JOINT MEETING OF ICHTHYOLOGISTS AND HERPETOLOGISTS

JULY 24-28, 2019
SNOWBIRD, UT - SNOWBIRD SKI AND SUMMER RESORT

ABSTRACTS

375 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Maria Sabando[1], Yannis Papastamatiou[1], Guillaume Rieucau[2], Darcy Bradley[3], Jennifer Caselle[3]

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Reef Shark Behavioral Interactions are Habitat Specific

Dominance hierarchies and competitive behaviors have been studied in several species of animals that includes mammals, birds, amphibians, and fish. Competition and distribution model predictions vary based on dominance hierarchies, but most assume differences in dominance are constant across habitats. More recent evidence suggests dominance and competitive advantages may vary based on habitat. We quantified dominance interactions between two species of sharks *Carcharhinus amblyrhynchos* and *Carcharhinus melanopterus,* across two different habitats, fore reef and back reef, at a remote Pacific atoll. We used Baited Remote Underwater Video (BRUV) to observe dominance behaviors and quantified the number of aggressive interactions or bites to the BRUVs from either species, both separately and in the presence of one another. Blacktip reef sharks were the most abundant species in either habitat, and there was significant negative correlation between their relative abundance, bites on BRUVs, and the number of grey reef sharks. Although this trend was found in both habitats, the decline in blacktip abundance with grey reef shark presence was far more pronounced in fore reef habitats. We show that the presence of one shark species may limit the feeding opportunities of another, but the extent of this relationship is habitat specific. Future competition models should consider habitat-specific dominance or competitive interactions.

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592 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Daniel Saenz[1], Toby Hibbitts[2], Cory Adams[1]

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Calling Phenology of the Southern Crawfish Frog (*Lithobates areolatus*)

The crawfish frog (*Lithobates areolatus*) spends most of its time in or near crawfish burrows, making it difficult to detect except when breeding. During the breeding season, however, they migrate to breeding wetlands and have exceptionally loud advertisement calls that allow auditory surveys to be conducted with relative ease. Our study is an attempt to learn about crawfish frog seasonal calling phenology, diel calling activity, and the exogenous factors that influence calling in the southern part of its range, the coastal prairie of Texas. We conducted auditory surveys for crawfish frogs and collected environmental data at the Attwater Prairie Chicken National Wildlife Refuge in Austin and Colorado Counties, Texas, from January 2013 through December

2018. After six years of daily surveys, our results revealed that there is an approximately 7-month window, each year, when crawfish frogs can call. However, crawfish frogs only call for a few days each year and there is significant inter-annual variation in the timing of the breeding activity. Our analyses suggest that the timing of crawfish frog calling activity is driven by several important abiotic factors. Breeding pond water depth, relative humidity, and rainfall have a significant positive relationship with crawfish frog calling and water temperature and wind speed are negatively associated. We suggest that crawfish frogs from the coastal prairies of Texas have an exceptionally long breeding season to be able to successfully breed when conditions are favorable in an unpredictable and sometimes harsh environment.

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793 Ichthyology Systematics II, Cottonwood A-D – The Snowbird Center, Sunday 28 July 2019

Michael Sandel[1], Andres Aguilar[2], David Neely[3], Thaddaeus Buser[4]

[1]The University of West Alabama, Livingston, Alabama, USA, [2]California State University Los Angeles, Los Angeles, California, USA, [3]Tennesee Aquarium Conservation Institute, Chattanooga, Tennessee, USA, [4]Oregon State University, Corvallis, Oregon, USA

Phylogenomic Interrelationships and Osteology of Baikal Sculpins with a Comparison of Perciform Adaptive Radiations

Lake Baikal is the oldest and largest freshwater ecosystem on Earth. The sculpins (Perciformes: Cottidae) of Lake Baikal represent the most diverse adaptive radiation of lacustrine fishes outside of the tropics. We present the first resolved phylogeny of 12 Baikalian sculpin genera with complete sampling of all extant species, inferred from complete mitochondrial genomes and over 100,000 single nucleotide polymorphisms (SNPs). We also report comparative analyses of 25 complete exomes, assembled from illumina sequencing over 300,000 capture targets. Results of phylogenetic analyses reveal non-monophyly of a number of taxa, including the family Abyssocottidae. We present a comprehensive set of osteological characters inferred from microCT scans, and map the evolution of osteological characters on the phylogeny. Results of comparative genomic analyses identify a number of important gene pathways shared with other perciform radiations. We discuss a subset of these pathways, including those involving neural crest development and oxidative phosphorylation, as they relate to the diversification of the Baikal Sculpin Radiation.

CANCELLED

81 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Theresa Santos[1], João Veloso[1], Bruno Macena[1,2], Fabio Hazin[1]

[1]Universidade Federal Rural de Pernambuco, Recife, PE, Brazil, [2]Universidade dos Açores, Horta, Faial, Portugal

Foraging aspects of Cookiecutter Shark (*Isistius sp.*) in an equatorial Mid-Atlantic archipelago

The Cookiecutter Shark (*Isistius sp.*) is a small squaloid shark found in the pelagic waters of tropical and sub-tropical oceans. The shark's unique mouth, teeth and tongue morphology leaves a circular bite on their preys. However, very little is known about their foraging ecology and population. The present study aimed to understand the Cookiecutter Shark foraging ecology through the patterns and frequency of bite scars on fishes in Saint Peter and Saint Paul Archipelago (SPSPA). Many pelagic fishes were caught by the commercial fleet that operates nearby SPSPA, some of them presented wounds from cookiecutter shark bites. The number of bites, diameter, and healing stage were assessed. Based on the high frequency of bite scars, the Wahoo (*Acanthocybium solandri)* was selected for further analysis. The estimated size of sharks that inflicted bites on pelagic fish was calculated from the diameter of bite scars, by using a linear regression of the shark's mouth width (MW) vs. total length (TL) $TL= 4.5 (MW) + 82.8$, where TL is shark total length (mm) and MW is shark mouth width (mm). A total of 100 Wahoos were analyzed; the wounds were found on lateral (71.6%), ventral (21.7%) and dorsal (6.7%) sides. The estimated size of the Cookiecutter Sharks that inflicted wounds ranged from 127 mm to 308 mm TL, and average size was 210 ±35 mm, suggesting the Wahoos were attacked by rather large sharks, for the species. The present study provides an insight into the foraging ecology of this elusive species.

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120 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Rachel Santymire[1], Allison Sacerdote-Velat[2], Andrew Gygli[3], Douglas Keinath[3], Sinlan Poo[4], Kristin Hinkson[4], Elizabeth McKeag[3]

[1]Conservation and Science Department, Lincoln Park Zoo, Chicago, IL, USA, [2]Chicago Academy of Sciences, Chicago, IL, USA, [3]US Fish and Wildlife Service, Wyoming Ecological Services Field Office, Cheyenne, WY, USA, [4]Conservation and Research Department, Memphis Zoo, Memphis, TN, USA

Using dermal cortisol to measure the stress physiology of wild and captive Wyoming toads (*Anaxyrus baxteri*)

We investigated disease, environmental conditions and stress physiology relationships in endangered Wyoming toads (*Anaxyrus baxteri*) using a novel, noninvasive dermal swabbing method to measure glucocorticoids. We aimed to validate use of dermal swabs to measure cortisol via enzyme immunoassay using adrenocorticotropic hormone (ACTH) challenge on 8 captive Wyoming toads (4 ACTH: 2M, 2F and 4 saline as controls: 2M, 2F); compare fecal glucocorticoid metabolites (FGMs) pre- and post-ACTH (1M, 1F); and investigate dermal cortisol across reintroduction sites with varying population success and disease prevalence. In females, saline resulted in two elevated swabs at 0 min (2.2-fold) and 60 mins (13.3-fold) and ACTH resulted in 2 (4.6-fold at 0 min and 3.0-fold at 90 min) and 3 elevated swabs (10.7-fold at 0 min, 3.4-fold at 30 min and 3.9-fold at 60 min). In males, saline resulted in 1 elevated swab

(8.6-fold) at 0 mins. For males, ACTH resulted in elevated swabs at 45 mins (4.9 fold) and 60 mins (3.1-fold) post-injection, respectively. Saline produced no change in FGMs post-injection; however, the male had elevated FGMs (7.6-fold) 2 days post-ACTH and female had elevated FGMs (1.6-fold) 4 days post-ACTH. Dermal cortisol was similar across reintroduction sites; however, wild males at the Mortenson site had higher (P=0.002) cortisol in August than June. Wild *Bd*+ toads (752.8 ±68.0 pg/ml swab) had higher (P=0.045) cortisol than *Bd*- toads (500.0 ±95.3 pg/ml swab). Dermal hormonal analysis is a novel tool to study amphibian stress physiology and may inform how environmental conditions impact population success.

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452 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Ralph Saporito[1], Sarah Bolton[2], Olivia Brooks[1]

[1]John Carroll University, University Heights, Ohio, USA, [2]The College at Brockport, State University of New York, Brockport, New York, USA

Maternal provisioning of alkaloid defenses in the dendrobatid poison frog *Oophaga granulifera*

Poison frogs sequester alkaloid defenses from a diet largely consisting of mites and ants. As a result, these frogs are unpalatable to many predators and protected against certain microbial infections. The strawberry poison frog *Oophaga pumilio* (Dendrobatidae) exhibits complex maternal care, wherein mothers transport recently hatched tadpoles to phytotelmata and return regularly to supply their developing tadpoles with unfertilized (nutritive) eggs as their only source of nutrition for ca. 6 weeks. Furthermore, female *O. pumilio* maternally provision their nutritive eggs with alkaloid defenses, providing protection to their developing tadpoles at a vulnerable life-stage. Here, we provide evidence that mother frogs of another species in the genus *Oophaga* (*Oophaga granulifera*), also provision alkaloid defenses to their tadpoles. We collected tadpoles of different developmental stages and females of *O. granulifera* from Costa Rica, and detected alkaloids in both life-stages. The quantity and number of alkaloids increased with tadpole mass and age; however, as with *O. pumilio*, we did not detect alkaloids in early stage tadpoles. Our findings suggest that maternal provisioning of alkaloids is not unique to *O. pumilio*, providing the first direct evidence that other members of *Oophaga* also provision alkaloids to their offspring.

CANCELLED

417 Amphibian Disease, Ballroom 3 – Cliff Lodge, Sunday 28 July 2019

Anna Savage, Jacob LaFond

University of Central Florida, Orlando, FL, USA

Rapid Immunogenetic Adaptation to Chytridiomycosis in Arizona Leopard Frogs

The lowland leopard frog (*Rana yavapaiensis*) is a desert southwest endemic that has declined considerably in recent decades. A major driver of these declines is chytridiomycosis, a fungal disease that has caused extirpations and extinctions in hundreds of amphibian species globally. *Rana yavapaiensis* has a highly variable response to chytridiomycosis, with some populations suffering major declines or extirpation, and others demonstrating adaptive tolerance. Previous research has demonstrated that this variation in susceptibility is due, at least in part, to genetic variation in certain major histocompatibility complex (MHC) immune genes, which play a key role in initiating adaptive immune responses. Specifically, allele Q of the MHC class IIβ peptide-binding region correlates with host survival in response to chytridiomycosis, and this allele is hypothesized to be under directional selection in some populations. However, whether a pattern of directional selection acting on beneficial alleles is occurring within extant populations has not been tested. Here, we utilize temporal sampling of seven natural *R. yavapaiensis* populations from 2006-2018 to test for positive and directional selection over a twelve-year period. We compare metrics of adaptive evolution, immunogenetic diversity, and population differentiation over time to assess whether, as predicted from earlier studies, beneficial MHC alleles are evolving in response to chytridiomycosis-induced directional selection in populations of *R. yavapaiensis* that are persisting with disease. Our study has the potential to inform management strategies for threatened amphibian species and to elucidate the importance of functional genetic diversity for population persistence in the face of rapid environmental change.

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789 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Amanda Schaaf, Jim Gelsleichter

University of North Florida, Jacksonville, Florida, USA

Exploring potential inshore habitat use by euryhaline elasmobranchs in a southeastern Atlantic river system utilizing fishery surveys and environmental DNA

Anthropogenic-induced changes to both climate and habitat can result in profound ecological consequences, affecting prey availability, timing of migration events, and changes in community structure. There has been a northward distribution expansion of many marine fish species in the North Atlantic Ocean and recent evidence of environmental changes leading to increased use of inshore habitats by Bull Sharks (*Carcharhinus leucas*) in the Southeast United States. The St. Johns River (SJR) is a large north-flowing system that empties into the Atlantic Ocean near Jacksonville, Florida and is an ideal system to study changing patterns of elasmobranch use due to the combined effects of upriver water withdrawals, dredging at the mouth of the river, and a warming climate that could induce a salinity gradient shift and thus establish better suited habitat for bull sharks and other euryhaline elasmobranchs, potentially including the Smalltooth Sawfish (*Pristis pectinata*). While preliminary observations did not yield any evidence of bull shark use, recent anecdotal reports and photographic evidence warrant a reinvestigation. To monitor species presence a bottom-longline survey will be conducted in conjunction with an environmental DNA (eDNA) survey targeting bull sharks and smalltooth sawfish. As species continue to expand their ranges and their distributions shift to stay within optimal conditions for growth and reproduction, many changes to the local ecosystem may accompany these shifts. It is important to understand these shifts due to possible trophic effects of increased abundance of an apex predator in a commercially important river system.

