Abstracts
Scribner-Zhuang

The Joint Meeting of
ASIH SSAR HL AES
Ichthyologists & Herpetologists

Austin 2017

Last Edited 5/11/2017

0412 Snake Biology I, Brazos, Sunday 16 July 2017

Jacob Scribner, Matthew Kwiatkowski

Stephen F. Austin State University, Nacogdoches, Texas, USA

Facial Stripes Influence Attack Frequency on Snake Models

Dark facial markings in vertebrates can serve a variety of functions, including glare reduction, social signaling, and aposematism. Dark facial markings in the form of stripes are common in some snake groups, but little is known about their function. It has been hypothesized that they may act as either social signals to conspecifics or as warning signals to potential predators. We tested the hypothesis that facial stripes act as signals to potential predators using plasticine models. Snake models were shaped with a plaster mold using brown plasticine that most closely matched the color of some local snake species. For half of the models, facial stripes were added using black plasticine. Models were placed at regularly spaced intervals, alternating those with and without facial stripes, along a little-used trail in the Stephen F. Austin Experimental Forest in eastern Texas. In an initial test, models were left for 72 hours, retrieved, and scored for attacks when visible markings from mammals or birds were present. Models with facial stripes had visible attack marks significantly more than models without stripes ($P = 0.002$). Our results seem to contradict the hypothesis that facial stripes act as a warning to predators. However, attacks on models were not random, suggesting that models with facial stripes were targeted. Models with facial stripes may have been perceived as more of a threat and were, therefore, attacked more frequently.

0525 ASIH STOYE ECOLOGY & ETHOLOGY II, Sabine, Thursday 13 July 2017

Jason D. Selwyn[1], Paolo Usseglio[2], J. Derek Hogan[1]

[1]Texas A&M University - Corpus Christi, Corpus Christi, Texas, USA, [2]Fundacion In-Nova, Castilla la Mancha, Spain

Fine-scale microhabitat usage of a putative habitat generalist reef dwelling goby, *Coryphopterus personatus*

Variability in habitat quality influences species both at the population level as well as the individual level. At the population level, habitat quality has been found to be a primary driver of metapopulations and dispersal dynamics, affecting the frequency and strength of dispersal polymorphisms. At the individual level, habitat quality affects the growth rate and reproductive output as well as the mortality rate, amongst other processes. A wide range of characteristics of any given habitat can be thought of as being either beneficial or harmful to any given species. As such, defining habitat quality needs to be done from the perspective of the species being studied. Using structure-from-motion photogrammetry we characterize fine-scale microhabitat usage across both habitat type and topographical features to determine microhabitat usage of a coral-reef goby, *Coryphopterus personatus*. Using a zero-inflated negative binomial analytical approach we find that both the presence of shoals and the density of individuals within shoals are significantly influenced by aspects of both habitat topography and type. Understanding the factors defining habitat quality in a habitat generalist provides an important baseline for assessing the potential effects of future habitat degradation as is predicted to occur on coral reefs. Furthermore, these findings provide the basis for future studies seeking to understand how variation in habitat quality influence both individual and population scale processes.

0381 Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Alexander Semenchenko

Far Eastern Federal University, Vladivostok, Primorskiy Territory, Russia

Phylogeny of the genus *Thymallus* (graylings) using complete mtDNA

Graylings (Thymallinae) are holarctic fishes, which have widespread distribution ranges across Eurasia and North American continents. As all salmonids, these fish live in rivers with pristine and cold water and often play an important role in game fishing and aquaculture. Despite such a great popularity, there are still many unresolved questions about taxonomic validity, phylogenetic relationships and biogeography of many grayling species. The recent phylogenetic studies have resulted in molecular trees with very poor resolution. Therefore, the goal of the current study is to reconstruct the phylogeny of grayling species collected from the distant locations in Siberia and in Far Eastern regions of Russia, including the additional data from Genbank. We sequenced the whole mitochondrial genome for each individual and used the Bayesian approach to build the phylogenetic tree based on the alignment matrix with the best-fitted gene partitioning scheme. Our analysis shows that the monophyletic group with two species, *Thymallus grubii flavomaculatus* and *T. tugarinae*, from the Amur River basin represents the most ancient divergence, which occurred about 5 Ma. Its sister lineage progressively expanded from Ponto-Caspian basin and Europe. The latter monophyletic group also included the lineages of several species/subspecies collected in the Amur River basin: *T. grubii*, *T. burejensis* and *T. baicalolenensis*, indicating that the common ancestor of all grayling species used in our study had lived in that watershed. Phylogeny of grayling fishes calibrated with the molecular clock approach provides us with a new knowledge about evolution and historical biogeography of freshwater fauna.

0882 Herp Ecology I, Pecos, Friday 14 July 2017

Jeffrey Seminoff[1], Lisa Komoroske[1], Peter Dutton[1], Miguel Donoso[2], Maike Heidemeyer[3], Gabriel Hoeffer[4], T. Todd Jones[5], Shaleyla Kelez[6], Garrett Lemons[7], Nelly de Paz[8], Juan Manuel Rodriguez Baron[9], Laura Sampson[10], Lucia Santos Baca[11], Joel Schumacher[1], Maria Vejar Rubio[12], Patricia Zarate[13], Alan Zavala[12], Brian Popp[14]

[1]NOAA-National Marine Fisheries Service, Southwest Fisheries Science Center, La Jolla, CA, USA, [2]Proyecto Laúd, Quilpué, Chile, [3]Asociación Programa Restauración de Tortuga Marinas, Tibás, San José, Costa Rica, [4]Comcáac community, Desemboque, Sonora, Mexico, [5]NOAA-National Marine Fisheries Service, Pacific Islands Fisheries Science Center, Honolulu, HI, USA, [6]Ecoceanica, Lima, Peru, [7]Department of Biology, San Diego State University, San Diego, CA, USA, [8]Areas Costeras y Recursos Marinos, Pisco, Peru, [9]Universidad Autonoma de Baja California Sur, La Paz, Baja California Sur, Mexico, [10]Department of Biology, Universidad del Valle, Cali, Colombia, [11]Department of Natural Resources, Centro de Investigaciónes Biologicas del Noroeste, La Paz, Baja California Sur, Mexico, [12]Istitutuo Politécnico Nacional, CIIDIR, Unidad Sinaloa, Guasave, Sinaloa, Mexico, [13]Instituto Fomento Pesquero, Valparaiso, Chile, [14]Department of Geology and Geophysics, University of Hawai'i at Manoa, Honolulu, HI, USA

Trophic Ecology of Green Sea Turtles Across the Eastern Pacific Ocean: Insights from Bulk Tissue and Compound Specific Stable Isotope Analysis

The trophic ecology of a species is among its most fundamental biological aspects. Patterns of resource use and niche width affect somatic growth and demography, and have important implications for species resilience and management. Green sea turtles (*Chelonia mydas*) are present throughout tropical to temperate marine habitats worldwide and historical paradigms suggest they are obligate herbivores in these areas with diets consisting of seagrasses and/or marine algae. In the eastern Pacific, stomach content data indicate that green turtles are opportunistic omnivores that may occupy multiple trophic levels; however, the spatial patterns of their resource use in this region are unclear. Here we use stable-carbon and -nitrogen isotope analysis of bulk epidermal tissue from 718 green turtles distributed among 16 foraging areas from the US to Chile to determine isotopic niche space. We also use compound-specific $\delta^{15}N$ analysis of amino acids of 21 turtles from seven of these sites to decipher the baseline influence on stable isotope values as well as to describe the trophic position of green turtles. Our findings support that green sea turtles are opportunistic omnivores whose diets adapt to local prey bases; our data also confirm that local isotope values are influenced by broad-scale nitrogen cycling patterns as well as local-scale anthropogenic impacts. To our knowledge, this is the largest database of stable isotope values ever assembled for a marine species. Our study underscores the value of individual and institutional collaboration across multiple countries and will hopefully provide an example for others to follow around the world.

0218 HL/SSAR/ASIH Symposium - The Science, Management, and Policy of Amphibian Conservation: Extending the Legacy of Ray Semlitsch, Glass Oaks, Saturday 15 July 2017

Raymond Semlitsch[1], Susan Walls[2], Jamie Barichivich[2], Katherine O'Donnell[2]

[1]*University of Missouri, Columbia, Missouri, USA,* [2]*US Geological Survey, Gainesville, Florida, USA*

A Comprehensive Multi-level Approach to Preventing Amphibian Extinction

A comprehensive view of population declines and their underlying causes is necessary to reverse species loss. Historically, in many cases, a narrow view may have allowed species declines to continue, virtually undetected, for long periods of time (perhaps even decades). We suggest that extinction debt is likely responsible for numerous (perhaps most) amphibian declines and that this perspective should be incorporated into the structure of amphibian research and management. Extinction debt, originally proposed to explain changes in species richness following environmental disturbance, may also refer to the proportion of populations of an individual species that is expected to eventually be lost due to habitat change. A conservation framework to address extinction debt focuses research on threats at the individual, population, and metapopulation levels. This approach will help enhance, restore, and protect specific processes and habitats at the proper scale by directing management to the most vulnerable level and stage of a species. We illustrate this approach using Flatwoods Salamanders, *Ambystoma cingulatum* and *Ambystoma bishopi*, which occurred historically throughout the Coastal Plain of the southeastern USA but have experienced a > 85% loss of populations in recent years. Reversal of these losses is possible only if conservation and recovery efforts encompass individual, population, and metapopulation levels. We illustrate our framework by outlining actions that could be taken at each of these levels to help guide conservation and management of amphibians with complex life cycles and provide options for how to prioritize conservation actions in the face of logistical and budgetary shortfalls.

0415 AES GRUBER AWARD I, Wedgewood, Thursday 13 July 2017

Emily Seubert[1], John Valentine[2], J. Marcus Drymon[1]

[1]*University of South Alabama, Mobile, AL, USA,* [2]*Dauphin Island Sea Lab, Dauphin Island, AL, USA*

Evaluating ecosystem resiliency through stable isotope analysis of common elasmobranchs across the northern Gulf of Mexico

Functional diversity and redundancy are important components of healthy ecosystems and can enhance ecosystem resiliency to environmental disasters. Predatory species often overlap trophic niches, thereby facilitating the ability of an ecosystem to rebound from a disturbance. Stable isotope analysis (SIA) is a non-invasive technique that can provide insight into the role of functional diversity within an ecosystem. To investigate the extent to which functional diversity of predatory species varies across the northern Gulf of Mexico, we applied SIA to tissues from common elasmobranch species in this region. Preliminary trials examined the 훿^{13}C and 훿^{15}N signatures of blood plasma and muscle of three common elasmobranchs from the Chandeleur Islands, Louisiana: Atlantic sharpnose shark (*Rhizoprionodon terraenovae*), blacktip shark (*Carcharhinus*

limbatus), and blacknose shark (*C. acronotus*). Across species, 훿^{15}N ranged from 13.74‰ to 15.54‰ in blood plasma and from 13.61‰ to 15.60‰ in muscle, indicating a high degree of predator functional diversity in the region. *R. terraenovae* blood plasma 훿^{15}N values were significantly higher than those values detected in the other shark species (mean ± SD, 15.10‰ ± 0.34‰), suggesting this species feeds at a higher trophic level, while *C. limbatus* and *C. acronotus* feed at similar trophic levels. With respect to carbon, a relatively narrow range of values was found (1.07‰ for blood plasma and 1.90‰ for muscle), suggesting these species occupy foodwebs with similar sources of primary production. These preliminary results indicate high predator functional diversity, as well as possible functional redundancy in this region, with further implications for ecosystem resiliency.

0784 Turtle Conservation, Sabine, Saturday 15 July 2017

H Bradley Shaffer[1], Jannet Vu[3], Phil Spinks[1], Robert Thomson[2]

[1]UCLA, Los Angeles, California, USA, [2]University of Hawaii, Honolulu, Hawaii, USA, [3]Stony Brook University, Stony Brook, New York, USA

The Turtle Tree of Life and how it Informs Global Conservation Priorities

During the past two decades, turtles have gone from the phylogenetically least well understood major vertebrate clade to one of, or perhaps the best resolved group. We present two phylogenetic analyses, each based on newly generated and analyzed molecular data, that provide novel views on the 220 million years of crown turtle diversity. A well resolved time tree for all families of chelonians based on a new 539-gene data set provides the backbone tree for chelonians—it is consistent with several other recent efforts, but provides a novel temporal view of living turtle diversity. A second, 15-gene analysis includes sampling for roughly 90% of the 330 species of the living turtles and tortoises, providing a comprehensive framework for species-level biogeography, diversification patterns, and conservation prioritization. We combine this species-level phylogeny with IUCN endangerment assessments to provide a first-ever map of global endangerment hotspots for turtles and tortoises that should help direct conservation efforts for the group.

0618 Herp Reproduction & Life History II, Pecos, Thursday 13 July 2017

Brian Shamblin[1], Mark Dodd[2], Michelle Pate[3], DuBose Griffin[3], Matthew Godfrey[4], Michael Coyne[5], Ruth Boettcher[6], Campbell Nairn[1]

[1]University of Georgia, Athens, Georgia, USA, [2]Georgia Department of Natural Resources, Brunswick, Georgia, USA, [3]South Carolina Department of Natural Resources, Charleston, South Carolina, USA, [4]North Carolina Wildlife Resources Commission, Beaufort, North Carolina, USA, [5]Seaturtle.org, Durham, North Carolina, USA, [6]Virginia Department of Game and Inland Fisheries, Machipongo, Virginia, USA

Nest Site Fidelity of Loggerhead Turtles Characterized Through Genetic Tagging

The scale of nest site fidelity (NSF) has important implications for population connectivity and the estimation of demographic parameters in marine turtle populations. We performed genetic tagging of the US loggerhead turtle Northern Recovery Unit through subpopulation-scale clutch sampling to make preliminary inferences about the scale of NSF. A single egg was sampled from each recorded loggerhead clutch from Georgia through Maryland and assigned to an individual female via microsatellite genotyping. We analyzed 10,152 intra-seasonal nesting records representing 6,650 females nesting in 2010 – 2015. Geographic variation in NSF was apparent across the study area and was temporally stable across the six years examined. Females nesting in the vicinity of the Cape Romain National Wildlife Refuge exhibited the highest NSF detected, whereas females nesting in the immediately adjacent Grand Strand and proximal North Carolina coast had the lowest NSF. This pattern suggests that coastal geomorphology and/or freshwater outflows may provide important nesting beach selection cues or affect recruitment patterns that shape NSF behavior. From 2011 through 2015, we detected 3,493 individual females during 3,912 remigrations. The mean displacement in median nesting latitude between years was 11.2 (10.2 – 12.2) km of latitude, suggesting relatively high fidelity. These preliminary results suggest limited connectivity across rookeries such that local sources of mortality near the nesting beach may have significant consequences for the resident nesting population. Analyses of related females' nesting ranges will provide an indirect assessment of the scale of natal site fidelity required for a more complete picture of population connectivity.

0279 AES Symposium: Applications of Physiological Ecology in Elasmobranch Research, Wedgewood, Saturday 15 July 2017

Ashley Shaw[1], Doug Adams[2], Amanda Barker[3], Chris Bedore[4], Jim Gelsleichter[5], David Portnoy[3], Eric Reyier[6], Bryan Frazier[1]

[1]South Carolina Department of Natural Resources, Charleston, SC, USA, [2]Florida Fish & Wildlife Conservation Commission, Fish & Wildlife Research Institute, Melbourne, FL, USA, [3]Texas A&M University-Corpus Christi, Corpus Christi, TX, USA, [4]Georgia Southern University, Statesboro, GA, USA, [5]University of North Florida, Jacksonville, FL, USA, [6]Kennedy Space Center Ecological Program, Cape Canaveral, FL, USA

Trophic ecology and condition of sympatric hammerhead species in nursery habitats in the Southeast U.S.

The Scalloped Hammerhead, *Sphyrna lewini*, and recently described Carolina Hammerhead, *Sphyrna gilberti*, are thought to be sympatric in estuarine and nearshore nursery habitats along the southeastern U.S. coast. Despite this coastal occurrence, little is known about the trophic ecology of these two morphologically indistinguishable species. We will examine the trophic ecology and condition factor of these two genetically identified hammerhead species in nursery habitats in estuaries and near coastal waters, using stomach content analysis and stable isotope analysis of four tissues. Analyses compare the trophic ecology of the two hammerhead species, and suggest regional differences in diet and trophic niche. In addition, the trophic ecology and condition factor of the hammerheads are compared across different nursery habitats.

0601 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Josh Sherwood, Jeff Stein

Illinois Natural History Survey, Champaign, IL, USA

Habitat and fish community changes in Champaign County, IL over the past 100 years

With data spanning over 100 years, the Fishes of Champaign County is a comprehensive, long-term investigation into the changing fish communities of east-central Illinois. The same 120 sites across the county have been sampled four times since 1928, which are compiled with data from an additional 40 sites sampled in the 1890's. Data from the surveys have produced a unique perspective into not only the fish communities of the region but changes to instream habitat. After a period of degradation, fish communities appear to be improving throughout the county, demonstrated by the return of two state-threatened species that had not been recorded since 1928. Our analysis of in-stream habitat indicates a general trend away from small streams of various substrate types towards wider, deeper streams with a more uniform substrate. Fish community data support the results, indicating a shift from typical headwater species to species that frequent streams with more stable flows and deeper streams. Long-term surveys such as this are rare and the data and analyses of these surveys can provide managers with valuable information to further restoration efforts using a historical prospective.

0542 AES GRUBER AWARD I, Wedgewood, Thursday 13 July 2017

Chelsea Shields[1], Jim Gelsleichter[1], Bryan Frazier[2]

[1]University of North Florida, Jacksonville, Florida, USA, [2]South Carolina Department of Natural Resources, South Carolina, USA

Reproduction of the tiger shark (*Galeocerdo cuvier*) off of South Carolina

Top ocean predators, such as large sharks, have shown trends of substantial population decline over the last few decades. Due to this, it is important to understand the life history of the species to determine if the population must be managed. This study examines the reproduction of tiger sharks off South Carolina using non-lethal methods, including ultrasonography and measuring hormone levels to understand the reproductive seasonality of the species. Blood samples and biological measurements

were collected from 55 animals along the southeast U.S. coast and ultrasonography was performed on mature females when possible. Female plasma estradiol concentrations showed an increased range of concentrations at size-at-maturity (310 cm TL). This likely indicates the hormonal differences between gravid and non-gravid animals. When estradiol level was compared to month in mature animals, certain (presumed non-gravid) animals showed significant levels of estradiol (above 600pg/ml) between June and October, while others (presumed gravid) maintained lower levels of estradiol through the summer. This shows that some of the animals are carrying offspring and some are not, indicating that the reproductive cycle of this species is at least biennial, if not triennial. Mating wounds were observed on several mature female tiger sharks in October and November, showing that mating is occurring. We found no clear pattern between levels of progesterone in females and size or reproductive stage. Not enough male tiger sharks have been sampled to date to form conclusions on changes in testosterone in males.

0026 AES Conservation & Management I, Pecos, Saturday 15 July 2017

David Shiffman

Simon Fraser University, Vancouver, BC, Canada

Trends in Elasmobranch Research 1985-2016: Methodolgies, Study Species, Conservation Framing, and Presenter Demographics

Here we present an analysis of how elasmobranch research has changed since the founding of the American Elasmobranch Society in 1985. Using abstracts from every past AES conference, we analyze trends in research methods used to study elasmobranchs, trends in the selection of study species, trends in the conservation framing of research projects, trends in presenter demographics, and more. We also include some predictions of where elasmobranch research may be heading.

0073 Herp Ecology I, Pecos, Friday 14 July 2017

Rick Shine[1], Claire Goiran[2], Paco Bustamante[3]

[1]University of Sydney, Sydney/NSW, Australia, [2]Université de la Nouvelle-Calédonie, Noumea, New Caledonia, [3]Université de La Rochelle, La Rochelle, France

Industrial melanism in a seasnake

The classic example of industrial melanism is the increase in black colouration among peppered moths during the industrial revolution in Europe, putatively driven by selection for camouflage against predators. We describe a similar correlation – melanism in anthropogenically disturbed habitats - in a very different taxon and location and infer a very different evolutionary mechanism. Most of the turtle-headed seasnakes (*Emydocephalus annulatus*) found in polluted bays beside the city of Noumea are jet-

black, whereas melanism is rare across the rest of the species' wide range except for an isolated reef in the Great Barrier Reef that is used as a bombing range. We identify a potential selective advantage to dark colouration in these polluted sites: melanin binds trace elements, which are voided when the snake sheds its skin. More broadly, industrial melanism in vertebrates may be driven by selective pressures very different from those experienced by the peppered moth in Europe.

0262 AES Ecology II, Glass Oaks, Sunday 16 July 2017

Oliver Shipley, Jill Olin, Michael Frisk

School of Marine and Atmospheric Sciences, Stony Brook University, Stony Brook, NY, USA

Environmental and biological drivers of intra- and inter-specific resource use among sympatric skates in the northwest Atlantic

Resource use and competition between marine predators support ecosystem structure and function and have large implications for resilience and diversity of global ecosystems. Understanding the environmental and biological divers of food-web structure can help inform management and conservation of marine predator species. Skates (order *Rajiformes*) are important mesopredators in benthic ecosystems worldwide, which provide important energetic linkages between lower trophic consumers and apex predators. In the last 60 years, skate populations have faced arguably the most considerable population declines of all elasmobranch species, and many are now listed as endangered, or critically endangered by the IUCN. Further life history and wider biological data is therefore required to inform management and conservation of these species. Here we used stable isotope analysis of carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) to understand the environmental (e.g. temperature, depth, latitude) and biological (e.g. age, sex, and size) drivers influencing the intra- and interspecific resource use of seven common skate species in the northwestern Atlantic. We present isotope data for winter (*Leucoraja ocellata,n* = 60), thorny (*Amblyraja radiate*, *n* = 48), little (*Leucoraja erinacea*, *n* = 78), smooth (*Malacoraja senta*, *n* = 4), rosette (*Leucoraja garmani*, *n* = 5), and barndoor (*Dipturus laevis*, *n* = 15) skates, collected from National Marine Fisheries Service's (NMFS) trawl surveys between 2001 and 2002. Although historic, these data provide insight into competition and niche width of sympatric skate species and provide a comparable baseline from which to generate present day community comparisons.

0027 Lightning Talks II, Glass Oaks, Friday 14 July 2017

Dustin Siegel[1], David Sever[2], Stanley Trauth[3]

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

The lack of nasolacrimal ducts in plethodontid salamanders

The nasolacrimal ducts drain excess products from tear production into the nasal cavity. The mass majority of terrestrial vertebrates possess nasolacrimal ducts. Recent studies concluded that nasolacrimal ducts were absent in plethodontid salamanders, but not from salamanders of every other family examined (Ambystomatidae and Salamandridae); however, only plethodontids from Plethodontinae and Spelerpinae have been examined. In the current study, we used histological preparations to survey nasolacrimal duct presence/absence from multiple representatives from all subfamilies of plethodontid salamanders (Bolitoglossinae, Hemidactyliinae, Plethodontinae, and Spelerpinae); thus, we tested the hypothesis that plethodontid salamanders lack a nasolacrimal duct.

0113 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Greg Sievert

Emporia State University, Emporia, Kansas, USA

Efficacy of Different Artificial Cover Objects in Reptile Surveys - A Long Term Study

Herpetologists commonly use cover objects in their surveys of terrestrial reptiles. It is widely assumed that the material used to create a cover object is relatively unimportant in study design; however, few studies have been conducted to validate this assumption. Differences in the numbers and types of reptiles attracted to different cover object materials have the potential to bias herpetological studies. I used arrays of cover objects to test for preferences between wood, tin, or tar paper cover objects by terrestrial reptiles. By monitoring these cover objects over five years and comparing captures of lizards and snakes to temperature data, I determined that reptiles collectively prefer tin cover object in early spring, but shift most usage to wooden cover objects in the summer. These shifts in cover object preference seem to be linked to thermoregulatory needs of the individual reptiles. Results of this study will assist herpetologists in choosing the cover object type best suited to their research objectives.

0069 ASIH STOYE GENERAL ICHTHYOLOGY III, Trinity, Friday 14 July 2017

Randy Singer[1], Jon Moore[2]

[1]Florida Museum of Natural History/iDigBio, Gainesville, FL, USA, [2]Florida Atlantic University, Boca Raton, FL, USA

Finding Dories: Variation in *Parazen pacificus* (Zeiformes: Parazenidae: Parazen) with the discovery of an undocumented reproductive strategy in a deep sea fish

Parazen pacificus (Parazenidae) is a monotypic genus of zeiform fish inhabiting bathydemersal (145-500 m depth) habitats along the continental slope of the Western Central Indo-Pacific and Atlantic Oceans. Despite high sampling of suitable habitat between its known ranges, no specimens have been collected from localities in the Eastern or Central Atlantic and Eastern Pacific Oceans. This highly disjunctive distribution raised suspicion that *Parazen pacificus* is not one, but two or more species. To explore this possibility, we compared morphological characters in Atlantic populations of *Parazen pacficius* to those from the Pacific Ocean. Morphological data support at minimum one undescribed species from the Caribbean Sea. During the course of specimen examination a reproductive strategy unique to Zeiformes was discovered. In addition, this trait is the first ever of its type found in a deep-sea fish. Until recently, the reproductive ecology of *Parazen pacificus*, like most species of Zeiformes, has remained largely understudied. It is difficult to observe reproductive behavior of deep sea fishes *in situ*, but most species have been assumed to be broadcast spawners. This discovery raises more questions as to the reproductive strategies across Zeiformes, as well as in other fish taxa and warrants further exploration. In addition, high resolution video from the Caribbean Sea via the NOAA Okeanos Explorer Océano Profundo Expedition has shed light on the feeding and swimming behavior of live *Parazen in situ*.

0728 HL GRADUATE RESEARCH AWARD, Pecos, Friday 14 July 2017

Shashwat Sirsi[1], Andrew R. MacLaren[1], Daniel H. Foley III[2], Michael R.J. Forstner[1]

[1]Texas State University, San Marcos, Texas, USA, [2]Sul Ross State University, Del Rio, Texas, USA

Comparing movement patterns and consequent management implications derived from Capture-Mark-Recapture, Telemetry, and Genetic Frameworks for the Rio Grande Cooter (*Pseudemys gorzugi*)

Freshwater turtles are among the most threatened vertebrates with ca. 42% threatened by unsustainable harvests and habitat loss. Gaining knowledge on the life-history of such threatened species is critical to enabling their management for conservation. Rio Grande Cooters (*Pseudemys gorzugi*) are a narrowly distributed and poorly-documented freshwater turtle species, restricted to the Rio Grande River and its tributaries. Habitat loss via modification to in-stream flow rates of these river systems represent a core threat to these turtles. Understanding movement patterns in such modified landscapes is important to determining population connectivity and spatial scale of management approaches. We compare the utility of three commonly used methods, Capture-Mark-Recapture (CMR), telemetry, and population genetics, in the assessment of movement rates. A raw examination of recapture locations from multi-year (2011 and 2014-2016) CMR data showed that individuals were sedentary. However, a POPAN formulation that generated a superpopulation estimate of 1019 + 241 individuals also estimated considerable probabilities (ca. 20-40%) of new entrants to the population at discrete occasions. This discrepancy provided the impetus to estimate movement in a subset of our population using telemetry. VHF transmitters coupled with GPS-enabled data loggers have revealed novel movement data with net movements of up to ca. 36 km. Movement data from telemetry is more comparable to previously completed genetic analyses which suggest the population is homogenous, with range-wide population connectivity maintained by occasional long-range movements. Each of these methods determine varying levels of connectivity and demonstrate a need for caution in management implementations from any single approach.

0454 HL/SSAR/ASIH Symposium - The Science, Management, and Policy of Amphibian Conservation: Extending the Legacy of Ray Semlitsch, Glass Oaks, Saturday 15 July 2017

David Skelly

Yale University, New Haven, CT, USA

Evolution in the Shade: the Microgeography of Thermal Adaptation in the Wood Frog

Understanding the distribution of species confronted with environmental heterogeneity is a fundamental goal of ecologists. The role of rapid-fine scale evolution as a driver for distributional patterns is poorly known. The wood frog (*Rana sylvatica*) exhibits wide tolerance of canopy conditions within the breeding ponds it selects. Overtopping by canopy imposes profound changes in conditions within small ponds including the thermal environment. Common garden experiments reveal that traits including critical thermal maximum, thermal preference behavior, and development rate vary with canopy. Open and closed canopy ponds are often in close proximity suggesting that divergence among breeding aggregations can occur at scales easily traversed by dispersing adults. Because canopy can change on decadal time scales, our evidence suggests that trait evolution can occur rapidly at microgeographic scales. While typical models of gene flow imply that even modest levels of dispersal between ponds differing in canopy should prevent divergence in traits, we see repeated evidence that such distinctions emerge and are maintained. The wood frog system suggests a powerful ecological role for localized adaptation. Because canopy surrounding wetlands is under active or passive management by humans, our findings illustrate unintended evolutionary consequences of environmental policies intended to conserve wildlife species.

0172 Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017; AES CARRIER AWARD

Rachel Skubel[1], Neil Hammerschlag[1], Yannis Papastamatiou[2], Jodie Rummer[3]

[1]University of Miami, Florida, USA, [2]Florida International University, Florida, USA, [3]James Cooke University, Queensland, Australia

From biochemistry to biotelemetry: An integrative framework for indicators of elasmobranch response to climate change

Elasmobranchs are a group of animals which have been subjected to major stressors including overfishing and habitat degradation, and now face the consequences of rising human carbon dioxide emissions – increased temperature and acidity, and decreased oxygen content in the oceans. Here, we systematically review the literature to assess characteristics of climate change vulnerability/resilience across (1) behavior, (2) hematology, (3) morphology, (4) cardiac and circulatory systems, (5) respiratory strategy and metabolism, (6) locomotion strategy, and (7) the nervous system. Environmental factors (biotic and abiotic habitat variability, prey, and human disturbance) are also explored with respect to their contributions to elasmobranch vulnerability and resilience to climatic change. An integrative framework to consider elasmobranch response to climate change is proposed, to contribute to the development of indicators for wide scale climate change risk assessments. We provide an overview of the state-of knowledge for the field of climate change responses of elasmobranchs, identify information gaps, and propose an integrative framework to consider elasmobranch response to climate change, to contribute to the development of indicators for wide scale climate change risk assessments.

