloporus arenicolus* (dunes sagebrush lizard) is a habitat specialist, endemic to the Mescalero-Monahans Sandhills of West Texas and southeastern New Mexico. With heavy oil and gas development occurring throughout its range, habitat fragmentation is an ongoing concern for the persistence of this species. We carried out a four-year mark-recapture study to quantify demography and movements of *S. arenicolus*. Two "super-grids" of pitfall traps were used to sample large landscapes in undisturbed and disturbed habitat. *Sceloporus arenicolus* was the third most common lizard species captured, with 549 individuals captured in the undisturbed site and 179 in the disturbed site. We modeled apparent survival and detection probability as a function of time, grid, and sex using Cormack-Jolly-Seber models in Program MARK. Top models showed apparent survival was a function of time, and detection probability was best modeled as an additive function of grid and time. There were no differences in survivorship between the two landscapes, but the population size was much smaller in the disturbed site. These results are interesting, because previous work demonstrated

that disturbance has a negative effect on *S. arenicolus* population size and persistence and it was clear in this study that the habitat in the disturbed area supports fewer *S. arenicolus* than in the undisturbed site. The reasons are complex and dependent upon site history, current site condition, and stochastic population fluctuations at the two sites.

**0467 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; STORER AWARD
ICHTHYOLOGY**

Ellie Wallace

University of Wisconsin-Stevens Point, Stevens Point, WI, USA

**Blood-Lactate Level Response to Potentially Stressful Activities Due to
Physical Exertion in Three Endemic South African Small-Bodied Shysharks
(Scyliorhinidae: Chondrichthyes)**

Angling exposes sharks to physical exhaustion and other types of stress. One of the many shark groups upon which angling has relatively unknown effects is the shysharks (F: Scyliorhinidae), endemic to the coast of South Africa, including the Puffadder Shyshark (*Haploblepharus edwardsii*), Dark Shyshark (*H. pictus*) and the Leopard Catshark (*Poroderma pantherinum*). Working with the RecFishSA program at the South African Shark Conservancy (SASC), I gathered and evaluated lactate levels in wild-caught shysharks experiencing voluntary stressors like actively foraging, involuntary stressors such as simulated angling by chasing, and also the effects of short recovery periods. I additionally defined and quantified several shark behaviors in video footage while the sharks were being subjected to chasing or foraging stimuli. These behaviors were indicative of physical exertion (i.e., line changes and tail whips), "psychological" stress (i.e., turning, circling, head raises, and suspensions), and interest (i.e., stimulus approaches). I hypothesized that blood lactate levels correlate with physical exertion and "psychological" stress in response to the two stimuli. There were no whole-blood lactate level differences among the species or sexes. Whole-blood lactate levels were higher in sharks experiencing chasing stimuli compared to foraging stimuli ($p < 0.0001$). The two behaviors indicative of physical exertion were positively correlated with blood lactate levels (p -values < 0.001). None of the behaviors indicative of "psychological" stress or interest significantly correlated with blood lactate levels. These data suggest that, in shysharks, blood lactate is primarily influenced by increased anaerobic metabolism during physical exertion rather than "psychological" stress.

0912 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Susan Walls¹, Katherine O'Donnell¹, William Barichivich¹, Joseph Reinman², Terry Peacock², Greg Titus², Jonathan Chandler²

¹US Geological Survey, Wetland and Aquatic Research Center, Gainesville, FL, USA,

²US Fish & Wildlife Service, St. Marks National Wildlife Refuge, St. Marks, FL, USA

Taking Action: Management and Recovery of Imperiled Flatwoods Salamanders at St. Marks National Wildlife Refuge, FL

Flatwoods salamanders (*Ambystoma cingulatum* and *A. bishopi*) historically occurred throughout the Coastal Plain of the southeastern U.S., but have declined by nearly 90% in recent years. St. Marks National Wildlife Refuge (SMNWR) in Florida is one of two remaining "strongholds" for *A. cingulatum*. Refuge land managers must decide how to restore and manage both aquatic and terrestrial habitats at SMNWR to maximize population persistence. We used structured decision making to develop a long-term approach to management and recovery of *A. cingulatum* at SMNWR. We also determined short-term actions needed to keep *A. cingulatum* on the landscape long enough to take advantage of improved future habitat conditions - an interim "emergency response." We used an adaptive management framework to address our habitat-related decision problem with state-dependent decisions, monitoring, and updating actions. For our emergency response, we decided to rear larvae to metamorphosis in mesocosms at SMNWR. We are actively engaged in conducting frequent growing season prescribed burns to restore upland and wetland habitat on the refuge, and have begun long-term monitoring of all known populations. In 2015, we set up cattle-watering tanks in which to head start larvae and, thus, boost survival to metamorphosis. SMNWR is committed to restoration of *A. cingulatum* habitat, coupled with head-starting larvae to boost survival, as means to stop and reverse this species' decline. Partnerships with state and other federal agencies are enhancing our ability to address complex challenges in conservation and management of this imperiled species.

1053 Fish Ecology II, Salon A-C, Saturday 9 July 2016

Christoph Walser¹, Sarah Walsh¹, Matthew Campbell², Helen Neville³

¹The College of Idaho, Caldwell, Idaho, USA, ²Idaho Department of Fish and Game, Eagle, Idaho, USA, ³Trout Unlimited, Boise, Idaho, USA

Distribution and movement of Columbia River redband trout, *Oncorhynchus mykiss gairdneri*, in an intermittent southern Idaho stream

The Columbia River redband trout (*Oncorhynchus mykiss gairdneri*) is native to the Columbia River Basin east of the Cascades. Throughout the region, the genetic structure of many redband trout populations has been influenced by introgression with hatchery stocks and by isolation due to migration barriers. Dry Creek is a small tributary of the Boise River and is characterized by large seasonal fluctuations in temperature and flow. The objective of our research was to describe trout distribution and movement patterns

and evaluate the potential effects of a road culvert on trout movement. During the summer of 2015, stream reaches throughout the watershed were surveyed for redband trout. Fish were collected via electrofishing and fin clips were taken from 243 individuals. Genetic analyses of fin clips were carried out at the Idaho Department of Fish and Game (IDFG), Fish Genetics Laboratory in Eagle, Idaho. Each fish was genotyped at 186 single nucleotide polymorphisms (SNPs). Genetic analyses using the program Colony identified 24 trout families (defined as three or more full-siblings). No full siblings were observed on opposite sides of the culvert. Most families were located above the culvert but one family of young of year fish was found below the culvert – providing the first evidence that trout use the lower reaches of Dry Creek for spawning. Mean distance of trout within families was 424-m. Given the recent establishment of a conservation easement for upper Dry Creek, the results of this study will assist efforts to design an effective watershed management plan.

0756 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Stephen Walsh¹, Frank Ribeiro², Lucía Rapp Py-Daniel³

¹U.S. Geological Survey, Gainesville, Florida, USA, ²Universidade Federal do Oeste do Pará, Santarém, Brazil, ³Instituto Nacional de Pesquisas da Amazônia, Manaus, Brazil

Revision of the South American Catfish Genus *Ageneiosus* (Siluriformes: Auchenipteridae)

The Neotropical family Auchenipteridae, commonly known as driftwood catfishes, currently includes about 118 species in 23 genera. The family is widely distributed throughout South America and includes two subfamilies, the Auchenipterinae (73 species) and Centromochlinae (45 species). *Ageneiosus* (barbelless or bottlenose catfishes) is the second most species-rich genus of the family and has been the subject of considerable study since Linnaeus (1766) described the first species (as *Silurus inermis*). Taxonomy of the *Ageneiosus* clade has been confounded by nomenclatural problems as well as cryptic and sexually dimorphic morphological features. Based on a comprehensive study of morphological variation, examination of type material, original descriptions, and other available evidence, we revise the genus *Ageneiosus* and recognize 13 valid species, four of which are described as new: *A. apiaka*, *A. intrusus*, *A. levis*, and *A. lineatus*, all from the Amazon River basin. *Ageneiosus* differs from the closely related genus *Tympanopleura* in having the gas bladder reduced and ossified, with the exception of *A. pardalis*, the only member of the genus that includes trans-Andean populations. *Ageneiosus inermis* reaches the largest body size of any species (> 45 cm), has the widest distribution, and is exploited for food in some regions. The center of diversity of *Ageneiosus* is in the Amazon basin (*A. ucayalensis* and other fork-tailed species). Additionally, there are species endemic to the Orinoco basin (*A. magoi*) and Paraná-Paraguay basin (*A. militaris*). *Ageneiosus* is absent from the São Francisco basin but occurs in a few coastal drainages of Suriname and Guyana.

0660 ASIH STOYE GENERAL ICHTHYOLOGY AWARD, Galerie 2, Friday 8 July 2016

Brandon Waltz, Kory Evans

University of Louisiana at Lafayette, Lafayette, LA, USA

Morphological and Molecular Variation in *Eigenmannia macrops* (Boulenger, 1897): A single widespread species or a cryptic species complex?

Neotropical fishes constitute the most species-rich continental ichthyofauna on Earth, and as in all biotas, evolutionary analyses and reliable measures of species richness depend on accurate alpha taxonomy. Because many species concepts ultimately come down to the presence of distinct gaps, it is necessary to understand the nature of variation as the basis for correct species delimitation. Here we examine morphological and genetic variation in the *Eigenmannia macrops* group (Sternopygidae, Gymnotiformes), a geographically widespread but phenotypically conserved taxon inhabiting both black and white water rivers throughout the Amazon, Orinoco, and Guianas region. We used geometric morphometric, osteological, and molecular genetic analyses to resolve a robust hypothesis of species-level taxa. We took homologous landmark data from 60 specimens spanning a large portion of the species distribution, followed by the implementation of a principle components analysis and Procrustes ANOVA. A minimum of four specimens per population were cleared and stained for osteological analysis, and 16 tissue samples were subjected to DNA extraction and amplification for phylogenetic and phylogeographic analyses across the Amazon and Orinoco river basins. Bayesian species delimitation under the multispecies coalescent model was implemented to test species limits and interrelationships. Two distinct morphotypes were recovered from the geometric morphometric analyses, each found in distinct water types. Snout length, eye diameter, head length, and head depth load most heavily on PC1 and PC2. Results of comparative osteology and molecular analyses suggest the existence of undescribed species in the genus.

0587 HL: Social Behavior in Reptiles Symposium, Salon E, Saturday 9 July 2016

Erik Wapstra¹, Tobias Uller², Geoff While¹

¹*University of Tasmania, Tasmania, Australia*, ²*University of Lund, Lund, Sweden*

The evolutionary ecology of family living in lizards

Family groups form the basis of social organisation across a wide range of organisms. Understanding the factors responsible for the evolutionary origins and diversification of family living has been a major challenge for biologists. Lizards offer a valuable system in this context because they provide us with a window into the very early stages of family life. Here I will report on a unique group of Australian lizards, the Egernia group, which provide a particularly useful system in this context. One of the most striking features of the Egernia group is that they include highly social lizards that form stable family

groups. While some species are largely solitary, in others males and females form long-term pair-bonds sometimes holding territories where juveniles can remain with their parents. In the most extreme cases this can lead to large communal groups of up to 30 related individuals, including non-breeding adults who stay within their parent's social group. The huge diversity in family structure across the Egernia group make them the idea model system to connect processes occurring across levels of biological organisation (from individuals to populations to species) and ultimately provide novel insights into the evolutionary origins of family life.

0261 General Herpetology, Balconies L & M, Sunday 10 July 2016

Jonathan Warner¹, Xander Combrink¹, Jan Myburgh², Colleen Downs¹

¹*School of Life Sciences, University of KwaZulu-Natal, Pietermaritzburg, KwaZulu-Natal, South Africa*, ²*Department of Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, Pretoria, Gauteng, South Africa*

Blood Lead Concentrations in Nile Crocodiles (*Crocodylus niloticus*) from South Africa

Crocodylians are apex, generalist predators that utilize both aquatic and terrestrial habitats, thereby exposing them to a potentially wide range of environmental contaminants. We collected blood from 34 free-ranging Nile crocodiles (*Crocodylus niloticus*) at three separate South African populations in order to analyze their blood lead concentrations (BPb). Concentrations ranged from below detectability ($< 3 \mu\text{g}/\text{dL}$, $n = 8$) to $960 \mu\text{g}/\text{dL}$ for an adult male at the Lake St Lucia Estuary. Blood lead concentrations averaged $8.15 \mu\text{g}/\text{dL}$ ($\text{SD} = 7.47$) for females and $98.10 \mu\text{g}/\text{dL}$ ($\text{SD} = 217.42$) for males. Eighteen individuals (53%) had elevated BPbs ($\geq 10 \mu\text{g}/\text{dL}$). Crocodiles had higher BPbs at Lake St Lucia than at Ndumo Game Reserve or Kosi Bay, which we attribute to lead sinker ingestion during normal gastrolith acquisition. No clinical effects of lead toxicosis were observed in these crocodiles, even though the highest concentration ($960 \mu\text{g}/\text{dL}$) we report represents the most elevated BPb recorded to date for a free-ranging vertebrate. Although we suggest adult Nile crocodiles are likely tolerant of elevated Pb body burdens, experimental studies on other crocodylian species suggest the BPb levels reported here may have harmful or fatal effects to egg development and hatchling health. In light of recent Nile crocodile nesting declines in South Africa we urge further BPb monitoring and ecotoxicology research on reproductive females and embryos.