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60 Herpetology Lightning Talks, Ballroom 3 – Cliff Lodge, Saturday 27 July 2019

Christopher Schalk[1], Michael Cove[2]

[1]Stephen F. Austin State University, Nacogdoches, TX, USA, [2]Smithsonian Conservation Biology Institute, Front Royal, VA, USA

Squamates as Prey: Predator Diversity Patterns and Predator-prey Size Relationships

Understanding the relationships between prey and their predators can provide important insights into evolution of defenses, foraging ecology, and functional roles within their ecosystem. Squamates (lizards and snakes) exhibit a wide range of morphological, ecological and behavioral variation and are model organisms for the study of the evolution of anti-predator traits, making them an ideal group to search for general patterns in predator-prey relationships. We compiled a squamate predator database that consisted of 1,152 squamate predation-prey interactions representing 396 lizard species from 30 families and 217 snake species from 13 families. We quantified the predator taxonomic diversity and explored the relationship between predator size and prey size. Both lizards and snakes were preyed upon by a greater diversity of squamate predators compared to avian and mammalian predators. Snakes appear to be more vulnerable to a broader size range of predators compared to lizards, which is likely attributed to differences in their body morphology. These results provide further support for the hypotheses that predation pressure may affect the evolutionary trajectory of squamate defenses.

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59 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Christopher Schalk[1], William Lutterschmidt[2], J.M. Weidler[3,2]

[1]Stephen F. Austin State University, Nacogdoches, TX, USA, [2]Sam Houston State University, Huntsville, TX, USA, [3]Bureau of Information and Telecommunications, Pierre, SD, USA

Hot Moments and Hot Spots in the Bayou: Patterns of Road Occurrence in a Louisiana Snake Assemblage

Quantifying temporal and spatial occurrence of road crossing activity by amphibians and reptiles has become increasingly important in conservation efforts. By documenting both the hot moments and hot spots of species and species assemblages, effective conservation strategies can help mitigate road mortality. We conducted a year-long survey of a snake assemblage on U.S.

Highway 51 along the Joyce and Manchac Wildlife Management Areas and the Manchac Land Bridge Area between Lake Pontchartrain and Lake Maurepas, Louisiana. A total of 78 road cruising surveys allowed us to investigate both the temporal and spatial occurrence of snakes. We found 409 snakes representing 12 species within two families, Colubridae and Viperidae. As expected, hot moments occurred in late spring or early summer, coinciding with the breeding season and mate searching behavior. Hot spots along Highway 51 were also detected at the assemblage level. However, we were also able to detect species-level hot spots most likely due to our large sampling occurrence. Both peak times and areas of snake activity are reported along U.S. Highway 51 and may serve to help define potential conservation efforts or at least considerations for mitigating or reducing wildlife road mortality.

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794 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Patricia Schellhammer, Michael Sandel

The University of West Alabama, Livingston, AL, USA

An Aquatic Melting Pot: Mapping Genetic Homogenization Among Bullhead Minnow Populations of the Tenn-Tom Waterway

The Tennessee and Mobile River Basins represent the two most biodiverse watersheds in North America. Unfortunately, the same rivers are now recognized for their imperilment, as they are home to a number of threatened and endangered species. Many fish populations of the Mobile River Basin are recognized as distinct endemic species. Genetic homogenization, therefore, represents a threat to native biodiversity in Alabama by the loss of heritable variation. In 1984, with the completion of the Tenn-Tom waterway, the Mobile and Tennessee River basins united hydrologically, providing an opportunity for gene flow between fish populations that had been separated for at least 5 million years. Examining mitochondrial DNA variation in the Bullhead Minnow (*Pimephales vigilax*) across in the Tennessee River, Mobile River, and neighboring watersheds along the Gulf Coast we find evidence for distinct native haplogroups with genetic exchange along the Tenn-Tom waterway.

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451 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Nicholas Schiwitz[1], Kasey Jobe[2], Krista Ward[2], Daniel Saenz[3], Christopher Schalk[1]

[1]Arthur Temple College of Forestry and Agriculture, Stephen F. Austin State University, Nacogdoches, TX, USA, [2]Department of Biology, Stephen F. Austin State University, Nacogdoches, TX, USA, [3]Southern Research Station, U.S. Forest Service, Nacogdoches, TX, USA

Does Instillation Method Affect Snake Entanglement in Erosion Control Blankets?

In the United States, roads are a ubiquitous feature of the landscape that need frequent maintenance. After a road construction project, erosion control blankets (ECBs) are installed to stabilize seed regeneration and prevent soil loss. While deployment of ECBs protects wetlands and decreases erosion potential, their presence on the landscape could negatively impact wildlife via entanglement. Snakes are at greater risk, with multiple accounts of snakes becoming entangled in ECBs that leads to sever injury or death. In particular, snakes are most prone to entanglement in plastic, monofilament ECBs with fused mesh corners. Many of these accounts note that entanglements occur on the edge of ECBs where multiple mesh layers are exposed. The objective of this research was to examine the effects of installation technique of ECBs on the risk of snake entanglement in an ECB with plastic monofilament mesh. We conducted an experiment to compare the likelihood of entanglement when 1) the edge of the ECB was exposed, and 2) when the edge of the ECB was staked down with metal stakes and buried. Fewer snakes became entangled when the ECB edge was buried compared to when it was exposed. Implementation of installation methods that minimize the amount of ECB edge exposed may reduce entanglement risk for snakes, especially in instances when ECBs with plastic monofilament mesh are deployed on the landscape.

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444 Herpetology Ecology, Primrose A&B – Cliff Lodge, Saturday 27 July 2019

Nicholas Schiwitz[1], Christopher Schalk[1], Daniel Saenz[2]

[1]Arthur Temple College of Forestry and Agriculture, Stephen F. Austin State University, Nacogdoches, TX, USA, [2]Southern Research Station, U.S. Forest Service, Nacogdoches, TX, USA

Activity Level and Predation Risk in a Tadpole Guild: Implications for Species' Distributions Along the Hydroperiod Gradient

The activity rate-predation risk tradeoff is pervasive amongst all animals. Increasing activity levels permits greater food intake for use towards growth and reproduction, consequently increasing predation risk. Larval anurans are model organisms to examine this tradeoff as they occupy a variety of lentic habitats. Ephemeral ponds have a low abundance and diversity of predators, allowing tadpole species to have high foraging rates for rapid development. Stable, permanent ponds possess a greater diversity and abundance of predators, with those tadpoles having a low activity rate or chemical defenses to minimize predation risk. The objective of this research is to examine how interspecific variation in activity rate corresponds to distributions of tadpole species along the hydroperiod gradient, and the influence of predation risk on the activity rate. We conducted a series of laboratory experiments where we quantified activity of 12 species of larval anurans native to East Texas. We further quantified how activity level changed through the addition of predator chemical cues, followed by alarm cues produced from a consumed conspecific. We found not all species altered their activity in the presence of predator cues or conspecific alarm cues. Species that maintained a high activity level, despite the threat of predation, utilize ephemeral ponds, where species that maintained low activity levels utilize permanent ponds. These results highlight that this tradeoff can have consequences on the life

histories of these, and other, species, providing insight to how it affects the organization of ecological communities.

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509 General Ichthyology II, Cottonwood A-D – The Snowbird Center, Saturday 27 July 2019

Ray Schmidt[1,2], Christian Barrientos[3]

[1]Randolph-Macon College, Ashland, VA, USA, [2]Research Associate, Division of Fishes, National Museum of Natural History, Washington, DC, USA, [3]Wildlife Conservation Society, Bata, Equatorial Guinea

Finding *Enteromius potamogalis*: discoveries and insights on the diversity of freshwater fishes from Equatorial Guinea

Rivers and streams in the mainland portion of Equatorial Guinea (Rio Muni) were virtually unexplored until the 1960s with few collections occurring since then. New collections from this region will assist with ongoing studies in the neighboring countries and are essential as it is the type locality for several fishes of taxonomic and nomenclatural importance. Most notable of these is *Enteromius potamogalis*; described from the area and only known from the type material. Genetic material from this species is necessary to resolve taxonomic uncertainty in the African barbs. A three-week expedition to the area in 2017 aimed to rapidly survey the freshwater fishes throughout the country, collect *E. potamogalis* from the type locality, and identify areas where further collections are needed. Specimens and tissue samples were collected at 42 localities across the county. The collections focused on the Rio Muni and Rio Mbini drainages, but most of the drainages and smaller coastal rivers were also sampled. *Enteromius potamogalis* from the presumed type locality (Rio Muni) and other coastal rivers were collected. Numerous undescribed species of cyprinids, mochokids, and characids were collected throughout the region and are being formally described. The expedition also collected several populations of wide-ranging species (e.g. *Enteromius camptacanthus, Amphilius longirostris*) which are contributing to revisions of these species complexes. Here we present the results from the expedition, highlight the diversity within some of the groups, and identify areas that need further study.

CANCELLED

711 Ichthyology Lightning Talks, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Eric Schneider[1,2], Brendan Talwar[1,3], Matthew Witt[4], Travis van Leeuwen[5]

[1]Cape Eleuthera Institute, Deep Creek, Bahamas, [2]University of Glasgow, Glasgow, United Kingdom, [3]Florida International University, Miami, FL, USA, [4]University of Exeter, Exeter, United Kingdom, [5]DFO Canada, St. Johns, Canada

Biomass Accumulation Around Anchored Fish Aggregation Devices (FADs): Utilizing Light Trapping and Fisheries Sonar to Quantify Colonization of Pelagic FADs

Fish aggregation devices (FADs) are an increasingly prominent tool in commercial fishing operations and facilitate over 50% of the annual tuna catch that is landed globally. Estimates suggest that upwards of 100,000 new FADs are deployed each year, yet management efforts surrounding FAD fishing are logistically difficult and often insufficient. While much of the research conducted around FADs focuses on commercially and recreationally important sportfish, little work has attempted to address the effects that FADs may have on smaller and lower trophic level organisms. To quantify biomass accumulation around two sub-surface FADs anchored in 600m of water, weekly transects were performed with an EK80 wide band echosounder from the surface to 250m deep in an array extending 1km in each cardinal and intercardinal direction away from the FAD for 9 months. Additionally, light traps were deployed on the FAD anchor line, 500m away and 1km away at depths of 10m, 200m, 400m and 600m to investigate the small mesopelagic fish and invertebrate community structure around the FAD. Results from these complementary methods will begin to shed light on whether anchored FADs incur fine-scale effects on pelagic fauna.

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803 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Tristan Schramer

Illinois Natural History Survey, Champaign, Illinois, USA

Into the Crayfish Burrow: The Ecology of Kirtland's Snake (*Clonophis kirtlandii*)

Kirtland’s snake (*Clonophis kirtlandii*) is a poorly known natricine inhabiting moist environs within Illinois, Indiana, Kentucky, Michigan, Missouri, Ohio, Pennsylvania, and Tennessee. Recent prospects of federal listing have been thwarted by the scarcity of information regarding its natural history, distribution, population size, and threats. Thus, more scrupulous and up-to-date information are needed for a constructive assessment of the current and future status of Kirtland’s snake. Aiding in this effort, this investigation aims to examine the ecology and zoogeography of *C. kirtlandii* in a new light. With the discovery of additional extant populations, novel data regarding the habitat use, community associations, and diet of Kirtland’s snake have also been unearthed. Coupling modern phylogenetics with these new ecological data may allow us to make inferences regarding unknown aspects of this species’ natural history, ecology, and evolution. Our knowledge of Kirtland’s snake has remained stagnant for decades now, but novel approaches may finally begin to conciliate the enigma shrouding *C. kirtlandii*.

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146 AES GRUBER AWARD I, Rendezvous A&B – The Snowbird Center, Thursday 25 July 2019

Gail Schwieterman[1], Daniel Crear[1], Danielle Lavoie[2], Brooke Andersen[3], James Sulkowski[3], Richard Brill[1]

[1]Virginia Institute of Marine Science, William & Mary, Gloucester Point, VA, USA, [2]Roger Williams University, Bristol, RI, USA, [3]University of New England, Biddeford, ME, USA

Interactions of Acute Temperature and pH Changes on Metabolic Rates and Hypoxia Tolerance: A Comparison Between Mid- and North-Atlantic Species

The increasing use of autonomous data recording devices has revealed that temperature, pH, and dissolved oxygen are extremely variable in temperate coastal and estuarine areas over both tidal and seasonal time scales. We hypothesized species inhabiting these areas likely possess species-specific physiological mechanisms which will allow them to withstand the environmental changes predicted under climate change. To test this hypothesis, we used intermittent-flow respirometry to measure changes in metabolism (*e.g.,* aerobic scope, standard metabolic rate) and hypoxia tolerance across multiple temperature and pH levels in clearnose skate (*Raja elganteria*), summer flounder (*Paralichthys dentatus*), and thorny skate (*Amblyraja radiata*). Our preliminary results suggest the two estuarine species native to the mid-Atlantic Bight (clearnose skate and summer flounder) are more tolerant of acute thermal stress than thorny skate (a species with a more northern and less environmentally-variable distribution). However, all three species exhibited an antagonistic, interactive effect of reductions in pH and increases in temperature on hypoxia tolerance. The differential responses to acute changes in temperature and pH conditions may have management implications under climate change, especially for the skates which are currently managed as a species complex.

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601 Ichthyology Ecology, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Fredys F. Segura-Guevara, Sonia E. Sánchez-Banda, Charles W. Olaya-Nieto

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

Trophic ecology of Blanquillo *Sorubim cuspicaudus* in the High Sinu River seven years after filling of Urra Dam, Colombia

Trophic ecology of Blanquillo *Sorubim cuspicaudus* in the Sinu River seven years after filling of Urrá Dam, Colombia, was studied. Individuals with total length (TL) ranged between 25.2 and 81.0 cm and total weight (TW) ranged between 72.0 and 3360.0 g were collected. The stomach contents were analyzed using the Proportion of empty stomachs, grade of digestion, Frequency of occurrence, numerical Frequency and Gravimetry. The Proportion of empty stomachs was high and most of the foods were half digested, identifying four food groups: Fishes, Crustaceans, vegetable Rests and Others. The evaluation of stomach contents showed that Fishes was the most common group, the most abundant group and the greatest group composition in weight and the main food in the Blanquillo´s diet. Fishes were consisted by species like *Andinoacara pulcher, Astyanax* sp., and *Cyphocharax magdalenae.* The results achieved in this study suggest

that Blanquillo is a carnivorous fish with piscivorous tendency which keeps its food preferences as it grows.