0529 Snake Biology I, Brazos, Sunday 16 July 2017

Cara Smith, Stephen Mackessy

University of Northern Colorado, Greeley, CO, USA

The Effects of Hybridization on Divergent Venom Phenotypes: Characterization of Venom from *Crotalus scutulatus scutulatus* × *C. oreganus helleri* Hybrids

Hybridization between divergent species can be analyzed to elucidate expression patterns of parental characteristics, as well as to provide information about the extent of reproductive isolation between species. A known hybrid cross between two rattlesnakes with highly divergent venom phenotypes provided the opportunity to examine occurrence of parental venom characteristics in the F1 hybrids, as well as ontogenetic shifts in the expression of these characters as the hybrids aged. The current study investigates both phenomena resulting from the hybridization of a male snake with type I degradative venom, *Crotalus oreganus helleri* (Southern Pacific Rattlesnake), and a female snake with type II neurotoxic venom, *C. scutulatus scutulatus* (Mojave Rattlesnake). SDS-PAGE, enzymology, Western blot and reversed phase HPLC (RP-HPLC) were used to characterize the venom of the *C. o. helleri* male, the *C. s. scutulatus* female and their two hybrid offspring as they aged. In general, *Crotalus o. helleri* × *C. s. scutulatus* hybrid venoms appeared to exhibit overlapping parental venom profiles, and several different enzyme activity patterns. The *C. s. scutulatus* × *C. o. helleri* hybrid male's venom profile provided the strongest evidence that type I and type II venom characteristics are expressed simultaneously in hybrid venoms, as this snake contained distinctive characteristics of both parental species. Ultimately, the chronological analysis of this known hybrid system reveals the most distinct characteristics that can be used in determining successful hybridization between snakes that follow the type I-type II trend in rattlesnake venom composition, namely the presence of metalloprotease activity and Mojave toxin.

0122 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Jaime E Smith[2], Joseph H.K. Pechmann[1], John Tupy[3]

[1]Western Carolina University, Cullowhee, NC, USA, [2]University of Southern Mississippi, Ocean Springs, MS, USA, [3]US Fish and Wildlife, Vero Beach, FL, USA

Effects of Litter Type and Algal Wafers on the Growth and Survival of Dusky Gopher Frog (*Rana sevosa*) Tadpoles

Growth and survival of *Rana sevosa* tadpoles is higher in open canopy than in closed canopy ponds. Litter substrates, which are dominated by herbaceous plant material in open canopy ponds and by pine and hardwood leaves in closed canopy ponds, may contribute to these differences. Supplemental food such as algae wafers may ameliorate any effects of substrate. We tested the effects of different combinations of the litters maidencane (*Panicum hemitomon*), juncus (*Juncus repens*), and leaves (*Pinus palustris, Liquidambar styraciflua*), both with and without weekly algae wafer additions, on *R. sevosa* tadpoles in outdoor tanks. Algae addition increased survival by 19%, decreased mean larval period by 25 days, increased metamorph mean snout-vent length (SVL) by 8 mm, and more than doubled metamorph mean mass. Without algae, survival averaged 53% lower for leaves alone, but with algae, survival averaged 43% lower for juncus alone, compared to other litters or litter combinations. Without algae, larval period averaged 8-23 days shorter for juncus and for juncus plus maidencane than for other litter treatments. With algae, substrate had no significant effect on larval period. Mass and SVL at metamorphosis were highest for juncus, lowest for leaves and leaves plus juncus, and intermediate for maidencane alone or combined with other substrates. *Rana sevosa* tadpoles did best overall with juncus plus maidencane and poorest overall with leaf litter and without algae addition. Use of substrates from open canopy ponds and algae wafers can improve growth and survival of *R. sevosa* tadpoles raised for translocation and population supplementation.

0189 AES GRUBER AWARD III, Wedgewood, Friday 14 July 2017

Kelcee Smith[1], Michael Kaller[1], John Carlson[2], Dana Bethea[3], Kevin Feldheim[4], William Kelso[1], Sabrina Taylor[1]

[1]Louisiana State University, Baton Rouge, LA, USA, [2]NOAA Fisheries Service - Southeast Fisheries Science Center, Panama City, FL, USA, [3]NOAA Fisheries Service -

Southeast Regional Office, St. Petersburg, FL, USA, [4]Field Museum of Natural History, Chicago, IL, USA

Combining capture and genetic data to estimate population size of juvenile endangered Smalltooth Sawfish (*Pristis pectinata*)

A fundamental parameter in mathematical models that underpin ecological, conservation, and evolutionary theory is population size. It can be estimated as census size (N_C), i.e. the number of individuals in a population, or effective population size (N_E), which only counts individuals contributing genes to future generations. Estimating both N_C and N_E allows for a better understanding of potential demographic, environmental, and genetic risks that populations face. However, both methods are rarely used together to examine components of population size. Here, we compare N_C and N_E estimates for the juvenile segment of endangered Smalltooth Sawfish, *Pristis pectinata,* population in Southwestern Florida, U.S. Capture-mark-recapture data (2000-2015) were analyzed in program MARK to estimate N_C with recapture probabilities and apparent survival from individual capture histories, assuming a closed population. Models with time dependent capture probability and constant recapture probability estimated an N_C of 261 (SE: $4.01X10^{-5}$) and 124 (SE: $2.69X10^{-5}$) individuals during the spring/summer and fall/winter seasons, respectively. This yields an annual N_C of 385 juveniles per year in this population. To estimate N_E, tissue samples (n = 375) taken from captured individuals were genotyped at 17 microsatellite loci. Estimates of N_E included temporal, linkage disequilibrium, and sibship methods. Overall, N_C can be compared to N_E to determine effects of harvest, environmental change, or species fitness. Monitoring imperiled species in this way can facilitate recovery by revealing specific issues not evident in estimates of N_C alone.

0626 Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Leo Smith[1], Chesney Buck[1], Sarah Gibson[1], Matthew Davis[2], Rene Martin[2], Matthew Girard[1]

[1]University of Kansas, Lawrence, KS, USA, [2]St. Cloud State University, St. Cloud, MN, USA

Techniques for the Improved Visualization of Vertebrate Anatomy

Following the recent discovery of fluorescence in living fishes, turtles, and amphibians, our laboratories procured the necessary equipment to explore the visual displays of these animals. Once the equipment was in the laboratory, it became clear that it had value that extended to the visualization of extant and fossil vertebrate anatomy. Previous work had highlighted the use of fluorescence in fossil vertebrates and of alizarin red autofluorescence in developmental studies of the Zebrafish. Herein, we highlight and expand on the value of alizarin red autofluorescence in comparative vertebrate anatomy. Further, we demonstrate the use of green autofluorescence with formalin-fixed soft tissues and fossilized vertebrate skeletons. Finally, we report on the use of a glycerine-gelatin matrix that allows for the temporary positioning of cleared-

and-stained vertebrates for imaging anatomical features in poses that are not possible in standard glycerine preparations. Although fluorescence microscopes can be expensive, we highlight less expensive setups that allow nearly any anatomical laboratory to take advantage of these techniques.

0753 ASIH STORER ICHTHYOLOGY; Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Shelby Smith, Devin D. Bloom

Western Michigan University, Kalamazoo, MI, USA

Evolutionary Ecology of Great Lakes alewives (*Alosa pseudoharengus*): a Population Genetic and Morphometric Analysis

Migratory animals have high dispersal ability and a propensity to colonize new areas. In some cases, migrators establish resident populations in new areas, which are subjected to rapid local adaptation. Native alewives, *Alosa pseudoharengus*, are primarily anadromous fishes occurring along the east coast of North America. Multiple native populations have also invaded inland lakes on the East Coast and become landlocked over hundreds to thousands of years. Alewives have been introduced in the Great Lakes, potentially via shipping canals or through accidental stocking. Studies comparing native landlocked populations of alewives to anadromous populations have revealed landlocked alewife populations restructured the size and composition of zooplankton communities, which subsequently drove alewife evolution. As a result, landlocked alewives have smaller gill raker spacing, gape widths, and body size compared to native anadromous populations. In this study, we used mtDNA sequencing to determine the origins of alewives in the Great Lakes and compared phenotypic traits of Great Lakes alewives with native anadromous and landlocked populations to determine the rate and patterns of morphological evolution. Our results show parallel evolution of gill raker spacing, gape width, and body size between Great Lakes and landlocked East Coast populations of alewives. We suggest that anadromy can facilitate colonization of novel geographic areas and result in rapid local adaptation.

0436 AES Ecology II, Glass Oaks, Sunday 16 July 2017

Matthew Smukall[1], Tristan Guttridge[1], Samuel Gruber[1]

[1]Bimini Biological Field Station Foundation, Bimini, Bahamas, [2]University of Alaska Fairbanks, Fairbanks, Alaska, USA

Seasonal and Ontogenetic Shifts in Movement and Trophic Position of Tiger Sharks *Galeocerdo cuvier* near Bimini, Bahamas

Tiger sharks *Galeocerdo cuvier* are presumed to fulfill important roles as apex predators across a wide range of tropical and temperate ecosystems. There has been documented

variation in their movements, habitat use, and diet, and these factors are likely affected by season, region, and ontogeny. Bimini, Bahamas provides an ideal location for assessing seasonal and ontogenetic shifts, as all age classes are abundant throughout the year. Changes in seasonal abundance, sex ratios, and size distributions were assessed with fishery-independent longline surveys. Vemco™ V16 acoustic tags were implanted in juvenile (n = 22, mean total length 118cm) and mature (n = 14, mean total length 332cm) sharks. Habitat usage, residency, and returns were monitored with 62 VR2W receivers stationed around Bimini. Long-range movement data was provided from detections on cooperative data sharing arrays and tag reporting through the National Marine Fisheries Service cooperative shark tagging program. Stable isotope analysis ($\delta^{13}C$, $\delta^{15}N$) of fin, muscle, and blood plasma samples were used to assess seasonal and ontogenetic shifts in trophic position. It is predicted movement of tiger sharks will predominately be driven by age and season. Trophic position is predicted to increase dramatically at early ages with noticeable short-term seasonal shifts. This information will provide a better understanding of the correlation between movement and trophic position for tiger sharks in this ecosystem.

0757 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Darrel E. Snyder, C. Lynn Bjork

Colorado State University Larval Fish Laboratory, Fort Collins, Colorado, USA

Larvae and Early Juveniles of Rio Grande Chub and Rio Grande Sucker

The Rio Grande Chub *Gila pandora* (RGC) and Rio Grande Sucker *Catostomus plebeius* (RGS) are medium-size fish (< 20-26 cm) native to the Rio Grande Basin (CO, NM, TX, and Mexico) and some adjacent closed basins. Both are now restricted mostly to tributary and headwater streams (and a few lakes for RGC). In Colorado, RGC is a species of special concern and RGS is endangered; in New Mexico, both are species of greatest conservation need; and in Texas, RGC are threatened. Reproductively, both are non-guarding, open-substrate lithophils, typically spawning over gravel or sand in spring or early summer. Eggs are demersal and adhesive with diameters of about 2.3-2.6 mm for RGC or (2.4-) 2.8-3.2 mm for RGS. RGC hatch as protolarvae at about 7 mm SL, complete yolk absorption at 8-9 mm, become metalarvae (have both the adult complement of principal median fin rays and pelvic-fin buds) at 11-12 mm, and become juveniles at 18-19 mm SL. Corresponding sizes for RGS are 7-9, 10-11, 15-17, and 23-25 mm SL. Recently hatched RGC have dark eyes and considerable dorsal body pigmentation, whereas recently hatched RGS have lighter eyes and no body pigmentation. Snout-to-vent (preanal) length is 66-73% SL for RGC larvae and 74-83% SL for RGS. Myomere counts to the posterior margin of the vent (preanal), after (postanal), and total are 27-31 + 11-15 = 41-44 for RGC and 31-37 + 7-11 = 41-45 for RGS.

0109 LFC Multi-Stressor Effects, San Marcos, Friday 14 July 2017

Jacob Snyder, Christopher Murray, Hannes Baumann

University of Connecticut, Avery Point, Groton, CT, USA

Maternal effects on offspring CO_2 sensitivity in a coastal marine fish

Many marine fish employ maternal provisioning as a strategy to better prepare offspring for changing environmental conditions. Whether maternal provisioning influences the sensitivity of fish early life stages to elevated CO2 conditions has yet to be determined. We reared offspring batches derived from five female Atlantic silversides (*Menidia menidia*) under contrasting CO2 conditions from fertilization to 16 days post hatch and quantified six response traits, including growth and survival. For most traits, we found strongly divergent responses (expressed as log-transformed response ratios, lnRR) between batches, and subsequently used fatty acid (FA) profiles of the unfertilized eggs to test for associations with the observed lnRRs. Multiple FAs were positively correlated (20:1n9, 22:5n3, 15:0) with survival lnRR's while others were negatively correlated (18:3n3, 18:4n3, 22:6n3) with length lnRR's. Maternal investment has been shown to be highly important to offspring survival, and this study shows that variable egg provisioning by mothers with certain FAs may influence offspring sensitivity to high CO2 environments. Our study also suggested that ocean acidification experiments on fish early life stages need to be based on a large number of spawners in order to avoid biases due to resulting from individual maternal effects.

0709 SSAR SEIBERT ECOLOGY II, Glass Oaks, Thursday 13 July 2017

Shawn Snyder[1], William Sutton[1], Christopher Howey[2]

[1]Tennessee State University, Nashville, TN, USA, [2]The Pennsylvania State University, University Park, PA, USA

Differentiation in Basking Habitat between Yellow and Black Morph Timber Rattlesnakes

Timber rattlesnakes (*Crotalus horridus*) have two distinct morphotypes across their range: a black morph and a yellow morph. If both morphs prefer to maintain similar preferred body temperatures, then black morphs may have a thermal advantage due to their increased melanin. If this is the case, then do yellow morphs use basking habitat that is more open? During 2016, we measured the preferred body temperature of snakes in the lab. We also radio-located 12 *C. horridus* (4 yellow morphs, 8 black morphs) between 6 June - 20 July in central Pennsylvania. Canopy closure was measured over top of basking rattlesnakes with a spherical densiometer and hemispherical photography. Further, we were able to measure the total incident solar radiation that reached each basking location based on hemispherical photographs within Gap Light Analyzer software. There was no difference in canopy closure between morphotypes or sex using either canopy measures. However, total incident solar radiation that each snake received did differ between morphotypes. These results suggest that although canopy openness does not differ between morph basking habitats, yellow morphs use sites that have more

open canopy that overlaps with the path of the sun; thus, permitting more incident solar radiation. We will discuss preferred body temperatures of snakes in the lab and field-active body temperatures of snakes. Further, these results suggest that yellow morph rattlesnakes might be able to behaviorally adapt to live in the colder northern part of their range by altering their habitat use.

0047 Fish Systematics, Trinity, Saturday 15 July 2017

Young Sun Song, Jin-Koo Kim

Pukyong National University, Busan, Republic of Korea

Cryptic Diversity of Hagfishes (Family Myxinidae) collected from Korea, Japan, Vietnam and Argentina

There are currently six recognized genera and 81 recognized species of hagfishes (Family Myxinidae). Most hagfish taxa have been described based on morphological data. Although hagfish have relatively simple bodies, providing limited morphological information, this is often sufficient to differentiate between hagfish species. In recent years, many new species have been reported and new classifications have been established using a molecular perspective to review phylogenetic relationships. However, it is difficult to clarify the relationships between hagfish genera because of their similar morphology and the comparative paucity of specimens. Hagfishes were recently collected from several countries (Korea, Japan, Vietnam and Argentina) and we analyzed their morphology and genetics (mtDNA COI and cytb sequences). Molecular results showed the existence of at least four cryptic species with distinct phylogenetic positions. *Eptatretus* sp. A from Korea, *Eptatretus* sp. B from Japan, *Eptatretus* sp. C from Vietnam, and *Notomyxine* sp. from Argentina were similar to *Eptatretus burgeri* (d=0.083), *Eptatretus okinoseanus* (d=0.026~0.031), *Eptatretus fernholmi* (d=0.052), and *Notomyxine tridentiger* (d=0.068~0.071), respectively. These four cryptic species were significantly distinct from other congeneric species based on morphological characteristics such as total cusps, slime pores, etc. Therefore, we suggest here the existence of four cryptic species of hagfishes, and further discuss their evolutionary history.

0365 Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017; AES CARRIER AWARD

Kelsey Spencer[1], Daniel Abel[1], Derek Crane[1], Neil Hammerschlag[2], Erin Burge[1], Caroline Collatos[1], Matt Larsen[1]

[1]Coastal Carolina University, Conway, SC, USA, [2]University of Miami, Miami, FL, USA

Coastal Shark Movements near Fishing Piers along the NE Coast of South Carolina: Early Results

Perceived increases in shark attacks/bites in the summer of 2015 focused attention on shark movements along beaches of the region and, more specifically, around fishing piers. Knowledge of shark movements around fishing piers has been strictly anecdotal. We implanted acoustic telemeters in pier-associated sharks to answer questions regarding the site fidelity of sharks to fishing piers in Northeastern South Carolina. Vemco V9-69 kHz transmitters were surgically implanted in 12 sharks [Blacktip (*Carcharhinus limbatus*, n = 4), Finetooth (*Carcharhinus isodon*, n = 2), Blacknose (*Carcharhinus acronotus*, n = 4), Tiger (*Galeocerdo cuvier*, n = 1), and Sandbar (*Carcharhinus plumbeus*, n = 1)] from July 14th through November 3rd, 2016. Three piers and two nearshore locations recorded 5,589 detections from July 25th, 2016 to January 5th, 2017. Three heterospecific individuals (Finetooth, Blacknose, and Blacktip), encompassed 96.3% of all detections. Site fidelity indices (number of days detected at piers / number of days detected) for the heterospecific individuals were 0.265, 0.025, and 0.463, respectively, indicating minimal site fidelity. A general linear model (GLM) revealed detection events (two detections within a 30-minute period) varied significantly ($p = 0.018$) with the interaction between bi-weekly catch per unit effort (CPUE) of potential prey caught on the piers and moon phase. Modeling results using standard selection criteria (BIC) indicated diel cycle, prey CPUE, and lunar percent illumination together best explained variation in presence/absence at piers. Results from the models demonstrate that the presence of sharks is dependent upon prey, which respond to moon phase among other factors.

0277 ASIH STOYE PHYSIOLOGY & PHYSIOLOGICAL ECOLOGY II, San Antonio, Thursday 13 July 2017

McKayla Spencer, C. M. Gienger

Austin Peay State University, Clarksville, TN, USA

Comparative Energetics and Responses to Feeding of Copperhead and Cottonmouth Snakes (*Agkistrodon*)

The breakdown of food and absorption of nutrients after feeding can be energetically costly for animals. Differences in response to feeding have been attributed to many factors such as temperature, foraging mode, and body shape. Habitat ecology has been less explored and differences in ecological attributes could lead to differences in important behaviors and physiological ecological interactions. We chose to compare post-feeding responses between two similar species with differing use of habitat; copperheads (*Agkistrodon contortrix*; a terrestrial species) and cottonmouths (*Agkistrodon piscivorus*; a semi-aquatic species). To make these comparisons we measured pre- and post-feeding metabolic rates (at 20, 25, and 30°C) and body temperature (T_b) selection by digesting snakes. Following the consumption of rodent meals, specific dynamic action (SDA) was affected by temperature but did not differ between species. Post-feeding, *A. contortrix* did not change their thermal behavior but *A. piscivorus* selected 5-6°C warmer temperatures. After feeding, *A. contortrix* had a longer duration of elevated metabolic rate at 25°C than at 30°C and selected a post-feeding temperature of 26°C. *A. piscivorus* had a longer duration of elevated metabolism following feeding at 30°C than at 25°C and selected a post-feeding temperature of 29°C. Overall, both species selected post-feeding temperatures that appear to physiologically result in a longer duration of elevated metabolic rate which may maximize net energy intake of a meal. The differences in the selected post-feeding temperatures between the species that results in physiological response differences is most likely a factor related to their differing use of habitat.

0676 ASIH STORER ICHTHYOLOGY; Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Zachary Sperstad[1], Peter Berendzen[1], Andrew Simons[2], Jonathan Armbruster[3], Emily Lemmon[4], Alan Lemmon[4]

[1]*The University of Northern Iowa, Cedar Falls, Iowa, USA,* [2]*The University of Minnesota, St. Paul, Minnesota, USA,* [3]*Auburn University, Auburn, Alabama, USA,* [4]*Florida State University, Tallahassee, Florida, USA*

Phylogenomics of Catostomidae

Catostomidae is a freshwater fish family within Cypriniformes, restricted to North America and Asia. This group contains about 78 species, which are hypothesized to have evolved from a single tetraploid ancestor. Phylogenetic reconstruction of the relationships within this family have been burdened by tetraploidy, therefore molecular systematics of this group have been largely restricted to mitochondrial gene regions. These studies have resulted in several conflicting hypotheses of the relationships among catostomids. The objective of this study is to generate a molecular hypothesis of the relationships within this group using a genomics approach with consideration of tetraploidy. An ultraconserved element dataset was generated using anchored hybrid enrichment. This dataset contains 179 loci, totaling 277,092 base pairs, for 43 catostomids and 11 outgroup species. All loci for the catostomids were phased for four alleles to account for tetraploidy. Phylogenies were reconstructed using species tree and maximum likelihood methods. To estimate the relative age of nodes, time-calibrated phylogenies were generated using fossil calibration. Preliminary results will be presented.

0321 Amphibian Behavior, Pecos, Friday 14 July 2017

Laura Springer[1], Cory Adams[2], Toby Hibbitts[3], Matt Kwiatkowski[1], Dan Saenz[2]

[1]*Stephen F. Austin State University, Nacogdoches, Texas, USA,* [2]*Wildlife Habitat and Silviculture Laboratory, Southern Research Station, USDA Forest Service, Nacogdoches, Texas, USA,* [3]*Texas A&M University, College Station, Texas, USA*

Home Range and Activity Patterns in the Southern Crawfish Frog

The crawfish frog, *Rana areolata*, has suffered declines across much of its range, primarily due to habitat loss, and is a candidate for protection in five of the states where it occurs. This species is a prairie specialist and prairies are one of the most rapidly disappearing landscapes in North America. Prairies in Texas have suffered a decline of 90%, with most of the loss occurring on the coastal prairie. In the northern part of their range, crawfish frogs are known to utilize crayfish burrows for shelter most of the year, but leave their burrow during the breeding season to travel to breeding ponds. We investigated movement patterns and burrow use of the crawfish frog in the southern part of their range where little is known about their biology. We tracked 24 crawfish frogs at the Attwater Prairie Chicken National Wildlife Refuge in southeast Texas from March 2015 to May 2016. We tracked 11 frogs back to burrows from their breeding ponds. Frogs traveled between 63 to 624 meters back to a burrow, for an average 315 meters. To monitor activity patterns of frogs at the burrows, we placed game cameras on five burrows. Frogs spent 75% of their time aboveground at the entrance of the burrow (69% of nocturnal activity, 81% of diurnal activity). These data suggest access to crayfish burrows in prairie habitat is key to the conservation of this species in Texas.

0514 Lizard Ecology, Trinity, Sunday 16 July 2017

Ariel Steele, Daniel Warner

Auburn University, Auburn, AL, USA

The Effect of Incubation Temperature on Sex and Morphology in a Lizard

The developmental environment plays a pivotal role in shaping phenotypes and fitness of all organisms. Perhaps the most enigmatic example of environmental effects is the influence of developmental temperature on an individual's sex, a phenomenon known as temperature-dependent sex determination (TSD). The first description of TSD was based on a study conducted 50 years ago on an African lizard (*Agama agama*). Although novel at this time of publication, this landmark study consisted of low sample sizes and provided a poor description of the sex-determining reaction norm in this species. Our goal was to revisit this work and better characterize the pattern of TSD in *A. agama.* In addition, we aimed to quantify the effects of constant and fluctuating incubation temperatures on a variety of fitness-relevant traits of offspring. Eggs were obtained from an invasive population of *A. agama* in Miami, FL, and randomly assigned to one of nine incubation treatments: six constant temperature treatments and three fluctuating treatments that mimic field conditions. We then measured hatchling morphology (snout-vent length, head size, mass), growth, and sprint performance as indicators of fitness. Size measurements were continuously taken every six weeks to determine the ontogenetic timing of sexual dimorphism and to determine if sexual dimorphism is influenced by incubation temperature. Preliminary data suggest that warm incubation temperatures produce mostly female offspring. This ongoing research will provide a critical evaluation of the long-term effects of developmental temperature on fitness-relevant traits, and provide insights into the adaptive significance of TSD.

0179 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

David Steen[1], Dawn Kelly[0]

[1]Auburn University, Auburn, AL, USA, [2]N/A, N/A, USA

A Cottonmouth and a Copperhead Engaged in Interspecific Combat in the Wild

Copperheads (*Agkistrodon contortrix*) and Cottonmouths (*A. piscivorus*) are relatively common viperid snakes occurring throughout the eastern and central United States. The two species are unlikely to encounter each other regularly, as Copperheads are associated with terrestrial habitats while Cottonmouths generally inhabit wetlands; thus, we know little about how the two species interact. In September 2016 both snakes were observed together outside Snowball, Arkansas and their behavior was recorded for approximately three minutes and forty seconds. The snakes' behavior in the video closely matches the stereotypical combat behavior demonstrated by males within the *Agkistrodon* genus and some other snake groups. We believe the video documents for the first time combat between two different snake species.

0174 Turtle Conservation, Sabine, Saturday 15 July 2017

David Steen[1], Orin Robinson[0]

[1]Auburn University, Auburn, AL, USA, [2]Cornell University, Ithaca, NY, USA

Estimating Freshwater Turtle Mortality Rates and Population Declines Following Hook Ingestion

Freshwater turtle populations are susceptible to declines following small increases in the mortality of adults, making it essential to identify and understand potential threats. Recent research has used x-ray technology to reveal that freshwater turtles ingest fish hooks associated with recreational angling; this is concerning because hook ingestion is a known source of additive mortality for sea turtles. We used a Bayesian-modeling framework, observed rates of freshwater turtle hook ingestion, and information from sea turtles to estimate there is a 1.2–11% chance that individual freshwater turtles of several species ingest fish hooks and consequently die. We then used our results and previously published life- history data for several species to demonstrate that currently observed rates of fish hook ingestion by freshwater turtles are likely sufficient to cause population declines. We believe we have identified fish hook ingestion as a serious yet generally overlooked threat to the viability of freshwater turtle populations.

0184 SSAR SEIBERT PHYSIOLOGY & MORPHOLOGY, Brazos, Friday 14 July 2017

John Stepanek[1], Natalie Claunch[1], Julius Frazier[1], Ignacio Moore[2], Ben Vernasco[2], Camilo Escallón[2], Emily Taylor[1]

[1]*California Polytechnic State University, San Luis Obispo, CA, USA,* [2]*Virginia Polytechnic Institute and State University, Blacksburg, VA, USA*

Corticosterone-Induced Color Change in Southern Pacific Rattlesnakes (*Crotalus helleri*)

Metachrosis, or color change, in reptiles has been of interest to herpetologists for a long time. Some species use it for thermoregulation or crypsis, but in many species the function and physiological mechanisms of metachrosis remain unknown. Anecdotes from herpetologists claim that some species, including rattlesnakes, undergo metachrosis when captured and placed in bags or buckets. A possible explanation for this color change is the release of their primary stress hormone, corticosterone. In this study, we implanted twenty-six wild Southern Pacific rattlesnakes (*Crotalus helleri*) intra-coelomically with either corticosterone or sham silastic implants. At 0 weeks (pre-implant), 2 weeks, and 4 weeks post-implant, the snakes were recaptured, bled, and photographed under standardized lighting in a curtained box. We used Adobe Photoshop to quantify light value of the dark and light bands of the snakes' tails and examined the relationship of these variables to baseline corticosterone levels. In addition, at 4 weeks post-implant, we assessed color change resulting from elevation of corticosterone from baseline levels after one hour of acute confinement stress. We found that baseline and acutely elevated corticosterone, regardless of implant treatment, were positively correlated with the lightness value of the light bands, but had no relationship with that of the dark bands. This ultimately led to increased contrast between the light and dark bands in snakes with higher corticosterone. This study is the first to quantify the relationship between corticosterone and color change in snakes, suggesting that hormones might mediate color change in response to stressors.

0086 AES Ecology II, Glass Oaks, Sunday 16 July 2017

Joshua Stewart[1], Christoph Rohner[2], Alessandro Ponzo[3], Daniel Fernando[4], Kerstin Forsberg[5], Brice Semmens[0]

[1]*Scripps Institution of Oceanography, La Jolla, CA, USA,* [2]*Marine Megafauna Foundation, Praia do Tofo, Mozambique,* [3]*Large Marine Vertebrates Research Institute Philippines, Jagna, Bohol, The Philippines,* [4]*The Manta Trust, Dorset, Dorchester, UK,* [5]*Planeta Oceano, Lima, Peru*

Trophic overlap in mobulid rays: insights from stable isotope analysis

Mobulid rays, a group of closely related filter feeders, are threatened globally by bycatch and targeted fisheries. Their habitat use and feeding ecology is not well studied, and most efforts have focused on temporally limited stomach content analysis or inferences from tagging data. Previous studies demonstrate a variety of different diving behaviors across species, which researchers have interpreted as evidence of disparate foraging

strategies. However, few studies have examined feeding habitats and diets of multiple mobulid species from a single location, and it is unclear if the proposed differences in diving and inferred foraging behavior are examples of interspecific variability or regional adaptations to food availability. We used stable isotope data from mobulids landed in fisheries to examine the feeding ecology of five species at three sites in the Indo-Pacific. Bayesian mixing models and analyses of isotopic niche areas demonstrated dietary overlap between sympatric mobulid species at all of our study sites. The degree of overlap may be inversely related to productivity, which is contrary to prevailing theories of niche overlap. Isotope data from two tissues allowed us to examine diet stability of *Manta birostris* and *Mobula tarapacana* in the Philippines, and we found evidence of diet switching in *M. birostris*. Our findings highlight challenges to bycatch mitigation measures for mobulid species, and may explain the multi-species mobulid bycatch that occurs in a variety of fisheries around the world.

0909 Amphibian Behavior, Pecos, Friday 14 July 2017

Meghan Still, Amanda Lea, Hans Hofmann, Michael Ryan

University of Texas Austin, Austin, Texas, USA

The Role of Chemical Cues during Courtship in Túngara Frogs, *Physalaemus pustulosus*

Chemo-sensation is among the least well-understood sensory modalities in anurans (frogs and toads). While vocalizations can mediate competitive interactions amongst males, chemicals (such as steroid hormones) leached in the water by calling males may also contain information that neighboring males within a chorus (an aggregation of males advertising for mates) can use to assess opponents during social interactions such as aggressive contests. To understand the influence of multimodal signaling displays on male courtship, we collected behavioral and physiological measurements from male túngara frogs (*Engystomops* = *Physalaemus pustulosus*) before, during, and after social stimulation. To permit repeated, non-invasive presentation of experimental stimuli and water borne hormone collection, we developed a unique testing chamber that allows for acoustic and chemical stimuli to be presented in isolation and in combination without directly handling the frog. Results demonstrate that the greatest calling effort and endocrine response (corticosterone and testosterone) occurs in response to the combined (acoustic + chemical) stimulus. Thus, an intriguing implication is that water, laden with peptide and hormonal secretions of neighbors, may act as a social cue that interacts with other social stimuli to influence aggressive interactions among chorusing males. Additional research is required to help elucidate the relative importance and ubiquity of chemical cues during male advertisement across anurans.