0674 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Mel Warren¹, Brooks Burr²

¹*Southern Research Station, USDA Forest Service, Oxford, MS, USA*, ²*Southern Illinois University, Carbondale, IL, USA*

Freshwater Fishes of North America: Update 2016

Over 1,200 native freshwater fish species occur on the North American continent, composing the largest temperate, freshwater fish fauna on Earth. The importance of freshwater fishes in North American ecosystem function, their direct value economically and as providers of ecological services, and the increasing need to conserve this fauna cannot be over emphasized. In the last 30 years, major scientific advances have been made for these fishes across disciplines of systematics, genetics, physiology, behavior, ecology, and conservation. These advances, however, are marked by increased specialization and resulting fragmentation of knowledge about the diverse North American fish fauna. Our book is the first-ever published, fully-illustrated multi-volume work synthesizing the diversity, natural history, ecology, and biology of 52 families of North American freshwater fishes (including several marine families with species occurring in fresh water). The coverage includes all of Canada, the coterminous United States, and Mexico (south to about the Isthmus of Tehuantepec). Chapter authors are synthesizing information on a set of standard topic areas for each family (see outline). Our emphasis is on near-comprehensive synthesis of existing information on freshwater fishes in North America. The book also covers non-taxonomic topics including evolution and ecology of fish assemblages, mating behavior, foreign fishes, fishes as models for scientific studies, and conservation overviews. Currently, 87 contributors are engaged in the book. Volume 1 was published by Johns Hopkins University Press in 2014. Volume 2 is slated for publication in 2017 and Volume 3 in 2018.

0910 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; STORER AWARD ICHTHYOLOGY

Brooke Washburn, David Eisenhour

Morehead State University, Morehead, Kentucky, USA

A Northern Fish in a Southern Land: Conservation Status of Trout-Perch (*Percopsis omiscomaycus*) in Tygart's Creek and Lewis County, Kentucky

The Trout-Perch, *Percopsis omiscomaycus*, is a fish species widely distributed in northern North America, extending south to northeast Kentucky. This study's purpose is to document the species' current distribution and population status in Kentucky and to identify habitat variables associated with the present occurrence of Trout-Perch. We investigated five drainages, Cabin Creek, Quicks Run, Salt Lick Creek, Kinniconick Creek, and Tygart's Creek, in three Kentucky counties, Lewis, Greenup, and Carter. The Lewis County sites and tributaries of Tygart's Creek were surveyed for Trout-Perch using a semi-quantitative protocol to assess Trout-Perch abundance by seining all pools

in a 200-300 m stream reach; habitat data were also taken from these sites. Additional sites in the mainstem of Tygart's Creek were sampled qualitatively. We detected Trout-Perch at 5 of 22 sites in Lewis County, all in the Quicks Run and Salt Lick Creek watersheds. In Tygart's Creek tributaries we detected Trout-Perch at 4 of 15 sites, three of which are new locality records. However, Trout-Perch were detected in only 1 of 7 Tygart's mainstem sites and were not detected in the Cabin Creek or Kinniconick Creek watersheds, which indicates Trout-Perch have declined in those watersheds when viewed alongside historical data. In sites with Trout-Perch present, Trout-Perch were associated with fine substrates, woody debris, and deep pools. Even when locally abundant, this species has a rather clumped distribution, making it difficult to detect; in Tygart's Creek tributaries, detection probability (p) of Trout-Perch was one of the lowest (0.243) of eleven pool-inhabiting species (range 0.239-1.00).

0667 Poster Session I, Acadia/Bissonet, Friday 8 July 2016

Mao Watanabe, Keisuke Furumitsu, Yu Umezawa, Naoki Yagishita, Atsuko Yamaguchi

Nagasaki University, Nagasaki, Nagasaki, Japan

Stable isotope and stomach contents analyses of *Aetobatus narutobiei* to clarify its feeding ecology and foraging impact on bivalve fisheries in Ariake Bay

The naru eagle ray *Aetobatus narutobiei*, inhabiting the southwestern coastal areas of Japan, has increased in numbers since 1990s. *A. narutobiei* feeds on bivalves and is considered to be responsible for the decrease in bivalve catches in coastal areas such as Ariake Bay. Our previous studies showed that *A. narutobiei* is a seasonal resident of Ariake Bay, however, detailed information on the feeding ecology and foraging impact of this species on bivalve fisheries, including bivalve cultures, is limited. In the present study, *A. narutobiei* (n = 188) were collected from Ariake Bay. Recognizable stomach contents were analyzed based on the mean weight percentage of each prey item. Muscle tissue samples of *A. narutobiei* and mollusk samples identified as prey items were analyzed for carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotopes. The main prey items identified by stomach contents analysis were bivalves such as *Scapharca kagoshimensis*, *Crassostrea gigas*, and *Ruditapes philippinarum*. There was no significant difference in isotopes between sexes and among months; however, significant differences were found among size classes for both $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$. The results of isotope analysis suggested that *Scapharca kagoshimensis* accounts for the largest proportion of the *A. narutobiei* diet. Moreover, comparative analysis of the stable isotopes in *Scapharca kagoshimensis* collected from cultured and wild areas showed that *A. narutobiei* likely feeds predominantly on the wild *Scapharca kagoshimensis*. This study demonstrates the possibility of using stable isotope analysis as a tool to determine both the feeding ecology and foraging impact of a predator species on bivalve cultures.

0718 Lightning Talks, Galerie 2, Saturday 9 July 2016

Heather Waye, Zach Smith

University of Minnesota Morris, Morris, MN, USA

Tiger salamander larval density and aquatic invertebrate communities in the prairie potholes of West-Central Minnesota

Tiger salamanders are a common inhabitant of aquatic habitats across much of North America. Despite their abundance, we know relatively little about their life history in the Prairie Pothole Region. Given the global interest in the health of amphibian species, we should be particularly interested in the environmental factors that influence survival and reproduction. We have recorded changes in larval Eastern Tiger Salamander (*Ambystoma tigrinum*) capture rates between years in certain ponds in west-central Minnesota. There are many factors that could affect larval survival rate, including availability and quality of food. The goal of this study is to examine prairie pond aquatic invertebrate communities in relation to tiger salamander population density. Three ponds were each sampled in June and August of 2015. Salamander density was estimated using the number of captures per trap-night, and aquatic invertebrates were sampled at each trap site using standardized sweeps. Invertebrates collected from the ponds and from salamander stomach contents were counted and identified to family. Salamander larvae density varied between ponds by an order of magnitude and June capture rates were more than double those in August. Pond invertebrates were similar between sites in June, but not in August. Salamander stomach samples were also similar in June, while differences in contents in August reflect variation in salamander size more than invertebrate availability. Major differences in invertebrate communities and/or larval diets between the ponds may point us in the direction needed to explore the variation in salamander reproductive success in seemingly similar pond habitats.

0768 Lightning Talks, Galerie 2, Saturday 9 July 2016

Alison Webb, Lori Neuman-Lee, Eleanor Watson, Susannah French

Utah State University, Logan, UT, USA

Timecourse of the immune response in non-model organisms, *Thamnophis elegans* and *Iguana iguana*

The time it takes for an animal's immune system to respond to and clear an infection is influenced by many factors and can ultimately affect disease resistance and survival. Studies of the time-course of an immune response and the relationship between immune components in non-model organisms are limited, but necessary for understanding the immune system in an ecological context. This study uses two non-model reptiles to assess the relationship between innate immune components following a primary injection with sheep red blood cells (SRBC's) and changes in immune response between primary and secondary injections of SRBC's. To assess the time-course of the immune

response, bacterial killing capacity, hemolysis, hemagglutination, and differential leukocyte counts were measured at days 0, 4, 8, 12, and 19 following both the primary and secondary injection. Bacterial killing capacity, hemolysis, and hemagglutination increased significantly following both primary and secondary injections. Of these variables, only hemagglutination increased significantly more following the secondary injection than the primary injection, suggesting some role of acquired immunity in these organisms.

0258 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: EVOLUTION, GENETICS, & SYSTEMATICS

Johanna Wegener¹, Adam Moreno², Jessica Atutubo¹, Jessica Pita-Aquino³, Jason Kolbe¹

¹University of Rhode Island, Kingston, RI, USA, ²Brown University, Providence, RI, USA, ³University of Puerto Rico, San Juan, PR, Puerto Rico

Genetic evidence of hybridization between the native green anole (*Anolis carolinensis*) and the invasive Cuban green anole (*A. porcatius*)

Anolis carolinensis, the only native anole in the United States, is closely related to *A. porcatius*, a naturalized species introduced to Florida from its native range in Cuba. The two species are morphologically and ecologically similar and the presence of *A. porcatius* in Miami is known from only mtDNA haplotypes. We genotyped six microsatellite loci and one mtDNA marker (ND2) to test for hybridization between *A. carolinensis* and *A. porcatius* in Miami. We genotyped 116 individuals from the potential hybrid zone in Miami and reference populations from *A. carolinensis* and *A. porcatius*. Results from a Bayesian cluster analysis reveal that the Miami population forms a distinct genetic cluster and individuals from this population share a high proportion of alleles with both the *A. carolinensis* reference population and *A. porcatius* from Cuba. We found both *A. carolinensis* and *A. porcatius* mtDNA haplotypes in the hybrid population and several individuals show a mismatch between nuclear microsatellite genotypes and mtDNA haplotypes. This reciprocal mismatch pattern is characteristic of hybrid populations. Hybridization may present a concern for the conservation of *A. carolinensis* since introgression can threaten the integrity of this native species.

0371 AES GRUBER AWARD, Balconies J & K, Thursday 7 July 2016

Ornella Celine Weideli^{1,4}, Yannis Papastamatiou², Mahmood Shivji³, Michael Heithaus², Rainer von Brandis⁴, Serge Planes¹

¹CRIOBE USR3278-EPHE-CNRS-UPVD, Perpignan, France, ²Florida International University (FIU), North Miami, FL, USA, ³Save Our Seas Shark Research Center (SOSSRC) NOVA University, Dania Beach, FL, USA, ⁴Save Our Seas Foundation D'Arros Research Centre (SOSF-DRC), D'Arros Island, Seychelles

Resource Partitioning and Competition in a Mutually Used Shark Nursery

Traditional theoretical approaches predict that resource partitioning is crucial to the coexistence of ecologically and morphologically similar species, as it minimizes competition among sympatric species. This partitioning may occur through divergence in resource use or through differences in spatial and temporal habitat use. Coastal reef sharks often use lagoons as nursery areas for their young, where inter-specific competition may be particularly high. At St. Joseph Atoll, Seychelles, two sympatric juvenile shark species, the sicklefin lemon shark, *Negaprion acutidens*, and the blacktip reef shark, *Carcharhinus melanopterus*, use shallow flats as a communal nursery. Both shark species are viviparous with no maternal care, therefore inexperienced and opportunistic behaviour is assumed to lead to niche overlaps and competition. Investigation of competition within shark nurseries at fine spatial scales are lacking, despite its importance for coastal nursery management. We investigated spatial and temporal niche partitioning using active tracking. We quantified dietary overlap using visual and molecular analysis of stomach contents (DNA barcoding), and analysis of stable isotopes (SIA) of red blood and plasma tissues. Preliminary results show various degrees of spatial and trophic segregation between the two species. If niche partitioning results through the avoidance of competition, or if it is shaped by species-specific food or habitat preferences, remains to be proven.

0948 SSAR SEIBERT AWARD CONSERVATION, Galerie 3, Friday 8 July 2016

Chava Weitzman¹, Franziska Sandmeier², C. Richard Tracy¹

¹University of Nevada, Reno, Reno, Nevada, USA, ²Lindenwood University - Belleville, Belleville, Illinois, USA

Presence and diversity of *Mycoplasma agassizii* in the threatened *Gopherus agassizii*

In 1990, the Mojave desert tortoise (*Gopherus agassizii*) was listed as threatened under the Endangered Species Act, partly due to the threat of an upper respiratory tract disease (URTD) that some feel has caused population declines. The bacterium *Mycoplasma agassizii* is a known cause of URTD, and in the last two decades, URTD has been extensively studied in the Mojave desert tortoise. There are still many gaps in our knowledge of this disease, and not much is known about the bacterium, *M. agassizii*, itself—its virulence, its strain diversity, its ecology, or its prevalence in local tortoise

populations. We have sampled nasal mucus from tortoises across the Mojave Desert. Here, we quantify spatially-explicit prevalence of *M. agassizii*, haplotype diversity of three genetic markers, and the relationship between tortoise encounter rate (as a proxy for density) and pathogen presence. This pathogen is found in all tortoise genotypes, although some sample sites had higher levels of prevalence than others. In three genetic markers of the pathogen—16S rRNA, 16-23S intergenic spacer, and rpoB—we found very little nucleotide diversity. Though *M. agassizii* is prevalent across the tortoise distribution, we do not know whether these levels are predictably stable across time. Our analyses suggest both new hypotheses about the host-pathogen relationship and ways in which tortoise populations may be managed.

0584 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Hannah Weller¹, Mark Westneat¹, Caleb McMahan²

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Dirt-sifting Devilfish: Diversity and Convergence of Winnowing Morphologies in Geophagine Cichlids

Winnowing, a substrate-sifting foraging strategy common in geophagine cichlids, is often assumed to be a stereotyped behavior similar to that of the distantly related surfperches (Embiotocidae), despite morphological and genetic diversity within the clade. Many geophagines possess an epibranchial lobe (EBL), a pharyngeal structure of unknown function that may be advantageous in feeding or mouthbrooding. With this study, we aim to investigate (1) whether winnowing is truly a stereotyped behavior comparable to that of embiotocids; (2) how morphological diversity within the clade scales with putative winnowing propensity, and (3) how, if at all, the mysterious EBL may be related to winnowing diversity. Winnowing behavior was characterized with high-speed video of *Satanoperca daemon*, and cranial and EBL morphology was analyzed in 18 species across 12 genera using PCA. We found that winnowing occurs in three distinct phases: strike, substrate is acquired through oral suction; winnowing, substrate and food are separated in the oral cavity and substrate ejected through the operculum; and oral ejection, large particulates are ejected through the mouth. While the first and last stages are fairly stereotyped, winnowing itself was found to be highly dynamic. PCA suggests a particular winnowing morphospace exploited differentially by particular morphologies. We also found a surprising amount of diversity in the EBL, which may function to filter out particulates of a certain size or density, optimizing winnowing efficiency at the cost of a more generalized feeding morphology.