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607 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Fredys F. Segura-Guevara[1], Glenys Tordecilla-Petro[2], Charles W. Olaya-Nieto[1]

[1]Fishery Biology Research Laboratory-FBRL, Department of Aquatic Sciences. University of Cordoba, Lorica, Cordoba, Colombia, [2]Institución Educativa Lácides C. Bersal. Lorica, Colombia, Lorica, Cordoba, Colombia

Reproductive biology of Chipe *Hoplosternum magdalenae* in the Cienaga Grande de Lorica, Colombia

Reproductive biology of Chipe *Hoplosternum magdalenae* in the Cienaga Grande de Lorica, Colombia was studied. Individuals with total length (TL) ranged between 9.2 and 13.5 cm and total weight (TW) ranged between 16.0 and 44.0 g were collected, and Sexual proportion, maturity index, spawning season, length at first maturity, ovocites's diameter and fecundity were estimated. It was found 132 females, 49 males and 20 undifferentiated individuals, with sexual proportion female: male 2.7:1, differently than expected. Length at first maturity was estimated in 11.1 cm TL for both sexes, oocites's average diameter were 1329 µm and average fecundity by spawning was estimated at 645 oocites, with better equation $F = 298.08\ WG^{1.27}$, $r = 0.81$. The results achieved in this study suggest that Chipe is a fish that has partial spawnings, with prolonged spawning season that extends throughout the year, with large oocytes and medium fecundity.

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632 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Jason Selwyn, Ashley Hamilton, Sharon Magnuson, Christopher Bird, J. Derek Hogan

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

First sequenced genome for a reef goby *Coryphopterus personatus* (Gobioidei: Gobiidae)

The ever-increasing number of fully assembled genomes is granting greater insight into the genomic architecture and evolutionary history of non-model species. However, despite the ever-decreasing cost of high throughput sequencing it is still challenging and expensive to *de novo* assemble a full species genome. Mapping sequencing data to a pre-existing genome from a different species can be problematic due to the evolutionary divergence between taxa and is further influenced by the quality of the genome used as a reference for mapping. Here we use tools to *de novo* assemble a novel genome for the goby *Coryphopterus personatus.* We used data that we collected for population genetic research to assemble the genome, demonstrating the multiple uses of RAD sequencing data. The population genetic data was supplemented with cheaply available shotgun sequencing to encompass the full genome. We assembled the genome using multiple reference genomes as guides. This has the benefit of not unduly increasing the cost of sequencing and avoids some of the pitfalls of reference mapping by using multiple distinct genomes of various evolutionary distances and assembly qualities to improve the overall assembly of our genome. This is the first genome assembly of a reef-dwelling goby species, and only the sixth of any member of the order Gobiiformes, representing one of the most specious taxa of vertebrates.

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165 AES Trophic Ecology I, Alpine A,B,C – The Snowbird Center, Sunday 28 July 2019

Emily Seubert[1], John Valentine[2], Sean Powers[3], Nigel Hussey[4], Marcus Drymon[1]

[1]Mississippi State University, Biloxi, MS, USA, [2]Dauphin Island Sea Lab, Dauphin Island, AL, USA, [3]University of South Alabama, Mobile, AL, USA, [4]University of Windsor, Windsor, Ontario, Canada

Not So Stable: Investigating the Trophic Flexibility of Predatory Species Using Stable Isotope Analysis

Throughout the Anthropocene, human influences have modified and altered marine seascapes, particularly in coastal regions. The northcentral Gulf of Mexico is a dynamic and diverse region with varying degrees of urbanization; yet it also supports large and variable populations of elasmobranchs. These species are often considered trophically redundant, occupying similar trophic roles in their ecosystems. Using two distinct gear types, bottom longline and demersal trawl, we sought to characterize the species composition of the predatory populations and their potential prey base across an east to west gradient of urbanization from Alabama to Louisiana, USA. To investigate seasonal as well as regional trophic variability, we used a fast turnover tissue, blood plasma, for stable isotope analysis of three distinct isotopes: $\delta^{13}C$, $\delta^{15}N$, and $\delta^{34}S$. Trophic overlap using all three isotopic signatures was calculated for seven dominant predatory species found across the sampling regions: Atlantic sharpnose shark (*Rhizoprionodon terraenovae*), blacktip shark (*Carcharhinus limbatus*), red drum (*Sciaenops ocellatus*), southern stingray (*Hypanus americanus*), blacknose shark (*C. acronotus*), spinner shark (*C. brevipinna*), and bull shark (*C. leucas*). Varying levels of trophic niche overlap were identified for the same species across different regions and seasons, suggesting these predator populations exhibit trophic flexibility across these habitats. Additionally, spatiotemporal variability was also detected in the trawl data, suggesting seasonal pulses of potential prey drive the shifts in predatory species catch composition. These findings underscore the fallacy of categorizing predatory species into the same trophic group and characterize an isotopically diverse predatory guild in the northern Gulf of Mexico.

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433 Herpetology Morphology and Systematics, Ballroom 1 – Cliff Lodge, Friday 26 July 2019

Brad Shaffer, Peter Scott

UCLA, Los Angeles, California, USA

Can 80 Genomes, 600 RADseq Libraries, the Best Museum Collections and 20 Herpetologists Resolve a Hard Species Delimitation Problem?

Most species are easy to delimit, but a small fraction are really hard. Those tough problems, including clades that have speciated recently, have some level of hybridization, or involve strong selection and potential convergence, are among the most interesting, and most frustrating in systematics. When those species are also endangered, resolution that reflects our best science is both challenging and essential. The turtle genus *Pseudemys* is one such clade. Current taxonomy divides *Pseudemys* into nine species, although the most recent molecular analysis, based on 10 nuclear and three mitochondrial genes, indicated that it may be badly oversplit. If correct, this previous work also suggests that two endangered species, *P. alabamensis* and *P. rubiventris bangsi*, may be invalid taxa. To address this problem, we sequenced the entire ~2.6 GB genomes of 80 individual turtles, with excellent geographic representation of all nominal taxa. Given its importance for the conservation community, we also collected RADseq data for a set of roughly 500 individuals, including population-level samples from all occupied rivers, of the federally endangered *P alabamensis* and co-occurring members of the *P. concinna* species complex. Finally, we organized a meeting in collaboration with the Florida Museum of Natural History where 20 experts examined specimens, characters, and their ideas on species limits in *Pseudemys.* Can this level of data and expertise fully resolve the systematics of this, and potentially other recalcitrant clades? We discuss this, and how to move forward as a community, in this presentation.

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466 AES Ecology, Rendezvous A&B – The Snowbird Center, Friday 26 July 2019

Rachel Shaw[1], Tobey Curtis[2], Gregory Metzger[3], Michael McCallister[1], Christopher Fischer[4], Matthew Ajemian[1]

[1]Florida Atlantic University, Harbor Branch Oceanographic Institute, Fort Pierce, FL, USA, [2]NOAA National Marine Fisheries Service, Atlantic Highly Migratory Species Management Division, Gloucester, MA, USA, [3]South Fork Natural History Museum, Bridgehampton, NY, USA, [4]OCEARCH, Park City, UT, USA

3D Movement and Habitat Use of Young White Sharks (*Carcharodon carcharias*) in the Northwest Atlantic Ocean

Recent research has confirmed the presence of a white shark (*Carcharodon carcharias*) nursery habitat off Long Island, New York; however, additional research is required to determine the habitat use and fine-scale movement patterns of young-of-the-year (YOY) and juvenile white sharks within this nursery. In order to identify what habitat characteristics are most often utilized, and to quantify diving behavior and diel activity patterns, YOY and juvenile white sharks were fitted with Smart Position or Temperature transmitting (SPOT) tags (n=19), and high-rate pop-up satellite archival tags (PSATs, n=7). Three-dimensional tracks were generated for four dual-tagged individuals. SPOT tags identified a majority of horizontal movements parallel to Long Island's southern shoreline at depths generally less than 40 m. PSAT logs showed mean swimming depths of 9 m (±6 m); however, vertical oscillations between the surface and depths as deep as 200 m were observed. Individuals swam in mean water temperatures of 19°C (±1°C), regardless of time of day, with preliminary results showing an increase in the number of dives performed during daylight hours. These results will help improve characterization of essential fish habitat used by YOY and juvenile white sharks and provide data that can be used by fisheries management to determine potential susceptibility to anthropogenic activities.

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759 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Caitlin Shea-Vantine, Stephen M. Kajiura, Marianne E. Porter

Florida Atlantic University, Boca Raton, Florida, USA

Puncture performance of the barbs from the Atlantic stingray, *Hypanus sabinus*

Many animals have venomous structures for defense against predators, such as bee stingers, male platypus spurs, and lionfish spines. A diagnostic characteristic of the Myliobatiformes is the presence of a barb located on the tail and used for defense. Stingray barbs are composed of mineralized collagen and are partially serrated. Barb cross-sectional shape, serrated length, and number of serrations vary across taxa and are correlated with ecology. The goal of this project was to determine the puncture performance of barbs from the Atlantic stingray, *Hypanus sabinus*. We used an Instron E1000 materials tester to quantify the puncture and withdraw forces of biologically relevant target materials: shark mouth skin and porcine skin, a common model for human skin. We hypothesized that stingray barbs would require greater force (N) to puncture and withdraw from shark mouth skin, due to the presence of embedded dermal denticles. To quantify puncture forces (N), barbs were driven into skin at 30 mm min^{-1} at a 90°angle until the barb embedded in the target tissue. The withdraw forces (N) were quantified by raising the barb at 30 mm min^{-1} until the tip was no longer embedded into the target material. We also incorporated micro-CT scanning to quantify the morphology of the barb as well as mineralization density. By investigating the puncture and withdraw mechanics of stingray barbs, we can quantify the effectiveness of the stingray defense system and compare true predator targets (sharks) with accidental targets (humans).

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311 SSAR SEIBERT CONSERVATION AWARD I, Ballroom 1 – Cliff Lodge, Friday 26 July 2019

Alexander Shepack, Alessandro Catenazzi

Florida International University, Miami, FL, USA

Demography and viability of amphibian populations recovering from chytridiomycosis related declines

Chytridiomycosis, caused by the fungal pathogen *Batrachochytrium dendrobatidis* (*Bd*), is widely believed to be responsible for amphibian declines and extinctions throughout the world. While the initial impacts of the epizootic wave on populations was widely documented, we are still struggling to understand the effects of the current enzootic disease-state on amphibian populations. Globally there are reports of recovering amphibian populations despite the continued presence of *Bd.* Our research focused on the demography, host-pathogen relationship, and genetics of several of these recovering populations. In central Costa Rica two such species, *Duellmanohyla rufioculis* and *Sachatamia ilex*, are recovering despite continued infection by *Bd* and consistent transmission throughout the community. Over 3 years we conducted a mark-recapture study on these species, concurrently sampling the community for *Bd*, and collecting samples for genetic analysis. Our results suggest that, despite high prevalence of infection in both species, individuals survive through reproduction and may be capable of surviving with *Bd.* Coupled with the mark-recapture results, population genetic analysis is illuminating the future viability of these populations as well as the consequences of epizootic declines and the longer-term enzootic effects. By studying the host-pathogen dynamics and biology of these recovering populations we can hope to understand the way populations and communities deal with pathogens across time-scales and can apply this knowledge to continued conservation efforts and in planning for other pathogen arrivals, like the related amphibian pathogen *Batrachochytrium salamandrivorans.*

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760 Herpetology Biogeography I, Ballroom 3 – Cliff Lodge, Friday 26 July 2019

Donald Shepard, Ryan Philobos, Pedro Simoncini, Cameron Robicheaux

Louisiana Tech University, Ruston, LA, USA

Demographic Responses to Pleistocene Climate Change in Interior Highlands Woodland Salamanders (Genus *Plethodon*)

The Pleistocene (~2.5 million to 12,000 years ago) was characterized by climate fluctuations and glacial cycles, which greatly impacted many species' distributions. Changes in population size associated with range expansion and contraction are expected to leave specific genetic signatures in populations. Closely related species occupying the same geographic area might be expected to respond similarly to climate fluctuations; however, growing evidence suggests that species often respond uniquely to environmental changes. The Interior Highlands (Ouachita Mountains and Ozark Plateau) of the United States are home to several species of plethodontid salamanders and experienced significant environmental changes throughout the Pleistocene. We used mitochondrial DNA sequences from seven species of Woodland Salamanders (Genus *Plethodon*) occurring in the Interior Highlands to test if species showed similar changes in effective population size (N_e) in response to Pleistocene climate change. We found that several species showed evidence of a recent increase in population size, likely as a result of range expansion following the retreat of glacial ice sheets after the Last Glacial Maximum. However, other species showed evidence of stable or slightly decreasing population size. Although some species appeared to have similar demographic responses to Pleistocene climate change, our results support the idea that species, even those closely related, will respond individually to environmental changes.