0590 Fish Conservation I, San Antonio, Sunday 16 July 2017

Andrew Stites, Joshua Sherwood, Jeremy Tiemann, Michael Dreslik

Illinois Natural History Survey, Champaign, IL, USA

Assessing the Distribution of Iowa Darters (*Etheostoma exile*) in Streams of Northern Illinois

Species distribution models are good tools for predicting the possible range of species that are rare or difficult to effectively sample for. Populations of the state-listed Iowa Darter (*Etheostoma exile*) have been declining in Illinois for more than a century. However, recent observations in headwater streams of northern Illinois with no previous records of Iowa Darters revealed the need to update its known distribution. We used MaxEnt, generalized linear, and random forest models, along with targetted field surveys, to estimate the historical and current distribution of Iowa Darters in Illinois. Our model of the historical distribution in Illinois estimates Iowa Darters were sporadically distributed in northeastern Illinois, focused in the Chicago metro and suburban region. Using the current distribution model, we selected and sampled 30 potential sites divided evenly between having low, medium, and high probabilities of Iowa Darter occurrence. We found nine new Iowa Darter localities during the surveys. We revised the distribution model with the findings and found the range of Iowa Darters in Illinois has substantially decreased from its historical range. However, areas of suitable habitat still exist and remain unsampled. Sampling and monitoring of these areas could guide potential conservation efforts and lead to additional populations.

0373 ASIH STOYE CONSERVATION II, San Antonio, Friday 14 July 2017

Joshua Stonecipher, Rebecca Blanton

Austin Peay State University, Clarksville, TN, USA

Conservation status and population genetic structure of the Smallscale Darter, *Nothonotus microlepidus*

The Smallscale Darter, *Nothonotus microlepidus,* occurs in four tributaries (Little, Harpeth, Red, and Stones rivers) to the middle and lower Cumberland River system in Tennessee and Kentucky. These tributaries are separated by the large-river mainstem of the Cumberland River, which lacks habitat typical of *N. microlepidus*. Because *N. microlepidus* is small-bodied, benthic, and lacks a gas bladder, large-river habitat conditions may limit dispersal and restrict gene flow among tributaries. Additionally, *N. microlepidus* has been petitioned for federal listing, but insufficient information is available to evaluate listing criteria. Therefore, the objective of this study was to assess the conservation status of *N. microlepidus* by documenting its current distribution and range-wide patterns of genetic diversity. We surveyed 20 historical localities to determine presence, and at two localities from each river system, the Jolly-Seber mark recapture method was used to estimate population size. Genetic structure was evaluated using twelve microsatellite loci examined for 30 individuals from two localities from each river system. *N. microlepidus* was present at 16 of 20 sampled localities. The Harpeth River had the largest population size estimates. The Stones River contained 3 of the 4 localities at which the focal species was not detected and showed a trend of lower population sizes and habitat

quality, indicating that populations in this system may be particularly vulnerable. Efforts to genotype all individuals and estimate the effects of distance, intervening mainstem habitats, and barriers such as dams on genetic structure are ongoing.

0205 General Ichthyology I, Trinity, Sunday 16 July 2017

Carla Stout, Jonathan Armbruster

Auburn University, Auburn, AL, USA

Molecular systematics of *Notropis* and related shiners (Cypriniformes: Leuciscidae)

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

0190 Amphibian Conservation I, Wedgewood, Sunday 16 July 2017

Miranda Strasburg, Michelle Boone

Miami University, Oxford, OH, USA

Examining the Role of Pesticide Exposure on Parasite Infections in Amphibians

Parasitic infection rates are rising across wildlife taxa for reasons that are not clear, which is increasing the importance of understanding how anthropogenic environmental stressors, like pesticides, alter host-parasite interactions. Because of their complex life cycle and aquatic origin, trematode parasites, like *Ribeiroia ondatrae* and *Echinostoma* *trivolvis*, and their hosts are at increased risk to pesticide exposure, which accumulate in aquatic systems through runoff, drift, and direct application. Trematodes negatively affect their host by altering behavior and development and can lead to mortality. Pesticides can influence these infections by affecting the host and the parasite through direct mortality, immunosuppression, or behavioral changes; these impacts may be asymmetrical so that either hosts or parasites could be more vulnerable to contamination. I tested the impact of environmentally relevant concentrations of two commonly used pesticides, *Bacillus thuringiensis israelensis* (Bti) and atrazine, on the likelihood of trematode infections in the northern leopard frog (*Lithobates pipiens*) and the Blanchard's cricket frog (*Acris crepitans blanchardi*). I hypothesized that pesticides would alter trematode infection rates through pesticide-mediated immunosuppression and behavioral changes in the host. Monitoring changes in host behavior after pesticide and parasite exposure, quantifying infection prevalence, and determining survival rates allowed us to determine if these pesticides affect amphibian-parasite dynamics. Preliminary results suggest that pesticides do not influence the effects of trematodes on these species. This complex system highlights the importance of understanding the influence of pesticide exposure on hosts and parasites as both may be distinctly impacted by exposure making overall outcomes difficult to predict.

0734 Snake Biology I, Brazos, Sunday 16 July 2017

Jeffrey Streicher[1], John Wiens[0]

[1]*Natural History Museum, London, UK,* [2]*University of Arizona, Tucson, AZ, USA*

Phylogenomic Analysis of More than 4000 Nuclear Loci Resolves a Difficult Branch of Squamate Reptile Phylogeny

Squamate reptiles (lizards and snakes) are one of the most diverse living groups of vertebrates with more than 9000 species. Despite considerable efforts to resolve higher-level relationships among major squamate lineages, some branches have remained difficult to resolve with strong support. These include relationships within a clade commonly referred to as Toxicofera (snakes, anguimorph lizards, and iguanian lizards), and the placement of snakes. The existence of Toxicofera itself has also been debated (as opposed to the traditional, basal placement of Iguania as sister to all other squamates). Here we used targeted sequence capture to obtain more than 4000 ultraconserved elements (UCEs) from 37 squamate taxa including representatives from all major extant groups. We sequenced an average of 2739 UCEs from each taxon and analyzed datasets including up to 1,530,015 nucleotides (from 4178 UCEs total). Data were analyzed using multiple analytical methods that included concatenated likelihood analysis and two major species-tree methods (ASTRAL and NJst). We found that UCE-inferred phylogenies of higher-level squamate relationships were largely congruent with previous molecular estimates (made from much smaller datasets), and showed overwhelming evidence against the basal placement of Iguania. We recovered strong support for a sister relationship between iguanian and anguimorph lizards across all

analyses, with snakes strongly supported as the sister group of these two clades. Thus, UCEs strongly resolve the difficult placement of snakes within squamates.

0498 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Jeffrey Streicher[1], Jack Davies[2], Natalie Cooper[1]

[1]Natural History Museum, London, UK, [2]University College London, London, UK

Amphibian Type Specimen Georeferencing and its Implications for IUCN Red List Classifications

We are currently in the midst of a 6th mass extinction. Species' extinction rates are 1,000-10,000 times higher than background rates, and these rates are predicted to increase as human activities and global change continue to intensify. If we want to prevent further extinctions, we need to know which species to conserve and where to conserve them. Unfortunately, these efforts may be hampered by inaccuracies in our knowledge of species geographic ranges. The International Union for Conservation of Nature (IUCN) Red List is widely used for assessing the conservation priority of species. The list is arranged by species and each account includes "species range" maps estimated by a panel of experts. These maps serve two purposes: (1) they are used to determine where species occur so that conservation areas can be prioritized, and what kinds of risks species may face in these areas; and (2) they are used to determine the range size of species, a factor that is incorporated into Red List extinction risk categories. Thus the accuracy of these maps is vital to conservation efforts. For some groups of vertebrates, however, these maps may contain inaccuracies due to poorly understood taxonomy of the species in question. One such group, which contains many imperilled species, is amphibians. Amphibian species that are widespread or have been described on the basis of few specimens are particularly likely to contain distributional inaccuracies. We compared georeferenced type localities (2000+ specimens) with IUCN spatial data to assess the accuracy of this crucial conservation resource.

0856 ASIH STOYE GENETICS, DEVELOPMENT, & MORPHOLOGY I, Trinity, Friday 14 July 2017

Jason Strickland[1], Miguel Borja[2], Andrew Mason[1], Darin Rokyta[3], Christopher Parkinson[1]

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

Venom evolution in Mojave Rattlesnakes, *Crotalus scutulatus*

Trait evolution can occur through changes in gene sequence via mutations that alter protein structure/function and through regulatory changes that alter gene expression

and relative proportion of proteins in the phenotype. It is hypothesized that changes in expression can occur on shorter time scales and will contribute more to variation among populations within a species. To understand the relative role of these mechanisms, we focused on snake venom in Mojave Rattlesnakes, *Crotalus scutulatus*, due to high intraspecific variability documented in their venom. We collected venom and tissue from 120 *C. scutulatus* from throughout their range, determined venom type using reversed-phase high-performance liquid chromatography, and sequenced the mitochondrial gene ND4 to estimate phylogeographic structure in the species. Using these data, we selected and sequenced the venom gland transcriptome (mRNA) and proteome (venom proteins) of 21 *C. scutulatus* from two populations that diverged ~2 mya. Within each population, animals of three venom types (hemorrhagic, neurotoxic, and "hybrid") were included. We estimated and compared gene sequence divergence and differential expression of orthologous transcripts to identify instances of nonsynonymous change and altered expression, respectively, among venom types and populations. Neurotoxic individuals from the two populations differed in the proportion of Mojave Toxin and myotoxins whereas hemorrhagic populations differed in the C-type lectins present. Among populations there were nonsynonymous mutations in several toxins including Mojave Toxin. Within populations, relative expression was different among individuals. Local adaptation is present but it is not solely driven by changes in expression in *C. scutulatus*.

0268 AES Life History, Pecos, Sunday 16 July 2017

Kristine Stump[1], David Die[2], John McManus[2], Tristan Guttridge[1], Samuel Gruber[1]

[1]*Bimini Biological Field Station, Bimini, Bahamas,* [2]*University of Miami - RSMAS, Miami, FL, USA*

Using a Long-Term Mark-Recapture Dataset to Investigate Effects of Habitat Loss on Survival Probability of Juvenile Lemon Sharks

Many shark species use nursery areas, increasing the probability of juvenile survival. The availability of suitable nursery habitat may be a limiting factor for some shark populations. The mangrove-fringed lagoons and creeks in Bimini, Bahamas serve as nurseries of the lemon shark (*Negaprion brevirostris*). Since 1997, one nursery has been subjected to large-scale anthropogenic disturbances, including dredging, mangrove deforestation and wetlands-filling. Using the Program MARK, we employed a long-term mark-recapture dataset to analyze models of recapture (p) and survival (Φ) probability of age 0, 1 and 2 lemon sharks in two adjacent Bimini nurseries. We first tested models in which recapture probabilities could vary with combinations of age, nursery and time, and found p varied with age. This model was subsequently used for the p component in a suite of candidate models for Φ, which differed in how survival could vary with major construction events (e.g., habitat alteration). Model selection based on Akaike's Information Criteria indicated that mangrove deforestation negatively affected probability of survival in juvenile lemon sharks, and young-of-the-year (YOY), in

particular. Model estimates of ΦYOY for the year of major disturbance are at or below published Leslie matrix approximations for population stability. These estimates suggest that in such years, anthropogenic effects may reduce the ability of the nursery to provide ample recruits to the adult population. Habitat loss is likely a significant threat to lemon shark populations. Future management scenarios and land-use planning should consider multiple life stages, including neonates and juveniles.

0306 ASIH STORER HERPETOLOGY; Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Jenny Sutherland[1], David Mifsud[2], Maegan Stapleton[2], Amber Stedman[1], Edward Roseman[3], James Boase[4], Andrew Briggs[4], Justin Chiotti[4], Katherine Greenwald[1]

[1]Eastern Michigan University, Ypsilanti, MI, USA, [2]Herpetological Resource and Management, Chelsea, MI, USA, [3]USGS Great Lakes Science Center, Ann Arbor, MI, USA, [4]US Fish and Wildlife Service, Waterford, MI, USA

Use of eDNA and Occupancy Modeling to Predict the Presence of Mudpuppies (*Necturus maculosus*) Along the St. Clair-Detroit River System

The mudpuppy (*Necturus maculosus*) is an elusive, 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 because of habitat loss and modification, pollution, lampricide use, and over collection. Land use practices along the St. Clair-Detroit River System (SCDRS) have altered habitat, but information on the status of mudpuppies along the SCDRS is lacking. In an effort to remove the St. Clair and Detroit Rivers as an Area of Concern some sites have undergone restoration and now provide suitable mudpuppy habitat. Mudpuppies are important indicators of good habitat quality and could be a gauge for restoration success. Mudpuppy occurrence was quantified at these sites, along with other sites along the SCDRS, using minnow trap and setline records. These data were then used in an occupancy model which predicts detection probability and occupancy. Additionally, we are investigating the utility of environmental DNA (eDNA) to aid future monitoring efforts at these locations. Environmental DNA could be a useful tool for monitoring because it is non-invasive and requires minimal fieldwork. We used eDNA sampling and quantitative PCR (qPCR) to determine mudpuppy presence at restored and unrestored locations and compared the results to trapping records. Results from this work will help document the occurrence of mudpuppies in the system and help prioritize management of mudpuppies on a local and range-wide scale, resulting in more successful conservation of this ecologically important species.

0628 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Emma Sutton, Anna Savage, Kate Mansfield, Matthew Lawrance

University of Central Florida, Florida, USA

A comprehensive approach to surveillance, epidemiology and genetic analyses of Chelonid Fibropapilloma-associated Herpesvirus in marine turtles

Of the seven extant marine turtle species, all are imperiled. The status of marine turtles is important when considering diseases that influence the survival of reduced populations. Fibropapillomatosis (FP) is a tumor disease of marine turtles that, while benign, can impact hosts by obstructing feeding and locomotion. The putative etiological agent of FP is Chelonid Fibropapilloma-associated Herpesvirus (CFPHV). The association between FP and CFPHV presence is not absolute, as CFPHV has been found within healthy turtles. This raises the question as to what factors may be important to the onset of FP, including variation in virus genetics. Previous research was stymied by small or narrowly focused sampling. We leveraged one of the strongest available sample sets of marine turtles, collected over three decades from Indian River Lagoon, Florida. Our sampling is comprehensive, incorporating hundreds of samples from both healthy and diseased turtles, from multiple tissue types including blood and skin, across multiple sampling seasons and from two species of marine turtle (*Chelonia mydas* and *Caretta caretta*). CFPHV was detected utilizing quantitative PCR, allowing for estimation of viral load as a proxy for disease intensity. From positive samples, we reconstructed the phylogenetic patterns of virus evolution using three viral loci (polymerase, capsid maturation protease, glycoprotein B), and utilized Bayes Factor testing to determine the robustness of putative phylogenetic trees. These results have utility in future efforts in explaining host coevolution as well as patterns of selection and differentiation on viral strains found across tissue and time.

0649 Fish Ecology I, San Antonio, Sunday 16 July 2017

Tracey Sutton[1], Jon Moore[2], April Cook[1], Andrea Bernard[1], Kevin Boswell[3], Ron Eytan[4], Kim Finnegan[1], Christopher Kenaley[5], Lacey Malarky[6], Ted Pietsch[7], Nina Pruzinsky[1], Mahmood Shivji[1], Max Weber[4], R. David Wells[4], Danté Fenolio[8]

[1]Nova Southeastern University, Dania Beach, FL, USA, [2]Florida Atlantic University, Jupiter, Florida, USA, [3]Florida International University, North Miami, FL, USA, [4]Texas A&M University Galveston, Galveston, TX, USA, [5]Boston College, Boston, MA, USA, [6]Oceana, Washington D.C., USA, [7]University of Washington, Seattle, WA, USA, [8]San Antonio Zoo, San Antonio, TX, USA

The Epi-to-Bathypelagic Ichthyofauna of the Gulf of Mexico: Recent Surveys Reveal Exceptional Diversity and Endemism, with 180 New Species Records

An ongoing research program has investigated the ichthyofaunal structure and dynamics of the oceanic northern Gulf of Mexico (GoM), from the surface to 1500 m depth. Prior to 2011 there was no inventory of the GoM bathypelagial (>1000 m depth) and that of the mesopelagial (200-1000 m) was largely limited to the eastern GoM. Extensive sampling and analysis since that time has revealed an exceptionally speciose

oceanic fish assemblage with inherent pelagic endemicity. Of the 794 fish species identified to date, 180 are new records for the GoM, including one newly described and 21 putative undescribed species. This increases the total fish species number for the entire GoM marine ecosystem by over 10%. Over half of all known fish species in the GoM use the oceanic habitat for part or all of their lives. The GoM now ranks among the most-speciose oceanic ichthyofaunal assemblages known in the World Ocean. This ranking likely results from: 1) the ecotonal nature of the oceanic GoM (low-latitude input, winter cooling); 2) high (non-limiting) oxygen at depth; 3) substantial use of pelagic habitat by juvenile deep-demersal and coastal fishes; 4) sampling intensity (the GoM stands as the world's most-studied bathypelagic system); and 5) the integration of morphological and genetic methodology used to increase taxonomic accuracy and precision. Despite extensive sampling, the species accumulation curve has not reached asymptote; more species will likely be recorded with more sampling.

0834 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

William Sutton[1], Chris McClure[2], Chris Edge[3], David Steen[4]

[1]Tennessee State University, Nashville, TN, USA, [2]The Peregrine Fund, Boise, ID, USA, [3]University of Toronto, Toronto, Canada, [4]Auburn University, Auburn, AL, USA

Landscape-Scale Snake Monitoring Studies: Work Hard or Work Smart?

Snakes represent an important and often maligned component of terrestrial and aquatic ecosystems. The often secretive activity patterns and cryptic coloration of snakes make it difficult to derive estimates abundance and population density for many species. In addition, local abundance and or detection rates may be so low that construction of accurate abundance/occupancy estimates is often impossible. Sampling methods for snakes are quite limited unless drift-fence arrays equipped with large box traps are employed. To this end, we acquired a series of snake occurrence/occupancy datasets from a variety of study sites throughout the southeastern United States (15 total snake occurrence datasets) to answer questions of sampling effort and approaches. We assembled all occurrence data into yearly presence/absence datasets for each snake species/species complex sampled. After correcting for landscape-scale habitat patterns, we evaluated a series of sampling and site-specific covariates that may potentially impact detection rates. Our analyses revealed that detection rates differ based on species evaluated and trap methodology employed. Collectively, our results are important for designing landscape-scale snake monitoring studies and determining the amount of sampling effort and techniques necessary for detecting both common and rare snake species.

0718 Amphibian Conservation IV, Wedgewood, Sunday 16 July 2017

William Sutton[1], Michael Osborne[2], Jeff Bailey[3], Thomas Pauley[4]

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

Impacts of Stream Disturbances on an Appalachian Stream Salamander Assemblage

Globally, amphibians are threatened by a variety of stressors, including landscape destruction and landuse change, emerging pathogens, aquatic pollution, and global climate change. 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 stream disturbance on stream salamander assemblage at 45 streams in West Virginia over a two-year period. We used a combination of transect and quadrat surveys to survey and capture salamanders. We used both multivariate approaches and N-mixture models to evaluate impacts of stream disturbances. We captured 463 adult salamanders and 1,535 larval salamanders representing 9 species throughout the study period. We found that salamanders in the genus *Desmognathus* had lowest abundance in degraded streams and reached greatest abundance in highest quality streams. The most commonly captured species, which included larval Northern and Southern Two-lined Salamanders (*Eurycea bislineata* and *E. cirrigera*), tended to reach greatest abundance at sites with intermediate disturbance levels. A variety of detection-level covariates impacted abundance estimates and included ecoregion of study site, date of survey, and survey technique. Collectively, agricultural and mountaintop-removal mining operations appear to be the greatest threat to salamanders in streams throughout the study region. 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.

0019 ASIH STORER HERPETOLOGY; Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Meredith Swartwout, J. D. Willson

University of Arkansas, Fayetteville, AR, USA

Disentangling Mechanisms of Decline for Litter Lizards at La Selva Biological Station, Costa Rica

In recent decades, increasing evidence has linked climate change to global lizard declines. The effects of climate change are complex, with both direct (e.g. disruption of thermal biology) and indirect components (e.g. changes in habitat structure and food webs) predicted to affect lizard populations. I conducted a pilot experiment to examine some of the indirect effects on lizards at La Selva, a lowland tropical rainforest site in Costa Rica where lizard populations have declined. I manipulated leaf litter depth and precipitation in forest plots, and measured densities of ants and other invertebrates that

may be predators or prey of leaf litter lizards. Because ants are important predators of lizard eggs, I also monitored ant recruitment and 12-hr bait mass loss at bait stations as a metric of ant predation levels across treatments. Ant densities were highest in control plots, and were positively correlated with bait mass loss ($p < 0.05$). Invertebrate densities followed the same general trend as ant densities, with both being lowest in irrigated and litter removal plots, which had the shallowest leaf litter. During the study, I encountered the most lizards on litter control plots. Preliminary results suggest that lizards may be selecting for a moderate or high leaf litter depth because of a tradeoff between prey availability and predation pressure. In future studies, I will validate the results presented here, evaluate how litter depth affects ant predation on lizard eggs, and construct models that evaluate sensitivity of population dynamics to indirect effects of climate change.

0180 Herp Biogeography & Phylogeography II, Sabine, Sunday 16 July 2017

Samuel Sweet

U C Santa Barbara, Santa Barbara, CA, USA

Drought and Terrestrial Plethodontids: Rediscovery of *Batrachoseps minor*

Mystery has surrounded the conservation status of the Least Slender Salamander (*Batrachoseps minor*) since its description in 2001. Regarded as common during the early 1970s in its limited distribution in the Santa Lucia Range of San Luis Obispo County, California, only three individuals were found in the 35 year interval 1976-2011 despite multiple attempts, some by the original collectors. Numbers found of the apparently microsympatric *B. nigriventris* remained roughly consistent in this interval. Current literature suggests that *B. minor* may have suffered a catastrophic population decline, with overcollecting or chytridiomycosis at its root, and a recent petition to USFWS seeks listing as Threatened. Beginning in 2011, field work has rediscovered *B. minor* at most of the historic sites, and at 6 new sites as well, augmenting its known range by about one third. True microsympatry with *B. nigriventris* occurs, but is rare; instead, *B. minor* is a habitat specialist favoring steep, heavily-shaded NE-facing slopes at moderate (not high) elevations, with limited leaf litter, shallow soils and exposed bedrock, usually with very dense stands of poison oak (*Toxicodendron diversilobum*, >15 stems/m^2). These patches are steeper, darker, rockier, and with shallower soils than sites favored by *B. nigriventris*, and additionally are inaccessible to individuals reactive to poison oak. Recent collectors have tended to avoid these sites, probably explaining the gap in records. The recent CBD listing petition is rife with errors - objectively, it is hard to imagine a species that would profit less from federal listing.

0778 AES GRUBER AWARD IV, Wedgewood, Friday 14 July 2017

John Swenson, Karen Crow

San Francisco State University, San Francisco, CA, USA

How the Devil Ray got its horns: The molecular evolution and development of the Myliobatid body plan

Batoids (skates and rays) are a diverse clade of cartilaginous fishes comprising over 550 recognized species. Sometimes called "flat sharks", their dorso-ventrally flattened bodies and anteriorly elongated pectoral fins distinguish batoids from sharks, while variations on this body plan differentiate batoid taxa from one another. Most batoids live a benthic lifestyle and generally exhibit round flexible pectoral fins that are used for both feeding and locomotion. In contrast, pelagic batoids of the family Myliobatidae have evolved diamond-shaped pectoral fins that are used solely for locomotion and an extra pair of anterior fins called cephalic lobes, which are used for feeding. Though the functional benefits associated with the unique myliobatid fin morphologies have been documented, little is known about the underlying genetic mechanisms associated with their evolution and development. Using RNA-Sequencing, we have examined gene expression among eight distinct fin domains in the cownose ray (*Rhinoptera bonasus)*, a derived pelagic myliobatid, at two different stages of early development. Our comparative transcriptomics approach has revealed both ancestral and novel gene expression pathways in the fins of cownose ray embryos, suggesting that the myliobatid body plan evolved by layering novel gene expression pathways on top of those that give rise to the ancestral batoid body plan.

0804 Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017; AES CARRIER AWARD

John Swenson, Karen Crow

San Francisco State University, San Francisco, CA, USA

How the Devil Ray got its horns: developmental staging of Myliobatid embryos

Devil rays and their relatives of the family Myliobatidae (manta rays, cownose rays, bat rays) are pelagic batoids that swim using a derived mode of locomotion termed ‘oscillatory swimming'. Morphological adaptations associated with the oscillatory swimming mode include distal elongation, a high aspect ratio, stiffened fin rays, and cephalic lobes, all of which are established prior to birth and may be observed in neonates. How and when, specifically, these features are established during gestation remains unknown, as no study to-date has described early development in any myliobatid taxon. By working with commercial fishermen, we collected embryos from a representative myliobatid species, the cownose ray, during early development. These specimens have revealed hitherto unknown aspects of myliobatid development, including cephalic lobes that develop as pectoral fin attachments, completely separate from the head, and pectoral fins that project outward from the body before the primary cartilage "zips up" to the gill arch. We conclude that the basic myliobatid body plan is

established within the first 1-2 months of gestation following a period during which development proceeds in a unique and often counterintuitive fashion.

0421 AES Trophic Ecology/Physiology, Wedgewood, Friday 14 July 2017

Brendan Talwar[1], Ian Bouyoucos[1], Jake Brownscombe[3], Cory Suski[4], Steven Cooke[3], John Mandelman[2], Edward Brooks[1]

[1]Cape Eleuthera Institute, Eleuthera, Bahamas, [2]Anderson Cabot Center for Ocean Life, New England Aquarium, Boston, MA, USA, [3]Carleton University, Ottowa, ON, Canada, [4]University of Illinois at Urbana-Champaign, Urbana, IL, USA

Comparative behavioral and physiological response to longline capture

The behavioral response to longline capture in fishes is poorly understood although it may be tightly linked with the magnitude of the physiological stress response, and, ultimately, may contribute to stress-induced mortality. We employed accelerometers, video cameras, and hook timers to analyze the behavioral response of wild subtropical fishes to experimental longline capture across varied capture durations, temperatures, and depths. We also sought to relate behavioral responses to the magnitude of physiological responses for longline-caught sharks. We found significant differences in fight intensity values across capture durations and species as well as between ventilation modes in sharks, with ram ventilators and blacktips *Carcharhinus limbatus* in particular emerging as those demonstrating the most pronounced fighting behavior. We found no effect of fish size or capture temperature on fight intensity values. In addition, we found evidence of behavioral responses influencing the magnitude of physiological responses. Our results suggest that the behavioral and physiological response to longline capture is species-specific and highly variable and may be linked to distinct evolutionary traits, providing a frame of reference for vulnerability and risk assessments.

0196 Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Milton Tan[1], Jonathan Armbruster[2]

[1]Emory University, Atlanta, GA, USA, [2]Auburn University, Auburn, AL, USA

Diagnosing Effects of Systematic Error and Phylogenetic Signal in Phylogenomics: A Case Study on the Order Cypriniformes

Although phylogenomics can help systematists overcome sampling error from limited data, conflict can arise due to systematic error (e.g. long branch attraction, base compositional heterogeneity, saturation), low phylogenetic signal, and from model choice (e.g. concatenation vs. coalescent-based analysis). Recently, the relationships of the Order Cypriniformes were clarified by use of anchored hybrid enrichment, however conflict arose with respect to relationships of *Gyrinocheilus*, Catostomidae, and Cobitoidei to *Paedocypris* and the remaining cyprinoids. It is possible that systematic

error confounds phylogenetic inference in this analysis. To assess this, we explore the sensitivity of phylogenomic analyses to systematic error by subsampling loci with respect to sources of noise and comparing their resulting trees to those from random permutations of loci, performing taxon exclusion experiments with concatenation analyses to assess the effect of long-branch attraction, and performed gene genealogy interrogation (GGI) to assess the effect of low phylogenetic signal in coalescent-based analysis. Many of the relationships of Cypriniformes are well supported across all analyses, even those on datasets with higher levels of noise, including the relationship of *Paedocypris* as sister to Cyprinoidei. Coalescent-based analyses and concatenation analyses generally differed on whether or not *Gyrinocheilus*, Catostomidae, and Cobitoidei were recovered as monophyletic. Exclusion of long-branched taxa in concatenation analysis and GGI-based coalescent-based analysis converged on a monophyly of this group, supporting the hypothesis these groups form a clade, and highlighting the effect of long-branch attraction, the anomaly zone, or both.

0374 AES Genetics, Systematics, & Biogeography, Pecos, Sunday 16 July 2017

Milton Tan[1], Al Dove[2], Tim Read[1]

[1]Emory University, Atlanta, GA, USA, [2]Georgia Aquarium, Atlanta, GA, USA

A New and Improved Genome Assembly of the Whale Shark (*Rhincodon typus*) and Comparative Genomics of Positive Selection

The genome sequence of the whale shark can be used to understand the evolution of its extreme body size, as a resource for conservation genomics of this species, and as a comparative resource in vertebrate genomics given the limited number of chondrichthyan genomes available. Previously, the whale shark genome was assembled using only short read sequences. We report on a new genome assembly based on *de novo* assembly of long-read PacBio sequences and polishing using Illumina sequences. Compared to our previous assembly, the new assembly is improved by multiple metrics, including having a higher contiguity, with orders of magnitude fewer contigs and orders of magnitude longer assembled fragments (N50), and higher conserved gene completeness (BUSCO2). The conserved gene completeness also compares favorably with other chondrichthyan genome and transcriptomes available. We also report on a new gene annotation informed by transcriptome sequences and protein homology. Finally, we perform genome-wide comparative genomic analysis to detect protein-coding genes under positive selection within the whale shark genome, and tested for a shift in positive selection associated with the evolution of gigantism in the whale shark.

0752 Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Kevin Tang, Hayley Schroeder, Rand Daboul

University of Michigan-Flint, MI, USA

Phylogenetic Relationships of Rabbitfishes (Teleostei: Siganidae)

The family Siganidae is a widespread group of marine fishes found in the Indo-Pacific Ocean and Mediterranean Sea, where they are typically occur in association with coral reefs. Of the 28 rabbitfish species, 24 were examined in this analysis. Additional acanthomorph species were used as outgroup taxa. 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 analysis. The results of these analyses found support for the monophyly of the family. Their evolutionary relationships, and how they might affect the classification and taxonomy of Siganidae, will be discussed.