1091 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

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Inter-observer Detection Error in Cricket Frog Auditory Surveys

Blanchard's Cricket Frog (*Acris blanchardi*) is declining throughout the northern part of its range and is Endangered in Wisconsin. It is currently only known from the southwest corner of the state. In order to monitor Wisconsin Cricket Frog populations, auditory surveys are traditionally conducted during the species' breeding period from May through August, by visiting wetland sites after dark to listen for and quantify frog calls. A possible alternative to this survey method is the use of automated recording systems (ARS) to collect acoustic samples rather than utilizing a human surveyor. In this study, ARS were utilized to obtain Cricket Frog call data at a focal site in southwest Wisconsin. One expert and 16 novice surveyors quantified presence/absence and calling intensity from recordings. Inter-observer agreement between expert and novice observers was generally high for species that call throughout much of the summer. Species displayed daily and seasonal calling patterns similar to previous studies. Specifically, anurans called more after sunset and species called more at different times throughout the season. Our data suggest that ARS are an effective method for collecting acoustic samples that can be used for monitoring calling behavior of this species. We address the potential for improving monitoring of this species by this method.

0090 AES Ecology & Behavior II, Balconies J & K, Saturday 9 July 2016

David Wells¹, Natalie Spear¹, Michael Kinney², Suzanne Kohin³

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Application of Chemical Tags to Age Validation Studies of Sharks in the Northeastern Pacific Ocean

Accurate age and growth models provide some of the most important biological parameters needed for stock assessment and fishery management. However, assumptions regarding band pair deposition rates used for age and growth models are often made without direct validation studies. As such, the purpose of this research was to validate vertebral band pair counts for three pelagic shark species in the northeastern Pacific Ocean. Species included shortfin mako (*Isurus oxyrinchus*), blue (*Prionace glauca*), and common thresher (*Alopias vulpinus*) sharks. Oxytetracycline (OTC) labeled vertebrae from each species were obtained from tag-recapture activities and used to determine centrum band pair deposition rates. Count results from band pairs distal to OTC marks indicate species- and life stage-specific band pair deposition rates for the three species investigated. Shortfin mako in this region exhibit biannual band pair deposition as juveniles (< 200 cm fork length, FL); males shift to annual deposition rates

at or near sexual maturity. In contrast, both blue and common thresher sharks appear to exhibit annual deposition rates over the juvenile and adult sizes examined. Given the uncertainty surrounding band pair deposition rates of shark vertebrae and the differences among species, life stages, and regions, it's important to continue validating the age and growth of sharks to ensure the most accurate biological parameters are being used to manage these ecologically and economically important predators.

0738 AES Sawfishes Symposium, Salon E, Sunday 10 July 2016

Monique Welten¹, Moya Meredith Smith³, Charlie Underwood⁴, Zerina Johanson²

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Teeth inside and outside the mouth: an X_CT analysis of topographic relationships in sawshark and sawfish dentitions (Elasmobranchii; Chondrichthyes)

The origin and evolution of teeth is still under debate, with competing hypotheses seeking to explain their evolutionary origins. Teeth and tooth-like structures, odontodes, are present both externally (skin denticles, scales) and internally (oropharyngeal teeth). Sharks and rays have been studied intensively to address evolutionary origins of teeth, since their dermal scales show great similarity to their oral teeth. According to the 'Outside in' theory, teeth evolved from skin denticles after the ancestral mouth cavity evolved by invagination of the skin. The 'Inside out' hypothesis however, suggests that teeth evolved independently from skin denticles. Tooth-like structures are also found on the elongate 'saw' in three chondrichthyan groups: the sawfish, the fossil Scelorhynchidae; and the sawsharks. These "teeth" differ from oral teeth and skin denticles, presenting a challenge in understanding their morphology and patterning, and relation to either skin denticles or oral teeth. We used Computed Tomography to study growth and replacement patterns of 'saw -teeth' in embryos, adults and fossils of these groups, to compare with their skin denticles and jaw teeth. Our results showed that in the sawfish 'saw-teeth' are of equal size and retained during life. By contrast, in sawsharks, the 'saw-teeth' are of various sizes; and are replaced irregularly, but in a size-specific manner. Strikingly, saw-teeth in the fossil sawfish *Sclerorhynchus* show many similarities in morphology to those of sawsharks, despite the lack of close phylogenetic relationships. We conclude that the saw "teeth" are specialized skin denticles, functioning as feeding and prey-obtaining structures.

0318 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: ECOLOGY, NATURAL HISTORY, DISTRIBUTION, & BEHAVIOR

Alexander Wendt, Jamie Roberts

Georgia Southern University, Statesboro, GA, USA

Population Genetic Structure and Dispersal of the Reticulated Flatwoods Salamanders (*Ambystoma bishopi*) on Eglin Air Force Base

Determining how landscape connectivity affects the distribution and abundance of species is vital for conservation efforts. The reticulated flatwoods salamander (*Ambystoma bishopi*) is an endangered pond-breeding species restricted to pine flatwoods habitats of Georgia and Florida. Some of the most extensive remaining habitat occurs on Eglin Air Force Base in Okaloosa County, Florida. We characterized variation of 12 microsatellite DNA loci among larval salamanders at 12 ponds on Eglin. Our objectives were to 1) delineate population genetic structure, 2) estimate dispersal rates among ponds, and 3) estimate the effective numbers of breeders contributing to each pond. We found an expected pattern of isolation-by-distance, with nearby groups of ponds showing higher connectivity and distant comparisons showing greater genetic differentiation. Connectivity also was reduced by anthropogenic landscape features such as roads and impervious surfaces as well as invasive vegetative overgrowth. Effective population sizes at ponds were small at most ponds, suggesting that few breeders contribute to a typical cohort. These findings will assist the Air Force with implementing effective habitat management measures on Eglin.

1031 Fish Conservation, Galerie 3, Sunday 10 July 2016

Julia Wester

University of Miami, Coral Gables, FL, USA

Opportunities in Hands-on Shark Outreach and Education

Experiential education and outreach programs can have valuable impacts on pro-environmental attitudes and behaviors as well as self-efficacy and interest in science. The Shark Research and Conservation Program at the University of Miami, is a research laboratory that has created an educational program combining classroom talks with hands-on experiences, engaging students in collecting real data in the field for ongoing shark research studies. The session will discuss this program and will cover the results of an ongoing study evaluating the impacts of these experiences on students' knowledge, attitudes, and behaviors toward sharks, science, and ocean conservation. The study combines a before and after survey design with student focus groups onboard the research vessels to provide a thorough and nuanced picture of how students are affected by their experiences and educational content. The findings highlight important lessons for several critical areas of modern marine science education, including strategies for conducting outreach around species with complex cultural representations

such as sharks and the differential impacts of experiential education on underrepresented communities in STEM. Finally, barriers and opportunities for developing these kinds of collaborative educational experiences between universities and high schools will be considered.

0636 Amphibian Ecology & General Herpetology, Salon F-H, Sunday 10 July 2016

Aundrea Westfall¹, Melissa Miller¹, Christopher Murray², Bryan Falk³, Robert Reed³, Lindsey Garner⁴, Frank Mazzotti⁴, Craig Guyer¹, Christina Romagosa⁵

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Morphological Plasticity of a Non-Native Parasite in Novel Snake Hosts

When a non-indigenous species (NIS) establishes in its introduced range, it can bring parasites capable of infecting native taxa. Parasites co-introduced with NIS may overcome the obstacles of infecting novel hosts in their invaded range by exhibiting phenotypic plasticity among hosts. Burmese pythons (*Python molurus bivittatus*) are well established in southern Florida and have introduced a lung parasite (*Raillietiella orientalis*) found within python's native range in Southeast Asia. Spillover of *R. orientalis* from pythons to native snakes has occurred, with two families and six genera of snakes infected in Florida. The mechanism through which *R. orientalis* infects such diverse taxa has not been explored. We utilized geometric morphometrics to evaluate the morphological plasticity of *R. orientalis* among infected south Florida snakes and pythons to investigate the parasites ability to infect a diverse array of novel snake taxa. A Procrustes ANOVA revealed significant variation in *R. orientalis* head shape ($F_{3, 64} = 2.27, P < 0.0001$) according to host taxa. Variation was not attributable to centroid size ($F_4 = 2.16, P = 0.09$). *Raillietiella orientalis* from semi-aquatic and aquatic native snakes exhibited the greatest morphological similarity. Morphological analyses of *R. orientalis* recovered from invasive pythons, native pitvipers, and terrestrial snakes each exhibited distinct groupings. Our results suggest *R. orientalis* exhibit significantly different morphology based upon host species infected. Additionally, we provide evidence of host-specific parasite head shape plasticity, an ability that may facilitate infection in a wide array of novel reptilian host species.

0700 Fish Systematics I, Salon F-H, Saturday 9 July 2016

Mark Westneat

University of Chicago, Chicago, IL, USA

Evolutionary history and global biogeographic patterns of reef fishes using all-species phylogenetic trees

Building large-scale phylogenies with all known species in various reef fish groups is now possible using a molecular backbone and a morphological trait matrix in tandem. All-species phylogenetic trees are presented for the Labridae (including the scarines and odacines), Chaetodontidae, and Pomacentridae. Anatomical characters play a key role in clade support and in placing rare taxa into the tree topology. The high resolution, species-level topologies for the three iconic reef fish families are used as a framework for mapping the evolutionary diversification of function and enhancing our understanding of biomechanical convergence in these groups. Finally, reconstructing global biogeographic patterns in the three families across major biogeographic provinces and from temperate to tropical seascapes show that these often sympatric fish groups show alternative patterns of phylogenetic dispersion history.

0397 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; STORER AWARD ICHTHYOLOGY

Courtney A. Weyand, Kyle R. Piller

Southeastern Louisiana University, Hammond, Louisiana, USA

Phylogeography of the Rosyside Dace (*Clinostomus funduloides*)

The genus *Clinostomus* (Teleostei: Cyprinidae) is an understudied genus of fishes in the order Cypriniformes. *Clinostomus* has a large geographic range occupying much of eastern North America. Currently, two species are recognized within *Clinostomus*: *C. funduloides* and *C. elongatus*. A previous morphological study recognized three subspecies within *C. funduloides*: *C. f. funduloides*, *C. f. estor*, and one undescribed subspecies, but these have not been universally recognized. Given the broad distribution and disjunct geographic range of this genus, a phylogenetic assessment of *Clinostomus* is needed to further resolve the taxonomic diversity within this genus. In particular, we focused on assessing diversity within *C. funduloides*. Multiple tissue samples of *C. funduloides* were obtained across the range. Sequence data was obtained from multiple mitochondrial and nuclear loci. Data were analyzed using Bayesian phylogenetic methods and constraint tree searches to investigate the diversity and phylogenetic relationships within the genus. Results of this study will give insight on the phylogenetic relationships, genetic differentiation, and taxonomic status of the populations within *C. funduloides*.

0007 AES GRUBER AWARD, Balconies J & K, Thursday 7 July 2016

John Whalen, Jim Gelsleichter

University of North Florida, Jacksonville, FL, USA

Multibiomarker evaluation of pollutant effects in Atlantic stingray (*Dasyatis sabina*) populations in Florida's St. Johns River

The goal of this study was to examine the potential health effects of polychlorinated biphenyl (PCB) and polycyclic aromatic hydrocarbon (PAH) exposure on Atlantic stingray populations in Florida's St. Johns River (SJR). Special emphasis was placed on identifying PAH- and/or PCB-related effects in stingrays from areas of the lower SJR basin that have been shown to possess elevated levels of these compounds, as well as characterizing baseline levels of pollutant exposure in other areas that may be subjected to dredging in the near future, potentially resuspending contaminated sediments and increasing pollutant associated effects. To accomplish this, we measured PCB and PAH biomarker levels in *D. sabina* collected from contaminated sites and reference locations. We specifically examined the biomarkers cytochrome P4501a1 (CYP1a1), a Phase I detoxification enzyme; glutathione-S-transferase (GST), a Phase II detoxification enzyme; fluorescent aromatic compounds (FACs), PAH bile metabolites; lipid peroxidation (LPO), cell membrane damage; and thyroid epithelial height (TEH), an assessment of endocrine disruption-induced hypothyroidism. Enzymatic activity of CYP1a1 and GST was measured using the EROD assay and a GST Assay Kit, while LPO was measured with an OxiSelect TBARS Assay Kit. FACs were measured using fixed wavelength fluorescence and TEH was analyzed histologically. Biomarker levels of individuals collected from contaminated sites were compared to individuals collected from reference sites. The data suggest that pollutant biomarker levels in SJR *D. sabina* did not differ significantly from those measured in individuals from reference locations. However, the close proximity of high biomarker levels to known contaminated areas suggests continuous exposure.

0350 AES Physiology, Paleontology, & Collections, Balconies L & M, Friday 8 July 2016

Catharine J. Wheaton¹, Andrew N. Evans², John M. Rimoldi³, Rama S. V. Gadepalli³, Bobbi R. O'Hara⁴, Natalie D. Mylniczenko¹

¹*Animals, Science and Environment, Disney's Animal Kingdom® and The SEAS with Nemo and Friends®, Lake Buena Vista, FL, 32830, USA*, ²*Department of Coastal Sciences, University of Southern Mississippi, Ocean Springs, MS 39564, USA*, ³*Department of Medicinal Chemistry, University of Mississippi, University, MS 38677, USA*, ⁴*Research and Development, Arbor Assays L.L.C., Ann Arbor, MI, 48108, USA*

Development and Preliminary Validation of a Monoclonal Antibody for Enzyme Immunoassay of the Steroid 1 α -hydroxycorticosterone in Selected Elasmobranch Species

Measurement of 1 α -hydroxycorticosterone (1 α OH-B), the putative primary stress and ionoregulatory hormone for shark and ray species has been of significant biological interest and a major scientific challenge for over 50 years. Previous research relied on measurements using techniques such as thin-layer chromatography, ultraviolet absorption spectra, or high-performance liquid chromatography of incubates from interrenal glands or large volumes of blood, often pooled from multiple individuals. Although commercial enzyme immunoassays (EIA) are available for corticosterone, those tested exhibit only low relative cross-reactivity to 1 α OH-B (3-5%). To improve measurement of 1 α OH-B, we developed a monoclonal antibody using a synthesized 1 α OH-B derivative for testing in a double-antibody EIA system. Relative displacements of cross-reactant compounds showed good sensitivity for 1 α OH-B and 11-dehydrocorticosterone with low reactivity to related steroids including corticosterone. Adjustment of incubation times and titration of the antibody and conjugate concentrations increased sensitivity of the EIA for 1 α OH-B (range 4-12 ng/ml, 90% binding). Banked serum and plasma samples from selected elasmobranch species managed at The SEAS with Nemo and Friends® were used to validate sample treatment and extraction protocols to optimize measurement of 1 α OH-B in <1 ml of sample. Improved measurement of 1 α OH-B in sharks and rays will be important for many aspects of collection, transport, medical treatment, and aquaria and conservation management of these charismatic and ecologically important species.