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119 ASIH STORER ICHTHYOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Andrew Sherman, Kyle Piller

Southeastern Louisiana University, Hammond, Louisiana, USA

Resolving Taxonomic Turmoil Among Aquarium Strains and Wild-Caught Samples of *Characodon* (Goodeidae)

Goodeid fishes (Cyprinodontiformes: Goodeidae) represent one of the most imperiled groups of freshwater fishes in North America. Changes in land-use, introduction of exotic species, and water removal represent some of the most substantial impacts to goodeid fishes. One of the most jeopardized groups in the family is the genus *Characodon*, a small group that currently includes two extant species, *C. lateralis* and *C. audax*, distributed in north-central Mexico. Taxonomic status of particular populations, for both species, are uncertain. Many of these populations are identified by locality, rather than taxonomic name, which has further lead to taxonomic uncertainty. As a result, the goal of this study is to examine mitochondrial DNA variation among populations of aquarium maintained strains of *Characodon* to attempt to clarify the nomenclatural boundaries. Fin clips were obtained from 13 aquarium strains of *Characodon* and we supplemented our sampling by including data from wild caught samples from known localities. DNA was extracted using a standard Qiagen DNEasy protocol and then used to PCR amplify a fragment of mtDNA (CytB). Mitochondrial data was used to construct a haplotype network and a maximum likelihood-based phylogeny, as well as several population genetic statistics. Our results provide clarity to the nomenclatural status of some of the aquarium strains, provide support for previous claims of a North-South clade in *C. lateralis*, and points to the possibility that populations previously believed to be *C. lateralis* are more closely related to *C. audax*.

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395 SSAR SEIBERT PHYSIOLOGY & MORPHOLOGY AWARD, Ballroom 3 – Cliff Lodge, Thursday 25 July 2019

Analisa Shields-Estrada, David Cannatella

University of Texas at Austin, Austin, TX, USA

Near Infrared Reflectance & Thermoregulation in *Epipedobates* Poison Frogs

Adaptive variation in color reflects a suite of organismal specific traits and behaviors, ranging from warning signaling to thermoregulation. However, how this variation is partitioned within the spectrum of solar radiation (300-2500nm) and why, remains unknown. The near-infrared reflectance (NIR) spectrum (700-2500nm) compromises 55% of all solar irradiance, yet spectral reflectance is rarely measured outside of the UV or visible spectra. Furthermore, extensive animal insensitivity to near-infrared wavelengths, makes this spectrum an ideal candidate for understanding the role spectral reflectance plays in ectotherm thermal physiology. The NIR spectrum may be less constrained by selection for warning signaling, camouflage, and sexual signaling, and may instead largely reflect thermoregulatory requirements. Our work examines the relationship between NIR, visible spectral reflectance, and thermoregulation, in a clade of *Epipedobates* poison frogs exhibiting a diverse range of color variation and thermal habitat regimes. We measured spectral reflectance of cryptic and conspicuous species throughout western Ecuador across elevational and temperature gradients in both the visible and NIR spectra (400-1100nm), and measured critical thermal maxima (CT_{max}) and body temperature of each individual. Our results show statistically significant differences between total reflectance in the NIR spectrum and the visible spectrum, indicating the possibility of different selective pressures on each spectrum, and emphasizing the need to consider multiple spectra when studying adaptive variation in color. Furthermore, we found inter-populational variation in CT_{max} and body temperature that may illuminate NIR's role in thermoregulation.

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10 AES Conservation & Management I, Rendezvous A&B – The Snowbird Center, Sunday 28 July 2019

David Shiffman

Simon Fraser University, Vancouver, BC, Canada

Global content analysis of shark conservation coverage in the popular press suggests biases contributing to public misunderstanding

There is significant public interest in chondrichthyan conservation, but many concerned citizens are misinformed about the threats facing sharks and the most effective solutions to protect sharks. This analysis considers how shark conservation threats and solutions are portrayed in an important information pathway, popular press coverage. Through an analysis of 1,808 popular press articles from 2008-2017 from across the English speaking world, we note that shark conservation threats and solutions are not covered in a factually accurate manner with appropriate context. A concerned citizen learning about shark conservation primarily through reading popular press coverage would wrongly believe that shark finning is the only major threat facing sharks and would wrongly believe that banning fishing for sharks and trade in their products are the only available solutions. Citizens' understanding of conservation threats and solutions to those threats influences what solutions they'll support, suggesting that these results are cause for concern if our goal is enacting science-based management policies for sharks.

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181 Session Honoring Contributions and Retirement of Pat Gregory, Ballroom 3 – Cliff Lodge, Sunday 28 July 2019

Richard Shine[1], Claire Goiran[2], Cathy Shilton[3], Gregory Brown[1]

[1]Macquarie University, Sydney, NSW, Australia, [2]University of New Caledonia, Noumea, Province Sud, New-Caledonia, [3]NT Dept Primary Industries and Resources, Darwin, NT, Australia

Have Sea Snakes Evolved Thicker Skins to Deal with Fouling Organisms?

Unlike its terrestrial and amphibious counterparts, an animal that spends its life underwater has to deal with fouling organisms (algae, barnacles, etc.) that attach to its skin and thus, compromise its hydrodynamics. Sloughing the skin can remove those organisms, but only if the skin is thick enough to include the attachment mechanisms of the epibionts. We thus predicted that fully aquatic snakes should have thicker skin than terrestrial or amphibious species; and that smaller species of sea snakes should have relatively thicker skin (because absolute not relative thickness determines vulnerability to fouling organisms). Measurements of 192 snakes of 44 species broadly supported those predictions, but with some surprising twists and turns.

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394 ASIH/HL/SSAR Symposium: The Expanding Role of Natural History Collections, Ballroom 1 – Cliff Lodge, Sunday 28 July 2019

Brian Sidlauskas

Oregon State University, Corvallis, OR, USA

Teaching Ichthyology Online with a Virtual Specimen Collection

For generations, organismal biologists have learned their craft in hands-on laboratories that teach anatomy, evolution, natural history, systematics and functional morphology through specimen collection, observation, comparison and manipulation. Though these activities teach the comparative method that lies at the heart of our discipline, students without access to specimen collections have been excluded from this foundational experience. To reach that underserved audience, I developed a virtual teaching collection of photographs and 3D specimen models, and designed entirely online version of courses in Ichthyology and Systematics of Fishes that draw heavily on that resource. The virtual collection allows students to illustrate and compare specimens in online labs, identify species from different habitats in a virtual field trip using

dichotomous keys, code characters, infer ancestry and locate synapomorphies on phylogenies, take online specimen-based practical exams, and help each other recognize adaptations and diagnostic features on threaded discussion boards. The classes built around the collection now educate more than 150 online students annually, most of whom have no other access to similar courses. Despite never handling physical specimens, their mastery of the material compares favorably to the face-to-face cohort. While we may never be able to replicate the aroma of oil-laden ethanol online, specimen virtualization opens access to experiential learning for an underserved and widespread audience, and allows new generations of students to develop crucial skills in observation, comparison and inference.

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134 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Shane Siers[1], William Pitt[2], Aaron Shiels[1], John Eisemann[1], Larry Clark[1], Robert Gosnell[3], Aaron Collins[3], William Coon[4], Michael Messaros[4]

[1]USDA APHIS WS National Wildlife Research Center, Fort Collins, CO, USA, [2]Smithsonian Conservation Biology Institute, Front Royal, VA, USA, [3]USDA APHIS Wildlife Services, Barrigada, GU, USA, [4]Applied Design Corporation, Boulder, CO, USA

Implementation of an Automated Bait Manufacturing and Aerial Delivery System for Landscape-Scale Control of Invasive Brown Treesnakes

The invasion of Guam by introduced Brown Treesnakes has caused substantial ecological damage and economic burden. High snake densities preclude recovery of Guam’s native birds and pose high risk of accidental introduction to other islands, including the Northern Mariana and Hawaiian Islands. Wildlife Services (WS) and its National Wildlife Research Center (NWRC) have demonstrated that treesnake numbers can be greatly reduced by the aerial application of dead neonatal mouse baits treated with 80 mg tablets of acetaminophen into forest canopy. To scale up to landscape-level operations, NWRC partnered with a private engineering firm, Applied Design Corporation, to develop a system for the automated manufacturing and aerial delivery of baits from a helicopter platform. The system can deliver up to 3,600 baits per payload at a rate of four per second. At an application rate of 120 baits/ha, the maximum approved by the EPA, 30 ha of forest can be treated within 15 minutes of firing time, with the system reloaded by a ground crew in two to three minutes. After a lengthy research and development phase, this technology has been transferred to the WS Guam State Office as a tool available to land managers. Operational snake suppression has begun in a 55-hectare snake exclosure, known as the Habitat Management Unit (HMU), with the intention of evaluating the feasibility of Brown Treesnake eradication and providing snake-free habitat for ecological restoration experiments. This transformative technology holds great promise for increased biosecurity and recovery of habitat for Guam’s native species.

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42 General Herpetology II, Primrose A&B – Cliff Lodge, Sunday 28 July 2019

Shane Siers[1], Amy Yackel Adams[2], Robert Reed[2]

[1]USDA National Wildlife Research Center, Hilo, HI, USA, [2]US Geological Survey, Fort Collins Science Center, Fort Collins, CO, USA

Changes in Behavior Following Ingestion of Large Meals by a Harmful Invasive Snake

Many snakes are uniquely adapted to ingest large prey at infrequent intervals. Digestion of large prey is physiologically costly, and prey boluses can impair locomotion, increasing vulnerability to predation. Cessation of foraging and sequestration in refugia conducive to digestion are expected to be strategies employed by snakes to cope with the demands of digestion while minimizing risk of predation. However, empirical observations of such submergent behavior from field experiments are limited. The brown treesnake (*Boiga irregularis*) is a nocturnal, arboreal, colubrid snake that was accidentally introduced to the island of Guam, with ecologically and economically costly consequences. Because tools for brown treesnake control rely on snakes being visible or responding to lures or baits while foraging, pauses in foraging after feeding would complicate management. We characterized differences in brown treesnake activity, movement, habitat use, and detectability following feeding of large meals (rodents 33% of the snake's body mass) via telemetry, trapping, and visual searching. Fed snakes showed drastic decreases in hourly and nightly activity rates, differences in refuge use, and a decrease in detectability by trapping and visual surveys. Depression of activity lasted 5–7 days, a period that corresponds to previous studies of brown treesnake digestion and cycles of detectability. Our results indicate that management strategies for invasive brown treesnakes need to account for cycles of unavailability, and underscore the importance of preventing spread of brown treesnakes to new environments where large prey are abundant and periods of cryptic behavior are likely to be frequent.

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566 AES GRUBER AWARD I, Rendezvous A&B – The Snowbird Center, Thursday 25 July 2019

D. Lorena Silva-Garay, Christopher G. Lowe

Department of Biological Sciences, California State University Long Beach, Long Beach, California, USA

Metabolic Thermal Sensitivity of the Round Stingray (*Urobatis halleri*)

Coastal ecosystems are considered highly vulnerable to the effects of climate change as diel and seasonal thermal fluctuations intensify. Understanding how the variations in sea temperature affect the metabolic demands and thermal sensitivity of species is key in the effort of improving local management and conservation strategies. The round stingray (*Urobatis halleri*) is an abundant benthic-predator of coastal habitats of Southern California, known for undertaking periodic movements across wide thermal gradients as a thermoregulatory strategy. Using

respirometry, we investigated the effects of temperature changes on the thermal sensitivity (Q_{10SMR}) and minimum metabolic demands of the round stingray. A total of 20 individuals (weight range=0.05–0.82kg) were acclimated at three temperature treatments (15°, 23°, 27°C) that resemble the seasonal thermal variability in Southern CA. Mass-adjusted resting oxygen consumption (MO_2, mgO_2/kg/min) was quantified as a proxy of their minimum aerobic metabolism. As a result, the average Q_{10SMR} value for the tested individuals was 3.43 ± 0.85; showing an increase in their thermal sensitivity with increasing temperatures (i.e. 2.99 ± 1.80 [15°-23°C], 2.90 ± 1.06 [15°-27°C], and 4.41 ± 5.81 [23°-27°C]). Mass-adjusted oxygen consumption rates showed significant differences among temperature treatments ($p<0.05$; ave. MO_2 (mgO_2/kg/min): 1.42 ± 1.02 at 15°, 2.64 ± 0.70 at 23°, and 4.31 ± 1.46 at 27°C). Our results contrast with thermal sensitivity values found for other rays' species of similar habitat association and suggest that drastic temperature changes in coastal habitats likely play a significant role on the energetic demands and the ecology of the round stingray.

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36 ASIH/HL/SSAR Symposium: The Expanding Role of Natural History Collections, Ballroom 1 – Cliff Lodge, Sunday 28 July 2019

Randal Singer

Michigan Museum of Zoology, Ann Arbor, MI, USA

Big Heads or Long Tails: How Every Fish Collection Matters in Collections-Based Biodiversity Research

The biodiversity collections community is largely lacking in quantitative data that can be used to communicate importance to administrators, funding agencies and potential stakeholders. Data for what is contained within US collections are typically only kept by those that curate the collections. Even less data have been collected to explore collection use and researcher data preference. Recently, some data from US fish collections have been collected from iDigBio in order to adequately explore collection holdings and give attribution to the collections that house the specimens. Additionally, a survey of over 430 fish biologists has been conducted to record data preferences. When used in concert, these data highlight some of the incredibly underappreciated and under supported data that small collections provide to the research community. From the data in iDigBio, over half of all fish records are contained in only 10 US collections, but the other half are housed in 28 other collections. Despite having fewer records, many of these smaller collections house unique resources like images, video, special preparations (e.g. cleared and stained specimens), tissues, and georeferenced localities in higher quantities than their much larger counterparts. These data are in high demand, but very few of these biologists know to look in these smaller collections to find it. Through looking closer at the data collections provide, it is possible to not only direct the future efforts of the larger collections with an eye towards what data biologists need, but also highlight the importance of maintaining many collections, even smaller ones.