0654 ASIH STOYE GENERAL HERPETOLOGY, San Antonio, Thursday 13 July 2017

Rebecca Tarvin[1], Cecilia Borghese[1], Wiebke Sachs[2], Juan Santos[3], Lauren O'Connell[4], David Cannatella[1], Adron Harris[1], Harold Zakon[1]

[1]University of Texas at Austin, Austin, TX, USA, [2]Universität Konstanz, Konstanz, Baden-Württemberg, Germany, [3]St John's University, Queens, NY, USA, [4]Harvard University, Cambridge, MA, USA

Evolution of Resistance to Epibatidine, a Potent and Toxic Analgesic Alkaloid, In Dendrobatid Poison Frogs

Poison frogs sequester hundreds of chemicals from their diet for anti-predator defenses. These amphibians must resist the effects of the bioaccumulation of these toxic chemicals or risk self-intoxication. Some alkaloids sequestered by poison frogs affect important nervous system proteins known as ion channels; resistance to such alkaloids often evolves via genetic changes in ion channels where alkaloids bind. Among these compounds is epibatidine, an analgesic alkaloid 200x more potent than morphine. Despite its therapeutic potential, epibatidine was never developed as a drug because it proved to be lethal at very low doses. Given epibatidine's potency, how have poison frogs evolved resistance to its bioaccumulation? We sequenced a nicotinic acetylcholine receptor (nAChR), the target of epibatidine, across Dendrobatidae. Using comparative phylogenetics we identified four amino acid replacements in two defended clades, *Epipedobates* and *Ameerega,* the only clades known to wield epibatidine. One replacement evolved convergently in both clades, but the other three replacements differ between groups. We tested whether the replacements provided resistance or altered nAChR function with *in vitro* electrophysiological assays. We found that two replacements provide resistance to epibatidine but at a cost of decreased sensitivity to acetylcholine. The other replacements improve nAChR sensitivity to acetylcholine, suggesting that they may have arisen after resistance evolved to fine-tune nAChR function. Both *Epipedobates* and *Ameerega* are relatively young lineages among poison frogs (<15 MYA) and appear to be diversifying rapidly; we hypothesize that the evolution of resistance to

potent toxins among defended lineages could play a part in facilitating their diversification.

0099 General Herpetology, Sabine, Sunday 16 July 2017

Samuel Tegge[1], Steve Huskey[1], Michael Smith[1], Christopher Anderson[2], Kenneth Barnett[3], Emily Hamilton[1], Kathryn Laslie[1]

[1]Western Kentucky University, Bowling Green, KY, USA, [2]University of South Dakota, Vermillion, SD, USA, [3]New York State Department of Environmental Conservation, Albany, NY, USA

The Behavioral Context and Mechanism of Biotremors in the Veiled Chameleon, *Chamaeleo calyptratus*

Communication, which is ubiquitous and diverse among all living organisms, is utilized to intra- and interspecifically transmit information via numerous mechanisms in myriad behavioral contexts. Vibratory communication, including biotremors, has convergently evolved in numerous animal groups, including insects, spiders, fishes, mammals, and was recently discovered in veiled chameleons. Using the veiled chameleon, *Chamaeleo calyptratus*, we have (1) determined some of the behavioral contexts in which biotremors are employed, and (2) investigated the mechanism by which they are produced. Behavioral data was collected during conspecific and individual trials. Throughout male-to-male behavioral trials, video recordings documented subtle head twitches while accelerometer data correlated twitches with the production of biotremors ranging from 50 – 100 Hz, with a mean pulse dominant frequency of 86 Hz. During individual trials, an experimental shaker, attached to a dowel with a free-moving chameleon perched on it, was employed to replicate conspecific biotremors through the production of artificial pulses. Chameleon movement rates while walking across the dowel were significantly reduced in response to pulses of 50 and 150 Hz (N=5; Wilcoxon signed-rank test; $^*P<0.05$), which are similar in frequency to conspecific biotremor production. Muscular and biotremor data were gathered simultaneously during vibration production. During intra-and intersexual interactions, surgically implanted electrodes recorded muscle electrical activity via electromyography (EMG), accelerometers detected the production of biotremors, and videography documented all behaviors associated with the vibrations. EMG data was then correlated with the accelerometer data to implicate the muscles responsible for the production of biotremors.

0607 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: EVOLUTION, GENETICS, & SYSTEMATICS; Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Panupong Thammachoti[1], Utpal Smart[1], Amir Hamidy[2], Irvan Sidik[2], Nia Kurniawan[3], Eric Smith[1]

[1]The University of Texas at Arlington, Arlington, TX, USA, [2]Indonesian Institute of Science, Cibinong, Indonesia, [3]Brawijaya University, Malang, Indonesia

Molecular Systematics, Species Delimitation and Divergence Time Estimates of The Common Sun Skinks (Scincidae: *Eutropis multifasciata* [Kuhl, 1820]) from Java and Sumatra

The Common Sun Skinks, *Eutropis multifasciata* are a widely distributed terrestrial scincid that ranges across the Indian subcontinent, Indochina, the Sunda shelf and Papua New Guinea. Originally described as multiple species and later synonymized to *E. multifasciata,* the taxonomy of this species, based exclusively on morphology, has been controversial. Several studies have investigated the molecular systematics of the genus, but the geographic sampling of *E. multifasciata* has been inadequate since samples from the type locality of West Java were absent. We thus set out to construct the first molecular phylogeny of *E. multifasciata* that employs sampling from the type locality and other hitherto unsampled areas of Java and Sumatra. To this end, we used a multilocus dataset comprising of two nuclear (NGFB and R35) and two mitochondrial (16S and ND4) loci, utilising supermatrix and coalescent phylogenetic approaches. To address the taxonomy, we also clarified species boundaries in the complex using Bayesian species delimitation methods. Finally, to shed light on the evolutionary origins of this species complex, we also performed divergence time analysis using a combination of molecular rates and calibration points based on the geological history of Sundaland. Our results recover multiple geographic clades within the Sumatran and Javan *E. multifasciata*. Our species delimitation analysis corroborates these populations as distinct species. Diversification within Sundaland was most likely driven by geographic changes in sea-level and habitat as well as global glacial events of the early Pliocene.

0624 Lizard Ecology, Trinity, Sunday 16 July 2017

Christopher Thawley, Jason Kolbe

University of Rhode Island, Kingston, RI, USA

Effects of Artificial Light at Night on Reproduction in Brown Anoles (*Anolis sagrei*)

Environments are changing rapidly due to human activity, and these changes have important costs and consequences for affected organisms. As human-impacted environments increase, artificial light at night (ALAN), an evolutionarily-novel stressor, affects many ecosystems and species worldwide. ALAN can impact physiological function, survival, and reproduction, yet this aspect of global change remains understudied, especially in reptiles. Anoles are adapted to specific photic environments and some species, such as the brown anole (*Anolis sagrei*), thrive in human-impacted habitats including cities where ALAN is prevalent. Previous research shows that photoperiod may drive reproduction in brown anoles and that lighting alters nocturnal activity in anoles, suggesting that ALAN may serve as a novel stressor and could impact reproduction in this species. We captured brown anoles at the beginning of the breeding season from remnant forest habitat in southern Florida and exposed them to natural light cycles or artificial light at night in the lab. We quantified impacts of ALAN on growth, body condition, and stress (plasma levels of corticosterone) in reproductive lizards. We also assessed ALAN's impacts on initiation of reproduction, inter-clutch interval, and reproductive investment. As the human populations grows and urban areas expand, artificial lighting is likely to impact many organismal traits, including reproduction, in a variety of organisms.

0188 Herp Morphology & Development, Brazos, Saturday 15 July 2017

Christopher Thigpen, Stanley Trauth

Arkansas State University, State University, AR, USA

Comparative Serous Gland Histology and Histochemistry in the Skin of North American Hylid and Ranid Frogs

The histology and histochemistry of serous glands of *Hyla chrysoscelis*, *H. cinerea*, *Rana palustris* and *R. sphenocephalus* are described, herein, for the first time. Light microscopy protocols using the stains hematoxylin counterstained with eosin, periodic acid Schiff counterstained with alcian blue, and Pollak trichome were used for examination of glands. The glands are merocrine, externally secreting and composed of a syncytium of secretory cells surrounding a central lumen bordered superficially by melanophores. Serous gland numbers and widths were compared within individuals and between species within a genus to test for differences between skin region and species with and without conspicuous coloration. Significant differences in serous gland size and number were found between regions within individuals and between species. These results suggest that concealed conspicuous coloration found in *H. chrysoscelis* and *L. palustris* is aposematic.

0662 ASIH STORER ICHTHYOLOGY; Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Dustin Thomas, Brook Fluker

Arkansas State University, Jonesboro, AR, USA

Analysis of body shape variation among restricted and widespread populations of the Southern Redbelly Dace, *Chrosomus erythrogaster*

The Southern Redbelly Dace (*Chrosomus erythrogaster*) has a widespread distribution throughout most of the eastern United States, with several disjunct populations in midwestern states and in the lower Mississippi River drainage. Of particular interest are potentially isolated populations on Crowley's Ridge in Arkansas and the Bluff Hills in Mississippi. Currently, it is unclear whether these populations share connections with larger core populations in the nearby Ozark and Eastern highlands, or represent isolated

populations on these "upland islands" within the Gulf Coastal Plain. This study used geometric morphometric techniques to evaluate body shape differences among *C. erythrogaster* from loess habitats of Crowley's Ridge and the Bluff Hills of Mississippi. In order to determine variation in body shape, focal populations were compared to populations from the Ozark and Eastern highlands, as well as populations from the Ohio, Green, and Rock River drainages. A Southwestern population was also included in the study for further comparisons. Preliminary analyses revealed variation in body shape across the geographic range, and the populations of interest seem to be showing patterns of intermediate body depth compared to other populations. In conjunction with an ongoing population genetic study, results from this study will provide valuable information about the distinctiveness of potentially isolated populations in Arkansas and Mississippi.

0545 SSAR SEIBERT ECOLOGY III, Glass Oaks, Friday 14 July 2017

Samantha Thomas

Western Kentucky University, Bowling Green, Kentucky, USA

Landscape Genetics of California Tiger Salamanders: Inferences from multiple methods

Landscape genetics is a rapidly growing field of study that compares patterns of gene flow among populations with habitat heterogeneity across a landscape to infer the interaction between dispersal of individuals and their physical environment. Empirical data generated from a landscape genetics study can be implemented for conservation and management purposes, making the field increasing popular. However, concerns have arisen that the field is expanding faster than the analytic framework that supports it. Multiple methods for generating estimates of the association among habitat types and dispersal (i.e., least-cost paths and resistance surfaces) have been proposed, and there is a debate as to which statistical methods are best for examining the genetic structure on a landscape. We use an integrated empirical- and expert-opinion-based strategy to generate a landscape resistance surface for the California Tiger salamander (CTS), *Ambystoma californiense*, which is a species of conservation concern. We utilize several alternative analysis methods (e.g., CCA, BIMR, GESTE and partial Mantel tests) to look for agreement among methods describing the relationship of landscape features and genetic variation. Our analysis revealed variation among methods for describing genetic structure in this CTS metapopulation, but all methods indicated the presence of genetic structure, to some extent, across the landscape. This empirical data set provides both a perspective on habitat management for the CTS and on the suitability of several novel analysis strategies for landscape genetics.

0020 ASIH STOYE PHYSIOLOGY & PHYSIOLOGICAL ECOLOGY I, San Antonio, Thursday 13 July 2017

Michelle E. Thompson, Maureen A. Donnelly

Florida International University, Miami, FL, USA

Thermal Quality Influences Habitat Use of Two Anole Species

Over the past several decades, human transformation of natural landscapes has become unprecedented in intensity and spatial scale and forest habitats and animal communities within forests are among the most highly impacted, globally. Forest destruction has been repeatedly documented as a driver of biodiversity loss. However, little is known about how animal communities respond when altered landscapes are abandoned and left to regenerate into secondary forests. To evaluate support for thermal quality as a mechanism driving reptile species distributions during secondary forest succession, we measured operative temperatures and occupancy in three successional forest stages (pasture, secondary forest, and old growth forest) for two anole species (*Norops humilis* and *Norops limifrons*). We then measured thermal preference in laboratory experiments and used operative temperature and temperature preference measurements to determine how thermal quality of habitat changes over the course of secondary forest succession and if occupancy varies as a function of thermal quality. We found that thermal quality was lowest in pasture because of a large frequency of temperatures above the thermal preference range. However, in low thermal quality pasture sites, riparian habitats provided a thermal refuge for species. Our results support thermal quality as a mechanism for reptile species distributions in altered landscapes and highlight the importance of the maintenance of riparian corridors.

0600 ASIH STORER HERPETOLOGY; Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Milinda Thompson[1], Tracy Langkilde[2], Christopher R. Tracy[1]

[1]*California State University Fullerton, Fullerton, CA, USA,* [2]*The Pennsylvania State University, State College, PA, USA*

Effect of Water Restriction on Corticosterone in the Herbivorous Lizard, *Dipsosaurus dorsalis*

Arid environments and their unpredictable rainfall events are a potential source of physiological stress because animals, like desert iguanas (*Dipsosaurus dorsalis*), must maintain water balance when the potential for evaporative water loss is high and water availability is limited. The stress hormone, corticosterone (CORT) could activate physiological systems to minimize the impact of dehydration to homeostasis. We predicted that CORT levels in populations of *D. dorsalis* from habitats with access to water from irrigated landscaping would have significantly lower CORT levels than lizards from a population with only natural precipitation. Thus, we measured hematocrit, as an indication of dehydration, and baseline CORT levels of two urban populations of *D. dorsalis*, one with access to water only from precipitation ("natural"), and one with access to irrigated landscaping, in Rancho Mirage, CA during the driest

portion of their active season. Hematocrit levels from the “natural” site were significantly higher than those from the irrigated site. However, there were no significant differences in baseline CORT between populations, even though, for a given hematocrit level, lizards without access to irrigation had higher baseline CORT levels than those with access to irrigation. While *D. dorsalis* from the “natural” site were dehydrated, our predictions about CORT were not supported. Dehydration may influence the acute stress response as well, so further analysis of *D. dorsalis* behavior and stress levels upon acute stress is needed to evaluate the entirety of their physiological stress responses to water restriction.

0034 SSAR SEIBERT PHYSIOLOGY & MORPHOLOGY, Brazos, Friday 14 July 2017

Jessica L. Tingle, Timothy E. Higham

University of California, Riverside, CA, USA

Morphological Correlates of Locomotor Specialization in Vipers

Ecomorphological studies of terrestrial vertebrates typically focus on limbed species despite the ecological diversity of some limbless taxa, particularly snakes. A few studies have uncovered body shape differences between arboreal and terrestrial snakes, but these generally considered few morphological characters and/or included few species. Additionally, they were limited by the available phylogenies and statistical methods. Using a recently published phylogeny that includes 79% of extant viper species, we tested whether arboreal or sidewinding specialists differ in body shape from terrestrial generalists. We took several measurements from museum specimens: snout-vent length (SVL); width and circumference at 25%, 50%, and 75% of SVL; tail length; head length and width; and number of pre-caudal vertebrae. We then calculated an elongation ratio by dividing the total length of the animal by the largest of the three width measurements and relative tail length by dividing tail length by SVL. We used phylogenetic PCA to determine whether arboreal or sidewinding species generally occupy different regions of morphospace than terrestrial generalists. We found that arboreal species differ from terrestrial species in overall body shape, with relatively longer tails, higher elongation, and lateral compression. While sidewinding species did not differ from terrestrial generalists in their average body shape, they occupied much less of the morphospace, perhaps as the result of ecological or functional constraint.

0383 AES GRUBER AWARD II, Wedgewood, Thursday 13 July 2017

Thomas C. TinHan[1], J. Marcus Drymon[2], Brett Falterman[3], Gregory W. Stunz[4], Matthew J. Ajemian[5], John A. Mohan[1], Eric R. Hoffmayer[6], William B. Driggers III[6], Jennifer A. McKinney[3], R. J. David Wells[1]

[1]Texas A&M University at Galveston, Galveston, Texas, USA, [2]University of South Alabama, Mobile, Alabama, USA, [3]Louisiana Department of Wildlife & Fisheries, Baton Rouge, Louisiana, USA, [4]Harte Research Institute for Gulf of Mexico Studies and Department of Life Sciences, Texas A&M University – Corpus Christi, Corpus Christi, Texas, USA, [5]Harbor Branch Oceanographic Institute, Florida Atlantic University, Fort Pierce, Florida, USA, [6]National Marine Fisheries Service, Southeast Fisheries Science Center, Mississippi Laboratories, Pascagoula, Mississippi, USA

Space Use and Habitat Preferences of Scalloped Hammerheads in the Northern Gulf of Mexico

The Scalloped Hammerhead (*Sphyrna lewini*) is a circumglobally distributed species common in coastal habitats ranging from temperate to tropical waters. Within the Gulf of Mexico (GoM), coastal and continental shelf waters are considered to be essential habitat for various life stages of *S. lewini*. However, there is limited information regarding individual patterns of movement and space use of *S. lewini* in the GoM, and those factors influencing habitat preference. From March 2013-November 2015, 38 *S. lewini* (102-220 cm fork length) were equipped with Smart Position or Temperature (SPOT) transmitting tags in the northern GoM. Mean squared distances from centers of activity and linearity indices calculated for individual tracks indicated the majority (53%) of sharks exhibited site fidelity to home ranges dispersed across the continental shelf and slope habitats within the GoM. Individual variation was observed in home range size, with core use areas (50% kernel density estimates) of 33.5 ± 95.6 km^2 (median ± IQR). Here we discuss the distribution and movement patterns of *S. lewini* in the northern GoM, and the results of generalized additive models and preference indices investigating the role of environmental variables (e.g. bathymetry, temperature, chlorophyll-a) in driving patterns of space use. These results may be used in the assessment of spatially or temporally explicit management strategies aimed at mitigating bycatch mortality of this species in the northern GoM.

0072 Herp Ecology II, Pecos, Friday 14 July 2017

Brian Todd, Justin Nowakowski

UC Davis, Davis, CA, USA

Meta-Analysis of Telemetry Studies Reveals Surprising Patterns of Home Range Scaling in Snakes

Home ranges increase in size with an animal's body size and subsequent energy needs. Mate searching can also drive an animal's space use, usually resulting in males having larger home ranges than females in most well-studied vertebrate groups. The extent to which these patterns apply generally to snakes remains untested, but a growing number of radio-telemetry studies in recent decades makes possible broad scale analyses for the first time. We obtained data on snake home ranges from nearly 100 published radio-telemetry studies, theses, and unpublished reports to examine which factors shape home

range size in snakes. As expected, home range size increased with body size of species, but the rate of this increase was much lower than that known for endotherms, possibly owing to the greater energy efficiency provided by ectothermy. On average, males also had larger home ranges than did females, with this relative difference paralleling that of body size between the sexes. After controlling for sexual size dimorphism, however, the extent to which males had larger home ranges than females was positively correlated with mean annual temperature and net primary productivity at study sites, suggesting, perhaps, that males are able to undertake more extensive mate-searching as energy becomes more plentiful in an area. Our results show that, although home range scaling in snakes is qualitatively similar to that of many other vertebrates, ectothermy and energy availability at a given site result in surprising macroecological and ecological patterns of space use scaling in snakes.

0227 AES Reproduction, Pecos, Sunday 16 July 2017

Taketeru Tomita, Ryo Nozu, Masaru Nakamura, Keiichi Sato

Okinawa Churashima Foundation, Motobu, Okinawa, Japan

Oxygen-diffusion capacity of the white shark uterus: Oxygen delivery to an embryo without a placenta

One of the mysteries of shark viviparity is how embryos acquire oxygen from their mother without a placental connection. It has been assumed that embryonic respiration in the viviparous shark mainly depends on oxygen from the uterine wall, although this hypothesis has not been tested quantitatively. Morphological observations and measurements of the uterine wall of the white shark (*Carcharodon carcharias*) provided the first quantitative evidence in support of the ability of the uterus to supply ample oxygen to the embryo of viviparous elasmobranchs. The uterine surface of the white shark is characterized by (1) uterine lamellae developed perpendicular to the uterine wall, (2) uterine lamellae folded in an accordion-like fashion, and (3) numerous micro-ridges developed on the lamellar surface. Because of these modifications, the surface area is increased 55-fold in comparison with that in species having smooth uterine surfaces, and the total surface area of a uterus was c.a. 20 m^2. Histological observations showed that the gas-diffusion barrier of the uterine wall is approximately 12 µm. Using these values, the oxygen-diffusion capacity of 1 cm^2 of the uterine wall of the white shark was estimated to be 59.5 $nmol \cdot min^{-1} \cdot torr^{-1}$. This value is 250-400 times greater than that observed in other viviparous sharks (*Squalus* spp.) and is comparable to that of fish gills.

0691 Herp Environment, Brazos, Saturday 15 July 2017

Brian Tornabene[1], Andrew Blaustein[2], Cheryl Briggs[3], Jason Rohr[4], Jason Hoverman[1]

[1]*Purdue University, West Lafayette, IN, USA,* [2]*Oregon State University, Corvalis, OR, USA,* [3]*University of California, Santa Barbara, Santa Barbara, CA, USA,* [4]*University of South Florida, Tampa, FL, USA,* [5]*University of Colorado at Boulder, Boulder, CO, USA*

Assessing the Influence of Spatial and Environmental Factors on Ranavirus Epidemiology in a California Amphibian Assemblage

A fundamental goal of disease ecology is to determine the spatial and environmental processes driving disease dynamics. Ranaviruses are emerging pathogens of amphibians, yet few studies have conducted comprehensive field surveys to assess potential drivers of disease dynamics on the landscape. Using field surveillance data, model selection, and multimodel inference, we examined the factors underlying patterns in site-level ranavirus presence and individual-level ranavirus infection in an amphibian assemblage in the East Bay region of California. Multiple spatial, abiotic, and biotic variables influenced patterns in ranavirus epidemiology. Wetlands in closer proximity to ranavirus-positive wetlands had a higher probability of ranavirus presence and infection suggesting that adult amphibians could play an important role in moving ranavirus between nearby ponds. We also found that ranavirus presence and infection were greater in wetlands with greater density indicating that transmission is density-dependent. Additionally, the probability of ranavirus presence and infection were higher in wetlands with greater total species richness and vertebrate richness, respectively, which provides evidence for an amplification effect. We also found several factors that were only associated with individual-level infections. Contrary to previous findings, bullfrogs reduced the risk of infection suggesting that they may function as dilution hosts. Collectively, our study demonstrates that an array of spatial and environmental factors can influence ranavirus epidemiology. Further investigations of these factors will help broaden our understanding of ranaviral disease dynamics in amphibian assemblages and wetland communities.

0860 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Ruben Tovar[1], Paul Gignac[2], Ron Bonett[1]

[1]*The University of Tulsa, Tulsa, OK, USA,* [2]*Oklahoma State University Center for Health Sciences, Tulsa, OK, USA*

Diffusible Iodine-based Contrast-enhanced Computed Tomography (diceCT), a novel approach to the comparative anatomy of degenerate neural structures; examples from the central Texas *Eurycea*

The paedomorphic *Eurycea* salamander clade of Central Texas exemplifes a continuum of morphological characteristics associated with aquatic-subterranean living: the surface-dwelling Texas salamander (*E. neotenes*) exhibits typical optic anatomy and acuity; the intermediate Comal blind salamander (*E. tridentifera*) maintains reduced but non-functional eyes; and the obligate subterranean Texas blind salamander (*E. rathbuni*) has an incompletely developed optic system. Together this genus represents a transformation series of karst phenotypes and a potentially exemplar system for using

comparative approaches to understanding vertebrate ocular evolution in the face of relaxed selective pressures. More than a century ago Eigenman described ocular histology in *E. rathbuni* adults as a focal troglodyte; yet, neither the extent of optic-nerve persistence in this taxon nor among its congeners has since been documented. In this study we employed gross and micro-scale imaging techniques to elucidate features of *Eurycea* optic anatomy with a particular interest in the central nervous system. Specimens from aforementioned taxa were fixed with 100% EtOH, contrast-enhanced with alcoholic iodine (I_2E), micro-CT scanned, and digital reconstructed using 3D rendering software for comparison to histological sections. Here we report on the 3D, internal soft-tissue systems of the eye in each taxon, documenting habitat-specific configurations of optic musculature and neuroanatomy for the first time—including for *E. rathbuni,* which surprisingly appears to retain complete bilateral optic nerves even though it lacks the mid-line decussations associated with an optic chiasm.

0031 Lightning Talks II, Glass Oaks, Friday 14 July 2017

Stan Trauth[1], Dustin Siegel[2], Steve Godley[3], Zachary Adcock[4], Roy McDiarmid[5]

[1]Arkansas State University, State University, AR, USA, [2]Southeast Missouri State University, Cape Girardeau, MO, USA, [3]Cardno ENTRIX, Riverview, FL, USA, [4]University of South Florida, Tampa, FL, USA, [5]National Museum of Natural History, Washington, DC, USA

Testicular Histology and Spermatogenic Stages in the Everglades Dwarf Siren, *Pseudobranchus axanthus belli* (Caudata: Sirenidae), from South-central Florida

We examined the testicular histology of 32 adult male Everglades Dwarf Sirens (*Pseudobranchus axanthus belli*) collected at Rainey Slough (Glades County), Florida, during 1974-75 and 1981. The salamanders were returned to the lab at the University of South Florida, euthanized in a dilute chloretone solution, fixed in 10% formalin, and deposited into the herpetological collection at the university. In 1982, the testes and attached kidneys were removed, measured, and massed by SET and JSG and prepared for light microscopy using routine histological techniques by SET. The Rainey Slough samples of *P. axanthus belli* are currently deposited at the Smithsonian Institution National Museum of Natural History. The process of spermatogenesis was evident throughout all regions of the testes and appeared to occur year-round. The testes contain numerous, spherical-to-oblong testicular lobules that vary greatly in size. Unlike all other salamanders, which exhibit cystic spermatogenesis along with a caudo-cephalic wave of maturing cell types (leading to spatial and temporal segregation of germ cells), spermatogenesis in *P. axanthus* lacks testicular cysts. Instead, the testicular lobules possess an assortment of different spermatogenic stages.

0659 Herp Genetics, San Antonio, Saturday 15 July 2017

Alexa Trujillo[1], Matthew Lawrance[1], Kiernan Oknefski[1], Richard Seigel[2], Anna Savage[1]

[1]*University of Central Florida, Orlando, FL, USA,* [2]*Towson University, Towson, MD, USA*

Evolutionary Dynamics of an Expressed Class II MHC Gene in Ranid Frog Populations Impacted by Emerging Infectious Diseases

A major cause of global amphibian declines is disease caused by infectious pathogens such as the fungus *Batrachochytrium dendrobatidis* (Bd) and the virus Ranavirus (Rv). Disease susceptibility and host immunogenetics are linked across a wide range of vertebrate animals. However, in amphibians, the relationship between host genetics and host susceptibility to disease is not well known for most taxa. Major histocompatibility complex (MHC) genes encode cell surface proteins that bind to and display pathogen antigens for T-cell recognition, and are therefore essential for generating acquired immune responses. In this study, we use amplicon sequencing to characterize an expressed class II MHC gene within and among populations of multiple North American ranid frog species. We also use quantitative polymerase chain reaction (qPCR) to measure prevalence and intensity of Bd and Rv for each individual. Subsequently, we test for significant associations between MHC genotype and the presence and intensity of Bd and Rv infection. To parse the roles of selection and demography in driving MHC evolution, we also sequence mitochondrial loci ND1 and ND2 across individuals as a metric of neutral population genetic diversity. Finally, we reconstruct a Bayesian genealogy of all recovered MHC alleles to assess trans-species polymorphism and lineage- and site-specific evidence of positive selection. Our study provides enhanced understanding of the link between adaptation to disease and MHC genotypes in North American amphibians, which can ultimately improve conservation and management efforts to prevent future declines.

0282 Herp Biogeography & Phylogeography I, Brazos, Sunday 16 July 2017

Derek Tucker[1], Jack Sites, Jr.[2], Tomas Hrbek[3], Adam Leache[13], Nelsy Rocío Pinto-Sánchez[4], R. Alexander Pyron[5], Miguel Rodrigues[6], Omar Torres-Carvajal[7], Giuseppe Gagliardi Urrutia[8], Pablo Venegas[9], Laurie Vitt[10], Fernanda Werneck[12], Guarino Colli[11]

[1]*University of West Florida, Pensacola, FL, USA,* [2]*Brigham Young University, Provo, UT, USA,* [3]*Universidade Federal do Amazonas, Manaus, Brazil,* [4]*Universidad de los Andes, Bogotá, Colombia,* [5]*The George Washington University, Washington, D.C., USA,* [6]*Universidade de São Paulo, São Paulo, Brazil,* [7]*Pontificia Universidad Católica del Ecuador, Quito, Ecuador,* [8]*Instituto de Investigaciones de la Amazonia Peruana, Iquitos, Peru,* [9]*Centro de Ornitología y Biodiversidad, Lima, Peru,* [10]*University of Oklahoma, Norman, OK, USA,* [11]*Universidade de Brasília, Brasília, Brazil,* [12]*Instituto Nacional de Pesquisas da Amazônia, Manaus, Brazil,* [13]*University of Washington, Seattle, WA, USA*

Species Boundaries and Phylogeography of the Widespread Giant Ameiva (*Ameiva ameiva*: Teiidae)

There has been a myriad of hypotheses put forth to explain the extreme biodiversity in the South American tropics. The Giant Ameiva (*Ameiva ameiva*) has an extremely large geographic distribution naturally occurring in much of South America east of the Andes as far south as northern Argentina. A lack of genetic data has resulted in taxonomic disagreement surrounding subspecies designations and species delimitation and its huge distribution across five major biomes suggests a complex phylogeographic history. We aim to generate the first rangewide genetic dataset for the *A. ameiva* complex to be used in combination with morphology to discover unique evolutionary lineages within the group and propose hypotheses about the origins of these lineages. Our complete alignment of the mitochondrial gene ND2 included 1,119 bp of DNA for 357 samples and recovered six well-supported clades. An examination of species boundaries using the GMYC model was supported by discriminant analysis of principal components and showed that *A. ameiva* may consist of up to six species, with mitochondrial divergences among these lineages ranging from 4.7–12.8%. Expectations of the riverine barrier hypothesis are not observed across much of the distribution, however, phylogeographic structure and divergence time estimates demonstrate that marine incursions or the presence of a large lake 'Lago Amazonas' that covered much of the Amazon basin may have played a role shaping genetic patterns. We have also generated a large SNP dataset for 280 individuals and are currently analyzing these data for comparison to the mtDNA.