0613 ASIH: Lessons From, and Visions For Symposium, Salon D, Sunday 10 July 2016

Kit Wheeler¹, Mary Freeman², Phillip Bumpers¹, Megan Hagler¹, Byron Freeman³, Seth Wenger¹

¹*River Basin Center & Odum School of Ecology, UGA, Athens, GA, USA*, ²*USGS Patuxent Wildlife Research Center, Athens, GA, USA*, ³*Georgia Museum of Natural History & Odum School of Ecology, UGA, Athens, GA, USA*

Rates Add Meaning to Long-term Monitoring Data

Ecologists commonly use long-term datasets to correlate environmental drivers with changes in community states, such as species richness or dominance by particular taxa. However, communities may arrive at the same state through differing processes, such as local extirpation as opposed to failure of species to colonize following an extreme event. An alternative approach is to explicitly estimate demographic process rates (extirpation, colonization, population growth) in relation to time or environmental covariates. This allows us to test hypotheses of actual mechanisms driving observed changes in community states. Here, we illustrate application of this process-based analytical approach using 20 years of annual surveys of shoal-dwelling fishes at multiple sites in the Conasauga River basin, GA. Our preliminary results showed substantial temporal variability among species in persistence (0.29-0.90) and colonization (0.24-0.89) rates and indicated population declines of some taxa. A comparative analysis of similar, long-term monitoring data for shoals in the nearby Etowah River basin suggested observed declines were restricted to the Conasauga River. By estimating process rates for multiple species simultaneously, we could more precisely infer trends for rare fishes for which it is otherwise difficult to distinguish non-detection from true absences. We suggest that process-based rates analyses provide a complementary framework for testing alternative hypothesized environmental drivers and for building predictive models of community change.

0863 AES GRUBER AWARD, Balconies J & K, Friday 8 July 2016

Connor White¹, Kady Lyon¹, Kevin Weng³, Chuck Winkler², Salvador Jorgensen³, John O'Sullivan³

¹*California State University Long Beach, Long Beach, CA, USA*, ²*Southern California Marine Institute, Terminal Island, CA, USA*, ³*Monterey Bay Aquarium, Monterey, CA, USA*

Movement of Juvenile White Sharks in Southern California: Predicting Future Nursery Habitat

The white shark, *Carcharodon carcharias*, is an apex predator with a circumglobal distribution and a low intrinsic growth rate that is listed as vulnerable by the IUCN. While considerable information is known for adults, there is limited information on the movements, environments, and distributions of juvenile white sharks (JWS).

Understanding this life stage is important as JWS experience considerable overlap with human activities and juveniles often have the highest mortality of any life stage. In an effort to quantify JWS movements and understand their distribution in the Southern California Bight, JWS were captured and outfitted with satellite transmitters (SPOT tags: n=20). There was a large amount of variability in number of geopositions rendered (Class 0-3: 645 locations; mean: 36, range: 0-130), with individuals having a higher probability of detection later in the day (1700-2000). Some individuals (n=9) displayed movements south of the United States border into Baja California, Mexico. A generalized linear model with a binomial distribution was used as a resource selection function to predict presence of individuals based on depth, distance to shoreline, and daily sea surface temperature (SST). Sharks were found to significantly select shallow habitats (<2500 m) close to land (<50km) at temperatures between 15.6 and 24.3C. The model predicts sharks to move to Baja California during winter and a higher probability of JWS in southern California during El Niño years.

0892 Amphibian Ecology & General Herpetology, Salon F-H, Sunday 10 July 2016

Elijah White, Joseph Pechmann

Western Carolina University, Cullowhee, North Carolina, USA

Life Cycles of a Facultatively Paedomorphic Salamander at High Elevation

Facultatively paedomorphic salamanders, including the mole salamander (*Ambystoma talpoideum*), respond to environmental conditions experienced as a larva by either metamorphosing into a terrestrial subadult or maturing in the aquatic environment as a paedomorph. There are two proposed selective mechanisms for the maintenance of paedomorphosis in salamanders: (1) "paedomorph advantage" (PA), in which a favorable aquatic habitat allows greater fitness than the terrestrial habitat and (2) "best of a bad lot" (BBL), in which paedomorphosis maximizes fitness in a growth-limiting environment by forgoing metamorphosis thereby allowing reproduction during the first breeding season. Paedomorphosis has been studied extensively in *A. talpoideum* in the coastal plain ecoregion, but the different environmental conditions at high elevations may affect breeding phenology and life cycles. This project characterizes the breeding phenology and seeks to determine which mechanism (PA or BBL) maintains paedomorphosis in high-elevation populations of *A. talpoideum* in the Nantahala Mountains of North Carolina. Field surveys revealed that high-elevation *A. talpoideum* populations are majority paedomorphic and breed from October-April as compared to September-March in Atlantic coastal plain populations. A mesocosm experiment found that water temperature did not affect growth rate, but growth was density dependent. All individuals remained paedomorphic or larval during their first breeding season, and those that metamorphosed the following spring attained a large body size prior to the metamorphosis event. This evidence supports the BBL hypothesis that maintenance of paedomorphosis in these high-elevation populations is a default strategy in a growth-limiting environment and that metamorphosis is favored when sufficient growth occurs.

1114 Poster Session I, Acadia/Bissonet, Friday 8 July 2016

Jared White¹, Michael Husak²

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New County Records and Range Expansion of the Mediterranean Gecko (*Hemidactylus turcicus*) in Oklahoma and Kansas

Prior to 2011, the introduced Mediterranean gecko (*Hemidactylus turcicus*) was known from 11 of Oklahoma's 77 counties. Following the discovery of a small breeding population in the city of Lawton, Comanche County, Oklahoma in 2011, I began surveys to determine the extent of *H. turcicus* established in Oklahoma and Kansas. Here we add 3 new county records to Kansas and 29 new county records to Oklahoma's previously described distribution.

0301 General Ichthyology II, Balconies J & K, Sunday 10 July 2016

Macaulay White¹, J. Derek Hogan¹, Luke Tornabene², Frank Pezold¹

¹Texas A&M University - Corpus Christi, Corpus Christi, Texas, USA, ²Smithsonian, Washington D.C., USA

Pelagic Larval Duration and Amphidromy Not Linked to Endemism in *Stiphodon* Gobies

Sicydiine gobies are a diverse group of freshwater fishes characterized by a unique life history and morphological features that allow them to inhabit oceanic island streams throughout tropical and sub-tropical regions. Larval dispersal is achieved by an amphidromous life history in which adults live and spawn in fresh water and larvae develop at sea. Sicydiine gobies often account for the majority of freshwater ichthyofauna in island streams, and many are endemic to particular regions. The subfamily Sicydiinae currently consists of nine genera of which the genus *Stiphodon* exhibits the most diversity and is widespread throughout the western Pacific. Many species of *Stiphodon* have very large distributional ranges, while others are more restricted. Dispersal plays a large role in the distribution of species, greater dispersal capabilities can lead to larger range sizes and vice versa. Variations in the number of individuals migrating to the sea may influence the dispersal capabilities, as well as the duration of time that larvae spend at sea. Variation in these traits may influence the geographic range size for a given species. To test these hypotheses, we counted daily growth rings from otoliths to determine the pelagic larval duration and used otolith chemistry to determine migratory behaviors of different *Stiphodon* species exhibiting different range sizes.

0928 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Mary White¹, Mark Merchant²

¹*Southeastern Louisiana University, Hammond, LA, USA*, ²*McNeese State University, Lake Charles, LA, USA*

Innate Immune System Genes of Crocodilians

Crocodilians have potent antimicrobial activity in their blood and tissue, attributed in large part to their serum complement proteins and other components of the innate immune system. Our previous work shows that crocodilians have two very different genes for complement C3, a vital component of complement activation. Birds and mammals have only a single C3 gene, and although snakes have multiple C3 genes, they encode very similar proteins. Among vertebrates, only fish are known to have such diverse C3 genes, and it was hypothesized that the diversity expanded the recognition repertoire of the innate immune system. Our current work continues investigation of the innate immunity of crocodilians, focusing on expression of the different complement C3 genes and other genes that may bolster the innate immune system.

0418 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Matthew White, Jenna Riemenschneider, Hannah Mohr

Ohio University, Athens, OH, USA

Genetic Differentiation of the Least Brook Lamprey in the Mississippi Embayment

The Least Brook lamprey is a non-parasitic species with a broad distribution in the eastern US. It displays limited variation in morphology and life history but is known to display considerable genetic differentiation among populations throughout its range. Notable is the variation observed among populations located along the Mississippi Embayment, particularly the Obion, Forked Deer, Hatchie, and Yazoo drainages. Samples of Least brook lamprey from additional streams in this region (Loosahatchie, Big Black, Bayou Pierre, Buffalo) were sequenced at two mitochondrial genes (Control region, ND3) for comparison to the larger data set. Consistent with previous work each population had a unique haplotype. Considerable variation (3-7% sequence divergence) was observed among populations in this region. The phylogeny observed confirmed the distinctiveness of the Hatchie River population. This pattern is consistent with that shown by the Least madtom (*Noturus hidebrandi*) suggesting a common history, likely a Hatchie/Tennessee River connection. In addition to variation among unique sequences these populations exhibited considerable variation in the sequence and number of tandem repeats in the mitochondrial Control Region. A major change in repeat structure was observed in populations south of the Yazoo River. The Hatchie River population and likely those found in several other streams (e.g., Obion) reflect undescribed species.

Additional surveys should be undertaken to determine if other species demonstrate differentiation in the Hatchie drainage.

0330 AES Sawfishes Symposium, Salon E, Sunday 10 July 2016

Stacia White¹, Katy Duke², Paula Carlson³, Alan Henningsen⁴, Katherine Hunter⁵, Richard Preziosi⁵, Jennifer Rountree⁵, Graham Hill², John Fitzpatrick⁶

¹Ripley's Aquariums, Inc., Myrtle Beach, SC, USA, ²The Deep, Hull, East Yorkshire, UK, ³Dallas World Aquarium, Dallas, TX, USA, ⁴National Aquarium, Baltimore, MD, USA, ⁵The University of Manchester, Manchester, UK, ⁶Stockholm University, Stockholm, Sweden

Making Connections for Sawfish: The Role of Public Aquaria in Sawfish Biology and Conservation

Aquaria are important partners in sawfish science and conservation. Important messages are communicated to millions of aquarium visitors by providing face - to - face encounters with living sawfish in a unique educational setting. The global decline of sawfishes is increasing the need for conservation of fragile coastal habitats. Public aquaria can build on these connections, to promote conservation solutions. Collaboration across many disciplines is vital for successful conservation of sawfishes, and aquaria can contribute alongside with academic institutions, conservation organizations, field research groups, government agencies and the local populations. All stakeholders can benefit from information exchange, and the implementation of knowledge on sawfish biology, ecology, and conservation. The IUCN Shark Specialist Group's Global Strategy for Sawfish Conservation provides a framework for collaborative sawfish conservation, including opportunities for aquaria to participate in conservation education, research and public awareness. The Association of Zoos and Aquariums' (AZA) Species Survival Plan and the European Association of Zoos and Aquaria (EAZA) Studbook, population management programs for pristids, provide member facilities a forum in which to share important data collected about their animals, and work collaboratively on sawfish husbandry, research and conservation. Current research at The Deep is developing non-invasive methods of DNA collection from elasmobranch species in collaboration with the University of Manchester. These methods have produced usable quantities of material for DNA analysis which the way forward for the establishment of a central identification DNA database of captive *Pristis* as proposed in the IUCN Strategy. These programs provide additional platforms for communication and collaboration with other stakeholders to promote sawfish science and conservation. Although the focus is on how aquaria have and can contribute to sawfish research and conservation, the greatest opportunity and need is for future collaboration with aquaria worldwide and other important stakeholders through existing as well as new programs and strategies.

0037 AES Sawfishes Symposium, Salon E, Sunday 10 July 2016

William White¹, Sharon Appleyard¹, Leontine Baje², Benthly Sabub²

¹CSIRO National Research Collections Australia, Hobart, Australia, ²National Fisheries Authority, Port Moresby, Papua New Guinea

Preliminary Investigation into Sawfish Catches in Papua New Guinea

During a larger project on the shark and ray fisheries of Papua New Guinea which commenced in 2014, records of sawfish catches were collated and anecdotal information from fishers collected. Tissue samples, photographs and morphometric measurements from dried rostra and/or fins were taken from any sawfish observed during artisanal surveys. Also, an observer program on prawn trawlers in the Gulf of Papua collected data and samples from any sawfish captures. All four species known to occur in the area (*Anoxypristis cuspidata*, *Pristis clavata*, *P. pristis* and *P. zijsron*) were recorded in the fishery catches. *Anoxypristis cuspidata* was by far the most abundant species caught. Most records were from the Gulf of Papua but records also taken from Manus, Rabaul and Bougainville. The difficulties in collecting such data in Papua New Guinea and the best way to continue acquiring good data and providing capacity building tools are discussed.