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40 ASIH STOYE GENERAL ICHTHYOLOGY AWARD II, Cottonwood A-D – The Snowbird Center, Friday 26 July 2019

Daniel Sinopoli[1], Donald Stewart[1], Jeremy Wright[2], Jay Palumbo[1]

[1]State University of New York: College of Environmental Science and Forestry, Syracuse, NY, USA, [2]New York State Museum, Albany, NY, USA

Morphological Variation of the Extant Bowfin (Amiidae: *Amia calva*) in the Mississippi River Basin: Taxonomic and Conservation Implications

The Bowfin genus *Amia* has been considered monotypic since 1896, when 12 nominal species were synonymized with *Amia calva* with no scientific analysis or rationale. In the 122 years since, only five studies have examined morphological or genetic variation within the genus, all of which did find some separation among populations. To test the 1896 monotypy hypothesis for the Mississippi River basin, we analyzed morphological variation in newly collected and museum archived Bowfins from Louisiana (LA: type localities of *A. marmorata, A. viridis*, and *A. subcoerulea*) and Illinois (IL: type localities of *A. reticulata* and *A. piquotii*); type locality for *A. ornata* from the Mississippi basin remains uncertain. Our analysis was based on 40 morphometric measurements and eight meristic counts, using standard multivariate and univariate statistics (e.g., PCA, ANCOVA, etc). There appear to be multiple morphotypes in both IL and LA waters of the Mississippi drainage and nearby Lake Pontchartrain system. We infer that there may be multiple taxa (or 'evolutionarily significant units') in the Mississippi basin. Additionally, two localities in Louisiana each appear to have two sympatric morphotypes. Therefore, we reject the 122-year-old monotypy hypothesis. The discovery of multiple Bowfin morphotypes (species?) has significant management and conservation implications; habitat loss, exotic competitors, and a developing Bowfin caviar fishery all could have harmful effects on population sizes and genetic variation.

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741 ASIH STOYE PHYSIOLOGY & PHYSIOLOGICAL ECOLOGY AWARD, Primrose A&B – Cliff Lodge, Friday 26 July 2019

Zachary Skelton, Philip Hastings

University of California, San Diego, San Diego, California, USA

A Cross-Species Comparison of Temperature Preference and Q10s of Three Species of Juvenile Sharks

Ectotherms, including sharks, must thermoregulate in order to maintain homeostasis and keep up with underlying biochemical and physiological demands. Sharks often utilize the warm, shallow waters of bays and estuaries as juveniles to facilitate growth, due to the abundance of prey, and to avoid predation. With persistent anthropogenic stressors around the bays of Southern California and increasing global ocean temperatures, uncovering how temperature may influence

the behavior and physiology of sharks at this life stage is important to understand how environmental changes might affect the distribution and movement of local species. Juvenile horn sharks (*Heterodontus francisci*), leopard sharks (*Triakis semifasciata*), and grey smoothhounds (*Mustelus californicus*) are among the most abundant species found in bays of San Diego County and were chosen as study species. The primary aim of this study is to use temperature as a proxy for habitat preference by isolating temperature as a single variable. The objectives of this study are threefold: 1) identify the temperatures juveniles prefer (and avoid), 2) assess how different temperatures affect metabolism via oxygen consumption (Q10), and 3) compare these results across species and between sexes. This study employs a shuttle tank to assess temperature preference and respirometry to assess Q10s. This baseline assessment will ultimately be paired with future in situ tracking to determine the role of these metabolic parameters on habitat selection in juvenile sharks.

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88 AES CARRIER AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Rachel Skubel[1], Jodie Rummer[2], Patricia Albano[3], Neil Hammerschlag[1]

[1]University of Miami, Coral Gables, FL, USA, [2]James Cook University, Townsville, Queensland, Australia, [3]University of Miami, Miami, FL, USA

Temperature and oxygen impact on sharks' hematological and stress response indicators at capture

With ongoing climate change, increasing water temperatures and declines in dissolved oxygen may amplify the stress response of sharks caught in commercial and recreational fisheries, which could affect mortality of sharks not retained by fishers. Species may experience less stress following fisheries interactions if their physiology permits high aerobic activity, such as experienced during capture, and/or they are able to recover from physiological perturbations associated with fishery capture. Across eight species of sharks sampled near Miami, Florida, we measured hemoglobin and hematocrit (and MCHC, mean corpuscular hemoglobin concentration) in blood from sampled sharks, to approximate blood-oxygen supply for aerobic activity, and whole-blood glucose and lactate as a proxy for the stress response. We compared these indicators with ambient water temperature, dissolved oxygen, and salinity, along with fight time. We found sharks' physiological indicators of stress were related to environmental conditions. The physiological indicators we measured were most strongly influenced by species. Lactate was additionally related to dissolved oxygen, and glucose to both temperature and dissolved oxygen. Hemoglobin was weakly related to temperature, while hematocrit and MCHC did not vary with either. Our results contribute to prior evidence of variation in the elasmobranch stress response with water temperature, highlighting the potential to mitigate accumulated stress through incorporating temperature and oxygen regimes in shark fisheries management. Moreover, these data suggest that climate-driven stressors on ocean ecosystems, such as increased temperatures and decreased dissolved oxygen, may affect species-specific stress responses to fisheries capture, with survival or fitness implications for animals released alive.

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74 AES Conservation & Management I, Rendezvous A&B – The Snowbird Center, Sunday 28 July 2019

Rachel Skubel, Meryl Shriver-Rice

University of Miami, Coral Gables, FL, USA

Multi-dimensional value of sharks influences policy creation and efficacy in the South Florida commercial shark fishery socio-ecological system

Historical overfishing of sharks in South Florida has necessitated policy interventions to restore populations to sustainable levels. Despite increases in some shark populations attributed to these regulations, there have been growing stakeholder conflicts over shark conservation measures. Here, we used ethnographic methods including semi-structured interviews and participant observation to characterize efforts of policy-makers to balance the needs of ocean-users with ecosystem health. As a result of user-group conflicts, there is an inconsistency of trust on the part of fishers towards management, scientific, and environmental advocacy organizations, impacting participation by fishers in the policy-making which directly affects their livelihoods and well-being. Our interviews and participant observation reveal conflicts arising from diverse views on the science behind policy interventions, and the efficacy of management organizations involved in designing and implementing these policies. These results demonstrate the complexity of communicating with resource stakeholders during the policy-making process, particularly when there is a diversity of strong relationships with, perceptions of, values from, and threats to, that resource. We recommend that management organizations streamline their goals towards regional wildlife and wildlife users, such as through integrating fishers in the collecting data on shark populations and increasing the ease of identifying and reporting illegal activity. By increasing the use and communication of how scientific information for regulating human interactions with sharks is collected and used, managers have the opportunity for more connection with their stakeholders, and for the continued resilience of both shark populations and the well-being of shark fishing communities.

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48 HL GRADUATE RESEARCH AWARD, Ballroom 1 – Cliff Lodge, Thursday 25 July 2019

Cara Smith[1], Stephen Mackessy[1], Drew Schield[2], Todd Castoe[2], Josh Parker[3]

[1]University of Northern Colorado, Greeley, CO, USA, [2]University of Texas at Arlington, Arlington, TX, USA, [3]Fresno City College, Fresno, CA, USA

Snakes on a Plain: Biochemical Ecology and Venom Variation in North America's Most Widely Ranging Rattlesnake (*Crotalus viridis*)

Snake venoms are complex mixtures comprised primarily of potent bioactive proteins used for prey incapacitation. Venom composition has been shown to vary taxonomically, geographically, with age, and with dietary preference. North America's most widely ranging rattlesnake, *Crotalus viridis* (Prairie Rattlesnake), is found from northern Mexico through the plains of the western United States to southern Canada. Coupled with its wide species range, *C. viridis* is also a habitat generalist and inhabits areas in close proximity to humans, increasing the likelihood of human encounters and bites from this snake. *Crotalus viridis* venom is known to induce hemorrhage and muscle degradation due to the presence of larger enzymes like snake venom metalloproteases (SVMPs) and snake venom serine proteases (SVSPs) and smaller nonenzymatic toxins targeting muscle (myotoxins). Though previous research on *C. viridis* has shown geographic variation in some venom toxins, to date, no analysis has investigated broad-ranging variation in the entire venom proteome of this species. The current project investigates venom variation in the *C. viridis* throughout its range in the United States by determining population-level patterns in abundance of major toxins using SDS-PAGE, high performance liquid chromatography, mass spectrometry and biochemical assays. The patterns observed straddle the Type 1-Type 2 venom compositional dichotomy previously characterized in rattlesnakes, as there appears to be a trade-off between dominantly enzymatic and nonenzymatic venom phenotypes. Ultimately, the patterns of venom variation in *C. viridis* can help inform snakebite treatment in addition to providing clues about foraging ecology and venom evolution of this wide-ranging rattlesnake.

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722 ASIH/HL/SSAR Symposium: Citizen Science in Herpetology: Productive Past and Promising Future, Ballroom 2 – Cliff Lodge, Sunday 28 July 2019

Christopher Smith[1], Don Becker[2], Mike Pingleton[3]

[1]HerpMapper, St. Paul, Minnesota, USA, [2]HerpMapper, Cedar Rapids, Iowa, USA, [3]HerpMapper, Champaign, Illinois, USA

Citizen Science 2.0: Implementing Bleeding-edge Technologies in Cooperative Biology

Community participation in herpetology has increased significantly in recent years, and the tools used to collect, manage, and analyze citizen-generated data are rapidly changing. HerpMapper is the largest volunteer-run nonprofit citizen-science project designed to collect and share amphibian and reptile data with conservation and research organizations around the world, with over 250,000 observations reported by more than 3,000 users. In response to demands from citizen scientists and professionals alike, HerpMapper is developing innovative tools to improve data quality, build citizen-scientist participation and capacity, and increase herpetological knowledge. We discuss completed improvements to the HerpMapper platform, discuss on-going project innovations, and describe future direction for HerpMapper and citizen science as a whole.

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453 ASIH STORER HERPETOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Jaime Smith[1,2], Joseph H.K. Pechmann[2], Robin Overstreet[1]

[1]University of Southern Mississippi, Ocean Springs, MS, USA, [2]Western Carolina University, Cullowhee, NC, USA

Can dusky gopher frogs acquire resistance to the Perkinsea clade parasite *Dermomycoides* sp.?

With a current population of < 200 breeding adults, the dusky gopher frog (*Rana sevosa*) risks extinction if shortened hydroperiods or disease greatly reduce natural metamorphic recruitment. The protist parasite, *Dermomycoides* sp., can cause mass mortalities in ranid tadpoles and is thought to have causedl years of near-zero recruitment in several *R. sevosa* populations. Acquired resistance in tadpoles previously exposed to a low dose of pathogen zoospores may explain survival of the few tadpoles not killed in mass mortality events. We experimentally exposed *R. sevosa* tadpoles at Gosner stage 25 to an initial high (~ 200 zoospore/µL), low (~50 zoospores/µL), or zero dose of zoospores of *Dermomycoides* sp. Two weeks after the initial infection, we exposed groups of tadpoles from each initial treatment to a challenge high, low, or zero zoospore dose. Survival was 100% in tadpoles initially exposed to the low zoospore dose and 92% in tadpoles initially exposed to the high dose, prior to infection with the challenge zoospore doses. All tadpoles died within 28 days of the challenge doses. There were no significant differences in days to mortality after the challenge dose among exposure or challenge treatments. This suggests that dusky *R. sevosa* are unable to develop an acquired resistance to infection of zoospores of *Dermomycoides* sp. This lack of resistance may be one explanation for mass mortality events observed in *R. sevosa* due to this parasite.

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122 AES Conservation & Management III, Rendezvous A&B – The Snowbird Center, Sunday 28 July 2019

Kelcee Smith, Dakus Geeslin

Texas Parks and Wildlife Department, Austin, Texas, USA

Updating the Status of Texas Elasmobranchs for Effective Conservation and Management

Species become imperiled for a variety of reasons, including: habitat loss, exploitation, and climate change. Besides these threats, inadequate funding and lack of data can result in misinformed management, limiting scientific research, and ultimately hindering recovery goals. Although many policies exist to protect imperiled species, if a species' conservation status is unknown, prioritizing recovery efforts and securing funding sources can be difficult. However, quantitative evaluation and periodic updating of a species' status can speed recovery efforts by guiding listing/delisting processes, directing conservation actions and research, and allowing for monitoring over time. In Texas, the Texas Parks and Wildlife Department is responsible for developing and managing two lists: State Threatened and Endangered Species and Species of Greatest Conservation Need. Currently, there are 45 species of elasmobranchs on these lists that

lack or require an updated status designation in the state. To evaluate the status of these species, abundance and trend data combined with specific threat vulnerability information was used to determine conservation status with the NatureServe® Conservation Rank Calculator. Working groups comprised of species experts were held to determine the accuracy of the ranking based on available data. Species were then sorted to the appropriate list based on their ranking and criteria outlined in the Texas Conservation Action Plan. This approach will aid the state of Texas in the refinement of its imperiled species lists and foster collaboration among other state agencies, since results will be used in a regional status assessment by the Southeastern Association of Fish and Wildlife Agencies.

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740 Ichthyology Systematics II, Cottonwood A-D – The Snowbird Center, Sunday 28 July 2019

Leo Smith

University of Kansas, Lawrence, KS, USA

The Phylogeny and Taxonomy of Scorpionfishes

During the last 35 years, ichthyologists have made tremendous improvements in our understanding of the relationships among scorpionfishes and their allies using explicit phylogenetic analyses of either morphological or molecular data. These studies have often resulted in the polyphyly of many traditionally recognized groups, and are often at odds with each other in various results. Further, molecular studies have grouped a diversity of other groups with the traditional scorpionfishes. Using a combination of genomic and morphological data, a revised phylogenetic hypothesis for scorpionfishes will be discussed in terms of the group's taxonomy and evolution.