0517 ASIH STOYE GENERAL ICHTHYOLOGY I, Trinity, Thursday 13 July 2017

A.J. Turner, Fernando Aldo, Prosanta Chakrabarty

Louisiana State University, Baton Rouge, LA, USA

Range-wide genetic and morphological variation in the sailfin molly, *Poecilia latipinna*

The sailfin molly, *Poecilia latipinna*, is part of the subgenus *Mollienesia* (Cyprinodontiformes: Poeciliidae) that diversified 1.1 – 4.0 Mya in Central America and expanded northward into Mexico and the Southeastern United States. Out of the 26 species within *Mollienesia*, *P. latipinna* has the northernmost distribution, which spans continuously from Mexico to Florida and reaches as far north as South Carolina. Across their wide distribution, sailfin mollies can be found in a variety of fresh and brackish water habitats. Living in such a variety of habitats has been known to facilitate phenotypic differences between populations, however, studies of this nature focused almost exclusively on variation at the local or regional scale, and the general patterns and drivers for this variation are unknown. The goal of this study was to test whether ecological or geographic barriers influence the morphological and genetic structure of *P. latipinna* throughout the species' entire range. Geometric morphometrics were used to identify morphological variation between different habitat types (e.g., freshwater streams and estuarine salt marshes) to explore if disjunct populations showed morphological convergence in similar environments. Genetic data were obtained to identify population structure throughout the range of *P. latipinna*, which provided further insights into the role that both geology and ecology played in shaping variation within this widely-distributed species.

0060 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Peter Uetz[1], Paul Freed[2], Jiří Hošek[3]

[1]Virginia Commonwealth University, Richmond, VA, USA, [2]The Reptile Photo Database, Scotts Mills, OR, USA, [3]Reptarium, Ostrava, Czech Republic

The Reptile Database: new developments

The Reptile Database (http://www.reptile-database.org) was founded in 1996 as EMBL Reptile Database and has evolved into a major online resource for systematic herpetology (for a brief history see Uetz 2016, *Herp. Rev*. 47: 330). Currently (March 2017) the database lists 10,520 species and 2,474 subspecies, although these numbers change almost daily. All species have distribution information and their original citations, with a total of 41,524 literature records of which 25,179 were linked to web sites where they can be obtained (many at the Biodiversity Heritage Library and other public sites). At the time of this writing, 3,373 species had diagnoses, 4,316 had etymologies, 10,208 had type localities (many with coordinates that are mapped to Google maps online), and 10,386 had type information (i.e. museum specimens). Currently the database receives ~ 35,000 visits and ~200,000 page views a month. This spring we exceeded 10,000 user-submitted photos representing 3,800 species. We also expect to make available maps to most reptile species world-wide this year. The database has enough data to make it useful for research projects, e.g. macro-ecology, species identification, or large-scale phylogenetics projects. Examples of ongoing research are presented.

0244 Fish Biogeography & Morphology, Trinity, Saturday 15 July 2017

Peter Unmack[1], Mark Adams[2], Christine Thacker[3]

[1]University of Canberra, ACT, Australia, [2]South Australian Museum, SA, Australia, [3]LA County Museum, CA, USA

Hemi-clonal unisexual carp gudgeons (Eleotridae: *Hypseleotris*): systematic clarification of species boundaries and various hybrid lineages in southeastern Australia

Carp gudgeons (Eleotridae: *Hypseleotris*) are the most abundant, widespread and biodiverse freshwater fishes in southeastern Australia, but the unacknowledged presence of multiple cryptic species and hemi-clonal unisexual lineages severely taints all research on this cornerstone group. Our goal is to help correct past taxonomic shortcomings and supply a valid framework for future study, by giving researchers a true picture of the group's biodiversity plus the means to accurately identify all sexual and unisexual forms in this key group. We used three genetic datasets including allozymes (52 loci), mtDNA (cytochrome b) and ddRADSeq (>10,000 SNP loci) to examine species and lineages across their entire range in southeastern Australia where most habitats contain 2-4 sympatric species and additional hemi-clonal lineages. One key finding was a single sexual population of Lake's carp gudgeon which is of critical conservation and research concern as every other population examined of Lake's carp gudgeon are F1 hemi-clonal hybrids. For more details all about this group you'll have to come and see my talk!

0243 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Peter Unmack[1], Mark Adams[2], Dean Gilligan[3], Andrzej Kilian[4]

[1]University of Canberra, ACT, Australia, [2]South Australian Museum, SA, Australia, [3]DPI Fisheries NSW, NSW, Australia, [4]Diversity Arrays Technology, ACT, Australia

Are specific populations of key threatened Murray-Darling Basin fishes native or introduced?

Many Murray-Darling Basin (MDB) freshwater fishes have experienced extreme declines, with around a quarter of the freshwater fishes threatened with extinction. Here we target three native fishes that were once widespread across the MDB, but today have all had significant declines (Purple Spotted Gudgeon, Olive Perchlet and Darling Hardyhead). Remnant populations are extremely geographically limited, with some recently discovered populations occurring outside of the perceived natural range of the species. Existing genetic data have been unable to clarify whether these populations are endemic or translocated. Recovery actions for remnant populations are consequently very difficult to prioritise. We are now applying genetic data from thousands of loci from next generation double digest RAD sequencing, coupled with comprehensive sampling from all potential source populations. Together this should unequivocally distinguish the native status of each population. It will also provide key information regarding each population’s genetic diversity, divergence between populations and whether any loci appear to be related to potential local adaptations. These results can then be used to guide reintroduction efforts and conservation strategies.

0022 Herp Morphology & Development, Brazos, Saturday 15 July 2017

Nicole Valenzuela, Srihari Radhakrishnan, Robert Literman

Iowa State Institution, Ames, IA, USA

Sexually dimorphic DNA methylation of sex-determining genes in TSD painted turtle hatchlings and their historic methylation revealed by genome-wide analyses

DNA methylation alters gene expression but not DNA sequence, mediates phenotypic plasticity, and depends on genomic CpG distribution. Temperature-dependent sex determination (TSD) epitomizes phenotypic plasticity. Yet, how extensive is the link between DNA methylation and TSD remains unclear. Here we test for broad differences in genome-wide DNA methylation between male and female hatchling gonads of the painted turtle *Chrysemys picta* (TSD) using Methyl DNA Immunoprecipitation sequencing (MeDIP-seq), to identify differentially methylated candidates for future study, including genes involved in vertebrate gonadal development and other potential mediators of TSD sex-specific development (genes of the epigenetic machinery, hormonal pathways, sensing responses). We also examine the genome-wide nCpG distribution in painted turtles, compare it other vertebrates, and test for historic methylation in genes regulating vertebrate sex determination/differentiation. We discuss our finding of sexually dimorphic DNA methylation in turtle gonads, its potential mediators and implications for the regulation of thermosensitive transcription in TSD vertebrates. Sexually dimorphic methylation of sex-determining genes in TSD turtle hatchlings and their historic methylation revealed by genome-wide analyses.

0671 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Maria C. Vallejo-Pareja[1], Juan D. Daza[1], Jessica A. Maisano[2], Monte L. Thies[1]

[1]*Sam Houston State University, Huntsville, Texas, USA,* [2]*The University of Texas at Austin, Jackson School of Geosciences, Austin, Texas, USA*

Consequences of Miniaturization in the Cranial Osteology of Lizards and Snakes

Miniaturization, the development of extreme body size, has evolved in at least 24 families within Squamata. In miniaturized skulls (~ 15 mm skull length or less), the space between the otic capsules is minimal. Given the large number of miniaturized groups, a general review of this evolutionary process and its consequences in the squamate skull is warranted. In this review, we assemble morphological changes previously attributed to miniaturization, together with new observations. General cranial features of miniaturized squamates include: 1) The relative increase in size of the neurocranium and its positioning at the same level as the dermatocranium; 2) the occipital condyle located at the posterior-most position of the skull; 3) the closure or reduction of the post-temporal fenestra; 4) the proportional expansion of the otic capsules; 5) elongation of the skull, with a 1:1 proportion between the snout and parietal units; 6) widening of the snout; and 7) short and stout paroccipital processes. Although a combination of these features is common among small squamates, at extreme miniaturization some groups exhibit morphological disparities. For example, small chameleons (*Brookesia minima*) have a short and anteroposteriorly compressed snout, resulting in a shortened skull, while small geckos have long (*Sphaerodactylus ariasae*) or shortened (*Chatogekko amazonicus*) snouts. Furthermore, while the majority of miniaturized squamates undergo closure of the post-temporal fenestra, in dwarf chameleons this opening remains open and proportionally large. Although miniaturization might also produce many convergent features among squamates (e.g., fossorial reptiles), in some groups (e.g., Chameleons) it results in distinctive morphologies.

0447 LFC Contributed III, San Marcos, Saturday 15 July 2017

Cindy van Damme[1], Niels Hintzen[1], Frank Kleissen[2], Loes Bolle[1], Matthias Kloppmann[3], Richard Nash[4]

[1]Wageningen Marine Research, IJmuiden, The Netherlands, [2]Deltares, Delft, The Netherlands, [3]Thünen Institute of Sea Fisheries, Hamburg, Germany, [4]Institute of Marine Research, Bergen, Norway

Improving Larvae Survey Indices: A case study of North Sea Herring

Recruitment is one of the major drivers of fish stock dynamics. Getting a correct perception of recruitment is therefore essential for fisheries management. Its prediction still is one of the most difficult aspects in fish stock dynamics to forecast, even if dedicated surveys are in place to sample larvae or juveniles. In the case of North Sea herring (*Clupea harengus*) there is a larvae survey (IHLS) for estimating the Spawning Stock Biomass and a later larvae survey (IBTS-MIK) for estimating recruitment. Once considered as a very good predictor of herring recruitment, in recent years the MIK index has become a poorer forecaster because the samples collected do not cover the offspring of the entire North Sea stock: only the autumn spawning component is sampled while the later winter spawning component is ignored. The mismatch is in that the IHLS gives an estimate of the whole North Sea stock, whereas the MIK recruitment index does not. A solution is to use a combination of larval drift modelling with data from the IHLS and including data from the MIK that was not previously used for estimating the recruitment index, along with simulation modelling to test if changes in survey design and the estimation procedures can provide more realistic estimates of SSB and recruitment. These simulations can also investigate whether it is advantageous to implement a new survey to estimate recruitment of the winter spawning component and thus, in combination with the standard MIK index, provide a recruitment index for the whole stock.

0783 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Robin Van Meter, Rose Adelizzi

Washington College, Chestertown, MD, USA

Pesticide and Fertilizer Effects on Corticosterone Production in Juvenile Amphibians

Agrochemicals, primarily pesticides and fertilizers, are used regularly to control damaging crop organisms and to increase crop productivity and yield. Their widespread use throughout agriculturally intensive landscapes makes these chemicals a risk factor for non-target organisms, both during and after application. Given the long-distance movement of amphibians to and from breeding ponds, often through croplands, exposure and susceptibility to agrochemicals is highly probable. In an effort to close our knowledge gaps on the combined effects of pesticides and fertilizers on terrestrial phase amphibians, this study was designed to explore bioaccumulation and stress response in Southern leopard frogs (*Rana sphenocephala*). Juvenile frogs were exposed to three agrochemicals in a factorial design including atrazine, alachlor and urea, 2 herbicides and a fertilizer, respectively, at the labeled application rate on natural soils for 8-hours. Following chemical exposure, all frogs were transferred into clean bowls filled with 150mL distilled water for 1 hour to measure stress response. Frogs were extracted as whole-body homogenates for pesticide analysis using GC-MS and water samples processed for corticosterone (stress hormone) production using Caymen Chemical ELISA kits. The mixture containing all 3 agrochemicals resulted in significantly greater corticosterone production (ANOVA p=0.002) indicating an elevated stress response among exposed frogs. Amphibians are most active during the same time of year that crops are grown and harvested, therefore gaining knowledge on the short- and long-term impacts of agrochemicals on terrestrial amphibians is essential for improved conservation efforts.

0814 AES Behavior, Pecos, Sunday 16 July 2017

Jeremy Vaudo[1], Heidi Dewar[2], Michael Byrne[1], Bradley Wetherbee[3], Mahmood Shivji[1]

[1]Nova Southeastern University, Dania Beach, FL, USA, [2]National Marine Fisheries Service, Southwest Fisheries Science Center, La Jolla, CA, USA, [3]University of Rhode Island, Kingston, RI, USA

Coupling of horizontal and vertical movements of shortfin mako sharks (*Isurus oxyrinchus*) in the eastern North Pacific Ocean

The pelagic environment represents a three-dimensional landscape, however, shark movement studies often focus on only two dimensions (i.e., horizontal movements). Combining data sets on horizontal movements with vertical movements provides a much more detailed view of movement behaviors and habitat use. The shortfin mako shark (*Isurus oxyrinchus*) is a wide ranging species found in temperate and tropical waters worldwide. Although horizontal and vertical movements of this species have been examined at various scales, there has been little work uniting these movements. To investigate the relationship between horizontal and vertical movements of juvenile mako sharks in the eastern North Pacific Ocean, 35 mako sharks (114 - 245 cm FL) were

double-tagged with Pop-up Archival and Transmitting (PAT) and Smart Position or Temperature Transmitting (SPOT) tags within the Southern California Bight between 2003 and 2008. We examined the depth distributions of these individuals after their horizontal movements were first classified into one of two behavioral modes (area-restricted movements or transiting) using a switching state-space model. During the transiting mode, proportion of daytime spent shallower than 10 m was relatively consistent (~57%) regardless of the thermal characteristics of the water column. Except for in the coolest water columns, mako sharks spent less time shallower than 10m while displaying area-restricted movements, possibly related to foraging.

0258 ASIH STORER ICHTHYOLOGY; Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Diego Vaz, Eric Hilton

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

Title: Morphological Variation of the Swimbladder of Toadfishes (Percomorphacea: Batrachoidiformes)

Batrachoidiformes, the Toadfishes, comprises 82 species of bottom-dwelling fishes that live in temperate and tropical coastal areas of all oceans around the world. These fishes are capable of a wide variety of vocalizations that are used for mating and nest defense. The sound is produced by sonic muscles attached to the swimbladders. The swimbladders of Batrachoidiformes are unique, being formed by two lobes. Previous studies proposed that a heart-shaped swimbladder is a synapomorphy of Batrachoidiformes, although there has yet to be a survey of this character across the diversity of Toadfishes. Morphological variation in this organ was examined through manual dissection of specimens of 34 species (in 16 genera) were examined, broadly representing the four currently accepted subfamilies of Batrachoidiformes. The level of separation between the lobes is variable among subfamilies: the lobes of the swimbladder of Thalassophryine, Batrachoidinae and Porichthyinae are separated anteriorly, but fused posteriorly. Species of Halophryinae share an almost complete separation of the lobes, with the left and right connected only by a small trunk in the postero-ventral surface of the swimbladder. Unlike all other subfamilies, which have rounded anterior edges of the lobes of the swimbladder, these lobes were found to be angular in representatives of Porichthyinae. Sexual dimorphism of the size of the swimbladder is present, with males usually having larger swimbladders than females. The sexual dimorphism, however, is not reflected in the degree of separation between lobes or in the shape of anterior edges of swimbladder.

0254 ASIH STOYE GENERAL ICHTHYOLOGY III, Trinity, Friday 14 July 2017

Diego Vaz[1], Eric Hilton[1], Adam Summers[2]

[1]*Virginia Institute of Marine Science, College of William & Mary, Gloucester Point, VA, USA,* [2]*Friday Harbor Laboratories, University of Washington, Friday Harbor, WA, USA*

Title: The Intermuscular Bones and Ligaments of Batrachoidiformes (Percomorphacea: Teleostei)

Intermuscular bones are ossifications that develop directly in the myosepta and generally are associated with series of ligaments. Intermuscular bones are categorized into three main series: epineurals (dorsal to the horizontal septum); epicentrals (in the horizontal septum); and epipleurals (ventral to the horizontal septum). Batrachoidiformes, the Toadfishes, is a monophyletic group of bottom-dwelling fishes described as having only the epineural series, in which the first epineural is enlarged and articulates with the cleithrum. Although the arrangement of the first epineural has been proposed as a synapomorphy of Batrachoidiformes, variation in the intermuscular complex across different species of toadfishes is unknown. Additionally, the interrelationships among species of Batrachoidiformes and its relationship to other percomorph fishes are unclear. To assess variation in this skeletal complex, representatives of the four sub-families of Batrachoidiformes were examined using CT-scans and cleared-and-stained specimens, with the goal of identifying characters that may be phylogenetically informative. The unique morphology of the first epineural was found in all examined species of Batrachoidiformes and seems unique among fishes. The second epineural (en2) in Halophryinae originates on the second neural spine; in Thalassophryinae, en2 articulates with the first neural spine; and in Batrachoidinae, en2 is is reduced. In Porichthyinae, the second and third epineurals are absent. Epicentrals, not reported previously in Batrachoidiformes, were found as both ligament (in all species) and bone (only in *Barchatus, Chatrabus*, *Colletteichthys*, *Halobatrachus*, *Perulibatrachus* and *Riekertia*). The implication of these characters for reconstructing the phylogenetic relationships within Batrachoidiformes will be discussed.

0221 LFC Contributed I, San Marcos, Friday 14 July 2017; LFC SALLY L. RICHARDSON BEST STUDENT PAPER

Sebastian Velez, Jon Moore

Florida Atlantic University, Boca Raton, Florida, USA

Larval and Juvenile Population Dynamics of Families Lutjanidae and Serranidae in the Gulf of Mexico, with Respect to the Loop Current and other Hydrographic Features

The Gulf of Mexico (GoM) is a dynamic environment with a variety of hydrographic features and oceanographic processes taking place. These features include; the Loop Current, cyclonic and anticyclonic eddies, and the Mississippi River Plume, all of which are important drivers of the biological processes in the GoM. Identifying the role these features play in the transportation of larval and juvenile nearshore species to offshore

environments is vital to resource managers. This information would allow managers to account for future changes to the environment and the effect large scale disturbances could have on economically important fish species. The long term larval and juvenile population dynamics of families Lutjanidae (snappers) and Serranidae (groupers) have been of great interest from a biological and economic perspective. These families represent many of the large predators found in reef ecosystems and are some of the most valuable fisheries in the GoM. Using data collected after the Deepwater Horizon Oil Spill (DWH) via the NOAA Natural Resource Damage Assessment in 2011 as well as from cruises conducted by the Deep Pelagic Nekton Dynamics of the Gulf of Mexico Consortium (www.DEEPENDConsortium.org) from 2015-2017. In comparing these two datasets we hope to identify the potential effects the DWH Spill had on these fishes and the role these oceanographic features play on their population dynamics.

0903 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Joaquin Villamil[1], Luciano J. Avila[2], Mariana Morando[2], Raul Manyero[1], Jack W. Sites, Jr.[3], Arley Camargo[4]

[1]Univ. de la Republica, Montevideo, Uruguay, [2]Centro Nacional Patagonico, Puerto Madryn, Chubut, Argentina, [3]Univ. de la Republica, Montevideo, Uruguay, [4]Brigham Young Univ., Provo, Utah, USA, [5]Univ. de la Republica, Rivera, Uruguay

Species limits and divergence times of lizards of the *Liolaemus wiegmannii* complex (Duméril & Bibron 1837) (Squamata: Liolaemidae)

Liolaemus wiegmannii together with 11 other species is part of the *wiegmannii* group, a clade of mainly arenicolous lizards whose monophyly is strongly supported. It is a species with wide distribution over several provinces of the center, center-south and northwestern of Argentina, as well as a great part of the coastal belt of southwestern and south of Uruguay. However, numerous authors have suggested that it could be a species complex. Here, we test the hypothesis of multiple species within *L. wiegmannii* and estimate the divergence times between independent lineages. We analyzed sequences of the cytochrome b gene and two nuclear loci (KIF24 and PRLR) with a Bayesian inference approach based on the multi-species coalescent. We infer species delimitation with Beast 2 STACEY, and the divergence times with the Beast 1.8 starBeast tool. The results support the hypothesis that *L. wiegmannii* includes at least four candidate species whose divergences would have begun in the early Pleistocene. The first split separated the complex into a sand-dune lineage, distributed in central-southern Argentina and Uruguay, and another present in no-dune habitats of northwestern Argentina. Thus, the early speciation of the complex may have been influenced by the expansion of the sand dunes in the Pampa and northern Patagonia during the last great Patagonian glaciation (approximately 1 million years ago).

0794 General Herpetology, Sabine, Sunday 16 July 2017

Andrea Villamizar-Gomez, William Keitt, Zachary Adcock, Dittmar Hahn, Michael Forstner

Texas State University, San Marcos, TX, USA

Prevalence of chytrid fungus (*Batrachochytrium dendrobatidis*) in the Jollyville Plateau Salamanders (*Eurycea tonkawae*) and its correlation with microhabitat

Batrachochytrium dendrobatidis (*Bd*), is a fungus that causes chytridiomycosis on infected amphibians, and has been implicated as a potential causative agent in some amphibian population declines. This study is a multi-year evaluation of prevalence of *Bd* in a population of salamanders, *Eurycea tonkawae*, in Central Texas across. We visited 7 sampling sites monthly (2013 - 2016) and evaluated possible relationships among microhabitat data and water chemistry measurements including temperature, pH, dissolved oxygen, turbidity, and conductivity to seasonal and site prevalence of *Bd* for more than 700 samples. Each salamander swab was assessed for the presence of the pathogen using a Taqman quantitative real-time PCR (*q*PCR) assay. Over the period the highest overall prevalence was 46% in 2013 and the lowest prevalence was 14% in 2014. It remains unknown if *Bd* has a harmful impact on this population of salamanders. Further monitoring of pathogen detection and the state of the population remain key components to determining how, or if, *Bd* affects the salamander population.

0430 ASIH STOYE GENETICS, DEVELOPMENT, & MORPHOLOGY II, Trinity, Friday 14 July 2017

Kirill Vinnikov, Kathleen Cole

University of Hawaii at Manoa, Honolulu, HI, USA

Exon Capture Sequencing of Amphidromous Gobies from the Genus Stenogobius (Teleostei: Gobiiformes)

Amphidromous gobies from the genus *Stenogobius* represent an extremely widespread group of Indo-Pacific fishes, which occur in almost every coastal freshwater stream of South-East Africa, South and South-East Asia and of most Central Pacific islands, including Hawaii. An amphidromous life cycle means that individuals live and reproduce in a freshwater environment during their adult stage. Larvae upon hatching passively drift to the ocean for a marine pelagic larval period, before returning to a freshwater stream and transforming into adult. It is still not clear whether marine larvae of *Stenogobius* species can disperse widely between the islands and archipelagos during a single life cycle, or whether they stay close to their natal streams. The goal of the current study is to investigate the population structure of *Stenogobius* species on selected Central Pacific Islands by using the exon capture sequencing approach. Here we provide our preliminary results on the population structure of *Stenogobius* and describe our experimental pipeline, which allows us to obtain a large amount of sequencing data for numerous coding regions, from hundreds of individuals. The pipeline consists of three steps: 1) transcriptome sequencing and annotation; 2) bait development and exon capture; and 3) exon sequencing with the following alignment of orthologs. The resulting dataset with >2,500 exons for 135 individuals provides the amount of necessary information for recovering fine scale population genetic structure, including genes under selection, and for estimating the larval dispersal pathways between islands of the Central Pacific.

0287 AES Ecology II, Glass Oaks, Sunday 16 July 2017

Liz Vinyard[1], Wally Bubley[1], Gorka Sancho[2], Bryan Frazier[1]

[1]South Carolina Department of Natural Resources, Charleston, South Carolina, USA, [2]The University of Charleston, South Carolina, Charleston, South Carolina, USA

Diet of the Finetooth Shark, *Carcharhinus isodon*, in coastal waters of the western North Atlantic Ocean

Diet and trophic interactions are becoming more important to understand ecological roles of organisms which can aid in current management decisions or future management approaches, such as ecosystem based methods. While the Finetooth Shark, *Carcharhinus isodon*, is one of the most abundant shark species in estuarine and nearshore waters in South Carolina, dietary information in the western North Atlantic (WNA) is limited to descriptive studies. This study provides the first quantitative diet study of the WNA Finetooth population using stomach content and stable isotope analysis to evaluate prey importance, trophic level, and to assess ontogenetic overlap. Stomach contents (n = 230) confirmed a teleost diet for all age categories (YOY, 99.8% Index of Relative Importance (IRI), juveniles, 99.8% IRI; adults, 99.9% IRI) with Atlantic Menhaden, *Brevoortia tyrannus,* as the most important prey species. Stable isotope analyses (n = 58) indicated juveniles had a significantly greater reliance on pelagic carbon sources while adults had significantly higher nitrogen ratios indicative of higher trophic level feeding. While dietary overlap between age categories was observed, each category maintained unique isotopic niche space. Juveniles had the smallest combined percentage of dietary niche overlap while adults had the largest. Even with a highly specialized diet, Finetooth Sharks display ontogenetic dietary shifts which have the potential to be driven by habitat usage and suggest the possibility of resource partitioning by age.

0714 Turtle Behavior, Pecos, Friday 14 July 2017

Richard C. Vogt[1], Camila R. Ferrara[0]

[1]Insituto Nacional de Pesquisas da Amazônia, Manaus, Amazonas, Brazil, [2]Wildlife Conservation International Brazil, Manaus, Amazonas, Brazil

Underwater Vocalizations in Freshwater Turtles and Seaturtles may be used for Management and Documenting Presence and Abundance Data

We have been documenting underwater vocalizations in both freshwater and marine turtles in nature for the last several years. We use the term vocalizations in that we now have video recordings of turtles vocalizing underwater and simultaneous muscle movements on the inferior posterior cephalic region suggesting the sounds are being produced in the buccal cavity. Although our most extensive work has been with one freshwater species, the Giant South American River Turtle (*Podocnemis expansa*) in the Brazilian Amazon Basin we have also documented vocalizations in many other freshwater species from both suborders in North and South America, Mexico, Australia and China, as well as all species of seaturtles. The propagation of low frequency sound underwater is an excellent media for long distance communication. We were able to call adult female *P. expansa* from one nesting beach congregation to another 4 km away by conducting underwater playback experiments using the vocalizations they emit when they are ascending the beach to nest. Now that we have verified that some marine turtles are vocalizing underwater during an arribada, we plan to use underwater speakers playing back the vocalizations of the arribada to call turtles into less concentrated nesting areas on the same beach to disperse the nesting activities; now the nests are concentrated in only a 5 km stretch of the 25 km beach in Escobilla, resulting in the loss of 100,000s of eggs due to females destroying nests during their digging of their own nest.

0040 ASIH STOYE CONSERVATION III, San Antonio, Friday 14 July 2017

Anthony W. Waddle, Jef R. Jaeger, Frank van Breukelen

University of Nevada, Las Vegas, Las Vegas, Nevada, USA

Emerging Infectious Disease and the Decline of the Imperiled Relict Leopard Frog

Chytridiomycosis is an emerging infectious disease of amphibians caused by the aquatic fungal pathogen, *Batrachochytrium dendrobatidis* (*Bd*). This pathogen has spread to every continent where amphibians occur, and has been linked to hundreds of species declines and many well-documented extinctions. Prior research into the thermal tolerance of *Bd* suggested that this invasive fungus may not be a threat in hot, arid regions. Recent contradictory evidence, however, prompted us to investigate the occurrence and impact of *Bd* in a frog species of conservation concern in the Mojave Desert. The relict leopard frog was historically more widespread, but now only exists naturally in thermal springs in two general areas in southern Nevada where high water temperatures may provide refuge from *Bd*. We sampled and detected *Bd* within the historical range of the relict leopard frog and in one population of the species. We subsequently performed *Bd* exposure studies to determine the susceptibility of this frog to chytridiomycosis. Our early efforts, using *Bd* strains isolated during die-offs of other anuran species in California, suggested that the pathogen might not be a substantial threat to the relict leopard frog. Our more recent efforts, however, show that *Bd* isolated from southern Nevada, including an isolate from a relict leopard frog, and *Bd* isolated from captive exotic amphibians increased mortality in the species. Our future research will borrow from the creativity of other *Bd* researchers in an effort to provide solutions to the management challenges for the relict leopard frog.

0290 Amphibian Conservation I, Wedgewood, Sunday 16 July 2017

Hardin Waddle[1], Michael Adams[2], Daniel Calhoun[3], Robert Fisher[4], Evan Grant[5], Daniel Grear[6], Brian Halstead[7], Blake Hossack[8], Jeffery Lorch[6], Erin Muths[9], Susan Walls[10], LeAnn White[6]

[1]U.S. Geological Survey, Lafayette, Louisiana, USA, [2]U.S. Geological Survey, Corvallis, Oregon, USA, [3]U.S. Geological Survey, Norcross, Georgia, USA, [4]U.S. Geological Survey, San Diego, California, USA, [5]U.S. Geological Survey, Turners Falls, Massachusetts, USA, [6]U.S. Geological Survey, Madison, Wisconsin, USA, [7]U.S. Geological Survey, Dixon, California, USA, [8]U.S. Geological Survey, Missoula, Montana, USA, [9]U.S. Geological Survey, Fort Collins, Colorado, USA, [10]U.S. Geological Survey, Gainesville, Florida, USA

A National Survey for *Batrachochytrium salamandrivorans* (Bsal) in the United States

Disease is one of many threats to amphibian populations worldwide. The emerging chytrid fungal pathogen *Batrachochytrium salamandrivorans* (Bsal) has caused widespread mortality among salamander species in Europe. Because of the high endemic diversity of salamander species in the U.S., Bsal has the potential to deal a major blow to global salamander diversity if it is introduced and becomes established here. Out of concern for the risk that Bsal poses to U.S. amphibians should it become established, the U.S. Geological Survey conducted a national survey for Bsal in 2016 and 2017. Our objective was to detect Bsal if it was present in wild populations of salamanders. We swabbed the skin of amphibians and used molecular methods (real time PCR diagnostic assay) to detect Bsal and *B. dendrobatidis* (Bd). We primarily sampled newts (*Notophthalmus* spp. and *Taricha* spp.) as they are widespread and abundant salamanders known to be susceptible to Bsal, but 39 other species including anurans were also sampled. Nearly 10,000 samples were collected from more than 390 sites representing 177 counties across 34 states. Whenever possible, a sufficient sample was collected at each site to ensure that Bsal would have been detected with 90% probability, even at a prevalence of 10% within the population. The results of this national survey provide information on the distribution of Bd and Bsal in the U.S. that can be used to update and refine risk assessments for these fungal pathogens.