0670 Amphibian Reproduction & Herp Conservation, Galerie 3, Saturday 9 July 2016

Steven Whitfield¹, Jacob Kerby³, Juan Abarca², Gilbert Alvarado⁴

¹Zoo Miami, Miami, FL, USA, ²Universidad de Costa Rica, San Pedro, Costa Rica, ³University of South Dakota, Vermillion, SD, USA, ⁴Universidade de São Paulo, São Paulo, Brazil

Enigmatic survival follows enigmatic amphibian decline - A turning point for amphibian conservation?

Amphibian chytridiomycosis (caused by the pathogen *Batrachochytrium dendrobatidis*, “Bd”) is an emerging fungal disease associated with apparent extinctions of perhaps more than 200 amphibian species. However, many amphibian species long presumed extinct have been recently rediscovered, and these rediscoveries are difficult to reconcile with the prevailing paradigm that an amphibian mass extinction has already transpired. Here, we synthesize information on amphibian rediscoveries, and present a new conceptual framework to classify rediscoveries that will improve clarity concerning mechanisms for host-pathogen co-existence relevant for efforts to mitigate Bd. We distinguish among four phenomena in rediscovery of amphibian populations. First, many rare amphibian species have been rediscovered after decades unseen by scientists, but are unrelated to chytridiomycosis. Second, some “relict populations” from chytridiomycosis-susceptible species exist in environmental refugia from chytridiomycosis (environments that are hostile for survival or growth of Bd). Third, recolonization of upland sites from lowland refugia is a second form of recovery, and is

widespread, but is not typical of the most severely threatened amphibian species or those presumed extinct. Finally, several species of amphibians highly sensitive to chytridiomycosis have populations surviving within ideal habitat for Bd yet persist with some unexplained resistance or tolerance to chytridiomycosis – the enigmatic survivors of amphibian extinctions. Enigmatic survival may result from evolutionary responses of hosts or pathogens, or shifts in the host community or community composition of the amphibian skin microbiome. Research on enigmatic survivors may inform strategies to mitigate wildlife emerging infectious diseases, including amphibian chytridiomycosis among others.

0092 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; AES CARRIER AWARD

Nicholas Whitney¹, Karissa Lear¹, Lindsay Gaskins¹, Adrian Gleiss²

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The effects of temperature and swimming speed on the metabolic rate of the nurse shark (*Ginglymostoma cirratum*, Bonaterre)

Sharks and other top predators have a substantial impact on their ecosystems through trophically mediated effects, and understanding the scope of this impact is essential to forming an accurate picture of energy flow within an ecosystem. One of the most important factors to consider when assessing a predator's impact is metabolic rate, which is dependent on a number of environmental, physiological, and anatomical characteristics. Standard (SMR) and routine metabolic rates (RMR) and swimming dynamics of the nurse shark (*Ginglymostoma cirratum*, Bonaterre) were assessed using a static respirometer over two experimental temperatures (23 and 30 °C). The metabolic rates measured here represent the lowest reported for any shark species to date. Mean (\pm SD) SMRs at 23 °C and 30 °C were 36 ± 8 and 60 ± 17 mg O₂ kg⁻¹ h⁻¹, and mean RMRs were 95 ± 15 and 138 ± 21 mg O₂ kg⁻¹ h⁻¹, respectively. The Q₁₀ for SMR was 2.42 between 23 and 30 °C. Minimum cost of transport (COT_{min}) at 23 °C was 68 mg O₂ kg⁻¹ km⁻¹, where swimming speed was 0.33 BL s⁻¹. The COT_{min} increased to 81 mg O₂ kg⁻¹ km⁻¹ at 30 °C, where swimming speed was 0.44 BL s⁻¹. The proportional cost of activity was greater compared to other elasmobranchs, and nearly twice that of most ram ventilating shark species. These results highlight the sedentary nature of nurse sharks and suggest that they are energetically suited for a minimally active lifestyle.

0560 AES Sawfishes Symposium, Salon E, Sunday 10 July 2016

Jeff Whitty¹, James Keleher¹, Adrian Gleiss¹, Brendan Ebner², Colin Simpfendorfer³, David Morgan¹

¹Murdoch University, Perth, Western Australia, Australia, ²CSIRO, Atherton, Queensland, Australia, ³James Cook University, Townsville, Queensland, Australia

Heterogeneous habitat use of the critically endangered largemouth sawfish (*Pristis pristis*) in a riverine nursery

Understanding the habit use and selection of a species is important for identifying environments and resources that it is dependent upon. However, these subjects can be complex and often involve a balance of multiple abiotic and biotic rewards and risks. This study used acoustic monitoring to assess the movements of 32 juvenile largemouth sawfish (*Pristis pristis*) in association with various abiotic and biotic variables in the Fitzroy River, Western Australia between 2008 and 2015, in order to determine which nursery habitats and resources are important to this critically endangered species. *Pristis pristis* demonstrated an affinity for deep-water runs and pools with high concentrations of large woody debris in the day-time, when activity was lowest, and for shallow-water habitats, such as glides, in the night-time, when movement and distance travelled significantly increased. Depth selection changed in response to the time of day, with individuals occupying deeper depths in the day-time and shallower depths in the night-time, moving between these depths in accordance with light intensity, regardless of the habitat type. Mean hourly depth of *P. pristis* also decreased through the dry season as temperatures increased and river stage height decreased. These results highlight that habitat use and selection of juvenile *P. pristis* are not static and that the species uses a range of riverine microhabitats. Given the threatened status of *P. pristis*, these habitats, which are largely unprotected in Australia, need to be strategically managed to promote juvenile survivorship and conservation of this species.

0917 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; STORER AWARD HERPETOLOGY

K.H. Wild, B. Bedal, C.M. Gienger

Austin Peay State University, Clarksville, TN, USA

External Parasites Influence Locomotor Performance of Male Eastern Fence Lizards (*Sceloporus undulatus*)

External parasites are common on wildlife and humans that inhabit forested areas. These ectoparasites may have a variable impact on the host species, from minimal effects to negative effects, that can alter the hosts physiology and potentially lead to influencing its overall health. Our objective is to quantify the effect of parasites (*Dermacentor variabilis*, American Dog tick and *Amblyomma americanum*, Lone Star tick) on male *S. undulatus* locomotor performance, a trait that is linked to health of an individual and

ultimately important for survival. *Sceloporus undulatus* is relatively common throughout the eastern U.S., and parasite load varies considerably among populations. We compared locomotor performance of lizards with attached ticks to lizards without ticks. We measured locomotor performance in two ways: maximum sprint speed and 2-meter run speed. Lizards with ticks had significantly lower maximum sprint speed and 2-meter run speed in comparison to lizards where ticks were absent.

0292 AES Sawfishes Symposium, Salon E, Sunday 10 July 2016

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¹Haven Worth Consulting, Palmetto, Florida, USA, ²NOAA Fisheries Service Southeast Regional Office Protected Resources Division, St. Petersburg, Florida, USA

Endangered Species Act Five-year Review and Recovery Plan Updates for US Smalltooth Sawfish, *Pristis pectinata*

The United States distinct population segment (DPS) of smalltooth sawfish (*Pristis pectinata*) was classified as Endangered under the US Endangered Species Act (ESA) in 2003. A recovery plan for the US DPS of smalltooth sawfish was published in 2009 detailing goals and actions necessary to meet identified recovery criteria. To monitor recovery efforts and ongoing threats to the species, the ESA requires the status of the species be assessed through regular 5-year reviews. The first review was completed in 2010 and, based on criteria established in the recovery plan, determined the species still warranted protections afforded by an Endangered classification. Recently a second ESA 5-year review was commenced and will determine if the listing classification of Endangered under the ESA is still appropriate. Changes to the recovery plan, including revised recovery goals and criteria, are also underway. Updating the plan, and the recovery criteria it contains, will help scientists and managers work toward restoring the sawfish population in the US to the point where it is a secure part of its ecosystem and protections under the ESA are no longer needed. Results of the second 5-year review and updated recovery plan will be presented.

0015 General Ichthyology II, Balconies J & K, Sunday 10 July 2016

Philip Willink¹, Gregory Jacobs², Dimitry Gorsky³, Zy Biesinger³, Andrew Kough¹

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Activity patterns of Lake Sturgeon (*Acipenser fulvescens*) in Lakes Erie and Ontario using Pop-off Archival Satellite Tags

Little is known about lake sturgeon (*Acipenser fulvescens*) movement and migration behavior in Lakes Erie and Ontario. In contrast to conventional survey methods, archival

tags allow the ability to record habitat variables, movement, and location throughout the year. The objective of this study was to characterize movement behavior of lake sturgeon in response to time and habitat variables during and after the spring spawning period. Pop-off Archival Satellite Tags (PSAT tags) were attached to 23 lake sturgeon in Buffalo Harbor, Lake Erie and 22 lake sturgeon in the Lower Niagara River, Lake Ontario during spring, 2014. PSAT tags measure location, depth, temperature, and activity until a programmed release date. After release, tags float to the surface where they communicate their data via satellite or may be recovered and their data downloaded directly. We evaluated migration behavior and positional accuracy of tag data on a daily time step. We then evaluated variation in tag acceleration and orientation across depth, temperature, and time to infer movement patterns. Migration patterns were difficult to assess as lake sturgeon tended to migrate relatively short distances during tag deployment. However, we do find patterns in the variation of lake sturgeon activity across environmental covariates.

0279 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Stuart Willis

Texas A&M University-Corpus Christi, Corpus Christi, TX, USA

Integrating disparate genetic data reveals a complex phylogeographic history and no resolution for species delimitation in the Amazon peacock bass cichlid *Cichla pinima* (Perciformes: Cichlidae) species complex

Species are often treated as fundamental units in biology, and their discovery and relationships are the principle goals of systematics. However, the delimitation of species is often ambiguous, and many forms of molecular data are often brought to bear on the question. Here we integrated analyses of genetic data from 11 microsatellites, mtDNA sequences, and sequences of 17 unlinked nuclear genes of 134 fishes from the *Cichla pinima* species complex. Four species were described from this complex, but later molecular analyses discovered two primary genetic clusters, neither of which corresponded well to the four described species. Our integration of these data with additional nuclear sequences showed that the complex exhibits a significant population structure, with moderate to high genetic divergence between most populations. Species delimitation under the multispecies coalescent supported the recognition of three species, with core distributions in the 1) Tapajós and Jari Rivers, 2) Trombetas, Nhamundá, and eastern tributaries of the Madeira River, and 3) the upper Uatumã River. However, approximate Bayesian computation favored models that included admixture in the lower Amazon between the Tapajós and Trombetas lineages. Continuous phylogeographic modeling also suggested that the two mitochondrial lineages (Tapajós vs. Trombetas+Uatumã), which are polyphyletic with respect to other *Cichla* clade A species, expanded recently from 'refugia' in the Tapajós and Madeira Rivers. These data are consistent with a hypothesis of sister populations that experienced significant isolation, followed by extensive range expansion and secondary

contact, and now exhibit an elaborate meta-population structure characterized by moderate isolation.

0277 Fish Genetics, Salon D, Sunday 10 July 2016

Stuart Willis, Jonathan Puritz, David Portnoy, John Gold

Texas A&M University-Corpus Christi, Corpus Christi, TX, USA

Low genomic divergence among King Mackerel (*Scomberomorus cavalla*) in northern temperate waters of the western Atlantic Ocean revealed by ddRAD sequencing

King mackerel is a migratory, coastal pelagic scombrid fish native to the Western Atlantic Ocean, including the Gulf of Mexico (Gulf). The species is highly targeted commercially in southern winter fisheries, and recreationally in northern summer fisheries. Demographic and otolith shape and microchemistry studies have identified distinct migratory groups along the U.S. Atlantic coast and in the northern Gulf, and it has been suggested that eastern and western migratory groups may exist in the northern Gulf as well. However, previous tagging studies have indicated little fidelity to migratory routes, and genetic studies have found few significant differences between migratory groups. We employed data from a reduced representation genomic library to test the hypothesis that migratory groups could be discriminated genetically. We surveyed a filtered set of over 1,000 haplotyped loci among king mackerel sampled from seven localities, six from the U.S. Atlantic and Gulf coasts and one from Campeche Bay (Mexico) in the southern Gulf. We found no evidence of genetic heterogeneity among localities, regions, or migratory groups (mean global G_{ST} of <0.001) and observed only a low probability in assigning individuals back to migratory group or region. The sample from Campeche Bay could not be distinguished from those in U.S. territorial waters. No significant F_{ST} 'outlier loci' were identified after rigorous filtering. We hypothesize that high migration rates and large effective population sizes have precluded divergence among king mackerel in the northern part of its contemporary range.

1014 Herp Conservation, Galerie 2, Sunday 10 July 2016

John Willson¹, Shannon Pittman², Tracey Tuberville³, Jeffrey Beane⁴, Michael Dorcas²

¹University of Arkansas, Fayetteville, AR, USA, ²Davidson College, Davidson, NC, USA, ³University of Georgia Savannah River Ecology Lab, Aiken, SC, USA, ⁴North Carolina State Museum of Natural Sciences, Raleigh, NC, USA

A Novel Approach to Estimating Density of Secretive Terrestrial Snakes

Accurate estimates of population density and individual detection probability are critical components of effective wildlife conservation and management. However, many

snake species are so secretive that their density cannot be determined using traditional methods such as mark-recapture. Thus, the status of populations of most terrestrial snake species remains completely unknown, presenting a substantial obstacle to wildlife inventory or management plans. Here we develop a novel simulation-based technique for estimating density of secretive snakes that combines behavioral observations of snake road crossing behavior (crossing speed), effort-corrected road survey data, and simulation-based analysis of spatial movement patterns derived from radiotelemetry, without relying on mark-recapture. Specifically, we use radiotelemetry data to parameterize individual-based movement models that estimate the frequency with which individual snakes cross roads and use information on survey vehicle speed and snake crossing speed to determine the probability of detecting a snake, given that it crosses the road transect during a survey. Snake encounter frequencies during systematic road surveys can then be interpreted in light of detection probabilities and simulation model results to estimate snake densities and to assess various factors likely to affect encounter rates. We demonstrate the applicability of this approach to a variety of rare, secretive, or poorly understood species through a case example of the imperiled Southern Hognose Snake (*Heterodon simus*) in the North Carolina sandhills.