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737 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Leo Smith[1], Kathleen Smith[2], Matthew Girard[1]

[1]University of Kansas, Lawrence, KS, USA, [2]ASIH, Lawrence, KS, USA

Copeia Improvements: Open Access, Publication Time, and Other Changes

Over the last decade, there have been a number of changes with *Copeia* that the *Copeia* Editorial Office wants to highlight. Among these changes, we highlight the diversity of open-access options and our improved publication and turnaround times. *Copeia* has a new open-access policy that allows authors to publish their articles with full open access for $500 for ASIH members. Additionally, all *Copeia* authors receive a personalized link to share that provides 50 days of free access to their article from the date of online publication. This link takes readers directly to the final version of the article and does not require registration or login. Finally, *Copeia* continued the trend of reduced review turnaround times in 2018 with an average of 46 days from manuscript submission until first decision. This compares favorably with data from ten years ago when turnaround time was closer to 80 days. Similarly, the number of days from manuscript submission to final publication averaged 273 days (often fewer than 200) in 2018. This also compares favorably with data from ten years ago when this same process averaged nearly 500 days. In this poster, we highlight these and other changes with *Copeia* and provide explicit data associated with timing of the various steps in the review process.

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340 AES Reproduction & Life History, Alpine A,B,C – The Snowbird Center, Friday 26 July 2019

Matthew Smukall[1,2], Natalie Mylniczenko[3], Andrew Seitz[2], Samuel Gruber[1], Tristan Guttridge[1]

[1]Bimini Biological Field Station Foundation, Bimini, Bahamas, [2]University of Alaska Fairbanks, Fairbanks, AK, USA, [3]Disney Animal Kingdom, Orlando, FL, USA

Body Condition and Energy Storage of Juvenile Tiger Sharks *Galeocerdo cuvier*

Body condition is likely to be a factor for key life history characteristics including foraging, growth, survival, reproduction, and movement. Maternally derived energy storages are thought to play an essential role for sharks during early life. Offspring rely upon these reserves as they become accustomed to their environment and hone foraging strategies. Traditionally, body indices based on morphometrics (girth, length, weight) have been used to infer condition of sharks. Recently, new methods including blood and metabolite analysis are being implemented to determine overall body condition and health in sharks. Therefore, accurate measures of body condition and health is of importance to fisheries managers and scientists. Here, we assess body condition indices and blood plasma and serum parameters (triglycerides, blood urea nitrogen, cholesterol, total protein, osmolality, and butyrate) for young-of-year and juvenile tiger sharks *Galeocerdo cuvier* from Bimini, The Bahamas. Plasma and serum parameters were compared to classical field morphometric measurements to determine the utility of these field measurements at inferring body condition. Additionally, blood plasma parameters of pregnant and recently post-partum females were assessed to determine the energetic demands of reproduction on body condition. These findings can help researchers to determine an effective measure of body condition and overall health for young sharks, which will ultimately improve conservation and management.

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627 Ichthyology Ecology, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Yeinny J. Solano-Rosario[1], William A. Pérez-Doria[1], Ángel L. Martínez-González[1], Fredys F. Segura-Guevara[1], Glenys Tordecilla-Petro[2], Charles W. Olaya-Nieto[1]

[1]*Fishery Biology Research Laboratory-FBRL, Department of Aquatic Sciences. University of Cordoba, Lorica, Cordoba, Colombia,* [2]*Institución Educativa Lácides C. Bersal. Alcaldía de Lorica, Lorica, Cordoba, Colombia*

Trophic ecology of Bagre rayado *Pseudoplatystoma magdaleniatum* in the San Jorge River, Colombia

To study the trophic ecology of Bagre rayado *Pseudoplatystoma magdaleniatum* in the San Jorge River, Colombia, we analyzed 168 stomachs of individuals collected between January and December 2013, with sizes between 32.1-101.5 cm TL and total weight (WT) between 158.0-9131.0 grams. The stomach content was analyzed using the Proportion of empty stomachs, Grade of digestion, Frequency of occurrence, numerical Frequency, Gravimetry and relative importance Index. The Proportion of empty stomachs was 57.1% and 43.9% of the foods were half digested, identifying four food groups: Fishes, vegetable Rests, Detritus and Others. Fishes were the most common group (69.4%), more abundant (58.2%) and with greater composition by weight (97.7%), respectively. The relative importance index indicates that Fishes is a trophic group with high relative importance in the diet of the species, while the other groups are circumstantial and with very low relative importance. The results obtained suggest that striped catfish is a carnivorous fish with a piscivorous tendency, which maintains its food preferences as it grows throughout the year, correlated with the hydrological cycle of the San Jorge river.

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585 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Graceann Sparkman[1], Oliver Shipley[2], Edward J. Brooks[3], Lucy Howey[4], Jim Gelsleichter[1]

[1]*University of North Florida, Biology Department: Shark Biology Program, Jacksonville, FL, USA,* [2]*University of Marine and Atmospheric Sciences, Stony Brook University, Stony Brook, NY, USA,* [3]*Shark Research and Conservation Program, Cape Eleuthera Institute, Eleuthera, Bahamas,* [4]*Microwave Telemetry, Inc., Columbia, MD, USA*

Mercury Concentrations in the Oceanic Whitetip Shark, *Carcharhinus longimanus*, off of Cat Island, Bahamas

Pelagic sharks have the tendency to accumulate the non-essential toxic metal mercury to levels that pose health risks to themselves, as well as human consumers of shark meat. Because of this, it is important to characterize mercury accumulation in these species; something that has been accomplished for many of the major pelagic shark species occurring in the western Atlantic Ocean. However, one pelagic shark species for which little data on mercury accumulation is available is the Oceanic whitetip shark (*Carcharhinus longimanus*), a species of high conservation concern that was recently listed as “threatened” under the U.S. Endangered Species Act. Therefore, the present study examined mercury accumulation in *C. longimanus*, making use of samples obtained non-lethally from sharks from Cat Island, Bahamas. Total mercury (THg) concentrations were measured in dried muscle, fin biopsies, and red blood cells. THg concentrations were found to be notably high in *C. longimanus* muscle (mean ±SD = 16.80 ±8.39 mg/kg dry weight, n = 24), exceeding prior reports of mercury accumulation in other pelagic

sharks from western Atlantic waters as well as most other shark species. Given this, there is potential for mercury to pose health risks to *C. longimanus* residing in the western Atlantic Ocean and perhaps even challenge recent efforts to conserve and rebuild these depleted populations. Correlations between THg concentrations in muscle with those in fin and red blood cells are also discussed as part of a larger study on the use of less invasive surrogates for measuring mercury accumulation in elasmobranchs.

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556 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Carol Spencer[1], Michelle Koo[1], Teresa Mayfield-Meyer[2], Emily Braker[3], Mariel Campbell[2], Carla Cicero[1], John Demboski[4], Andrew Doll[4], Kyndall Hildebrandt[5], Angela Linn[5]

[1]Museum of Vertebrate Zoology, UC Berkeley, Berkeley, CA, USA, [2]Museum of Southwestern Biology, University of New Mexico, Albuquerque, NM, USA, [3]University of Colorado Museum of Natural History, Boulder, CO, USA, [4]Denver Museum of Nature & Science, Denver, CO, USA, [5]University of Alaska Museum of the North, Fairbanks, AK, USA

Arctos: A Collaborative Collection Management Solution

Arctos (arctosdb.org) is a collaborative collection management solution serving global data on +3.5 million biodiversity and cultural records and 775,000 media objects from more than 158 collections. Pioneered in 1999 and hosted at the Texas Advanced Computing Center, the portal (arctos.database.museum) provides tools and services to manage data and make them publicly available. For herpetology and ichthyology, it is especially rich; its standardized shared data have led to innovations in relating objects within or between collections (e.g., predator-prey, host-parasite), promoting data discovery and interdisciplinary research. Arctos is a knowledge network reciprocally linking external web services with collaborators, including Barcode of Life, GBIF, GenBank, iDigBio, Global Genome Biodiversity Network, Global Names Architecture, MorphoSource, National Center for Biotechnology Innovation, World Register of Marine Species, and VertNet. Arctos is a community of biodiversity professionals who collaborate on best practices and trainings, and work together to improve data richness, develop workflows for data cleaning and publication, and expand functionality. Arctos collection members have the opportunity to participate in its development through the Arctos Working Group. A robust research infrastructure, Arctos integrates biological, earth science, and cultural data as well as emerging data types such as environmental DNA and microbiomes for use by museum scientists, researchers, students, government agencies, NGOs, and the public. At a time when data discovery is imperative for research and conservation, Arctos provides a uniquely collaborative platform and community for bridging gaps between museum collections, informatics specialists, and researchers.

CANCELLED

689 ASIH STOYE ECOLOGY & ETHOLOGY AWARD II, Primrose A&B – Cliff Lodge, Friday 26 July 2019

Megan Sporre

College of Charleston, Charleston, SC, USA

Frequency of Multiple Paternity Varies with Population Sex-Ratio in an Estuarine Turtle Species (*Malaclemys terrapin)*.

Variation in the incidence of multiple paternity in conspecifics is common, caused by differences in rates of mate encounter. Past studies have shown interspecific variation in the occurrence of multiple paternity under a range of female biased diamondback terrapin populations. The frequency of multiple paternity in a male dominated diamondback terrapin population was determined by amplifying eight microsatellite loci in 102 mothers and 106 clutches of *Malaclemys terrapin*. Thirty-seven clutches (35%) showed evidence of multiple paternity, and 50% of females who laid more than one clutch showed evidence of sperm storage. Fathers did not contribute to clutches equally, and the primary father sired between 50 to 89% of offspring in a single clutch. Comparisons to other studies of multiple paternity and sex-ratios show that mating strategy differences between species of turtles may be driving opposing increases in the frequency of multiple paternity. Unequal paternal contribution may be evidence of increased sperm competition and second male fertilization advantage. The use of a SNP panel for parentage analysis will be tested by comparing panels and results of a *de novo* assembly and a mapped assembly, with implications for future parentage research in which little information about the species genome is known.

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273 SSAR HUTCHISON PHYSIOLOGY & MORPHOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Natasha Stepanova, Aaron Bauer

Villanova University, Villanova, PA, USA

Comparative Cranial Morphology in *Acontias* and Other African Burrowing Skinks

Burrowing squamates are characterized by a unique morphology including limb reduction, body elongation, and modifications to streamline and reinforce the skull. While differences between burrowing and non-burrowing squamates are well-known, studies on variation within burrowers are much more limited, with the majority of work done on amphisbaenians. Scincidae is another group that shows many semi-fossorial and fossorial forms. I investigated the skull morphology in 7 genera of African skinks (*Acontias*, *Typhlosaurus*, *Scelotes*, *Sepsina*, *Feylinia*, *Typhlacontias*, and *Mochlus*) from 3 skink subfamilies representing independent derivations of fossorial lifestyles. I focused on variation within *Acontias* and also compared *Acontias* to other genera. I expected convergence in overall skull shape with variation correlated with burrowing substrate, but that the morphology of individual elements would vary between clades. Using computed tomography (CT) scans, I examined characters and used morphometrics to evaluate variation in skull morphology. Although some morphological features were unique to acontine skinks, they

were not found uniformly in *Acontias*. For example, only some acontines showed frontal processes that bordered the nasals laterally. Other features, such as the loss of the upper temporal arch, were found in many burrowers but not in all species of *Acontias*. There was also variation in the general shape of the skull within *Acontias*, with some species showing broad skulls similar to *Sepsina* and others showing flatter, pointed skulls more similar to *Typhlosaurus*. My study revealed variation in both individual elements and overall shape within *Acontias* that in many cases was convergent with the other genera examined.

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138 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Phillip Sternes, Kenshu Shimada

DePaul University, Chicago, IL, USA

Diversity and evolution of body forms in dogfish sharks (Elasmobranchii: Squaliformes)

Squaliformes (dogfish sharks) is a large elasmobranch order with six families (Centrophoridae, Dalatiidae, Etmopteridae, Oxynotidae, Somniosidae, and Squalidae) and over 100 species. Recent molecular-based phylogenetic studies have shown that Squalidae is the basal-most squaliform family, and that Oxynotidae is nested within Somniosidae; regardless, the squaliform monophyly is generally supported. All squaliforms are said to exhibit one basic body plan unlike most other shark orders that may be represented by multiple body forms. Here, we used landmark-based geometric morphometrics to investigate if Squaliformes is represented by only one body plan, and if any evolutionary patterns can be discerned. We examined the outline of all extant squaliform species in lateral view and conducted three separate analyses: (1) a full body analysis (precaudal body + caudal fin), (2) precaudal body analysis, and (3) caudal fin analysis. Our results indicate that each squaliform family has its own unique general body plan, but all squaliforms as a whole are indeed represented by only one basic body plan. Although Centrophoridae is determined to have the most generalized body form within Squaliformes, a slender body with a mid-body position of the first dorsal fin seen in Squalidae represents the most pleisomorphic condition. 'Oxynotids' are regarded as highly derived somniosids, but our study indicates that, although they have a unique precaudal body shape, oxynotids retain the basic caudal fin plan of Somniosidae. The caudal fin is represented by two alternative apomorphic conditions characterized by Etmopteridae and Somniosidae. Within Squaliformes, Dalatiidae has evolved the widest range of body forms.