0169 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Brian Waldron[1], Shawn Kuchta[2], Cari Hickerson[1], Maggie Hantak[2], Carl Anthony[1]

[1]*John Carroll University, University Heights, OH, USA,* [2]*Ohio University, Athens, OH, USA*

Genetic Analysis of Distinct Lineages of *Plethodon cinereus* at a Secondary Contact Zone in Northeast Ohio

Contact zones between species, subspecies, or potentially diverging lineages offer important insights into the processes that maintain reproductive isolation. *Plethodon cinereus*, a highly abundant and wide-ranging terrestrial salamander found in the northeast United States and Canada, provides an excellent model system for studying secondary contact zones. Using mtDNA, six distinct clades have been identified across the range of *Plethodon cinereus*. Populations of two such clades, the Ohio (OH) clade, which dispersed through central Ohio following receding glaciers of the Last Glacial Maximum, and the Pennsylvania (PA) clade, which dispersed through Pennsylvania and then west through northern Ohio, can be found approximately 9.4 km apart in Lorain County, Ohio. I collected tissue samples at 25 sites along an approximate north-south transect following the Black River between two populations with known clade assignment (OH-north and PA-south clades). Ten microsatellite loci and restriction-fragment length polymorphisms of mtDNA were examined to characterize the genetic structure of the contact zone between and surrounding the known populations. Twenty-three sites contained only members of the PA clade and only two sites contained a mixture of members of both the OH and PA clades. Population structure from microsatellite data analyzed suggests either 2 or 6 genetic clusters, although given the available data, it is not clear if these clusters correspond to clade membership. My results suggest that the contact zone extends northward toward Lake Erie or west of the present sampling area and should be further sampled to test gene flow and genetic clines between these two clades.

0469 AES Trophic Ecology/Physiology, Wedgewood, Friday 14 July 2017

Cathy Walsh[1], Jess Restivo[1], Timothy Polk[2], Hannah Reid[3], Carl Luer[1]

[1]*Mote Marine Laboratory, Sarasota, FL, USA,* [2]*University of South Florida Sarasota-Manatee, Sarasota, FL, USA,* [3]*University of Tampa, Tampa, FL, USA*

Preliminary Studies to Transform Elasmobranch Immune Cells into a Continuous Cell Line

Research in our laboratory has demonstrated that 72-96 hr cultures of immune cells derived from shark epigonal organs secrete compounds into the surrounding culture medium that will kill human tumor cells *in vitro* by inducing apoptosis (programmed cell death) via a mechanism that preferentially targets cancer cells compared to normal cells. Studies are underway to transform elasmobranch immune cells into a continuous cell line, with the goal of generating tumor cell inhibitory compounds from cells in

culture. These efforts represent the first application of hybridoma technology with elasmobranch cells and explore the feasibility of co-culturing allogeneic populations of immune cells to stimulate cell transformation via polyethylene glycol (PEG)-mediated cell fusion. Methodology gained from preliminary studies using peripheral blood leukocytes from Atlantic stingrays (*Dasyatis sabina*) has been applied to epigonal cells isolated from bonnethead sharks (*Sphyrna tiburo*), where one allogeneic population of cells stained with green fluorescing dye and the other stained with red fluorescing dye were co-cultured. The interaction between populations of stained cells was examined by fluorescent microscopy and cell cycling was analyzed using cell flow cytometry. Analyses of stained cell mixtures were performed before and after PEG treatment, with PEG treatment resulting in an increase in cells whose fluorescent properties were consistent with a fused cell population. Cell cycle profiles demonstrated the persistence of replicating cells (S-phase) for up to 4 weeks in the mixed cells/fused cells treated with PEG, with a decline in replicating cells in the absence of PEG.

0345 General Ichthyology I, Trinity, Sunday 16 July 2017

Brandon Waltz[1], Fernando Alda[2], Prosanta Chakrabarty[2], James Albert[1]

[1]*University of Louisiana at Lafayette, Lafayette, LA, USA,* [2]*Louisiana State University, Baton Rouge, LA, USA*

Addressing the Achilles Heel of Biodiversity: UCEs Indicate Cryptic Speciation in the Neotropical Electric Fish *Eigenmannia macrops*

Understanding biodiversity is fundamental to elucidating the relationships of life on Earth and understanding evolutionary patterns and processes. Evolutionary analyses and reliable measures of species richness depend on accurate alpha taxonomy; therefore, it is necessary to understand the nature of variation as the basis for correct species delimitation. However, the vast majority of species have been described based solely on morphology, leaving out a key source of variation and leading to the "Achilles heel" of biodiversity: undocumented cryptic diversity. Metapopulations face a variety of evolutionary processes contributing to lineage divergence and independence, including processes traditional morphological practices would be unable to recognize. Environmental conditions may exert strong stabilizing selection on aspects of morphology, resulting in maintenance of similar morphology throughout and after speciation. Additionally, and likely alongside stabilizing selection, the diversification of non-visual mating cues can result in undetected diversity. *Eigenmannia macrops* is a freshwater fish present in abundance throughout three large Neotropical river basins and possesses a weakly-electric signal used for non-visual communicative, reproductive, and foraging behaviors, making *E. macrops* an excellent candidate species to assess cryptic diversity. Furthermore, preliminary genetic analyses suggest the presence of undocumented diversity within the nominal taxon *E. macrops*. Here we present a case study examining the evolutionary patterns associated with cryptic speciation. Utilizing 101 samples from across the Amazon, Orinoco, and Essequibo basins, we examine the evolutionary history of *Eigenmannia macrops* using next generation target enrichment methods coupled with Bayesian species delimitation and validation methods.

0025 LFC Nutrition, San Marcos, Friday 14 July 2017

Jian Wang, Wen-Xiong Wang

The Hong Kong University of Science and Technology, Hong Kong, Hong Kong

Understanding the role of rotifer in micro-element nutrition to marine fish larvae

Rotifer has been widely used as the mouth-open diet for many marine fish larvae, whereas its role on micro-element nutrition has been seldom investigated. In present study, bioaccessibility of micro-elements in rotifer (enriched or non-enriched) was evaluated through an in vitro fractional method. Radio-tracer technique was adopted to study the specific micro-element (i.e., Zn and Fe) and macro-element (i.e., C) transfer from rotifer (enriched or non-enriched) to two different staged marine medaka larvae (*Oryzias melastigma*). The results showed that enrich rotifer with green algae (*Nannochloropsis gaditana*) can significant ($p<0.05$) increase Co, Mn and Fe content in rotifer and retained more micro-elements in the non-skeleton fraction (bioaccessible fraction). Fe assimilation efficiency (AE) by fish was significantly increased (ca. 1 fold) when fed with enriched rotifer. The digestive ability of madaka larvae increased from 5 dph to 25 dph, which in lined with the increased AE of C (ca. 1 fold). However, only a slight increase of both Fe and Zn AE proceeded over this period. The overall study suggested high bioaccessibility of micro-elements in rotifers and stressed importance of algae enrichment in the enhancement of larval fish micro-element nutrition (especially Fe). The assimilation of micro-elements by larval fish was unlikely limited by their digestive abilities, but the presence of certain bioavailable elemental species mattered.

0360 ASIH STOYE CONSERVATION II, San Antonio, Friday 14 July 2017

Brooke Washburn, Mollie Cashner, Rebecca Blanton

Austin Peay State University, Clarksville, Tennessee, USA

Islands in the stream, is that what we are: assessing the spatial scale of genetic diversity in the endangered Tuxedo Darter, *Etheostoma lemniscatum*

The federally endangered Tuxedo Darter, *Etheostoma lemniscatum*, occupies a 38.6 km reach of the Big South Fork Cumberland River where it is associated with shallow, slow-moving water with large substrate, generally located near riffles. This habitat is patchily distributed and separated by long sections (>1 km) of deep pools that are thought to be unsuitable for the species. Given intrinsic features of the species, which suggest it may have limited dispersal potential, we examined whether optimal habitat patches are functionally islands (or metapopulations), resulting from restricted gene flow. Fin clips

were taken from *E. lemniscatum* collected while snorkeling. A total of 232 individuals were observed; of these, 165 individuals were captured and fin clipped from 18 distinct habitat patches encompassing its range. Sixteen variable microsatellite loci were identified and optimized for PCR amplification. A subset of individuals (n=72) from 15 habitat patches have been genotyped. Preliminary results show weak, but significant (F_{ST}=0.012), genetic structure among populations upstream and downstream of an 11 km disjunction in their distribution and overall higher allelic diversity from the upstream reach (downstream: N_a=4.06; upstream: N_a=4.88). These results suggest long distances or reaches with unsuitable habitat may limit gene flow. The lower bound of the N_e estimate indicates the overall breeding population could be as low as 376 individuals; higher than the last census estimate (N_c) of 300 individuals. Efforts to genotype the remaining individuals at all loci to further elucidate genetic structure among sample localities are ongoing.

0392 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Dennis Wasko, Stephan Bullard

Hillyer College, University of Hartford, West Hartford, CT, USA

Analysis of Mass-Media Reported Venomous Snakebites in the U.S., 2011-2013

A common perception exists in some cases that in the United States, most venomous snakebites are "illegitimate," resulting from victims' deliberate interaction with snakes (such as attempting to move or kill the animal). While many studies have addressed snakebite epidemiology, victim demography, and clinical presentation, there is relatively little quantitative information available regarding the conditions under which bites actually occur. We compiled a dataset of snakebites occurring in the U.S. between 2011 and 2013, as reported by popular news outlets. A total of 332 reported snakebites were recorded, 307 occurring under natural circumstances and 25 under captive-care conditions. Most victims were adult males, and the majority of cases were considered "legitimate", usually resulting from accidentally stepping on or putting the hands near a snake. Sex was significantly associated with bite legitimacy, with males being more likely to intentionally interact with venomous snakes. While bias in popular-media snakebite reporting is likely and some results should be interpreted with caution, we consider this a useful complementary methodology. Across the United States, "legitimate" bites from unseen snakes appear to be the norm.

0802 Herp Reproduction & Life History II, Pecos, Thursday 13 July 2017

Andrew R. Wastell, Stephen P. Mackessy

University of Northern Colorado, Greeley, CO, USA

Desert Massasauga Rattlesnakes in Colorado

Massasauga Rattlesnakes (*Sistrurus catenatus*) are threatened over much of their historic range and occur from SE Canada to SE Arizona. Desert Massasauga Rattlesnakes (*S. c. edwardsii*) in southeastern Colorado were studied over a ten year period. Mark–recapture data for 770 snakes indicated a population size of >3,500 snakes in an area of approximately 4,800 ha. Field growth rates and size class frequency distributions showed that average snake age was 3 yr; 4 yr old snakes were frequently encountered, but less than 4% were 5 yr or older, suggesting low survivorship beyond this age. Conversely, initial growth was rapid; snakes grew an average of 0.57 mm/day in their first full year. Desert Massasaugas mated in fall and spring, producing 2–7 (mean 3.3) young in late August-September, and reproduction appeared to be biennial. Desert Massasaugas showed maternal attendance for at least 5 days post-parturition, and neonate dispersal corresponded with the first shed. Desert Massasaugas used rodent burrows as hibernacula, and within 50 m of Desert Massasauga hibernacula, eight snake, five anuran, and two turtle species use the same area for hibernation. Stable hibernation conditions are the primary resources attracting a diverse assemblage of species to this area, which serves as a critically important winter refuge for numerous species and supports the largest known population of Desert Massasaugas. This population is considered stable at present; however, because of rapidly changing climatic conditions, habitat loss and degradation, anthropogenic disturbance, and shifts in prey abundance, it may become threatened in the near future.

0713 LFC Nutrition, San Marcos, Friday 14 July 2017

Ken Webb, Lee Fuiman

University of Texas at Austin, Port Aransas, TX, USA

Tissue DHA Content of Red Drum (*Sciaenops ocellatus*) Larvae is Affected by Factors Other than Maternal Egg DHA Concentration

Previous research on red drum larvae in our lab has shown that the ability of red drum larvae to accumulate docosahexaenoic acid (DHA) in their tissues is affected by the level of DHA present in the egg. Research into the mechanisms underlying this “metabolic programming” have shown that while egg DHA content is a strong determinant, there are other factors involved. In the current experiment, we performed growout studies using eggs from two broodstock groups fed dissimilar diet regimes producing eggs of similar DHA content. While one group performed as expected with larval DHA accumulation predicted by egg DHA level the other group did not perform as expected. In order to examine these differences, eggs and larval tissues were analyzed using a number of approaches. First, eggs and larval tissues were analyzed for total fatty acid content. In order to better understand how the eggs differed, they were additionally analyzed for differences in neutral and polar metabolic compounds using mass spectrometry (LC-MS/MS) and magnetic resonance spectroscopy (MRS). Finally, the RNA profile of eggs and larval tissue was examined via tag based RNA-Seq (TagSeq) in order to examine differences in key metabolic markers.

0467 ASIH STOYE PHYSIOLOGY & PHYSIOLOGICAL ECOLOGY II, San Antonio, Thursday 13 July 2017

Denita Weeks, Matthew Parris

University of Memphis, Memphis, TN, USA

Immunity is Skin Deep: Considering Microbial Pesticides as a Disease Mitigation Strategy for Chytridiomycosis

Chytridiomycosis is an infectious amphibian disease caused by the pathogenic fungus *Batrachochytrium dendrobatidis* (*Bd*). *Bd* attaches to keratin on the dermis, invades skin cells, and may lead to pathogenesis in susceptible individuals. However, susceptibility differs within and among species. While this is due to many factors, the skin microbiome is a large contributor to disease resistance. Amphibians form symbiotic relationships with environmental microbes on the skin surface, some of which produce antifungal agents effective against *Bd.* Interestingly, many agricultural biopesticides utilize the common soil-dwelling bacteria, *Bacillus thuringiensis.* These bacteria are also known to produce antifungal metabolites and volatile organic compounds that inhibit growth of fungal plant pathogens. Through agricultural use, these bacteria increase in environmental abundance and provide opportunity for amphibian exposure. Additionally, *Bacillus* spp. appear in amphibian skin microflora, some of which inhibit *Bd*. Yet, *B. thuringiensis* has never been considered as a biological control agent for *Bd*. In vitro exposure to *B. thuringiensis* subsp. *kurstaki* significantly inhibited growth of *Bd*. We have also assessed the potential for *B. thuringiensis* colonization on *Lithobates sphenocephalus* and the subsequent effects on *Bd* susceptibility. Furthermore, while the bacteria alone may be beneficial, the toxicity of commercial formulations has been scarcely tested on amphibians. We found that eggs and premetamorphic tadpoles of *L. sphenocephalus* are sensitive to high doses of one commercial formulation. However, prometamorphic tadpoles and adults do not experience mortality. Ongoing research will assess the utility of these biopesticides in the microbial immunity of amphibians.

0747 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Nicholas Wegner[1], Laura Schwebel[1], John Hyde[1]

[1]NOAA Fisheries, La Jolla, CA, USA, [2]University of San Diego, San Diego, CA, USA

Reduced swimming and metabolic fitness of aquaculture-reared California Yellowtail (*Seriola dorsalis*) in comparison to wild-caught fish

Aspects of swimming and metabolic physiology were measured in aquaculture-reared California Yellowtail (*Seriola dorsalis*) in comparison to wild-caught individuals in order to examine potential reductions in health and fitness associated with captive rearing, and to help identify areas for targeted improvement in *Seriola* aquaculture. Incremental swimming velocity trials using a swim tunnel respirometer showed that aquaculture-

reared yellowtail had a significantly slower mean maximum sustainable swimming speed (U_{crit}) (4.16±0.62 BL s^{-1}) in comparison to that of wild-caught fish (4.80±0.52 BL s^{-1}). In addition, metabolic ($\dot{M}O_2$) measurements at varying swimming speeds allowed for estimation of standard metabolic rate, which was significantly higher in aquaculture-reared yellowtail (7.36±2.28 vs. 3.97±1.62 mgO_2 kg^{-1} min^{-1}). Aquaculture fish also had a reduced aerobic scope (9.16±3.40 mgO_2 kg^{-1} min^{-1}) in comparison to wild-caught yellowtail (15.77±5.78 mgO_2 kg^{-1} min^{-1}), which likely contributed to their reduced capacity for fast sustainable swimming. Reduced physical fitness is commonplace in aquaculture-reared fishes, and the examination of wild-caught yellowtail in this study provides baseline metrics that can be used to gauge the health and fitness of future *S. dorsalis* production. In particular, the lower standard metabolic rate and higher aerobic scope of wild-caught fish represent desirable metabolic characteristics that if achievable in aquaculture through better-rearing practices should allow for more efficient and potentially faster growth. At a minimum, a 50% reduction in standard metabolic rate (to that observed for wild-caught yellowtail) would result in increased feed conversion efficiencies and substantial cost savings for aquaculture operations.

0755 SSAR SEIBERT ECOLOGY III, Glass Oaks, Friday 14 July 2017

Chava Weitzman[1], Sarah Snyder[3], Franziska Sandmeier[2], C. Richard Tracy[1]

[1]University of Nevada, Reno, Reno, Nevada, USA, [2]Colorado State University, Pueblo, Pueblo, Colorado, USA, [3]Bard College at Simon's Rock, Great Barrington, Massachusetts, USA

Co-infection Does Not Predict Disease in *Gopherus* Tortoises

In disease ecology, the host immune system interacts with environmental conditions and pathogens to determine the manifestation of disease. Pathogens can also interact inside a host to facilitate or inhibit other pathogens' growth, and pathogens interact with different hosts in different ways, allowing individuals to be carriers of pathogens that can cause harm to others. We investigated co-infection patterns of two *Mycoplasma* pathogens (*M. agassizii* and *M. testudineum*) and the association of infection with clinical signs of disease in four congeneric tortoise host species (*Gopherus*) in the United States to detect differences in infection risk and disease dynamics. By examining frequencies of infection and co-infection for each host species, we found that Mojave desert tortoises (*G. agassizii*) were more likely to have detectable amounts of one or both pathogens than other tortoise species. In some species, but not all, the presence of each pathogen influenced the infection intensity of the other. These two *Mycoplasma* pathogens interact differently within, and with, different hosts. Neither infection nor co-infection was associated with clinical signs of disease. Experimental inoculation studies, as well as recurrent resampling of wild individuals, would help further to decipher disease dynamics in this system.

0871 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017; HL/SSAR/ASIH SYMPOSIUM - THE SCIENCE, MANAGEMENT, AND POLICY OF AMPHIBIAN CONSERVATION: EXTENDING THE LEGACY OF RAY SEMLITSCH

Allison Welch, Amber Ruby, Emily Beam

College of Charleston, Charleston, SC, USA

Salinity Tolerance Across Life Stages in Southern Toads, *Anaxyrus terrestris*: Transitions and Carryover Effects

Salinization of freshwater ecosystems is an emerging environmental concern, as rising sea level, intensified storm surge, road deicing salts, and land use changes can contribute to increased salinity in freshwater habitats. Elevated salinity can increase the demands of osmoregulation in freshwater organisms, and amphibians are particularly at risk due to their semi-aquatic life cycle and permeable skin. Tolerance to environmental challenges may vary across the life cycle, with individual- and population-level impacts dependent on the timing of exposure relative to the timing of vulnerability. Further, environmental challenges experienced early in development may alter performance during later stages, through acclimatization, compensatory effects, or cumulative effects. We assessed salinity tolerance of embryos, tadpoles, newly metamorphosed juveniles, and adults of the southern toad, *Anaxyrus terrestris*. Among these life stages, embryos were the most sensitive to salinity, while both terrestrial stages were able to withstand moderately elevated salinities without dehydrating. We also tested for carryover effects of salinity exposure during embryonic development, and found that elevated salinity during the embryo stage resulted in reduced performance during the subsequent larval stage. Our results suggest that elevated salinity is most likely to affect population dynamics when experienced during embryonic development, when even transient exposure to elevated salinity can be detrimental. Further, the difference in tolerance between tadpoles and newly metamorphosed individuals suggests that salinity tolerance increases before or during the metamorphic transition. Finally, this study demonstrates that tolerance to elevated salinity may be overestimated unless carryover effects are considered.

0874 Lightning Talks II, Glass Oaks, Friday 14 July 2017

Allison Welch, Jessica Hinson, Sylvia Davila, Wendy Cory

College of Charleston, Charleston, SC, USA

Shining a Light on Prozac's Effects on Amphibians: Fluoxetine and its UV Phototransformation Products Reduce Growth and Activity of Toad Tadpoles

Pharmaceutical pollution is an emerging environmental concern, with a wide variety of medications appearing in surface waters around the world. In the environment, UV radiation can cause many pharmaceuticals to transform into related molecules, which may be more toxic than the original compound. Despite increasing attention to the

effects of various pharmaceuticals on aquatic life, very little is known about the ecotoxicology of these pharmaceuticals' transformation products. This study examined the effects of the widely-prescribed antidepressant fluoxetine (Prozac) and its transformation products on amphibian larvae. Throughout larval development, tadpoles of the southern toad (*Anaxyrus terrestris*) were exposed either to untransformed fluoxetine or to fluoxetine that had undergone UV phototransformation. Tadpoles experienced similar growth reduction in the two treatments, even though the total concentration of fluoxetine and its transformation products was lower in the phototransformed treatment. This result suggests that tadpole growth was more strongly affected by the transformation products than by fluoxetine itself. By contrast, tadpoles exposed to untransformed fluoxetine showed a more dramatic reduction in activity than did those in the phototransformed treatment, suggesting that the effects on activity were mostly attributable to fluoxetine rather than its transformation products. Because UV phototransformation of fluoxetine results in compounds that may be more harmful than fluoxetine itself, levels of these transformation products, as well as fluoxetine, should be monitored in the environment. More generally, when evaluating the risks posed by pharmaceuticals in the environment, their phototransformation products must also be considered.

0388 Fish Systematics, Trinity, Saturday 15 July 2017

Stuart Welsh[1], Dean Jerry[2], Damien Burrows[2], Meaghan Rourke[3]

[1]West Virginia University, Morgantown, WV, USA, [2]James Cook University, Townsville, QLD, Australia, [3]NSW Dept. of Primary Industries, Narrandera, NSW, Australia

A New Species of Eel-tailed Catfish from New South Wales, Australia

A new species of *Tandanus* is described based on specimens from four river drainages (Bellinger, Macleay, Hastings, and Manning rivers) of the mid-northern coast of New South Wales, Australia. Previously, three species were recognized in the genus *Tandanus*; *T. tropicanus* of the wet tropics region of northeast Queensland, *T. tandanus* of the Murray-Darling drainage and coastal streams of central-southern Queensland and New South Wales, and *T. bostocki* of southwestern Western Australia. The new species is distinguished from all congeners by a combination of the following morphologic characters: a high count of rays in the continuous caudodorsal and anal fins (range 153-169, mode 159), a high count of gill rakers on the first arch (range 35-39, mode 36), and strongly-recurved posterior serrae of the pectoral fin spine. Additionally, results from previously-conducted genetic studies corroborate morphologic and taxonomic distinctness of the new species.

0482 ASIH STOYE GENETICS, DEVELOPMENT, & MORPHOLOGY I, Trinity, Friday 14 July 2017

Alexander Wendt, James Roberts

Georgia Southern University, Statesboro, GA, USA

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

Determining how landscape connectivity affects the demographics and evolution 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 10 microsatellite DNA loci among larval salamanders at 12 ponds on Eglin from two years. Our objectives were to delineate population genetic structure, estimate the effective numbers of breeders contributing to each pond, and determine how landscape structure influences gene flow among ponds. We found an expected pattern of isolation-by-distance, with nearby groups of ponds showing higher genetic similarity and distant ponds showing greater genetic differentiation. Estimated effective population sizes were small at most ponds and positively related to pond area. However, larvae showed few sibling pairs, indicating relatively widespread reproductive contributions to the sampled cohorts. Gene flow showed some relationship to various landscape features such as land cover, roads and elevation. These findings will help managers monitor the status of breeding populations, prioritize ponds and surrounding areas for habitat restoration, and design appropriate translocation plans for *Ambystoma bishopi* on Eglin and elsewhere.

0209 AES Symposium: Applications of Physiological Ecology in Elasmobranch Research, Wedgewood, Saturday 15 July 2017

Kevin Weng[1], Gen Del Raye[2], Dan Crear[1]

[1]Virginia Institute of Marine Science, Gloucester Point VA, USA, [2]University of Hawaii, Honolulu, HI, USA

How Do You Know When a Shark is in Love? It's all in the Heart (Rate)

Heart rate, the rhythm of animal life, is one of the most important biological rates. It may also offer a proxy for metabolic rate, and provide clues to the ecological activities of species that are difficult to observe (such as elasmobranchs). We used a recently developed implantable ECG tag (Star-Oddi, Iceland) in captive sandbar sharks and cobia. The tag measures electrical signals with external electrodes and performs on-board processing to determine heart rate. High noise and error may be introduced by nearby non-cardiac muscles and other electrical activity, so the heart rate measurements can be erroneous. To provide an independent measure of heart rate we also used an ultrasound machine to image the heart directly. The ECG tag performs well in cobia but is very difficult to use in sandbar sharks, due to the different morphology of the cardiac region in elasmobranchs.

0593 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Steven Werman

Colorado Mesa University, Grand Junction, CO, USA

Aspects of the Cephalic Anatomy of the Bushmaster (*Lachesis)* with Phylogenetic Considerations

The cephalic soft tissue anatomy of the Bushmaster (*Lachesis)* is described from dissection and previously published studies. Osteological features are included where appropriate. This assessment of anatomy is based primarily on myology, but nerves and cephalic circulatory structures are included where observed. Comparisons are made to the anatomy of other New World pitviper genera where known. A phylogentic assessment is developed to determine if there is support for existing phylogenetic hypotheses based on molecular or other types of data sets.

0237 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: ECOLOGY, NATURAL HISTORY, DISTRIBUTION, & BEHAVIOR; Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Samantha Wesnak[1], Todd Pierson[2], Jennifer Deitloff[1]

[1]Lock Haven University, Lock Haven, PA, USA, [2]University of Tennessee, Knoxville, TN, USA

Mating Behaviors of *Eurycea wilderae*

Mating behaviors between many organisms include mate-guarding, where a male aggressively defends a female. These behaviors vary among and within a species. In *Eurycea wilderae*, there are two morphs, referred to as Morph A and Morph wilderae. Morph A has a larger temporal musculature on the lateral side of the head, while Morph wilderae has a smaller head, longer cirri, and a mental hedonic gland. We hypothesized that, due to these differences, there would be a significant difference between these males' behaviors. We tested this hypothesis using courtship, mate-guarding, and y-maze trials. The courtship and mate-guarding trials were used to observe the mating behaviors between the two morphs along with aggressive behaviors and Y-mazes were used to test seeking behavior. From statistical analysis of the courtship and mate-guarding trials, we concluded that there was no significant behavioral difference between Morph A and Morph wilderae; however only Morph A individuals performed aggressive behaviors during mate-guarding trials. From Y maze trials, we found there was no significant differences between the morphs' seeking behaviors. From this experiment, we found that though there was no statistical difference in mate-guarding behaviors between these morphs, we think that since only Morph A performed mate-guarding behaviors, there is some evidence that these morphs display differences in their reproductive behaviors. This data was consistent with studies done using *Eurycea*

aquatica, which have large temporal musculature and display mate-guarding behaviors; however, more work must be done to determine the extent of these behaviors in Morph A of *E. wilderae*.

0604 Lizard Conservation, Sabine, Saturday 15 July 2017

Michael Westphal[1], Alex Filazzola[2], Amanda Liczner[2], Taylor Noble[2], Deborah Woolett-Smith[3], Christopher Lortie[2]

[1]US Bureau of Land Management, Marina, California, USA, [2]York University, Toronto, Ontario, Canada, [3]Working Dogs for Conservation, Three Forks, Montana, USA

Nonrandom association of blunt-nosed leopard lizards (*Gambelia sila*) with California jointfir (*Ephedra californica*) in a high-elevation refugium

Gambelia sila is endemic to the newly-described San Joaquin Desert of central California. Due to loss of over 90% of its habitat and the threat of further habitat loss due to climate change, the need to identify components that provide a resilient landscape for the species is urgent. We investigated use of a perennial shrub, *Ephedra californica*, by *G. sila*. Using trap cameras, scat-detecting dogs, and radiotelemetry, we found compelling evidence for an ecological association between *G. sila* and *E. californica*. We also investigated the resilience of *E. californica* to environmental change using historical photography, experimental plantings, and removal of whole shrubs. We found individual *E. californica* shrubs to be exceptionally long lived (>50yrs) and individual shrubs readily resprouted following complete destruction of surface foliage by fire and direct removal. We conclude that *E. californica* may be an important target for restoration of robust habitat for *G. sila*.

0759 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Michael Westphal[1], Michael Izumiyama[2], Ken Oda[3], Kristine Lesyna[3], Steven Morey[4], Karen Crow[2]

[1]US Bureau of Land Management, Marina, California, USA, [2]San Francisco State University, San Francisco, California, USA, [3]California Dept. of Fish and Wildlife, Monterey, California, USA, [4]US Fish and Wildlife Service, Portland, Oregon, USA

Geographic variation in life history characteristics of the calico surfperch, *Amphistichus koelzi*

An ongoing comparative study focusing on life history traits among the three species in the genus *Amphistichus* (*A. argenteus, A. rhodoterus, A. koelzi*) suggests a delay in timing of reproduction in *A. rhodoterus* relative to the other two species. Because the data for *A. rhodoterus* came from samples far to the north of the other two species, it is unclear whether observed differences are due to interspecific variation or simple latitudinal variation arising from plasticity in life history attributes. We assessed variation in

timing of reproduction as a function of embryo size at a set date in samples of *A. koelzi* gathered from the length of its range along the California coast. We found some evidence for latitudinal variation in *A. koelzi* but conclude that *A. rhodoterus* is nonetheless more divergent than would be expected under simple plasticity.

0526 ASIH STOYE GENERAL ICHTHYOLOGY II, Trinity, Thursday 13 July 2017

Courtney Weyand, Kyle Piller

Southeastern Louisiana University, Hammond, Louisiana, USA

Phylogeography of the Rosyside Dace, *Clinostomus funduloides* (Teleostei:Cyprinidae)

The genus *Clinostomus* is an understudied genus of fishes in the family Cyprinidae. *Clinostomus* has a large geographic range occupying much of eastern North America. Currently, two species are recognized within the genus: *C. funduloides* and *C. elongatus*. A previous morphological study identified multiple subspecies within *C. funduloides* and later, one additional undescribed taxon was proposed (Smoky Dace). 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 the Rosyside Dace (*C. funduloides*). Multiple tissue samples of *C. funduloides* were obtained across the range. Both mitochondrial and nuclear DNA sequence data were obtained and the data was analyzed using Bayesian phylogenetic methods to investigate the diversity and phylogenetic relationship within the species. Here we present the first comprehensive molecular phylogenetic hypothesis for *C. funduloides* using multiple unlinked loci. Using a multilocus approach, our results recovered several divergent clades within the species and exhibits substantial sequence divergences between clades, which may be indicative of move diversity within genus *Clinostomus*.