0657 Poster Session I, Acadia/Bissonet, Friday 8 July 2016; SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: ECOLOGY, NATURAL HISTORY, DISTRIBUTION, & BEHAVIOR

Audrey Wilson, Steve Johnson

University of Florida, Gainesville, FL, USA

Habitat Use of Invasive Cane Toads (*Rhinella marina*) in Florida

Cane toads (*Rhinella marina*) were accidentally introduced to Florida through the pet trade in the 1950s. They are now common in disturbed habitat throughout much of south and central Florida, and are particularly prevalent in residential areas. However, there are few records of cane toads in natural areas in Florida. It is unclear if the lack of records in undisturbed habitat indicates a true absence or if it results from insufficient sampling effort. We deployed thirty-eight autonomous recording units (ARUs) in four natural areas and nearby neighborhoods to identify cane toads calling in summer and fall 2015. We scanned recordings with Song Scope software using an automated recognizer, and then manually to focus on periods of heavy rain. Cane toads were not detected in any of the natural habitats, though they were recorded calling at four of five residential sampling locations. Although two of the four sites experienced abnormally low rainfall, other species called regularly. Species frequently heard calling in natural areas included southern toads (*Anaxyrus terrestris*), oak toads (*Anaxyrus quercicus*), Cuban tree frogs (*Osteopilus septentrionalis*), green tree frogs (*Hyla cinerea*) and eastern narrowmouth toads (*Gastrophryne carolinensis*). Additional ARUs will be deployed spring 2016 to examine cane toad presence along a disturbance gradient.

0778 Lightning Talks, Galerie 2, Saturday 9 July 2016

Thomas Wilson, Brad Reynolds, Margaret Dempsey, Alexandra Korshun, Ashton Mitchell, Erin Shrenker, Richard Schwartz, Team Salamander

University of Tennessee at Chattanooga, Chattanooga, TN/SEUSA, USA

The Development and Implementation of a Natural Science Living and Learning Community and a Case for Hands-On Herpetology Utilizing the Biological Field Stations at UT-Chattanooga

The University of Tennessee at Chattanooga (UTC) is a regional metropolitan university that is exploring new and exciting ways to better engage and prepare students for careers. Pedagogically speaking, the traditional approach of pairing lectures and laboratories is not always effective when compared to research approaches utilizing problem-based learning with design process thinking. The latter has received some traction at UTC and is a dynamic way to prepare students for productive careers in science. Our Natural Science Living and Learning Community (NSLLC) will be a residentially based research opportunity that focuses on a particular aspect of natural science. In 2004, UTC officials began drafting a plan to acquire properties to be used as biological field stations (BFS) so that faculty could better engage students in education, research, outreach and conservation. UTC's BFS are pivotal for this NSLLC because they provide the frame work for students to better understand wildlife-habitat relationships in urban systems. By using existing elements of the curricula and university infrastructure, we have devised a plan to integrate the BFS into a four semester curriculum so that students can gain hands-on experience in scientific research. The NSLLC will be tied to the current research being performed at the BFS because it provides an excellent jump-off platform that dovetails flawlessly within a realistic problem based learning environment. In closing, the NSLLC will build capacity for undergraduate research, facilitate partnerships among community stakeholders, and foster active yet collaborative learning by studying the urban ecology of the Chattanooga area.

0290 HL GRADUATE RESEARCH AWARD, Galerie 2, Friday 8 July 2016

Kristin Winchell¹, Elizabeth Carlen², Liam Revell¹

¹*University of Massachusetts Boston, Boston, MA, USA*, ²*Fordham University, New York, NY, USA*

Urban Habitat Partitioning by Two Common Species of Puerto Rican Anoles

Ecology and evolution of herpetofauna in urban areas is an important aspect of global change. Urbanization leads to significant habitat modification and species differ in their ability to utilize and adapt to human-altered landscapes. In Puerto Rico, *Anolis cristatellus* is abundant in urban areas where it frequently utilizes manmade substrates. Our previous work demonstrated that this urban habitat use is correlated with phenotypic shifts in fitness-related traits. Yet not all species present in urban areas

utilize anthropogenic habitat extensively. *Anolis stratulus* is frequently found in urban areas across Puerto Rico but rarely utilizes manmade substrates. We quantified differences in habitat use for these two species to better understand partitioning of urban habitat. We found that *A. cristatellus* and *A. stratulus* discriminately utilized different portions of the habitat. Specifically, *A. stratulus* chose patchy, remnant natural habitat such as trees and shrubs while *A. cristatellus* used anthropogenic habitat such as buildings and fences with high frequency. Aspects of the observed habitat discrimination are similar to patterns in natural sympatric populations: *A. stratulus* perched higher than *A. cristatellus*, preferring sites with lower temperatures and greater canopy cover. However, the use of manmade substrates by *A. cristatellus* and not *A. stratulus* reduces niche overlap. The avoidance of manmade substrates by *A. stratulus* may reduce inter-specific predation and competition or may reflect less flexible habitat requirements. Our results have implications for long-term persistence of these species in urban habitats and suggest loss of natural habitat elements may lead to non-random species extirpations as urbanization intensifies.

0507 SSAR SEIBERT AWARD CONSERVATION, Galerie 3, Friday 8 July 2016

Stephanie Winton¹, Christine Bishop², Karl Larsen¹

¹Thompson Rivers University, Kamloops, British Columbia, Canada, ²Environment and Climate Change Canada, Delta, British Columbia, Canada

Assessing the Relationship between Habitat Temperature and Rattlesnake Road Mortality

Road mortality poses a severe threat to many wildlife species, and effective mitigation requires a fundamental understanding of why animals occupy roads in the first place. Research has recognized that snakes are particularly susceptible to roadkill due to distinct life history traits, even being shown to have a preference for road habitat in some cases. However, little research has attempted to identify the driving factors behind snake occurrences on roads. As ectotherms at the northern extent of their range in British Columbia, western rattlesnakes (*Crotalus oreganus*) exhibit behavior that is highly influenced by the need to thermoregulate, and paved roads likely offer preferential habitat at certain times of the day or season compared to the surrounding shrub-steppe. We are examining a population of western rattlesnakes through mark-recapture and radio-telemetry work. Regular road and habitat surveys are conducted throughout the active season with concurrent monitoring of environmental conditions such as substrate temperatures. The goal of this research is to identify predictors of snake behavior relating to road thermodynamics, as well as quantify overall roadkill impacts on the population. Preliminary analysis indicates that there is a positive relationship between road temperature and the presence of rattlesnakes on roads, although the combination of multiple factors is being explored. It is anticipated that this research will reveal important movement corridors and roadkill 'hot-spots' as well as identify conditions associated with incidence of roadkill. Being able to predict when, where and for how

long snakes are occupying roadside habitat will contribute to successful mitigation measures.

0953 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Van Wishingrad, Anthony Barley, Robert Thomson, Amber Wright

University of Hawaii, Honolulu, Hawaii, USA

Evidence-based threat assessment: lessons from California herpetofauna

Mitigating threats to species of conservation concern requires accurately determining causes of decline. While many studies have assessed common threats across taxa, little attention has been paid to the standards for evidence used to determine threats. We used reptiles and amphibians in California, USA as a case study for determining both the threats causing imperilment and the evidence used to support identification of threats. We reviewed the original listing documents and relevant literature for all taxa that are endangered, threatened, or special concern at the state and/or federal level (64 taxa). For each cited threat we scored whether evidence existed for that threat from observational or experimental data, and whether that evidence was replicated across space, time, or research groups. Threats supported only by expert opinion were scored as lacking formal evidence. Overall, the most commonly cited threats were habitat degradation (92% of taxa affected), climate change (72%) and introduced species (50%). We identified 186 combinations of threat and taxon, and in over half of these cases (54%) there was no empirical evidence for the threat. When evidence was available, it was usually from observational data only (54/85 cases with evidence), and a quarter of cases with empirical evidence were unreplicated (22/85). The call for evidence-based conservation has been growing, with an emphasis on decision-making regarding alternative interventions. Our analysis shows that little evidence is contributing to identifying threats in the first place, potentially leading to inefficient conservation actions. Our analysis highlights key research gaps for conservation of California herpetofauna.

0599 ASIH STOYE AWARD CONSERVATION, SALON E, Thursday 7 July 2016

Calvin Won, Larry Allen

California State University, Northridge, Northridge, California, USA

Moonlit Summer Love: Exploring the lunar effect on spatial patterns of spawning Barred Sand Bass

Spawning aggregations are essential to commercial and recreational fish harvest. Predictability of aggregations in both time and space allows for plentiful yield with relatively low fishing effort. However, this places certain species at risk of overharvest.

The Barred Sand Bass (*Paralabrax nebulifer*), a resident California species, has been exhibiting the characteristics of an aggregation-based fishery that is on the verge of collapse, as annual catch estimates have declined by more than 90% within a 10-year period. Population declines of aggregation-based fisheries have a tendency of going unnoticed, as fishery-dependent stock assessments do not generally account for spatial or temporal variability. Spatial variability and behavior of many fish species is mediated by physical environmental factors. This study aims to investigate the spatial tendencies of Barred Sand Bass spawning aggregations in relation to lunar periodicity. Lunar phase-dependent transect surveys were performed using active acoustic technology (BioSonics® DT-X split beam echosounder, 206 kHz) during the summer of 2014 spawning season. These data revealed a possible lunar-dependent depth pattern, as Barred Sand Bass were detected over shallower environments during new moon events and over deeper environments during full moon events. This pattern may be related to variations in water column illumination, which has previously been shown to alter the schooling behaviors of the Northern Anchovy (*Engraulis mordax*), a common prey species to the piscivorous Barred Sand Bass.

1116 Herp Conservation, Galerie 2, Sunday 10 July 2016

Dustin Wood¹, Erika Nowak², Randy Jennings⁵, Bruce Christman⁵, Iain Emmons², Jeff Servoss⁴, Amy Vandergast¹

¹U.S. Geological Survey, San Diego, CA, USA, ²Northern Arizona University, Flagstaff, AZ, USA, ³U. S. Geological Survey, Flagstaff, AZ, USA, ⁴U.S. Fish and Wildlife Service, Tucson, AZ, USA, ⁵Western New Mexico University, Silver City, NM, USA

Genetic Connectivity of Mexican and Narrow-headed gartersnakes across the major US watersheds using genome-wide SNP data

The Northern Mexican Gartersnake (*Thamnophis eques megalops*) and the Narrow-headed Gartersnake (*Thamnophis rufipunctatus*) are highly aquatic species inhabiting the major perennial watersheds throughout central and southern Arizona, western New Mexico, and Mexico. Although historically common and widespread throughout their range, remaining populations in the United States are largely disjunct and isolated from one another and from populations in Mexico, suggesting that gene flow is nonexistent or impeded. Given the fragmented state of the remaining populations, it is critical to understand the genetic structure and diversity of existing populations to ensure long-term viability. We used data from hundreds of independent nuclear markers (Single Nucleotide Polymorphisms) to (1) determine whether there is significant genetic structure among watersheds, (2) assess the levels of genetic diversity and gene flow dynamics within and among watersheds, (3) and identify suitable source populations for potential re-establishment efforts. In both species we found evidence for strong genetic partitioning both within and among watershed and multiple genetic clusters within each species. Using comparisons of genetic diversity and effective population size estimates, we discuss how patterns of genetic diversity can inform conservation management decisions and the recovery planning efforts for both species.

0470 Fish Ecology I, Salon A-C, Saturday 9 July 2016

Kirsten Work, Melissa Gibbs

Stetson University, DeLand, FL, USA

How effective is discharge management on maintaining Florida spring fish assemblage structure?

Over the past forty years, Florida springs have been increasingly impacted by reductions in water quantity and quality and by invasions of exotic species. Those springs near high population densities have been disproportionately impacted. Volusia Blue Spring is a first magnitude spring (> 100 mgd/day) and a major manatee refuge in Central Florida and its springshed is almost entirely municipal. The St. Johns River Water Management District adopted a Minimum Flow Regime (MFR) in 2007 to provide an administrative means for maintaining discharge and the ecological health of the spring. This study was part of the periodic evaluation of the ecological integrity of the spring for the MFR and its purpose was to determine whether there were relationships between discharge and stage, water quality, and biological parameters. Over the course of one year, we assessed (among other parameters) fish density and diversity monthly with seine and snorkel counts. We evaluated spatial, seasonal, and annual changes in the assemblages and compared the data collected in 2014-2015 to data collected in 2007-2008 and in 2001-2003. Low discharge combined with high stage and salinity in 2014-2015 produced a fish population with a lower density and diversity than in previous years. As a result of the strong relationships between variation in discharge and an array of chemical and biological characteristics of the spring, we suggest that maintaining the historical discharge rate is important for preserving the ecological integrity of Volusia Blue Spring.