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445 ASIH/HL/SSAR Symposium: Citizen Science in Herpetology: Productive Past and Promising Future, Ballroom 2 – Cliff Lodge, Sunday 28 July 2019

Sean Sterrett[1], Rachel Katz[2], William Fields[3], Evan Grant[4]

[1]Monmouth University, West Long Branch, NJ, USA, [2]U.S. Fish and Wildlife Service, Hadley, MA, USA, [3]U.S. Geological Survey, Turners Falls, MA, USA, [4]US Geological Survey, Turners

Falls, MA, USA

The Contribution of Road-based Citizen Science to the Conservation of Pond-breeding Amphibians

Roadside amphibian citizen science (CS) programs bring together volunteers focused on collecting scientific data while working to mitigate population declines by reducing road mortality of pond-breeding amphibians. Despite the international popularity of these movement-based, roadside conservation efforts (i.e. "bucket brigades" and "toad patrols"), direct benefits to conservation have rarely been quantified or evaluated. As a case study, we used a population simulation approach to evaluate how volunteer intensity, frequency and distribution influence three conservation outcomes (minimum population size, population growth rate and years to extinction) of the spotted salamander (*Ambystoma maculatum*), often a focal pond-breeding amphibian of CS and conservation programs in the United States. Sensitivity analysis supported the expectation that spotted salamander populations were primarily recruitment-driven. Thus, conservation outcomes were highest when volunteers focused on metamorph outmigration as opposed to adult in-migration—contrary to the typical timing of such volunteer events. Almost every volunteer strategy resulted in increased conservation outcomes compared to a no-volunteer strategy. Specifically, volunteer frequency during metamorph migration increased outcomes more than the same increases in volunteer effort during adult migration. Volunteers during the first adult in-migration had a relatively small effect compared to most other strategies. This study demonstrates a need to evaluate the effectiveness of focusing CS mitigation efforts on the metamorph stage, as opposed to the adult stage. Current amphibian CS programs will be challenged to balance implementing evidence-based conservation measures on the most limiting life stage, while retaining social and community benefits for volunteers.

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613 Ichthyology Life History/NIA, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Carly Lynn Strange, Nicholas Partington, Melanie Herrera, Madison R. Martin, Antony S. Harold

College of Charleston, Charleston, SC, USA

Seasonal Variation in Patterns of Abundance of Early Life History Stages of Fishes Associated with the *Gracilaria vermiculophylla*

We present an update on our ongoing study of the patterns of abundance of post-metamorphic juvenile stages of fishes in the Charleston Harbor estuary (southeastern United States). In order to probe the effects of bottom coverage by an invasive benthic red alga, *Gracilaria vermiculophylla,* we focused on two microhabitats, between June 2018 and January 2019. Samples were obtained by a fine-mesh beach seine hauled along a 15 m transect through dense or sparse algal beds. All fishes captured were identified to the lowest taxonomic level possible. A total of 5,609 specimens were caught, with 4,095 (26 taxa total) of those from dense sites and

1,514 (25 taxa) from sparse, and most fishes caught were smaller than about 20 mm SL. During the summer months (June/July) the assemblage was dominated by, in decreasing rank of abundance, *Anchoa mitchilli, Mugil curema, Eucinostomus* sp., *Syngnathus fuscus*, and *Menidia menidia*, whereas in late fall and early winter (Dec/Jan) there was a shift to *Leiostomus xanthurus, Lagodon rhomboides, Archosargus probatocephalus, Anchoa mitchilli*, and *Micropogonias undulatus*. These species all had higher abundances in the dense algal beds, with the one exception being *Archosargus probatocephalus*. Overall, dense sites support much higher fish abundances in comparison to sparse. Based on our study to date, it is apparent that *Gracilaria vermiculophylla* provides important nursery resources for many of the ecologically and economically important fish species of the region. There are likely negative impacts of this alga on the fish communities but they remain to be identified.

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516 SSAR SEIBERT ECOLOGY AWARD I, Ballroom 2 – Cliff Lodge, Thursday 25 July 2019

Miranda Strasburg, Michelle Boone

Miami University, Oxford, OH, USA

Effects of Trematode Parasites on an Anuran Host across a Predator Gradient

The role that parasites play in populations and communities varies across environmental gradients. In amphibian-parasite systems, predators can decrease a host's probability of becoming infected by parasites through direct parasite consumption or by acting as alternative hosts. Conversely, amphibian predator-avoidance mechanisms, like decreased activity, can increase a host's probability of becoming infected. We hypothesized that larval exposure to predators (crayfish [*Orconectes rusticus*], bluegill sunfish [*Lepomis macrochirus*], or mosquito fish [*Gambusia affinis*]) in mesocosm communities would alter the effects of the trematode parasite, *Echinostoma* spp., on northern leopard frog (*Lithobates pipiens*) by mediating changes in behavior, development, and survival through overwintering. When exposed to predators and parasites, tadpoles reduced their activity, increasing their risk of being detected by parasites. While parasites reduced tadpole survival when crayfish or no predators were present, the influence of fish on survival was less straightforward. Exposure to bluegill sunfish reduced survival dramatically, obscuring any parasite effects, whereas mosquito fish did not impact survival even with parasite exposure. By acting as alternative hosts and parasite consumers, mosquito fish may reduce the number of parasites available to infect tadpoles, minimizing parasite effects. By reducing larval survival, exposure to parasites and predators also influenced size at metamorphosis, which contributed to changes in behavior in the terrestrial environment. Terrestrial growth but not survival was also influenced by these factors, suggesting that larval exposure to stressors influences terrestrial condition in sublethal ways. This study highlights the importance of community composition in regulating the outcome of parasitic infections in aquatic systems.

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768 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Cailla Strobel[1], Sarah Noonan[2], Jim Gelsleichter[1]

[1]University of North Florida, Jacksonville, FL, USA, [2]University of Tampa, Tampa, FL, USA

Preliminary observations on the uptake of microplastics in the Atlantic sharpnose shark (*Rhizoprionodon terraenovae*) and the Atlantic stingray (*Hypanus sabina*)

There has been a growing concern about the presence of microplastics in the aquatic environment. Microplastics are pieces of plastic that are smaller than 5 mm in size, and originate from direct manufacturing for use in commercial products or are formed through chemical breakdown/physical fragmentation of larger plastics. Because of these concerns, a number of studies have recently examined the uptake of microplastics in a variety of aquatic organisms. However, few studies have been conducted on microplastic uptake in elasmobranchs, important members of coastal and marine communities. Therefore, the purpose of the current study was to examine the occurrence of microplastics in the gastrointestinal system of coastal sharks and rays, focusing on two species abundant in nearshore areas on the southeastern U.S. coast, the Atlantic sharpnose shark (*Rhizoprionodon terranovae*) and the Atlantic stingray (*Hypanus sabina).* Young-of-the year Atlantic sharpnose sharks and adult Atlantic stingrays were collected from multiple locations on the southeast U.S. coast, including sites in South Carolina, Georgia, northeast Florida, and northwest Florida. The presence of microplastics in the gastrointestinal tract was determined using microscopy, following hydrogen peroxide-based digestion of organic gut contents and filtration. Microplastic presence was also confirmed via polymer analysis using Fourier transform-Infrared (FTIR) microscopy. Microplastics were found in 100% of individuals, ranging in levels from 1 to 16 pieces per individual. All microplastics observed in the present study were categorized as microfibers. FTIR microscopy provided partial validation of the composition of fibers, however weathering presents challenges for conclusive identification of suspected microplastics.

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684 General Ichthyology I, Cottonwood A-D – The Snowbird Center, Saturday 27 July 2019

Mikayla Struble[1], Cassandra Donatelli[2], Emily Standen[3], Alice Gibb[1], Jaida Elcock[1]

[1]Northern Arizona University, Flagstaff, AZ, USA, [2]Tufts University, Medford, MA, USA, [3]University of Ottawa, Ontario, Canada

Burial Behavior in Elongate Fishes of the Salish Sea

The ability of an organism to move through its environment is a key aspect of its ecology. Fish occupy a large breadth of niches and have subsequently developed a wide range of locomotor abilities, including burial which has independently developed multiple times in acinopterygians. The Zoarcoids, a group of marine elongate fishes, typically display strong shelter-seeking

tendencies which range from cave-dwelling in wolfish, sea-grass habitation in gunnels, burrowing behavior in wrymouths, and intertidal burial in pricklebacks. To observe and quantify burial behavior in these elongate fishes, we collected individuals representing five species of Zoarcoids found in the Salish Sea (San Juan Island, Washington), performed a behavioral analysis in captivity, and compared burial biomechanics between these species. We documented disparities in burial tendencies which suggest that while some fishes that are reluctant to bury may lack a morphological or biomechanical means to move into sediments, other fishes are biomechanically capable of burial but are not behaviorally inclined towards this behavior. This may suggest a relatively recent behavioral shift in habitat preferences. We found that elongate fishes bury themselves using a variety of behavioral processes, several of which have not previously been described in fish. Although elongate fish burial-behavior shares similarities with both terrestrial and aquatic locomotion it possesses features which are not present in either other locomotor pattern. Our results document burial behavior as a novel locomotor activity and suggest burial in the elongate fishes is behaviorally and biomechanically versatile between species occupying differential ecological niches.

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681 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Jaida Elcock[1], Mikayla Struble[1], Alice Gibb[1], Cassandra Donatelli[2], Emily Standen[3]

[1]Northern Arizona University, Flagstaff, Arizona, USA, [2]Tufts University, Medford, Massachusetts, USA, [3]University of Ottawa, Ottawa, Ontario, Canada

Burial Kinematics of the Rock Prickleback

Locomotion is a key factor in determining how an organism interacts with its environment. One relatively poorly understood mode of locomotion is aquatic burial, or the ability to penetrate and move through the substrate in an aquatic environment. *Xiphister mucosus* (the rock prickleback) is an elongate fish found in the Eastern Pacific. *X. mucosus* individuals bury in intertidal regions to acquire food, avoid predators, protect eggs, and remain moist when buried above the tideline. To quantify how this species interacts with its environment, we introduced specimens into a tank containing approximately 2.5 cm of clear acrylic beads covered in water and a clear plexiglass panel pressed over the beads under which the animal could bury; the combination of clear plexiglass and beads permitted us a clear view of the animals as they buried. We collected data from fine (1mm), medium (2mm), and large (3mm) grain “sediments” and performed and kinematic analysis from video recordings of the burial events. We documented stages of this relatively complex burial process (including a packing, tail-push, and fossorial stage), several aspects of which have not been previously described in fish. We also recorded deviances in this biomechanical pattern as correlated with grain size. Burial behavior plays a vital role in the rock prickleback’s life history. In this study we shed light on environmental limitations that may restrict this species’ biogeographic range and biomechanics adaptations that likely allow this species to bury in larger grain sizes in rocky intertidal regions.

481 AES Physiology II, Alpine A,B,C – The Snowbird Center, Sunday 28 July 2019

Wm. Kirk Suedmeyer, Brian Stockinger

Kansas City Zoo, Kansas City, MO, USA

Clinical hypoiodinism, goiter and treatment in a group of white spotted bamboo sharks

A group of ten white spotted bamboo sharks (*Chiloscyllium plagiosum*) presented with anorexia and soft tissue swelling of the submandibular region seven months after introduction to a newly constructed touch tank exhibit. The exhibit is a 38,000 gallon display with ozonation, sand filters and protein skimmers. Water quality is evaluated daily. One shark died shortly after presentation. Two sharks did not exhibit soft tissue swelling. All sharks were evaluated for total plasma iodine and tetraiodothyronine (T4) levels. All sharks had detectable levels of iodine (20 - 42 ng/mL) but were considered low when compared to iodine values of 55 - 120 ng/mL for other animal species. Six of the eight sharks had undetectable (<0.1 ug/dL) levels of T4. Two sharks, one with visual and palpable submandibular swelling, and one without had minimally detectable levels of T4 (0.8 ug/dL and 0.13 ug/dL). Sharks were treated by bathing in a calculated (0.08 mg/dL) sodium iodide supplemented pool two hours daily for seven days. Total iodine after the last treatment demonstrated extreme levels of total iodine (2,100- > 10,000 ng/mL). Iodine baths were discontinued and tube feeding was initiated with 300mcg T4 and one tablet of commercially available vitamin/mineral supplement providing 200mg calcium iodate. Sharks were returned to the exhibit pool after each treatment. All sharks were removed to a nonozonated holding tank for further treatment and evaluation. All sharks demonstrated an increase in T4. Within six weeks of treatment, all sharks had visibly reduced swelling and began eating.

390 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Sarah Sullivan[1], Jeffrey Hudgins[2], Jim Gelsleichter[2]

[1]University of North Florida, Jacksonville, FL, USA, [2]University of North Florida, Jacksonville, FL, USA

An Evaluation of the use of Red Blood Cells as a Surrogate for Measuring Mercury Contamination in Sharks and Rays

Elasmobranchs (sharks and rays) have been shown to bioconcentrate the toxic metal mercury (Hg) to concentrations that may pose health risks to themselves as well as human consumers of shark meat. Because of this, many studies have investigated Hg accumulation in a number of elasmobranch species, often through lethal sampling and the analysis of muscle or other tissues/organs such as liver or kidney. However, while muscle samples can be obtained through non-lethal biopsies, the evaluation of Hg uptake in threatened and endangered elasmobranchs may still be challenged by restrictions on use of such moderately-invasive techniques. Therefore, in the current study, we evaluated the potential use of erythrocytes obtained through routine blood sampling as a less-invasive surrogate for assessing Hg accumulation in sharks and rays. Total Hg (THg) concentrations were measured in paired dried muscle and erythrocyte samples from multiple species, including Atlantic sharpnose shark (*Rhizoprionodon terranovae*), blacktip shark (*Carcharhinus limbatus*), and Atlantic stingray (*Hypanus sabinus*). Correlations between THg concentrations in muscle and erythrocytes were examined to determine relationships that could be used to predict Hg burden from blood sample analysis. THg concentrations in erythrocytes from 15 additional elasmobranch species are presented.