0012 AES GRUBER AWARD IV, Wedgewood, Friday 14 July 2017

John Whalen, Jim Gelsleichter

University of North Florida, Jacksonville, FL, USA

A multibiomarker analysis of pollutant effects on Atlantic stingray populations in Florida's St. Johns River

The goal of this study was to examine the potential health effects of organochlorine (OC) and polycyclic aromatic hydrocarbon (PAH) exposure on Atlantic stingray (*Dasyatis sabina*) populations in Florida's St. Johns River (SJR). Special emphasis was placed on identifying OC- and/or PAH-related effects in stingrays from areas of the lower (LSJR) and middle (MSJR) basins that have been shown to possess elevated levels of these

compounds, as well as characterizing baseline levels of pollutant exposure in the LSJR shipping channel, which may be subjected to dredging in the near future, potentially resuspending and redistributing contaminated sediments and increasing pollutant-associated effects. To accomplish this, we measured OC and PAH biomarker levels in stingrays collected from contaminated and reference sites. Data was analyzed using the Integrated Biomarker Response (IBR), which synthesizes data from multiple biomarkers, allowing for a comparison of samples by site. The data suggested that biomarker values from the SJR were variable, with elevated levels from Lake Jesup, intermediate levels from Lake Monroe and the LSJR, and low levels from Lake George. Biomarker levels from the LSJR were low compared to reference estuaries. This indicates that residing in portions of the MSJR is detrimental to stingray health, but residing in the LSJR is not. Data also suggested that individuals from Lake Monroe experienced reduced contaminant input over time, while the opposite was indicated for Lake Jesup. This study has developed a baseline for biomarker levels in the LSJR, allowing for the identification of dredging-induced changes to the system.

0605 Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Jim Wharton[1], Sandra Elvin[2], Debborah Luke[2]

[1]Seattle Aquarium, Seattle, WA, USA, [2]Association of Zoos and Aquariums, Silver Spring, MD, USA

Unified Conservation Messaging for Zoos and Aquariums

The Association of Zoos and Aquariums (AZA) is a nonprofit organization dedicated to the advancement of zoos and aquariums in the areas of conservation, animal welfare, education, science, and recreation. Saving Animals from Extinction (SAFE) is an AZA conservation initiative with a mission to combine the power of 183+ million annual visitors with the resources and collective expertise of AZA members and partners to save animals threatened with extinction. AZA has chosen 10 signature species (or complexes) to lead this new initiative. For each species, AZA institutions are working with conservation partners to develop collaborative, 3-year Conservation Action Plans (CAPs) built on existing conservation plans for the species. The CAP for sharks and rays includes seven conservation projects—public engagement, sustainable products, community-based conservation, multimedia, policy, research, and responsible animal management—each led by a coordinator from an accredited AZA institution. This poster will share some of the early work of the public engagement project. This work includes: developing a team of collaborators from AZA institutions and their partners, an informal baseline survey of AZA institutions to understand existing messaging around shark and ray conservation, and a collaborative process to develop a set of consensus shark and ray conservation messages and actions that may be shared and amplified through the exhibits and programming in over 200 accredited zoos and aquariums. Additional background and details on other shark and ray CAP projects will be shared, with opportunities for engagement by AES members.

0083 Fish Conservation I, San Antonio, Sunday 16 July 2017

Justine Whitaker[1], Amy Brower[1], Margaret Hunter[2], Alexis Janosik[1]

[1]University of West Florida, Pensacola, Florida, USA, [2]US Geological Survey, Wetland and Aquatic Research Center, Gainesville, Florida, USA

Retracing the phylogeographic structure of the lionfish (*Pterois volitans* and *P. miles*) invasion: a two marker approach that elucidates hidden diversity.

To examine population connectivity in the invasive range of lionfish (*Pterois volitans* and *P. miles*), published *P. volitans* d-loop sequences were compiled with newly sequenced lionfish (n=145). Lionfish tissue samples were collected from across their invasive range from Jacksonville (n=37), Bahamas (n=20) and Key Largo (n=30), to newly sampled locations, including Pensacola (n=23), St. Petersburg (n=20) and Trinidad and Tobago (n=15). Targeted regions for amplification included two mitochondrial genes: d-loop (control region) and the cytochrome oxidase I (COI). Based on the d-loop sequences, all samples were identified as *P. volitans* and none corresponded to *P. miles*. However, based on the COI sequences, one sample from the Bahamas corresponded to *P. miles*. This is the first known record of *P. miles* in the Bahamas and it would have been overlooked without inclusion of the COI marker, suggesting that previous studies using the d-loop alone may have overlooked the presence of *P. miles*. Additionally, rare haplotype H03, found in the northern region of the invasive range, was identified in one sample from Trinidad and Tobago, which may be evidence of a secondary introduction. Haplotype composition and genetic diversities confirmed lower genetic diversity in the invasive than the native range, and indicated differentiation between the northern and southern region within the invasive range. This study suggests employing multiple markers, with a specific focus on identification of *P. volitans, P. miles*, and potential hybrids, is necessary to gain further insight into the highly successful invasion of lionfish.

0584 Lightning Talks I, Glass Oaks, Friday 14 July 2017

Mary White

Southeastern Louisiana University, Hammond, LA, USA

Venom Proteins, Genomics and Predicted Sequences

Do crocodilians have venom proteins? It's hard to imagine. However a search of Genbank turns up the predicted sequence for alligator "*A. superbus* venom factor 1-like mRNA." This predicted sequence corresponds to one of the two alternative versions of the crocodilian Complement C3 genes. Co-option and the perils of predicted sequences will be discussed.

0154 SSAR SEIBERT ECOLOGY III, Glass Oaks, Friday 14 July 2017

Nicole White[1], Betsie Rothermel[3], Kelly Zamudio[4], Tracey Tuberville[2]

[1]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA, [2]Savannah River Ecology Lab, University of Georgia, Aiken, SC, USA, [3]Archbold Biological Station, Venus, FL, USA, [4]Department of Ecology and Evolutionary Biology, Cornell University, Ithaca, NY, USA

Male Size Drives Siring Success in the Gopher Tortoise (*Gopherus polyphemus*)

Male size can be a determining factor in siring success. Strains on populations such as changes to density may interact with existing reproductive biases allowing advantaged individuals to dominate mating opportunities, skew rates of siring success and lower effective population sizes and genetic diversity. The Gopher Tortoise (*Gopherus polyphemus*) has experienced range-wide population declines due to habitat loss and fragmentation, resulting in changes to natural population densities. We evaluated the rate of multiple paternity and the effects of male size on likelihood of siring offspring and how many offspring a sire in a high-density (~6/ha) population of gopher tortoises at Archbold Biological Station in Florida. We collected a total of 29 nests in 2015 and 2016 and incubated the eggs through hatching. Using previously-developed microsatellite markers, we genotyped all hatchlings (n = 220) and most potential dams and sires in the population (n = 101). We used programs CERVUS and COLONY to assign each hatchling to the most likely dam and sire. We observed multiple paternity in 24% of clutches, within range of previously reported rates. We used a zero-inflated Poisson model to evaluate the effect of size on probability of siring and number of offspring sired. Larger males were significantly more likely to sire offspring than smaller males. Additionally, size was positively correlated with number of offspring sired though this trend was not significant. Understanding factors influencing reproduction of this declining species may be important for developing management strategies under high-density scenarios caused by habitat loss or translocations.

0522 HL/SSAR/ASIH Symposium - The Science, Management, and Policy of Amphibian Conservation: Extending the Legacy of Ray Semlitsch, Glass Oaks, Saturday 15 July 2017

Howard Whiteman[1], Alycia Lackey[1], Michael Moore[2], Jacqueline Doyle[3], Nicole Gerlanc[4], Ashley Hagan[1]

[1]Murray State University, Murray, KY, USA, [2]Case Western Reserve University, Cleveland, OH, USA, [3]Towson State University, Towson, MD, USA, [4]Eunice Kennedy Shriver National Institute of Child Health & Human Development, Bethesda, MD, USA

Understanding the Evolution of Alternative Life Histories Using Long-term Population Monitoring

Understanding the evolution of phenotypic variation in response to environmental change is a fundamental question in evolutionary ecology that has consequences for the production and maintenance of biodiversity. Some salamanders facultatively express two adult morphotypes, terrestrial metamorphs and aquatic paedomorphs, in response to environmental variation experienced as larvae. Size-structured populations create demographic variation such that early larval cohorts inhibit the development of later cohorts via cannibalism and competition, subsequently influencing morph production and fitness. We parameterized Structural Equation Models using 27 years of population data for Arizona Tiger Salamanders (*Ambystoma mavortium nebulosum*), to investigate how larval growth, inter-cohort interactions, and other environmental parameters influence this polyphenism. Because previous results suggested that most paedomorphs in this population were smaller as larvae than those becoming metamorphs, and because paedomorph dispersal is limited, we predicted that paedomorphs would exhibit increased reproductive effort to mitigate the fitness costs associated with smaller sizes and reduced dispersal. We also predicted that fitness of both morphs would be mediated by inter-cohort interactions such that adults from early cohorts would mature at larger sizes and older ages than later ones. We found that the two morphs ultimately reach equivalent fitness, on average, but through different paths. Paedomorphs tend to reproduce earlier, while metamorphs have longer life spans. These tradeoffs, however, depend on cohort position, which tends to impact the fitness of paedomorphs more than metamorphs, perhaps because inter-cohort interactions continue after maturity within ponds. Thus, inter-cohort interactions provide spatiotemporal variation that helps maintain alternative life histories.

0578 Amphibian Conservation II, Wedgewood, Sunday 16 July 2017

Steven Whitfield[1], Jacob Kerby[2], Juan Abarca[3], Gilbert Alvarado[4]

[1]Zoo Miami, Miami, FL, USA, [2]University of South Dakota, Vermillion, SD, USA, [3]Centro de Investigación en Estructuras Microscópicas, Universidad de Costa Rica, San Pedro, Costa Rica, [4]Faculdade de Medicina, Veterinária e Zootecnia, Universidade de São Paulo, Sao Paolo, Brazil

Ecology and Conservation of Relict Amphibian Populations in Costa Rica

The emergence of the amphibian chytrid fungus (*Batrachochytrium dendrobatidis* “Bd") has been linked to mass mortality events, rapid population declines, and widespread extirpations of amphibians in the Neotropics. In Costa Rica, dozens of amphibian species were presumed extinct following the emergence of Bd, yet in the past decade many of these species have been rediscovered in relict populations in small parts of their historic range. Here, we overview the ecology and conservation of several relict and recovering amphibian populations in Costa Rica. We distinguish among species persisting within environmental refugia (*Craugastor ranoides*, *Craugastor taurus*) within climates hypothesized to be intolerable to Bd, and species that persist within habitat suitable to Bd (*Lithobates vibicarius*, *Incilius holdridgei*, *Agalychnis lemur*, *Agalychnis annae*). We distinguish among species that are persisting at low population sizes (*Incilius*

holdrigei, *Craugastor taurus*) and species that appear to be recovering and recolonizing their former ranges (i.e., *Lithobates vibicarius*). We show that rates of infection by Bd are highly variable among species, and among sites. Ranavirus - which is not typically given high conservation interest in Central America, is present at most sites occupied by relict populations. While some relict populations occur within relatively pristine areas and protected reserves, other relict populations occur outside of protected areas or occur in highly disturbed environments. We discuss integrative conservation strategies to protect relict populations, both in Costa Rica and around the world.

0177 ASIH STORER HERPETOLOGY; Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

K.H. Wild, C.M. Gienger

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

Between-year Repeatability of Locomotor Performance of Eastern Fence Lizards (*Sceloporus undulatus*)

Locomotor ability is a common metric used to assess whole-animal performance, and the ability to effectively traverse the environment plays an important role in individual fitness. The repeatability of phenotypic traits across time has been used to understand the heritability of performance traits, such as speed and endurance. Generally, it is expected that selection will remove variation and thus decrease heritability and repeatability of a phenotype. More precisely, selection will typically result in reduced additive genetic variation. *Sceloporus undulatus* is a sexually dimorphic forest lizard that is relatively common throughout the eastern United States. To assess the repeatability of locomotor performance, individuals were captured and raced in 2014 and again in 2015. Locomotor performance was highly and significantly repeatable across years (maximum sprint speed, $r = 0.74$, $p < 0.01$; 2-meter run, $r = 0.47$, $p = 0.01$). Our results are noteworthy due to the difficulty of capturing the same individuals over the course of consecutive study seasons, and to our knowledge is the first study to observe individual between-year repeatability in performance of free-ranging *Sceloporus undulatus*.

0611 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Alex Will, Julie Cobb, Zachary Gellner, David Rostal

Georgia Southern University, Georgia Southern University, USA

Endocrine influence on signalling in the Central Bearded Dragon (*Pogona vitticeps*)

The Central Bearded Dragon exhibits many types of behavioural signals from arm waves to head bobs. Males will also display a colour signal in the form of a darkened

"Beard" which exhibits physiological colour change. This study examined the effects of two hormones, testosterone and corticosterone, on the time spent performing each signal along with colour expression. A captive group of nine adult male and four adult female lizards were used. Trials were randomised. Two lizards were placed into an enclosure and separated by an opaque barrier. They were given 24 hours to acclimate to the new enclosure. After 24 hrs the barrier was removed and they were allowed to interact for 1 hour. The interaction was recorded using a video camera and direct observation for signalling behaviours. An Ethogram of behaviours was developed and frequency plus duration of behaviours was recorded. Blood samples were taken from the caudal vein before and immediately after trials, and colour expression was recorded immediately after blood draws using a digital camera and a spectrophotometer. Blood samples were assayed by ELISA to determine hormone concentration. Testosterone and corticosterone levels will be correlated with beard colour changes and behaviour duration and frequency.

0720 Lizard Conservation, Sabine, Saturday 15 July 2017

Dean Williams, Amanda Hale, Ashley Wall, Daniella Biffi

Texas Christian University, Fort Worth, TX, USA

Conservation genetics of Texas horned lizards (*Phrynosoma cornutum*)

The Texas horned lizard (*Phrynosoma cornutum*) has experienced declines in the state of Texas due to habitat loss and the introduction of invasive red fire ants (*Solenopsis invicta*). We conducted a statewide population genetics study to aid in future reintroduction and captive breeding initiatives in the state. We used 11 nuclear microsatellite loci and the mitochondrial d-loop to genotype 707 individuals. Bayesian clustering indicated the presence of three population clusters that correspond to 1) South Texas Plains and Coastal Prairie ecosystems, 2) High Plains, Rolling Plains, Edwards Plateau, and Pecos ecoregions, and 3) Chihuahua Desert ecoregion. Genetic diversity is high in protected areas but is significantly lower in populations that occur in small towns. Towns act as islands, isolating lizards from surrounding populations, resulting in low genetic diversity and low effective population size (Ne). A detailed study within a small town revealed restricted home ranges (usually within a town block), rare movement across roads, and significant genetic structuring on either side of major roads suggesting these roads serve as barriers to gene flow. Although data on local adaptation are currently lacking, we suggest the correspondence between genetic structure and major ecoregions warrants a cautionary approach to translocation and captive breeding strategies. Captive-bred Texas horned lizards should only be repatriated to their region of origin and translocations should only occur within the three major genetic clusters. Lizards located in small towns should not be used in captive breeding programs or in translocations due to their lower genetic diversity.

0256 Fish Ecology II, San Antonio, Sunday 16 July 2017

Stuart Willis[1], Christopher Hollenbeck[1], Jon Puritz[2], John Gold[1], David Portnoy[1]

[1]*Texas A&M University-Corpus Christi, Corpus Christi, TX, USA,* [2]*University of Rhode Island, Kingston, RI, USA*

Dispersal is limited by distance and depth in young-of-the-year, deep-water snappers (Lutjanidae) in the U.S. Caribbean as revealed by ddRAD population genomics

Genetic diversity and relatedness were surveyed in consecutive cohorts of young-of the-year recruits (age 0-1) of three, deep-water snapper species (*Lutjanus vivanus*, *L. buccanella*, and *Rhomoplites aurorubrens*), sampled from ten sites along the west coast of Puerto Rico. These species, especially *L. vivanus*, support important fisheries in U.S. waters of the Caribbean Sea. Individuals were genotyped at >2,100 single nucleotide polymorphisms (SNPs) contained in >1,000 haplotyped contigs (loci). The results indicate spatiotemporal variation in patterns of genetic diversity in recruits for all three species. Differences in within-sample genetic diversity and elevated relatedness were observed in samples of silk snapper from two marine protected areas (MPAs). The two MPAs, an island and an ocean bank, are separated from the coastal shelf by deeper water (>100 m) and results suggest these sites have partially decoupled recruitment processes relative to shelf sites. Spatial autocorrelation was observed on spatial scales of less than 20 km in silk snapper, and less than 15 km in the other two species, likely indicating common sources for settling recruits at these small spatial scales. This would suggest that recruitment along the west coast of Puerto Rico originates from multiple, semi-independent units of spawners whose contribution to individual sites varies in space and time. We suggest that management of these resources protect spawning adults distributed across the entire western shelf rather than in a few specific areas.

0253 Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Stuart Willis[1], David Saenz[2], Gang Wang[2], Christopher Hollenbeck[1], James Cai[2], David Portnoy[1], Kirk Winemiller[2]

[1]*Texas A&M University-Corpus Christi, Corpus Christi, TX, USA,* [2]*Texas A&M University-College Station, College Station, TX, USA*

RNA-seq analysis to decipher mechanisms of osmoregulatory adaptation to divergent physicochemical conditions and its role in diversification of Amazon fishes

Despite considerable study of osmoregulatory mechanisms in fishes, little is known about how populations adapt to new osmotic regimes. Consequently, the types of constraints that will impair the ability of freshwater fishes to respond to novel physicochemical challenges, including those resulting from climate change, remain uncertain. In the Amazon most meta-population lineages are closely associated with distinct physicochemical environments, so-called white, clear and black waters, that

differentially challenge fish osmoregulatory physiology. However, closely-related lineages often show complementary distributions in different water types, suggesting that adaptation to novel osmotic regimes and the transition between habitats are diversifying forces. Nonetheless, the observation that most species are not broadly tolerant of multiple water types, a necessary intermediate stage for expansion to new habitats, implies costs to plasticity such that osmoregulatory strategies across environments are often mutually exclusive. Lineages with populations adapted to different water types, or with plastic and non-plastic populations, provide ideal study systems for understanding this process; however, a prerequisite is clear delimitation of lineage boundaries and population structure. One group of Amazonian fishes for which these data are available is the tucunarés, or peacock bass cichlids, of the genus *Cichla*. Two lineages, *C. orinocensis* and *C. ocellaris 'monoculus'*, exhibit populations in both heterogeneous and homogeneous blackwater regions, with the latter populations being phylogeographically derived. Here, we present results of an RNA-seq analysis of gill tissue from the offspring of wild *C. oc. 'monoculus'* exposed to white and black water conditions in the laboratory.

0665 Lightning Talks II, Glass Oaks, Friday 14 July 2017

John Willson[1], Shannon Pittman[2]

[1]University of Arkansas, Fayetteville, AR, USA, [2]Davidson College, Davidson, NC, USA

A Novel Approach to Estimating Density of Burmese Pythons in Everglades National Park

The Burmese python has rapidly become one of the most high profile invasive species in North America. Despite growing evidence that pythons are having dramatic effects on native wildlife in South Florida and numerous attempts to develop and refine capture methods for pythons, efforts to manage or eradiate pythons are hampered by lack of an accurate estimate of python density or population size. Here we use a novel simulation-based technique to estimate density of Burmese pythons in Everglades National Park. Specifically, we combine behavioral observations of snake road crossing behavior (crossing speed) and simulation-based analysis of spatial movement patterns derived from radiotelemetry to estimate the probability of detecting pythons as they cross roads. We then use data on detection probability to translate python encounter rates during systematic road surveys to density, without relying on mark-recapture. The density estimates we provide fill a critical knowledge gap in understanding python impacts, control, and spread.

0441 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Hannah Wilson[1], Erika Nowak[1], Dustin Wood[2]

[1]*Northern Arizona University, Flagstaff, AZ, USA,* [2]*U.S. Geological Survey, San Diego, CA, USA*

Unusual Reproductive Events in *Thamnophis rufipunctatus*

In the fall of 2013, Northern Arizona University paired one female ("46") *Thamnophis rufipunctatus* with two male siblings in order to determine the possibility of breeding this threatened species in captivity. All the snakes were from the same litter from a wild-caught female. The following summer, 2014, 46 gave birth to six inbred offspring. All offspring were kept together as they were thought to be too small and young to be sexually mature. After nearly one year (in 2015), one of the female offspring ("Big Red") was observed mating with one of her siblings. She was removed immediately. In summer 2016, both 46 and Big Red began developing embryos. Both snakes aborted the partially-, or under-developed litters close to the expected birth date, and 46 was confirmed to have an oviduct infection at the time. Genetic samples from all of the 2014 litter and the failed 2016 litters were used for sibship and paternity analyses to investigate the possibilities of multiple paternity, long term sperm storage and/or parthenogenesis. 46's ability to become pregnant two years after being with a male, and the possibility of multiple paternity in the first litter provide novel observations of reproductive abilities in a federally threatened reptile. This information can be used to inform future decisions in captive breeding programs with *T. rufipunctatus.*

0527 Fish Ecology II, San Antonio, Sunday 16 July 2017

Kirk Winemiller[1], Pitagoras Piana[2], Eduardo Cunha[3], Angelo Agostinho[3], Luiz Gomes[3]

[1]*Texas A&M University, College Station, TX, USA,* [2]*Universidade Estadual do Oeste do Paraná, Toledo, PR, Brazil,* [3]*Universidade Estadual de Maringá, Maringá, PR, Brazil*

Using Fish Functional Traits for Individual-based Modeling to Simulate Food-web Dynamics in River-floodplain Systems

A major challenge for predicting ecosystem dynamics is the fact that species respond differently to environmental variation. Species with different life history strategies respond to environmental variation in ways not captured by food-web models that focus solely on networks of consumer-resource interactions. I will describe development of a spatially explicit, individual-based model that simulates hydrology and food-web dynamics in the last undammed stretch of the Upper Paraná River, Brazil, a system that has extensive empirical data needed to support model construction, calibration and testing. The model accepts landscape and hydrologic data and simulates fish populations based on functional traits and constraints identified by a periodic table of niches. Our ultimate goal is to create individual-based models for other river floodplain systems for which there is less empirical data but pressing needs to assess current and future human impacts, such as large hydroelectric dams and water diversions, on fish biodiversity, fisheries productivity and other important ecosystem services.

0657 Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Leann Winn, Brooke Flammang

New Jersey Institute of Technology, Newark, NJ, USA

Investigating the Fluid Dynamics of Chondrichthyan Egg Cases

Chondrichthyan development within an egg case may take multiple years before hatching. During the development of the embryo, flow is required through the egg case to move oxygenated water and metabolic wastes in and out of the egg case. In the egg cases of some skates and chimaeroids the embryo actively pumps water through the case by undulating its tail; however, some catsharks (*Apristurus* and *Parmaturus*) do not actively ventilate their egg cases and the water within the case is passively pumped through by hydrodynamic forces. The relationship between permeability, functional morphology, and fluid dynamics of egg cases are yet to be fully understood and are poorly represented in the literature. Here we show basic flow models pertaining to the effects of morphology and environmental factors on fluid dynamics surrounding egg cases. Using 3D printed models of egg cases and volumetric flow analyses, we established a previously unknown metric of flow probabilities based on morphological properties. Findings from this work contribute to the understanding of the effective relationship between an organism and its environment.

0910 AES Ecology I, Glass Oaks, Sunday 16 July 2017

Brent Winner

Florida Fish and Wildlife Research Institute, Saint Petersburg, FL, USA

A Multi-decadal Analysis of Distribution, Relative Abundance, and Habitat Utilization of the Cownose Ray, (*Rhinoptera bonasus*), in the southeastern United States

Cownose rays inhabit coastal waters from Chesapeake Bay through Brazil including much of the Gulf of Mexico. In some regions, their durophagous feeding strategy and schooling behavior result in bioturbation and depletion of economically-important shellfish beds. Subsequently, exploitation of cownose ray populations for bait and human consumption have increased to ameliorate these perceived negative impacts to shellfish fisheries. State or federal regulations on the harvest of cownose rays are currently lacking, so there is a critical need for ecological and abundance data, to support assessment and management. We summarize 27 years of standardized fisheries-independent monitoring data collected within eight estuaries along Florida's Atlantic and Gulf coasts. Samples were collected using a stratified-random multi-gear sampling design. From 1990 through 2016, 99,000 net hauls collected 19,051 cownose rays, ranging in size from 200 to 1,031 mm disc width. Cownose rays were collected year-round, suggesting that not all cownose rays undergo long distance winter migrations in Florida.

Peak abundance generally occurred during spring/summer months, with reduced abundance in northern estuaries during winter. Juvenile recruitment typically occurred during spring and early summer, with some latitudinal variation among Gulf estuaries. Young-of-the-year rays were rarely collected in Florida's Atlantic coast estuaries. Cownose rays were widely distributed throughout most estuaries over a variety of habitats, temperatures (13.8 - 37.1 °C), and salinities (2.2 - 42.9 ppt). Long-term trends in relative abundance varied among Florida's Gulf estuaries, with generally stable or slightly declining abundance since 2000, although cownose ray abundance was typically low along the Florida Atlantic coast.

0439 AES Conservation & Management I, Pecos, Saturday 15 July 2017

Sabine Wintner[1], Sven Kerwath[3]

[1]KZN Sharks Board MCoE, Umhlanga Rocks, South Africa, [2]Biomedical Resource Unit, University of KwaZulu-Natal, Durban, South Africa, [3]Department of Agriculture, Forestry and Fisheries, Rogge Bay, South Africa, [4]Department of Agriculture, Forestry and Fisheries, Rondebosch, South Africa, [5]Department of Animal Sciences, Stellenbosch University, Stellenbosch, South Africa

Cold Fins, murky Waters and the Moon: What Affects Shark Catches in the Bather Protection Program of KwaZulu-Natal, South Africa?

The influence of environmental variables on shark catch in bather protection program along the South African East Coast was investigated for eleven commonly caught species (*Carcharhinus limbatus*, *C. obscurus*, *C. brachyurus*, *C. plumbeus*, *C. brevipinna*, *C. leucas*, *Carcharodon carcharias*, *Carcharias taurus*, *Sphyrna lewini*, *S. zygaena*, *Galeocerdo cuvier*). Data for the period 1986-1994 were analysed using General Additive Models and General Additive Mixed Models. The influence of temporal and spatial factors, respectively, was considered and removed within a standardisation procedure to investigate and predict the influence of lunar cycle, sea surface temperature (SST) and water visibility on daily catch. The catches of *C. taurus* and *C. brevipinna* were significantly affected by all three factors. All other species' catches were affected by at least one of the three factors. The results suggest that measurable, predictable relationships exist between environmental conditions and presence and consequently catch of shark species in this fishery. Understanding these relationships could be useful to mitigate against unwanted catch and to further reduce risk for bathers.

0433 ASIH STOYE GENETICS, DEVELOPMENT, & MORPHOLOGY I, Trinity, Friday 14 July 2017

Nicole Witzel, Ali Taheri, William Sutton

Tennessee State University, Nashville, Tennessee, USA

Detecting the Presence and Abundance of Streamside Salamanders (*Ambystoma barbouri*) in Middle Tennessee Using Environmental DNA

Amphibians represent the vertebrate taxa that has experienced the greatest declines globally. Declines tend to occur in species with geographically-isolated and/or fragmented populations. This is specifically true for the Streamside Salamander (*Ambystoma barbouri*), an Ambystomatid salamander that occurs in Middle Tennessee. This species is active during winter and spring months when it emerges to breed in low-order, ephemeral streams. As these animals are cryptic and only surface-active for several months, they can be difficult to detect using traditional survey methods. Surveys that target environmental DNA (eDNA) in the form of DNA sloughed into their aquatic environment could provide an effective method for detecting the presence of this species. Water samples were collected in 50 meter stretches of 17 streams across the *A. barbouri* range once per month for 4 months (December - April 2017). Stream segments were searched for all life-stages of salamanders using rock-turning and visual surveys. We used real-time PCR to quantify DNA amounts using an *A. barbouri* species-specific primer. We used Generalized Linear Mixed Models to evaluate relationships between adult, larval, and egg counts and biomass at each site and evaluated the change in eDNA amounts across the active season of *A. barbouri*. Primary outputs from this study include a replicable eDNA approach to identify *A. barbouri* populations in Tennessee and sampling guidelines for appropriate times to collect eDNA survey data for *A. barbouri*. This information will provide a method which can be used by wildlife agencies to further the knowledge and conservation of this species.

0647 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: EVOLUTION, GENETICS, & SYSTEMATICS; Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Nicole Witzel, Ali Taheri, William Sutton

Tennessee State University, Nashville, Tennessee, USA

Development of an Environmental DNA Protocol to Detect and Quantify Streamside Salamanders (*Ambystoma barbouri*) in Low-order Streams of Middle Tennessee

The Streamside Salamander (*Ambystoma barbouri*) is an Ambystomatid salamander that occurs in Middle Tennessee where it is geographically isolated from other populations. This salamander species is active during the winter and spring months when it emerges to breed in low-order, ephemeral streams. As these animals are cryptic and only surface-active for several months, they can be difficult to detect using traditional survey methods. Surveys that target environmental DNA (eDNA) sloughed into their aquatic environment provide a potentially effective method for detecting the presence of this species. However, before this method can be used, it is essential to develop species-specific genetic primers that will correctly target key segments of DNA. The initial objective of this study is to identify a primer that is specific to and will successfully

amplify only the DNA of *A. barbouri* without amplifying DNA of congeners. Primers were selected by choosing *A. barbouri* cytochrome B mitochondrial DNA segments with base pairs that differed from *A. texanum*, a closely related sibling species. These primers were used to amplify *A. barbouri* DNA and tested for specificity among other Ambystomatid congeners in Tennessee. Following initial tests of specificity, we used this data to develop a probe to conduct quantitative PCR to evaluate the quantity of environmental DNA in stream water samples. The long-term goal of this study is to provide a replicable eDNA approach to identify *A. barbouri* populations in Tennessee. This information will provide a method which can be used to further the knowledge and conservation of the species.

0100 Herp Genetics, San Antonio, Saturday 15 July 2017

Jared Wood[1], Stephanie Dowell[2], Todd Campbell[3], Robert Page[4]

[1]Southwestern Adventist University, Keene, TX, USA, [2]U.S. Fish & Wildlife Service, Lamar, PA, USA, [3]University of Tampa, Tampa, FL, USA, [4]Texas A&M University-San Antonio, San Antonio, TX, USA

Insights into the Introduction Histories and Population Genetic Dynamics of the Nile Monitor (*Varanus niloticus*) and the Argentine Black-and-White Tegu (*Salvator merianae*) in Florida

Invasive species are a leading cause of the ongoing biodiversity crisis because they frequently disrupt community function. Florida is prone to invasion by reptiles due to its climate, frequency of disturbance, and exotic pet industry. Two of the largest invasive lizards in Florida are the Nile monitor (*Varanus niloticus*) and the Argentine black-and-white tegu (*Salvator merianae*). Currently, there are self-perpetuating populations of these species in more than one region of Florida; however, little is known about the histories of these populations or the degree to which they are connected by gene flow. To address these issues, we used microsatellites to investigate genetic diversity and intra-specific gene flow between *V. niloticus* and *S. merianae* populations in Homestead, Cape Coral, and West Palm Beach (*V. niloticus*) and Hillsborough and Miami-Dade Counties (*S. merianae*). Our results show that there is limited genetic diversity in all of these populations and that there is not gene flow among regions in *V. niloticus*. However, we did find evidence for limited admixture in *S. merianae*. Use of approximate Bayesian computation (ABC) suggested that all three *V. niloticus* populations resulted from separate introduction events. Conversely, in *S. merianae*, ABC suggested that the Hillsborough and Miami-Dade populations are most likely derived from a population that was not sampled. Our results indicate that wildlife managers should treat each population of *V. niloticus* and *S. merianae* as an independent management unit, and that managers should follow up on sightings of both species--even in areas where there are not documented populations.