1016 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Amber Wright

University of Hawaii at Manoa, Honolulu, HI, USA

Competition in Novel Lizard Communities: *Anolis* vs. *Phelsuma* in Hawaii

Novel communities are increasingly being formed by factors such as climate change and species introductions. Predicting the outcome of interactions in novel communities is of paramount practical importance, and also addresses fundamental questions in ecology about community assembly. The arboreal, diurnal lizard fauna of Hawaii is comprised of the ecologically similar but distantly related anoles and day geckoes, providing an ideal study system for predicting the outcome of novel species interactions. The two anoles (*A. carolinensis* and *A. sagrei*) have a well-documented competitive interaction: where they co-occur they partition habitat, and *A. carolinensis* abundance declines. Therefore, I can use the traits of the anoles and their expected competitive outcome as a

reference to predict how the novel player, *P. laticauda*, fits into the community. Here I report preliminary data on functional trait variation, observational data from the field, and data from experimentally assembled communities. When alone, any of the three species can be abundant, but in sympatry only one is abundant. *A. carolinensis* is still abundant and uses lower perches in sites recently colonized by either of the other species compared to sites with longer co-occurrence. In 10 m x 10 m experimental enclosures, interactions between the two anoles are consistent with previous studies. Interactions between *Phelsuma* and the anoles seems to depend on whether 1 or 2 anole species are present: *P. laticauda* perches much higher in the presence of both species compared to all other combinations. These results suggest that these taxa are indeed competing in Hawaii.

1067 Herp Ecology, Salon F-H, Sunday 10 July 2016

Amber Wright¹, Gregory Pauly², Anthony Barley¹, Robert Thomson¹

¹University of Hawaii at Manoa, Honolulu, HI, USA, ²Natural History Museum of Los Angeles County, Los Angeles, CA, USA

Historical Resurveys of Lizard Communities in the Mojave Desert

In seminal work on lizard ecology, Eric Pianka surveyed distribution, abundance, and species traits of flatland, Mojave Desert lizard communities in the 1960s. This work combined with surveys by Benjamin Banta during the same period resulted in the collection of over 3,500 specimens. Since then, this region has experienced increased development and a warming climate, with such trends expected to continue into the future. We resurveyed 5 of these historical sites to determine changes in lizard communities over the last 50 years. We found slight changes in species richness at most sites. For the two most common lizards, *Aspidoscelis tigris* and *Uta stansburiana*, for which historical abundance data were available, we found decreases in abundance at most sites. Future work will expand to resurveys of the full transect of Pianka localities in the Sonoran and Great Basin deserts, and analysis of trait variation over time. Our resurvey will provide an important benchmark for future studies of environmental change in the Mojave Desert.

0610 AES Sawfishes Symposium, Salon E, Sunday 10 July 2016

Barbara Wueringer¹, Teagan Marzullo¹, Vera Schluessel²

¹Sharks And Rays Australia, Bungalow, Queensland, Australia, ²University of Bonn, Institute of Zoology, Bonn, Germany

Sawfish research in Queensland, Australia

For four species of sawfish, i.e. the green sawfish *Pristis zijsron*, the dwarf sawfish *Pristis clavata*, the freshwater sawfish *P. pristis* and the narrow sawfish *Anoxypristis cuspidata*,

the waters of Northern Australia are likely to represent their last global stronghold. The organization Sharks And Rays Australia is currently undertaking a project assessing the distribution and abundance of these four sawfish species in Northern Queensland, focusing on Far North Queensland, the Cape York region and the coastline of the Gulf of Carpentaria. The region north of Cairns is only sparsely populated by approximately 28,000 people. A large percentage of the 2500 km coastline and rivers are believed to be an important habitat for sawfish. The aim of Sharks and Rays Australia will be to determine the status quo and review the limitations of the current knowledge on the occurrences of sawfish within this region. The methods of our study, including a tagging study, collaborations with local indigenous rangers and the involvement of the public, will be presented together with preliminary results and future aims for the expansion of this study.

1062 AES Morphology & Reproduction, Balconies L & M, Friday 8 July 2016

Jennifer Wyffels, Linda M. Penfold

South-East Zoo Alliance for Reproduction & Conservation, Yulee, FL, USA

Comparative Morphology of Shark Sperm Using Light and Electron Microscopy

Elasmobranch spermatozoa studied so far are characterized by a conical acrosome, helical nucleus, long mitochondria-rich midpiece, and helical tail. Semen was collected from 5 sharks (*Carcharias taurus*, *Chiloscyllium plagiosum*, *Chiloscyllium punctatum*, *Mustelus canis*, and *Carcharhinus limbatus*) for comparative light and scanning and transmission electron microscopy. Spermatozoa had a species-specific number of gyres or twists (*C. plagiosum* 32, *C. taurus* 17, *M. canis* 11, and *C. limbatus* 5) that continued into part of the midpiece for *C. plagiosum*, *C. punctatum*, and *M. canis*. The midpiece was composed of glycogen granules and mitochondria with concentric cristae. A cytoplasmic sleeve, analogous to the cytoplasmic droplet of other vertebrates, was located at the junction of the midpiece and flagellum and was shed via movement down the flagellum over time after semen collection. For all species the flagellum contained two ovoid longitudinal columns adjacent to the axoneme at doublets 3 and 8. In contrast to the other sharks, the nucleus of *C. limbatus* underwent changes with cell death that manifested as foci of nuclear expansion from DNA decondensation. *C. punctatum* and *C. plagiosum* spermatozoa were observed to be capable of both forward and backward motility. Reverse motility for spermatozoa is a remarkable feature not reported for other species.

0835 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Amy Yackel Adams¹, Bjorn Lardner², Elden Holldorf³, Justine Kaseman³, Lea Bonewell¹, Rod Adams⁴, Adam Knox¹, Michelle Collier¹, Bryan Falk¹, Emma Hanslowe¹, Julie Savidge², Robert Reed¹

¹U.S. Geological Survey, Fort Collins, CO, USA, ²Colorado State University, Fort Collins, CO, USA, ³Cherokee Services Group, Fort Collins, CO, USA, ⁴Front Range Community College, Fort Collins, CO, USA

Camera Traps as a Tool in Reptile Research

Advances in trail camera technology, coupled with decreasing costs, have led to a dramatic increase in camera trap use in wildlife research. There is immense potential for camera traps to deliver new data types. In our invasive reptile research program, we use cameras to understand tegu brumation behavior, species presence, and snake activity around mouse-baited traps. We report on the use of trail cameras to record behaviors of invasive brown treesnakes around conventionally-used snake traps on Guam. Our results provide circadian rhythm information and trap-entry rates of snakes that approach traps. Camera trap use, while extremely challenging in field settings for reptiles, can provide important information on reptile biology as well as control-tool efficacy for invasive reptiles.

0816 Herp Conservation, Galerie 2, Sunday 10 July 2016

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Can Detectability of Brown Treesnakes Reveal its Ability to Predict When it is Worth Foraging?

Invasive Brown Treesnakes (*Boiga irregularis*) have caused extinction or extirpation of many native vertebrates on Guam, a U.S. territory in the western Pacific Ocean. We study control, containment, and detection of this species. One of the primary objectives of our research is to obtain comprehensive estimates of snake detection probability – a parameter of paramount interest for optimizing invasive species management. In a 5-ha enclosure, we used mark-recapture and nocturnal visual searches to evaluate detection determinants that reflect (1) human ability to detect an active snake (e.g., wind, rain, searcher) and (2) differences in snake activity (e.g., sex, size, body condition, prey, and an individual's recent detection history). Snake size affected individual detection in a predictable manner, but also interacted in a novel way with our sighting rates of prey: small snakes were more detectable on nights when their gecko prey were frequently sighted, whereas large snakes were more detectable on nights when their rat prey were frequently sighted. Nightly gecko and rat sighting rates were not correlated. We suspect that the snakes cannot sense the activity of prey species directly, but likely use proxies

(e.g., high humidity, dark of moon, etc.) that they have come to associate with good hunting. However, our modeling of known proxies suggests the existence of additional unidentified factors. Knowledge of modulators of snake activity and their covariates can be useful for not only enhancing the precision and reducing the bias of monitoring and control activities, but also for exploring ecological questions.

0228 SSAR SEIBERT ECOLOGY AWARD, Galerie 2, Friday 8 July 2016

Katharine Yagi¹, David Green²

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Mechanisms of Density-Dependent Dispersal in Juvenile Fowler's toads, *Anaxyrus fowleri*

Dispersal is a necessary process for any species living in a fragmented landscape, but it is unknown precisely how body size is related to dispersal. If displacement is in some way size-dependent, then by manipulating larval density conditions to produce juvenile toads of varying sizes in the same adult habitat, we should see a correlation between displacement and body size among individuals. To address this, we reared Fowler's toad tadpoles in eight density treatments in artificial ponds located in the Long Point National Wildlife Area. After about two weeks post-metamorphosis, we measured toadlet body length and relative leg length and released individuals into the adult habitat. Toadlets were recaptured in the terrestrial landscape the following spring and identified using photographs of their dorsal spot patterns. Displacement rate was measured using the linear distance between the initial release coordinates and the coordinates of their first recapture the following season, divided by the number of active season days in between each encounter. We hypothesized that if larger toads have more energy stores to move longer distances at a faster rate, then we should find a positive relationship between body size and relative displacement rate. Similarly, if longer legged animals jump proportionally longer distances than those with shorter legs, relative leg length should positively correlate with relative displacement rate. The results show that relative leg length is a better predictor for relative displacement rate than body length, suggesting that tadpole density may influence dispersal indirectly, by influencing leg length of toadlets.

0596 Poster Session I, Acadia/Bissonet, Friday 8 July 2016

Naoki Yagishita¹, Takahiro Kusaka², Hara Koujirou¹, Keisuke Furumitsu¹, Shinji Uehara³, Yuta Yagi³, Atsuko Yamaguchi¹

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Microsatellite DNA analysis of population structure of a Japanese common skate *Dipturus cf. kwangtungensis* in Japan

A Japanese common skate *Dipturus cf. kwangtungensis* is distributed in the coast of Japan from Hokkaido southward to Kyushu, the East China Sea, Korean Peninsula, and Taiwan, inhabiting depth of 20 to 320 m. The populations around Japan of the species are indicated to be structured by mitochondrial DNA analyses. We investigated population structure of *D. cf. kwangtungensis* based on polymorphism of microsatellite (simple sequence repeat: SSR). Samples of *D. cf. kwangtungensis* were collected from the Pacific Ocean (northern part of Honshu), the Sea of Japan (Niigata and Kyoto Prefs.), the East China Sea (Goto Islands and Danjo-gunto Islands). Polymerase chain reactions were carried out to amplify four SSR loci (LERI21, 34, 44, 50; El Nagar et al. 2010). The number of alleles per SSR locus within samples varied from 2 to 13 with a mean of 5.5. The H_o ranged from 0.182 to 0.909 with a mean of 0.611, and the H_e ranged from 0.385 to 0.939 with a mean of 0.703. The pairwise F_{st} values between northern part of Honshu and each of the other four geographic populations were high (0.157–0.252) and significant after Bonferroni correction ($P < 0.001$), while the values between each of the geographic populations in the Sea of Japan and the East China Sea were low (from -0.026 to 0.013) and not significant ($P > 0.05$). The genetic differentiation was suggested between population in the Pacific Ocean and the group containing populations in the Sea of Japan and the East China Sea.

0654 Poster Session I, Acadia/Bissonet, Friday 8 July 2016

Atsuko Yamaguchi, Kojiro Hara, Noriko Omori, Keisuke Furumitsu

Nagasaki University, Nagasaki, Japan

Two hammerhead sharks, *Sphyrna lewini* and *S. zygaena* in Ariake Bay, Japan: size and age composition, feeding habits, and migration

Hammerhead sharks of the genus *Sphyrna* play an important role as predators in ecosystems. However, very few studies exist on the species of *Sphyrna* in Japan, including Ariake Bay, the largest bay in Kyushu. Here, we report the assessment of biological and behavioral aspects of two hammerhead sharks, *S. lewini* and *S. zygaena*, such as age composition, feeding habits, and migration, based on the specimens collected in Ariake Bay from 2006 to 2016. *S. lewini* specimens collected were 429-3290 mm in total length (TL) with aged 0-33; however, specimens aged 2-8 were not collected. *S. zygaena* specimens collected were 548-1590 mm TL; however, specimens of mature

animals were not collected. The stomach contents of both species comprised primarily teleosts, cephalopods, and crustaceans. Of those, teleosts were predominant; the two *Sphyrna* spp. were therefore considered to feed primarily on teleosts in Ariake Bay. The investigation of movement and migration revealed that small *S. zygaena* individuals enter the bay incidentally. In contrast, *S. lewini* was considered to visit the bay to breed in early summer and leave after giving birth and mating. Juvenile *S. lewini* appeared to move to the open sea in autumn after inhabiting the shallow areas of the bay through the summer. We estimate that they inhabit the open sea and do not return to the bay until they reach sexual maturity. Ariake Bay was thus regarded as playing an important role as a nursery ground for *S. lewini*.

0308 Fish Systematics II, Salon F-H, Saturday 9 July 2016

Lei Yang, Gavin Naylor

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Mitogenome Sequencing and the Tree of Life of Chondrichthyan Fishes

The present study is aimed at resolving the phylogenetic relationships among chondrichthyan fishes based on the largest taxon sampling to date and the mitogenome sequences. A preliminary Neighbor-Joining tree was estimated from mitochondrial ND2 sequences derived from more than 12,000 tissue samples collected as part of a NSF funded Tree of Life project. Representative samples of lineages identified as distinct in the Neighbor-Joining analysis were subsequently subjected to library preparation. Cross-species gene capture of nuclear genes and the mitogenome were then performed separately using three different sets of specially designed RNA baits (one for nuclear genes, two for mitogenomes). Captured genes of pooled samples were then sequenced on an Illumina MiSeq. Only results from mitogenome sequences are shown here. Partitioned Maximum Likelihood searches and bootstrap analyses were performed for the concatenated dataset of the protein-coding genes of the mitogenome sequences obtained. Most nodes were resolved with high bootstrap support in the tree. Topology of the tree was compared with those from previous studies and relationships among major lineages of sharks and batoids were discussed. Molecular dating based on multiple well-characterized chondrichthyan fossils and diversification analyses were performed.

0341 Poster Session I, Acadia/Bissonet, Friday 8 July 2016

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Estimation of Spatial Distribution of North Pacific Spiny Dogfish *Squalus suckleyi* using Generalized Additive Models

The distribution of North Pacific spiny dogfish *Squalus suckleyi* is not well known in the whole North Pacific, in particular around Japan. Our objective is to demonstrate the dogfish habitat in the North Pacific and to evaluate the effect of sea surface temperature (SST) and prey availability. A total of 14,893 gillnet operations were conducted in the North Pacific from 1972–2011 and the presence/absence of dogfish in each gillnet were analyzed by the generalized additive models with a binomial error distribution. Our results supported the previous study that the probability of dogfish presence was highest around the Gulf of Alaska and presented the following new findings; (1) the area with a high probability of presence also exists off Japan, (2) the distribution is continuous between two areas. Though the waters in the Tsugaru Strait has been considered as a primary habitat area for this species, our results showed that the area with higher probability located in the Sea of Japan off Hokkaido Island than the Tsugaru Strait. The spiny dogfish probability of the presence was high ranging 6 to 12 °C in SST, and the probability was higher if the prey co-exist. These results indicate that the factors both distribution of prey species and SST affect to the dogfish habitat, and the evaluating the habitat of this species could be available for rational management.

0340 AES Sawfishes Symposium, Salon E, Sunday 10 July 2016

Kara Yopak¹, Barbara Wueringer², Kirk Feindel³, Shaun Collin¹

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What you Saw Isn't always What you Get: Patterns of Brain Organization in Sawfishes

Broad variability has been documented within cartilaginous fishes regarding the size and complexity of the brain and its major components (olfactory bulbs, telencephalon, diencephalon, mesencephalon, cerebellum and medulla). This variability is often

associated with habitat or specific behavior patterns, even in phylogenetically unrelated species that share certain lifestyle characteristics. However, few studies to date have examined the brain in species that have convergently evolved morphological specializations, such as the protruded “saw” rostrum of sawfishes and sawsharks, which is used for detecting and/or manipulating prey. This study examined the brains of four species of sawfishes, including representatives from the *Anoxypristis* and *Pristis* genera, in comparison to the sawshark *Pristiophorus cirratus* and an existing dataset of approximately 100 other chondrichthyan species, which differed with respect to their phylogeny and ecology. Brains were assessed in these critically endangered species using magnetic resonance imaging (MRI), which allowed for non-invasive interrogation of the organization of the central nervous system and the quantification of different brain regions. Results show dramatic differences in both relative brain size and brain morphology between sawfishes and sawsharks, which reflect their phylogenetic and ecological divergence. Of particular note is the variation in size and complexity of the corpus cerebellum, a region of the brain thought to be responsible for executing fast and efficient movement in these ancient predators. Results support the assertion that the saw-like rostrum may serve different functions in these two divergent taxa and that their brain organization may reflect a range of behavioral and ecological specializations.

0498 Herp Morphology & Genetics, Galerie 3, Sunday 10 July 2016

Bruce Young, Dawei Han

Kirksville College of Osteopathic Medicine, Kirksville, MO, USA

The dynamic middle ear of the water monitor lizard (*Varanus salvator*)

Many reptiles have internally-coupled ears in which the two eardrums, or tympana, are linked by relatively large open passageways through the skull. This morphology produces novel sound localization cues arising from both the timing and amplitude of tympanic activation. Which of these two cues a reptile uses is determined, in part, by the fundamental frequency (or tension) of the tympanic membrane. Anatomical investigations of the water monitor lizard (*Varanus salvator*) revealed a small skeletal muscle capable of tensing the tympanum, as well as a band of elastic tissue bordering one edge of the tympanum. Experimental analyses using muscle stimulation and laser doppler vibrometry demonstrate that contraction of the muscle is associated with displacement of the tympanum, and that this displacement alters how the eardrum responds to presented tones. Monitor lizards actively alter the air pressure between the tympana by regulating the contractile state of hypobranchial muscles. Experimental analyses reveal that pressurizing the inter-tympanic connection results in displacement of the tympana and changes how the membrane responds to presented tones. The monitor lizards can actively modulate, through skeletal muscle, the tension (and thus fundamental frequency) of the tympana, which will determine the relative levels of the temporal and amplitude cues available for sound localization. This represents a novel form of modulating the auditory system, as it is mechanical not neural, and based on the middle ear not the inner ear.

0800 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Nadege Zaghoudi-Allan¹, Mark Roberts², Andrew Coleman³, Fernando Manzano-Cervantes⁴, Irma Galván⁴, Kathryn Levasseur², Laura Kiehn⁵

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Preliminary characterization of a poorly understood nesting population of the critically endangered Kemp's ridley sea turtle

Once nearly extinct, Kemp's ridley sea turtles have made an impressive comeback. Despite this, it remains the most endangered of all sea turtles, and the total impact of the 2011 oil spill on the species is still unclear. Currently, most conservation efforts are centered around Rancho Nuevo (RN), MX and Padre Island, US; however, efforts to protect important additional beaches are one of the priorities of the NMFS Bi-National Recovery Plan for the species. A comparatively poorly understood nesting population at Tecolutla, Veracruz (~ 330km S of RN) represents a potentially important nesting beach due to its relatively large nesting population size and the possibility that it is isolated from the RN nesting population. Additionally, temperature controlled hatchling sex ratios produced at Tecolutla could be different from those produced at RN - as they are in other marine turtle species separated by a similar distance. Dispersal models indicate that local currents promote the successful pelagic recruitment of Kemp's ridley hatchlings from Tecolutla as effectively as from RN, further stressing the need to characterize this population. A Mexican NGO has conducted surveys for a number of years that focus on counting and protective relocation of nests. In 2014 a study was initiated to characterize the nesting beach (beach profile and sediment grain size analyses), establish nest temperature profiles, estimate genetic diversity, characterize the morphology of nesting turtles, and develop a rigorous tagging program. Here we present nesting history at Tecolutla from 2000-present as well as initial results of the recent study.

0049 Poster Session I, Acadia/Bissonet, Friday 8 July 2016

Ilena Zanella, Andrés López

Misión Tiburón, Guanacaste, Costa Rica

Identification and Protection of Critical Habitats for Scalloped Hammerhead Shark (*Sphyrna lewini*), in Golfo Dulce, Costa Rica

The scalloped hammerhead shark, *Sphyrna lewini*, is threatened by human activities. In 2008 the IUCN Red List classified as Endangered, and in 2013 it was included on the CITES Appendix II list. Neonates and juveniles live in nursery areas located in coastal

waters, where nutrient waters provide food and protection from predators. The adults migrate to open waters, returning to nursery areas for mating and pupping. Scientific study is needed to identify nursery areas and provide evidence-based recommendations for the development of successful conservation management plans. Fisheries-dependent biological data was gathered for *S. lewini* during artisanal fishing trips between May 2010 and May 2011 in Golfo Dulce. Catch per unit effort (CPUE) throughout the year was also estimated from catch data. We sampled a total of 315 sharks. Mean total length was estimated at 74.3 ± 17.4 cm. Total length and relative abundance of *S. lewini* had opposite tendencies, with the smallest TL recorded during July-August, when CPUE was highest. Based on the fisheries dependent data from on board observations, three aggregations sites were selected to deploy acoustic receivers and tag ten hammerhead sharks. Between June 2011 and July 2012, the receivers recorded almost 40,000 detections. All the sharks tagged were reported, showing daily movements between receivers. Our field research during this project has identified critical habitats within Golfo Dulce, and acted to improve the management plans for their protection. Through our efforts we have discovered the first evidence of a biological connection for *S. lewini* between critical coastal habitats and Cocos Island.

0894 AES Ecology & Behavior I, Balconies L & M, Thursday 7 July 2016

Patricia Zarate, Carlos Montenegro, Daniel Devia

Instituto de Fomento Pesquero, Valparaiso, Chile

Preliminary results on the horizontal and vertical movements of *Lamna nasus* in the South East Pacific

Spatial dynamics are poorly understood for pelagic sharks despite the decline of many species due to overfishing. For many species with low population abundances, however, little progress has been made in identifying space use patterns. Porbeagle sharks *Lamna nasus* stocks from North and South West Atlantic Ocean and Mediterranean Sea have severely declined in population sizes resulting in the listing of this species in CITES' Appendix II. In the South East Pacific Ocean, particularly in Chilean waters, porbeagles are the third most common species incidentally caught by swordfish fisheries in Chile. Here we described the movements, diving behavior and habitats (vertical thermal) occupied by a juvenile female porbeagle in the Southeast Pacific Ocean using pop-up satellite-linked archival transmitters (PSATs). The shark named "Violeta" was tagged on November 2015 and tracked for 90 days. Violeta displayed a clear southward movement of approximately 1500 km after being tagged off Coquimbo in the north coast of Chile (36° latitude). Shark occupied a broad vertical depth range (0 - 552 m) and water temperatures (8° - 19 °C). This study described for the first time the diving behavior and habitats occupied by porbeagle sharks in this region of the Pacific Ocean.

0171 Poster Session II, Acadia/Bissonet, Saturday 9 July 2016

Jeffrey Zeyl, Carol Johnston

Auburn University, Auburn, AL, USA

Comparative and developmental patterns of amphibious auditory function in salamanders

Early amphibious tetrapods lacked tympanic ears, which restricted the detection of air-borne sounds to low frequencies and high intensities. In these taxa, aquatic hearing adaptations could have pre-equipped aerial function, depending on the extent of acoustic transmission between air and unspecialized tissues. Salamanders lack tympanic middle ears, but may use sound-induced lung vibrations to detect aquatic sound pressure. Therefore, they could be useful models for the functional constraints and evolutionary responses of the early tetrapod auditory system to the aquatic-terrestrial boundary. We collected amphibious auditory evoked potential audiograms in five phylogenetically and ecologically distinct salamanders (*Amphiuma means*, *Notophthalmus viridescens*, *Ambystoma talpoideum*, *Eurycea cirrigera*, and *Plethodon glutinosus*) to: (1) assess the diversity of auditory carryover across media, and (2) examine whether terrestrial niche and metamorphosis are associated with higher aerial sensitivity. Relative to its aquatic audiogram, aerial sensitivity of *A. means* was maximized at 100 Hz, but constrained at higher frequencies. In contrast, *A. talpoideum* and *E. cirrigera* showed best aquatic-aerial sensitivity carryover at 400-500 Hz, while auditory thresholds in *N. viridescens* were shifted uniformly across frequencies. Aerial thresholds of terrestrial *P. glutinosus* were similar to paedomorphic *A. talpoideum* and adult *E. cirrigera*, but lower than *N. viridescens* and *A. means*. Metamorphosis was not associated with higher aerial sensitivity in *N. viridescens* or *A. talpoideum*. The results fail to support significant specialization of the salamander ear for terrestrial auditory function. Additionally, aerial performance is contingent on aquatic performance, but to varying degrees for different species.

0909 Fish Morphology & Biogeography, Salon A-C, Sunday 10 July 2016

Nicholas Zielinski, Ian Bollinger, Ryan Lavoie, Julianne Rawson, Jeff Eble

University of West Florida, Pensacola, Florida, USA

The Black Triggerfish (*Melichthys niger*): A Circumtropical Species or Species Complex?

There are more than 15,000 known species of marine fishes, yet only 284 are believed to be truly circumtropical. Of these, nearly all (83%) are either pelagic and highly migratory as adults or inhabit the bathypelagic zone where few barriers to dispersal exist. The ability to maintain genetic connectivity and high similarity across major marine biogeographic provinces (Atlantic, Indo-Pacific and East Pacific) is rare among reef fishes. Only 2% of circumtropical fish are reef associated and depend on a pelagic larval stage as a means of dispersal. *Melichthys niger*, the black triggerfish, is a reef fish

found commonly across the tropics. The purpose of this study is to address whether *M. niger* is truly a circumtropical species or a species complex through a comparative genetic survey. Mitochondrial (CO1 and d-loop) and nuclear (S7-1) loci in 250 individuals from 17 globally distributed sites were analyzed. Results indicate high genetic connectivity throughout the range of *M. niger*, including ongoing or recent gene flow between the Indian and Atlantic Oceans, and throughout the closely-associated islands of the East Indian and West Pacific Oceans (Indo-Pacific region). The lack of deep-genetic subdivision and apparent high gene flow indicates *M. niger* is an exceptional disperser, with the relatively unique ability among reef fishes to maintain genetic connectivity between sites separated by tens of thousands of kilometers.

**0646 ASIH STOYE AWARD ECOLOGY & ETHOLOGY, SALON D, Thursday
7 July 2016**

Erin Zylstra¹, Robert Steidl¹, Don Swann², Blake Hossack³

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Population Dynamics and Dispersal of Canyon Treefrogs in Desert Mountain Canyons

Understanding the biotic and abiotic factors that govern variation in demography is essential for conservation and management of amphibians, many of which have declined in response to a broad array of anthropogenic activities. Canyon treefrogs (*Hyla arenicolor*) inhabit arid canyons in the Sky Island region of southern Arizona, environments where the amount of surface water is highly dynamic and predicted to decrease with climate change. We used visual encounter (n = 56-74 surveys at each of 5 sites) and mark-recapture surveys (n ≥ 10 surveys/site) to characterize demography and movements of treefrogs in 2014-2015. Counts of adult (range = 0-695 frogs/survey) and juvenile (0-736) treefrogs varied markedly over time, reflecting seasonal variation in both abundance and surface activity. Treefrogs reproduced in both spring and summer, but recruitment varied with availability of surface water and failed during spring when pools dried before the onset of monsoon rains. We marked >1800 adult and subadult frogs; of those individuals recaptured, most were observed < 30 m from their original capture location. Movements > 100 m along drainages or between canyons were rare, comprising < 6% of movements. Apparent monthly survival varied seasonally and was highest during winter (>0.90) and lowest during summer (<0.50), indicating that most frogs live < 1 year after reaching subadult stages. Low rates of adult survival suggest that persistence of treefrog populations depends on high rates of recruitment, immigration, or both in these dynamic environments. Reductions in surface water and hydrologic connectivity will likely increase risk of local extinction.