0506 ASIH STOYE ECOLOGY & ETHOLOGY II, Sabine, Thursday 13 July 2017

Matthew S. Woodstock, Christopher A. Blanar, Tracey T. Sutton

Nova Southeastern University, Dania Beach, FL, USA

A Comparison of the Parasite Fauna and Trophic Ecology of Vertically Migrating and Non-migrating Mesopelagic Fishes in the Northern Gulf of Mexico

Mesopelagic (open ocean, 200-1000 m daytime depth) fishes are important consumers of zooplankton and are prey of oceanic predators. Two dominant mesopelagic fish families, Myctophidae and Sternoptychidae, occupy a similar daytime depth, but different nighttime depths. Myctophids undertake diel vertical migrations, while the sternoptychid genus *Sternoptyx* does not. The relationship between parasites and gut contents provides insights into ecological processes occurring within assemblages, as prey items are often vectors for parasites. This study examined the differences between the prey contents and parasite fauna of these two contrasting families in the Gulf of Mexico. Results showed that the non-migrating *Sternoptyx* fed upon a broader range of taxa than myctophids and appeared to transition from a zooplanktivorous to a micronektonivorous feeding style with increasing size. Calanoid copepods were the primary prey item observed in all size classes of the vertically migrating myctophids, but their ration increased with body size. In both families, parasites were more abundant among higher size classes. The more diverse feeding predators, *Sternoptyx* sp., harbored a lesser diversity of parasites than the more selective feeding predator. These data will be used to enhance models aimed at understanding ecosystem structure and population connectivity of oceanic ecosystems.

0326 NIA Contributed/Fish Ecology, Brazos, Friday 14 July 2017

Kirsten Work

Stetson University, DeLand, FL, USA

From Snapper to Darters: Video Surveys of 26 Florida Springs

Florida springs are highly prized as "aquatic gems", both for their clear water and their biotic assemblages. However, most Florida springs are threatened by reductions in water quantity and quality and by invasions of exotic species. Despite this confluence of appreciation and threat, very few studies have been published on fish assemblages in Florida springs, although certainly data on spring fish exist in targeted studies by state and federal agencies. To create a broad-scale picture of Florida spring fish assemblages, albeit a coarse one, I surveyed fish assemblages in 26 springs along the Suwannee River, the Santa Fe River, and the St. Johns River. For each survey, I traversed the spring run with a GoPro camera mounted underwater near the front of a kayak. I also stopped at up to five sites along the spring run, depending upon its length, to film fish with two GoPro cameras mounted on tripods in shallow water on either bank. I analyzed the

videos for presence/absence of fish species, for rough prevalence (the proportion video segments that contained each species), and for rough density (the maximum number of individuals of each species observed in one frame) and I analyzed these data with hierarchical cluster analysis. Many springs clustered based on proximity and morphology; for example, most of the Suwannee springs, which tended to be dominated by algae, were more similar to each other than to springs with less algae and/or abundant macrophytes.

0474 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Elijah Wostl, Eric Smith

University of Texas, Arlington, Arlington, Texas, USA

New Species and Phylogeographic Relationships of Sunda Shelf *Philautus* (Anura: Rhacophoridae)

Between 2012 and 2016, we conducted a series of large-scale herpetological surveys of the highlands of Java and Sumatra, the most intensive effort at documenting the herpetological diversity of these islands to date. From material collected during these surveys, we used a combination of morphological, molecular, and bioacoustic data to describe several new species of frogs in the genus *Philautus* and generate a nearly comprehensive phylogenetic analysis of the genus on the Sunda Shelf. We also use complete mitochondrial genomes to explore the phylogeographic relationships of the genus on the islands of Borneo, Java, and Sumatra and estimate when each island was colonized. We find that the genus is taxonomically underrepresented on Java and Sumatra. Moreover, the diversity of the genus on each respective island is largely composed of previously unrecognized monophyletic radiations. We also uncover a unique phylogeographic relationship between the islands of Java and Borneo.

0789 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Ian Wright, Travis LaDuc

University of Texas at Austin, Austin, TX, USA

Diet of the Spot-tailed Earless Lizard, *Holbrookia lacerata*

Diet composition is an important indicator of habitat use and can be of tremendous value to conservation efforts. Unfortunately, diet breadth, composition, and preference are not always known, especially for rare or threatened taxa. Such is the case for the spot-tailed earless lizard, *Holbrookia lacerata*; a species of greatest conservation need in Texas. As this species is near-threatened and encounters are no longer common in the field, we utilized historical collections to describe its diet. We dissected 129 *H. lacerata* specimens collected from across Texas and northern Mexico over the last 110 years and identified their stomach contents as well as recorded volumetric data for each prey item.

The diet of this lizard is dominated by grasshoppers (40% relative volume), followed by beetles (16% relative volume), spiders (14% relative volume), and 10 other arthropod orders. There is little sexual or ontogenetic variation in this diet makeup, however juveniles tended to eat higher proportions of very small-bodied arthropod groups than adult lizards. The results of these stomach dissections indicate that *H. lacerata* is a generalist and an opportunistic forager; focusing on large-bodied grasshopper prey, but taking smaller meals when other arthropods are encountered. These results deepen our understanding of habitat utilization in spot-tailed earless lizards and may help aid conservation efforts in the recovery of this species.

0655 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Jessica L. Wright[1], Juan D. Daza[1], Miguel T. Rodrigues[2], Tony Gamble[3], Aaron M. Bauer[4]

[1]Sam Houston State University, Huntsville, TX, USA, [2]Universidade de São Paulo, Instituto de Biociências, São Paulo, SP, Brazil, [3]Marquette University, Milwaukee, WI, USA, [4]Villanova University, Villanova, PA, USA

Skull variation in pug-nosed gecko *Chatogekko amazonicus* (Gekkota: Sphaerodactylidae)

The monotypic genus *Chatogekko* was recognized only six years ago to include South American forms that exhibit extreme snout reduction. *Chatogekko amazonicus* is widely distributed in the Northeast of South America, including Venezuela, Guyana, Suriname, French Guiana, Brazil, and possibly Bolivia. Previous molecular studies have indicated that *C. amazonicus* includes several multiple species-level lineages (at least five), but previous attempts to diagnose such groups have been ineffective. Here we study the skull anatomy of specimens throughout its distributional range to provide a basis for distinguishing these species. Besides extreme morphological changes associated with the species complex, such as an elongation of the premaxillary ascending process separating entirely the nasals, posterior displacement of the osseous naris approaching the frontal, development of deep choanal grooves in the palatine. Specimens from the Northeast of Brazil, Guyana, and Surinam differ from other localities in having a very broad ascending nasal process and in lacking the squamosal bone. The premaxilla ascending nasal process and the nasal shape shows tremendous variation, which might be influencing disparity in the snout across groups; for instance, specimens from central-northern parts of the amazon basin have a narrow projection on the premaxilla while some southern and central tend to have a notched ascending nasal process (M-shaped). More material needs to be examined to corroborate these patterns and continuous data is being taking to quantify differences in the snout, which might have some ecomorphological significance to understand the diversification of *C. amazonicus* in South America.

0576 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Chi-Shiun Wu, Jun-Jie Ma, Chang-Ye Yang

Chinese Culture University, Taipei, Taiwan

Does Salinity Experienced during Embryonic Development Affect Survival and Metamorphosis of Taiwanese Tadpoles Living in Coastal Areas?

The effects of salinity on amphibian physiology and ecology has drawn more attention in recent decades. Salinity conditions experienced early in development have immediate effects and potentially lasting consequences throughout ontogeny in amphibians. We conducted two experiments. In Experiment I, we reared embryos of *Fejervarya limnocharis* in freshwater, 3ppt, 6ppt, and 9ppt to access the salt tolerance of embryos. In Experiment II, we assigned tadpoles hatching from different salinities (freshwater, 3ppt, and 6ppt) to freshwater, 3ppt, and 6ppt (3x3=9 treatments) and measured survival, metamorphic traits, and post-metamorphic morphology of tadpoles, to test if salinity experienced during embryonic development influences survival and metamorphosis of tadpoles. Results showed that high salinity decreased hatching success but salinity experienced during embryonic development did not influence survival and post-metamorphic morphology of tadpoles. However, tadpoles expressed different patterns in metamorphic traits under the same salinity treatments if they experienced different salinities during embryonic development. Under 6ppt, time to metamorphosis of tadpoles experiencing 3ppt during embryonic development was shorter than that of tadpoles experiencing freshwater and 6ppt during embryonic development, but size at metamorphosis did not vary among these treatments with different initial salinities. This result suggests a medium salinity experienced during embryonic development helps tadpoles to adapt to higher salinity afterwards. In addition, tadpoles experiencing high salinity during embryonic development metamorphosed later and at a smaller body size when exposed to high salinity. Together, our results indicate that salinity condition experienced early in development is critical because it influences metamorphic trait of tadpoles under salinity stress.

0754 Reptile Conservation, Trinity, Sunday 16 July 2017

Amy Yackel Adams[1], Bjorn Lardner[2], Adam Knox[3], Julie Savidge[2], Robert Reed[1]

[1]U.S. Geological Survey, Fort Collins, CO, USA, [2]Colorado State University, Fort Collins, CO, USA, [3]Maui Invasive Species Committee, Makawao, HI, USA

Evaluating searcher fatigue and taxon-bias during nocturnal visual encounter surveys for reptiles on Saipan, Commonwealth of the Northern Mariana Islands, USA

Visual encounter surveying is a standard animal inventory method, modifications of which (e.g., distance sampling and repeated count surveys) are used for modeling population density. However, a variety of factors may confound visual survey results. We evaluated a group of observers for signs of fatigue and for individual biases in what

taxa (lizards and small mammals) they detected in 4 hours following twilight. Detections of sleeping (diurnal) Emerald Tree Skinks, *Lamprolepis smaragdina*, exhibited a small but significant decline as the evening progressed; a pattern consistent with searcher fatigue (tiredness and/or loss of concentration). Surprisingly, detections of sleeping (diurnal) Green Anoles, *Anolis carolinensis*, increased significantly as the evening progressed. Detections of nocturnal geckos (several species pooled) showed a weak and non-significant declining trend. Small mammal sightings (rats, shrews, and mice) declined significantly over the course of an evening, suggesting an effect of their circadian rhythm on top of any surveyor fatigue. Observers were biased in taxa detected, with particularly strong differences among persons in the ratio of Emerald Tree Skinks to Green Anoles that they spotted. Yet, across the four analyzed taxonomic classes, the skills of some observers appeared to be consistently above average; others consistently below average. We conclude that neither short-term nor long-term observer fatigue is of concern for visual searches, but that differences among observers may hamper efforts to statistically evaluate survey results.

0213 Fish Reproduction & Development, San Antonio, Saturday 15 July 2017

Alora Yarbrough, Karen Martin

Pepperdine University, Malibu, California, USA

Effects of Increased Air and Water Temperatures on the Embryonic Development of the California Grunion

As the earth's atmosphere becomes warmer, more organisms are being affected at varying stages of their life history. *Leuresthes tenuis* is a beach spawning silverside that is endemic to the Pacific Coast of North America from Point Conception, CA to Punta Abreojos, Mexico. *L. tenuis* may be uniquely affected by climate change due to their unusual embryonic development occurring in a terrestrial environment rather than a marine one. To examine the effects of embryonic development of *L. tenuis* under temperature stress, we examined the effects of exposure to high temperatures for only a portion of the day coupled with a rest period of a lower temperature overnight. Little has been done to compare the incubation of *L. tenuis* in water versus air, so we also describe the developmental differences observed between eggs incubated in sand versus seawater. Eggs were incubated in either sand or water in three temperature conditions of constant 20°C, constant 30°C, and alternating 30°C for eight hours and 20°C for sixteen hours resulting in a mean temperature of ~23°C. The eggs were examined under a microscope daily, hatching success testing began at 6 days post fertilization and hatchling length was measured. The eggs incubated in water showed more frequent deformities, slower embryonic development, lower hatching success, and shorter hatchling length than those incubated in sand across all temperature treatments. Future studies should focus on the factors behind what causes the developmental deficiencies in eggs incubated in water.

0207 AES Conservation & Management II, Pecos, Saturday 15 July 2017

Chelsey N. Young[1], Margaret H. Miller[1], John Carlson[2]

[1]NOAA National Marine Fisheries Service Office of Protected Resources, Silver Spring, MD, USA, [2]NOAA National Marine Fisheries Service Southeast Fisheries Science Center, Panama City, FL, USA

Understanding the U.S. Endangered Species Act and Examining Trends in Elasmobranch Petitions and Listings

The purpose of the U.S. Endangered Species Act (ESA) is to conserve threatened and endangered species and their ecosystems. Currently, there are over 2,300 species listed under the ESA. Each of these species have met the criteria for listing under Section 4(a)(1) of the ESA and are considered to be endangered or threatened as defined by the ESA. Recently, the National Marine Fisheries Service has seen an influx of petitions to list various elasmobranch species under the ESA. Since 2010, we have received 24 elasmobranch petitions covering 56 species, including 33 species that are found solely outside of U.S. waters and 23 species that may occur within U.S. jurisdiction. Prior to 2010, we received only 2 petitions (in 1999 and 2009) requesting the listing of elasmobranch species. Currently, a total of 23 elasmobranch species (includes distinct population segments) are either listed or proposed for listing under the ESA. The listing process under the ESA, including the criteria for listing, is often misunderstood and sometimes conflated with other organizations' criteria for listing species (including the International Union for the Conservation of Nature's Red List and the Convention on International Trade in Endangered Species). Therefore, we will provide an overview of the ESA listing process, describe key factors considered in making listing determinations, and summarize specific case studies of recent elasmobranch petitions and their outcomes.

0387 HL/SSAR/ASIH Symposium - The Science, Management, and Policy of Amphibian Conservation: Extending the Legacy of Ray Semlitsch, Glass Oaks, Saturday 15 July 2017

Melissa Youngquist[2], Michelle Boone[1]

[1]Miami University, Oxford, OH, USA, [2]University of Minnesota, St. Paul, MN, USA

Understanding species distributions: the effects of landscape composition, configuration, and scale

Species distributions are a function of the availability of suitable habitat and an individual's ability to disperse to and colonize suitable habitat patches. These factors depend on the composition and configuration of land cover types across the landscape. Equally important to our understanding of species distributions is the scale at which patterns of occupancy are described. We investigated the influence of habitat and dispersal on Blanchard's cricket frog (*Acris blanchardi*) distribution in Ohio, USA, at two spatial scales. First, we assessed which land cover types were predictive of presence and population genetic structure at a small spatial scale (county-wide). Second, we used habitat suitability models to assess if the same factors affecting presence at small scales were predictive at a larger spatial scale (state-wide); we then used logistic regressions to evaluate whether habitat suitability or landscape connectivity were most predictive of cricket frog presence across Ohio. We found that land cover is moderately predictive of cricket frog presence at all scales and that highways limit gene flow. When comparing models of cricket frog presence, we found that habitat suitability, not landscape connectivity, best explains cricket frog distribution. Our results show that cricket frog distribution is primarily a factor of habitat availability and is not limited by dispersal in the Ohio landscape. Assessing the relative importance of habitat suitability versus landscape connectivity is vital for effective species management because it can help direct conservation effort towards the most important factors affecting species distributions in a given area.

0408 Poster Session II, Rio Grande Exhibit Hall, Saturday 15 July 2017

Melissa Youngquist[1], Sue Eggert[2], Anthony D'Amato[3], Brian Palik[2], Robert Slesak[1]

[1]University of Minnesota, St. Paul, MN, USA, [2]USDA Forest Service Northern Research Station, Grand Rapids, MN, USA, [3]University of Vermont, Burlington, VT, USA

Potential effects of emerald ash borer invasion on wetland community composition

Forested wetlands provide vital habitat to a range of taxa and yet, they are one of the most threatened habitat types in North America. In the Great Lakes Regions, black ash wetlands are at risk from invasion by emerald ash borer (EAB; *Agrilus planipennis*); widespread infestation by EAB will dramatically alter the physical environment within and around these wetlands, with consequences for the biotic community. However, to date, relatively little is known about the aquatic community within these habitats. Our objectives were to 1) characterize the amphibian community within black ash wetlands and 2) to understand how amphibians might respond to EAB invasion. Using calls surveys and quantitative larval sampling, we documented the amphibian community within black ash wetlands across northeastern Minnesota; we also sampled amphibians within experimental ash plots that were clear-cut to mimic EAB die-offs. We found six species of anurans within the study area; however only three anuran and one salamander species used the ephemeral pools within ash stands for breeding. There was no difference in larval amphibian composition between in-tact ash stands or clear-cuts. Taxon richness was positively correlated with pond hydroperiod and area. Our results suggest that, on a small spatial and temporal scale, aquatic communities may be resistant to EAB invasion.

0056 Fish Biogeography & Morphology, Trinity, Saturday 15 July 2017

Hyo Jae Yu, Jin-Koo Kim

Pukyong National University, Busan, Republic of Korea

Clarifying the Effects of a Sister Species and Dispersal of Ichthyoplankton on the Population Genetic Structure of Goldeye Rockfish, *Sebastes thompsoni* (Pisces, Sebastidae)

Sebastes thompsoni is an important component of the commercial rockfish catch in the northwest Pacific Ocean. This species is most closely related to *Sebastes joyneri*, based on both morphology and genetics. To clarify the population genetic structure of Korean *S. thompsoni* and its relationship with *S. joyneri*, we analyzed a mitochondrial DNA (mtDNA) control region and eleven polymorphic microsatellite DNA (msDNA) loci of 215 *S. thompsoni* and 48 *S. joyneri* specimens collected from Korean waters. *S. joyneri* individuals were clearly distinguished from *S. thompsoni* by the mtDNA control region and msDNA results. Analysis of mtDNA revealed no distinct subpopulations within *S. thompsoni*. The msDNA results, in contrast, showed two distinct subpopulations of *S. thompsoni*: one distributed along the entire coast of Korea, and the other restricted to the Dok-do Island and Wangdolcho Reef off its coast, in the East Sea. One factor that may limit gene flow between subpopulations is the early dispersal of this species in the East Sea, where the circulating Tsushima warm current may inhibit transport to other locations. In this study, *S. thompsoni* larvae and juveniles were mainly observed near the coast, where their dispersal is restricted by various ocean current patterns (e.g., upwellings, eddies). Our results indicate that the two subpopulations of Korean *S. thompsoni* may be differentiated primarily by the characteristics of local marine environments and consequent effects on the dispersal of larvae and juveniles, rather than by hybridization between *S. thompsoni* and *S. joyneri*.

0057 Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Hyo Jae Yu, Jin-Koo Kim

Pukyong National University, Busan, Republic of Korea

Is the Family Sebastidae (Pisces, Scorpaenoidei) Monophyletic According to Molecular Data?

In 1994, Ishida first proposed the new family Sebastidae (eight genera: *Sebastes*, *Sebastiscus*, *Hozukius*, *Helicolenus*, *Adelosebastes*, *Sebastolobus*, *Trachyscorpia* and *Plectrogenium*), which, based on myological and osteological characteristics, is clearly distinct from other families in the suborder Scorpaenoidei. Due to their fairly recent speciation, species groups within this family exhibit few or only minute morphological differences, rendering their phylogenetic relationships potentially confusing. Also, Ishida's (1994) new classification has not yet been broadly accepted. This study aims to clarify Sebastidae phylogeny using genetic data to test whether this family is a reciprocal monophyletic group and, if so, to determine which genera it includes. Here, two mitochondrial (mt) DNA sequences (1002 bp of cytochrome b and 559 bp of 16S rRNA) and two nuclear (n) DNA sequences (655 bp of RAG2 and 956 bp of RNF213) from 29 species in six genera in the family Sebastidae (excluding *Trachyscorpia* and *Plectrogenium*), as well as 27 outgroups, collected from the northern Pacific Ocean, were used to confirm the interrelationships among Sebastidae taxa. Bayesian inferences based on mtDNA and nDNA produced similar phylogenies, suggesting that the family Sebastidae is monophyletic. Furthermore, the basal position of *Sebastolobus* within Sebastidae as revealed by molecular phylogeny was highly consistent with the previous morphology-based tree. However, because some researchers recognize *Sebastolobus* as a separate family (Sebastolobidae, sensu Nakabo, 2013), more diverse sampling and additional data are required to resolve the problem.

0694 Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017

Joshua Zacharias, Robert Cerrato, Michael Frisk

Stony Brook University, Stony Brook, NY, USA

Habitat Preference and Spatial Interactions of the NW Atlantic Skate Complex

The seven resident northwest Atlantic species of skates; barndoor (*Dipturus laevis*), clearnose (*Raja eglanteria*), little (*Leucoraja erinacea*), rosette (*L. garmani*), smooth (*Malacoraja senta*), thorny (*Amblyraja radiata*) and winter (*L. ocellata*) possess life history traits that make them vulnerable to overexploitation, such as slow growth, late maturation and low fecundity. The various species occupy overlapping habitats and often migrate long distances throughout the year. While their ecological role as benthic marine generalists and common geographic ranges are known, wider habitat use of these species is poorly defined. The goal of this study was to examine habitat preference and overlapping space use between the seven species of skate in the northwest Atlantic. National Marine Fisheries Service (NMFS) bottom trawl survey data from 1963-2009 was analyzed to assess conspecific and interspecific spatial overlap for all seven species. Within a species, we focused on measures of aggregation within the surveyed area as well as within the sampled fish distributions with emphasis upon temporal and abundance variation. We found evidence of population density based range expansion/retraction in several species. Our interspecies analysis focused upon indexes of collocation between each possible combination of species pairs. The highest index values, indicating a higher degree of spatial overlap, were found amongst sympatric species pairs. These results highlight spatial preference amongst skate species and a possible reference point to aid management in understanding population movement and exploitation vulnerability.

0385 Fish Behavior, San Antonio, Saturday 15 July 2017

Nathaniel Zbasnik, Steve Huskey

Western Kentucky University, Bowling Green, Kentucky, USA

The Impact of Invasive Lionfish, *Pterois volitans,* on the Feeding Performance of Endemic Spotted Scorpionfish, *Scorpaena plumieri*

In 1985, *Pterois volitans*, red lionfish, were introduced off the coast of Florida. Without natural predators, they have rapidly reproduced while negatively impacting native populations and ecosystems. The impacts lionfish have on Atlantic and Caribbean ecosystems, specifically their reproduction and utilization of resources, have been well studied. Here, the presence of lionfish was assessed for its influence on the feeding success of an endemic family member, the spotted scorpionfish, *Scorpaena plumieri*. Wild-caught individuals were transported to the lab where we employed three experimental treatments: isolated, intraspecific competition, and interspecific competition. Isolated scorpionfish were maintained in individual tanks during feeding trials and were used to establish baseline feeding performance. During intraspecific and interspecific trials, a scorpionfish was housed with either another scorpionfish or a lionfish. Several key-feeding kinematic variables (e.g. timings, durations, excursion distances, and angles), as well as negative buccal pressure, were recorded and analyzed with high-speed videography and a Millar pressure catheter, respectively, for all six scorpionfish across all treatments. We also quantified the overall success (i.e. prey-capture rate) of scorpionfish feeding with competitors present and absent. Preliminary data suggest lionfish directly impact the feeding success of spotted scorpionfish. Scorpionfish are forced to modulate their feeding behavior and performance to be competitive in the presence of lionfish. While the impact of lionfish on endemic fishes is overwhelmingly negative, their impact on a family member, with whom they overlap greatly ecologically, is likely even more significant.

0319 Fish Ecology II, San Antonio, Sunday 16 July 2017

Zachery D. Zbinden[1], William J. Matthews[2]

[1]*University of Arkansas, Fayetteville, AR, USA,* [2]*University of Oklahoma, Norman, OK, USA*

Beta Diversity of Stream Fish Assemblages: Partitioning Variation Between Spatial and Environmental Factors

Studies that analyze the structure of assemblages across spatial scales, in order to determine generalizable patterns, can be used to guide efforts that allocate resources meant to conserve regional biodiversity. Beta diversity can shed light on the underlying factors that drive variation of assemblage structure including spatial and environmental influences. We examined fish beta diversity in southeastern Oklahoma by sampling 65 wade-able stream reaches and measuring 30 environmental factors at each sampling location. Variation of fish assemblage structure was partitioned between environmental and spatial predictors using RDA. Species turnover was separated into its two additive components of spatial turnover and nestedness to determine which of these two accounted for the most turnover across the drainage. Spatial and environmental factors

combined accounted for 25.5% of fish beta diversity. Environmental factors alone accounted for 20.1%, while spatial factors alone only accounted for 3.5% of the variation. Nine environmental factors were significantly related to fish beta diversity: 1) elevation; 2) stream order; 3) stream width; 4) percent riffle habitat; 5) water temperature; 6) conductivity; 7) turbidity; 8) gravel substrate; and 9) current speed. Overall species turnover was driven mostly by spatial turnover rather than nestedness. This pattern was found to be the same across multiple spatial scales (entire drainage, sub-drainage, mainstem) and despite several techniques used to extract turnover coefficients. These results suggest that fish assemblages-particularly in headwater streams-are structured by environmental filtering and that these assemblages tend to be compositionally distinct, rather than being nested derivatives of one another.

0884 Herp Ecology II, Pecos, Friday 14 July 2017

Amanda J. Zellmer[1], Gregory B. Pauly[2]

[1]*Occidental College, Los Angeles, CA, USA,* [2]*Natural History Museum of Los Angeles County, Los Angeles, CA, USA*

Citizen Science Elucidates Urban Habitat Usage by *Batrachoseps* Salamanders

Urban environments are often associated with a loss of biodiversity due to widespread habitat modifications. Yet many organisms including some amphibians and reptiles continue to make use of urban habitats, from large city parks down to even the smallest gardens and backyards. Studying habitat use within urban environments however is a challenge because of limited access to private property. Using a combination of field surveys and data from the RASCals citizen science project, we document the presence of two species of salamanders, *Batrachoseps nigriventris* and *Batrachoseps major*, in urban habitat across Los Angeles. The presence of these species throughout the city raises the question of whether these are isolated remnant populations of *Batrachoseps* or if urbanization has instead resulted in an expansion into newly created habitats where irrigation has led to year-round availability of moist soil in a historically seasonally dry landscape. We test these hypotheses using fine-scale species distribution models by comparing the role of natural versus urban environmental variables in the distributions of these salamanders. Our results illustrate the importance of all urban green spaces and demonstrate a need to manage and conserve urban habitat regardless of habitat size. Further, our results highlight the utility of citizen science projects for studying urban species.

0524 Poster Session I, Rio Grande Exhibit Hall, Friday 14 July 2017; AES SYMPOSIUM – APPLICATIONS OF PHYSIOLOGICAL ECOLOGY IN ELASMOBRANCH RESEARCH

Casey Zender, James Gelsleichter

University of North Florida, Jacksonville, Florida, USA

Exploration of Plasma Indicators for Predicting Post-Release Mortality in the Blacktip Shark (*Carcharhinus limbatus*)

Catch-and-release fishing as well as the release of fisheries by-catch are often regarded as sustainable fishing approaches. However, recent studies have shown that a higher degree of post-release mortality may be occurring in sharks captured and released in these fisheries than previously expected. To determine the amount of capture-related mortality, previous studies have used electronic tagging and measurement of blood-borne secondary indictors including pH, concentrations of lactate, and dissolved CO_2. These methods may not be the best fit, as electronic tagging can be costly, and some secondary stress markers may consistently correlate with post-release mortality. For this reason, there has been a call for study of new indicators. To partially address this call, this study examined if plasma concentrations of malondialdehyde (MDA), a by-product of lipid peroxidation (LPO), and 8-hydroxy-2′-deoxyguanosine (8-OHdG), an indicator of DNA oxidation, were useful as indicators of capture stress and post-release mortality in blacktip sharks. LPO and DNA oxidation are the processes in which lipids and DNA respectively are damaged during oxidative stress, which can occur during capture. We measured plasma levels of MDA and 8-OHdG in blacktip sharks that were collected for a prior capture stress study, and compared these values to data obtained using more traditional forms of stress assessment, including electronic tagging and secondary stress indicators. Preliminary data suggests that levels of MDA may not be closely correlated with the expression of traditional indicators, although additional testing is needed. Development of new indicators are imperative to provide new mortality data for fisheries management.

0761 Herp Morphology & Development, Brazos, Saturday 15 July 2017

Mingna V. Zhuang[1], Anthony P. Russell[2], Heather A. Jamniczky[2], Timothy E. Higham[1]

[1]UC Riverside, Riverside, CA, USA, [2]University of Calgary, Calgary, Alberta, Canada

Evolution of the gecko ankle in relation to the acquisition of frictional adhesion: A geometric morphometric analysis of the mesotarsal joint

Among terrestrial vertebrates, foot morphology and locomotor function are closely associated. A prominent example of this is the pedally-based adhesive system of geckos. Although the integumentary aspects of this complex are well-studied, its skeletal elements are not. The mesotarsal ankle joint of limbed squamates, situated between the astragalocalcaneum and fourth distal tarsal, is complex and governs the patterns of foot motion during propulsion. Among geckos, pad-bearing taxa have different limb and ankle kinematics from ancestrally padless forms, and we predicted that such kinematic differences are reflected in skeletal anatomy. To explore whether evolutionary changes in the morphology of the ankle joint have accompanied the acquisition of adhesive function, we obtained 3D micro CT images of the hind foot of 28 genera of the

Gekkonidae and six outgroups. Our sample represents seven origins of the adhesive apparatus. We used 3D geometric morphometrics and phylogenetic comparative methods to compare shape variation in the ankle joint among ancestrally padless and pad-bearing lineages. Preliminary results suggest that the ankle joint of pad-bearing lineages differs from that of ancestrally padless lineages in having a shallower astragalocalcaneal groove and a shorter ventral peg on the fourth distal tarsal. This is suggestive that flexion and rotation of the crus about the foot are decoupled in pad-bearing lineages. Our results have important implications for the function of the adhesive system and gecko locomotion, and also provide evidence relating to how superficial and deep anatomy change in parallel in association with function.