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668 SSAR SEIBERT SYSTEMATICS AND EVOLUTION AWARD I, Ballroom 2 – Cliff Lodge, Friday 26 July 2019

Alexandra Sumarli[1], Bradford Hollingsworth[2], Annie Peralta-García [3], Jorge Valdez-Villavicencio[3], Tod Reeder[1]

[1]San Diego State University, San Diego, CA, USA, [2]San Diego Natural History Museum, San Diego, CA, USA, [3]Conservación de Fauna de Noroeste, Ensenada, Baja California, Mexico

Species Delimitation of the Common Chuckwalla (*Sauromalus ater*): Implementation of an Integrative Approach

Accurately delimiting species remains a contentious issue within modern systematic biology despite recent advancements in genomic high-throughput sequencing techniques and analytical approaches to species delimitation. We apply an integrative approach that uses multiple lines of evidence (i.e., genomic data, morphology, and climatic data) to elucidate the species limits and evolutionary diversification history of the currently recognized geographically widespread Common Chuckwalla (*Sauromalus ater*). Given the unique ecology, geographic morphological variation, and evidence of at least four well-supported mtDNA lineages, we explore and test alternative hypotheses that involve multiple species within *S. ater*. Phylogenetic and multispecies coalescent analyses of our RadSeq data (~1000 loci) of ~90 individuals from throughout the range of *S. ater* confirm the presence of at least two major lineages (i.e., peninsular and continental clades), as well as the continued recognition of morphologically distinct insular *S. varius* and *S. hispidus* which are nested within *S. ater*. Subsequent population membership and principal component analyses demonstrate substantial to moderate phylogeographic structure within the continental and peninsular lineages (K=5 and K=2, respectively). We assess the level of statistical congruence between the purely genomic species hypothesis and integrative species hypotheses by implementing the newly developed genealogical divergence index (*gdi*) metric. Incorporating the *gdi* provides a quantitative rather than qualitative measure to compare of the strengths/impacts of using multiple sources of data when evaluating alternative species hypotheses. Taken together, our results highlight the need for taxonomic revision within *S. ater* and we demonstrate the utility of using an integrative species delimitation approach.

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459 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

John Swenson[1], Dovi Kacev[2], Charlotte Boyd[3], Michael Kinney[2], Kevin Feldheim[4], Lisa Komoroske[1]

[1]University of Massachusetts, Amherst, MA, USA, [2]Southwest Fisheries Science Center, La Jolla, CA, USA, [3]Alaska Fisheries Science Center, Seattle, WA, USA, [4]Pritzker Laboratory for Molecular Systematics and Evolution, The Field Museum, Chicago, IL, USA

Next-Generation Mark-Recapture: Evaluating Close-Kin Mark-Recapture as a Tool for Abundance Estimation in Elasmobranchs

Successful marine resource management relies on population assessments that evaluate the status of marine fisheries stocks and species of concern. These assessments require data that can be challenging to obtain, hindering reliable population assessments for these species. Close-kin mark-recapture (CKMR) is an emerging approach that uses genetic data in a mark-recapture framework to estimate key demographic parameters in populations for which such estimates were previously unreliable or infeasible. However, like any new method, before the CKMR framework can be broadly applied, it first needs to be validated in different biological systems to examine its ability to reliably produce robust parameter estimates that can be incorporated into population assessments and stock projections. This project tests central assumptions of the CKMR framework using simulation and genetic data drawn from a tractable population of Lemon Sharks that has been exhaustively sampled and intensively studied for over 20 years. Specifically, we are assessing the sensitivity of abundance and survival parameters to sampling effort and comparing results under varying degrees of data richness. This research will help establish best practices for designing and implementing a CKMR experiment, and is expected to demonstrate the utility of CKMR for informing management and conservation of elasmobranch species.

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29 AES GRUBER AWARD I, Rendezvous A&B – The Snowbird Center, Thursday 25 July 2019

John Swenson[1], Jeff Klomp[2], Robert Fisher[3], Karen Crow-Sanchez[4]

[1]University of Massachusetts, Amherst, MA, USA, [2]University of North Carolina, Chapel Hill, NC, USA, [3]Virginia Institute of Marine Science, Gloucester Point, VA, USA, [4]San Francisco State University, San Francisco, CA, USA

Zipping and Zagging: The Story of Cownose Ray Fin Development

One of the central goals of evolutionary-developmental biology is to understand the processes by which diverse forms and features evolve. Cownose rays (*Rhinoptera bonasus*) and their relatives (bat rays, eagle rays, manta rays) have a unique body plan that includes broad triangular-shaped pectoral fins that are used for propulsion and a seemingly separate set of fins near the mouth called "cephalic lobes", which are used for feeding. The partitioning of swimming and feeding behaviors into distinct fin domains is associated with a suite of morphological modifications relative to other batoids. These modifications are likely correlated with the evolution of oscillatory swimming and shift to a more pelagic lifestyle in cownose rays and their relatives. With this study, we describe for the first time the evolutionary-developmental processes underlying pectoral fin remodeling in developing cownose ray embryos, including anterolateral expansion of the fin and subsequent 'zipping' to the body. We also find that cephalic lobes, which appear as independent appendages in adults, develop as anterior pectoral fin domains that 'zag' ventrally towards the mouth near the shoulder before fusing to the underside of the rostrum. Finally, we reveal multiple candidate genes that likely play a key role in cephalic lobe development, including several that are known to underlie development of claspers, the male reproductive organs in elasmobranchs. Overall, we find that the eccentric body plan of cownose rays and their relatives likely evolved via stepwise changes to existing mechanisms during development.

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275 AES GRUBER AWARD II, Rendezvous A&B – The Snowbird Center, Thursday 25 July 2019

Dominic Swift[1], Dean Grubbs[2], Dana Bethea[3], Bryan Frazier[4], Fernando Márquez-Farías[5], Liliana Cuervo-López[6], Tristan Guttridge[7], Alexei Abierno[8], David Portnoy[1]

[1]Texas A&M University-Corpus Christi, Corpus Christi, Texas, USA, [2]Florida State University, St. Teresa, Florida, USA, [3]NOAA, Panama City, Florida, USA, [4]South Carolina Department of Natural Resources, Charleston, South Carolina, USA, [5]Universidad Autónoma de Sinaloa, Culiacán, Mexico, [6]Coordinadora Regional de la Unidad de Posgrado, Poza Rica, Mexico, [7]Bimini Biological Field Station, Bimini, Bahamas, [8]Universidad de la Habana, Havana, Cuba

Population Genomics Assessment of Blacktip Shark Structure Across National Boundaries in the Gulf of Mexico and western North Atlantic Ocean

Population genomics approaches can be used to characterize population structure of exploited species and limit localized overfishing by facilitating appropriate management. The blacktip shark (*Carcharhinus limbatus*) is a large coastal shark found in warm temperate to tropical regions of the Gulf of Mexico and western North Atlantic Ocean. Many coastal sharks, including the blacktip, return faithfully to coastal sites within their region of birth for parturition. This phenomenon, known as regional philopatry, could contribute to the formation of distinct populations by limiting dispersal and gene flow. In U.S. waters, blacktip sharks comprise a substantial portion of landings in commercial and recreational fisheries. Shark fishing is also legal in Mexico and Cuba but is prohibited in the Bahamas. Blacktip sharks are highly migratory and likely traverse national boundaries, thus multinational collaboration may be required for appropriate management. Blacktip shark population structure and connectivity have been characterized in U.S. waters, but these assessments have been not extended beyond national boundaries. Therefore, we sampled over 700 young-of-the-year, juvenile, and mature blacktip sharks from the United States (Texas, Alabama, Florida, South Carolina), Mexico, Cuba, and the Bahamas (Andros and Bimini) to characterize population structure using high-throughput sequencing and population genomics techniques. In addition, we investigated the movement of mature blacktip sharks across national boundaries and assessed if males are more frequently dispersing from their region of birth than females. The implications of collaborative research to promote and inform coordinated management of straddling stocks will be discussed.

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599 Ichthyology Lightning Talks, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Brendan Talwar[1,2], Eric Schneider[2,3], Jeremy Kiszka[1], Michael Heithaus[1]

[1]Florida International University, Miami, FL, USA, [2]Cape Eleuthera Institute, Eleuthera, Bahamas, [3]University of Glasgow, Glasgow, United Kingdom

Preliminary research on juvenile silky sharks in the eastern Bahamas

Silky sharks, particularly juveniles, are commonly caught as bycatch in numerous fisheries around the world and have experienced regional declines in abundance across the Gulf of Mexico and wider Caribbean and western Atlantic regions. Research is limited on the role that these animals play in the wider pelagic food web as well as their diving behavior, feeding ecology, and movements. My research seeks to build off of data being collected through the satellite tagging of juvenile silky sharks to develop a better understanding of silky shark ecology in subtropical oligotrophic ecosystems during a critical life stage. This work is taking place in the eastern Bahamas and is still in its early stages.

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795 General Ichthyology II, Cottonwood A-D – The Snowbird Center, Saturday 27 July 2019

Milton Tan[1], Jonathan Armbruster[2]

[1]Illinois Natural History Survey, Champaign, Illinois, USA, [2]Auburn University, Auburn, Alabama, USA

Shape Evolution and Diversification in North American Leuciscidae (Cypriniformes)

In North America, minnows of the family Leuciscidae are a dominant component of the fish fauna. The diversity of North American minnows comprises four subfamilies. From highest to lowest diversity in North America, these subfamilies are the Pogonichthyinae (shiner clade defined by an open posterior myodome), Laviniinae (a primarily western US clade), Plagopterinae (creek chub-plagopterin clade), and the Leuciscinae (represented only by *Notemigonus crysoleucas*). Hence, the four clades of North American Leuciscidae differ considerably in their taxonomic diversity. Previous research has demonstrated that diversification rates increased within the Pogonichthyinae corresponding to a shift from benthic to pelagic habits. It has also been found that the ecomorphological evolution in the Pogonichthyinae experienced more convergence than expected under neutrality (e.g. Brownian Motion). However, how this applies outside of the Pogonichthyinae has not been studied. First, we estimated rates of diversification across the subfamilies of North American Leuciscidae based on a new time-calibrated phylogeny. Next, we estimated morphological diversity across clades using a geometric morphometric approach and explored the phylomorphospace occupied across clades. Finally, we studied the rates of multivariate shape diversification using multiple comparative phylogenetic approaches, and compared these to the rates of diversification across leuciscid subfamilies.

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743 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Kevin Tang[1], Jade Henckel[1], Christopher Fielitz[2]

[1]University of Michigan-Flint, Flint, MI, USA, [2]Emory & Henry, Emory, VA, USA

Phylogeny of Moray Eels (Anguilliformes: Muraenidae)

The eel family Muraenidae consists of 16 recognized genera and over 200 species. Moray eels are predominantly marine fishes found in tropical and temperate waters worldwide, where they are important predators. Muraenids are characterized by a high posterior nostril and the absence of pectoral fins. Previous studies have found widespread polyphyly for several genera (e.g., *Echidna*, *Gymnothorax*). Sequence data from four mitochondrial genes (12S, 16S, cytochrome *b*, and cytochrome *c* oxidase I) were analyzed for over 100 muraenid species representing 15 genera (*Anarchias*, *Channomuraena*, *Diaphenchelys*, *Echidna*, *Enchelycore*, *Enchelynassa*, *Gymnomuraena*, *Gymnothorax*, *Monopenchelys*, *Muraena*, *Pseudechidna*, *Rhinomuraena*, *Scuticaria*, *Strophidon,* and *Uropterygius*) from both subfamilies, Muraeninae and Uropterygiinae. Additional anguilliform and elopomorph taxa were included as outgroups. Our results found that genera like (e.g., *Echidna*, *Enchelycore*, *Gymnothorax*, and *Uropterygius*)

were not monophyletic, which corroborates earlier studies. The family and the two component subfamilies are each monophyletic.

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738 SSAR SEIBERT SYSTEMATICS AND EVOLUTION AWARD II, Ballroom 2 – Cliff Lodge, Friday 26 July 2019

Walter Paulin Tapondjou[1,2], Kaitlin Allen[1], Legrand Gonwouo[2], Rafe Brown[1]

[1]University of Kansas, Lawrence, Kansas, USA, [2]Cameroon Herpetology – Conservation Biology Foundation, Yaounde, Cameroon

Phylogeography of the mountain endemic chameleons of the Cameroon Volcanic Line (Chamaeleonidae: *Trioceros*)

The Cameroon Volcanic Line (CVL) possesses the highest diversity of the genus *Trioceros* within Central and Western Africa. Species delimitation and gene flow between *Trioceros* populations have been poorly studied and the chronology of their colonization of the mountains of the CVL has never been assessed. We used molecular data, two mitochondrial genes (16S, ND4) and one nuclear gene (RAG1), to understand *Trioceros* species diversification in the CVL. The taxa involved in this study are *T. cristatus, T. montium*, *T. pfefferi*, *T. serratus*, *T. wiedersheimi*, *T. perreti*, *T. quadricornis quadricornis*, *T. q. eisentrauti*, and *T. q. gracilior*. Our results suggest that the species *T. serratus* and *T. montium* represent two possible species complexes. The *T. quadricornis* complex is actually a complex of two subspecies instead of three as previously recognized and the subspecies *T. quadricornis gracilior* should be elevated to the species level. The results of our dated phylogeny generated with BEAST2 concur with the theory stating that the *Trioceros* clade migrated toward Central Africa from eastern Africa during late Eocene, and mountain endemic species began to diversify in the CVL during late Miocene-Pliocene. The interspecific divergences between CVL *Trioceros* lineages are estimated to be about four Mya, consistent with an end of Pliocene and beginning of Pleistocene origin of these montane endemics. Multiple, overlapping geographic events (climate and/or geomorphological changes) might account for speciation patterns in *Trioceros* given the dating results.

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712 ASIH/HL/SSAR Symposium: Professional Women in Herpetology: Lessons and Insights, Ballroom 1 – Cliff Lodge, Saturday 27 July 2019

Rebecca Tarvin

University of California Berkeley, Berkeley, CA, USA

What ten years in the tropics has taught me about frogs and society

Field biology is an exciting but demanding career, as the rewards and challenges are both professional and cultural. In my talk I will review my career path and research through several vignettes of international field trips. Initially driven to study Neotropical frogs, I have become fascinated by the evolution of chemical defenses, especially in dendrobatid poison frogs. Through fieldwork I have learned that failure can be serendipitous, that local communities are key, and that everyone can learn to love the frogs in their back yards. As I begin my new lab, the roles and value of diversity, equity, and inclusion are ever on my mind. Science is a unique and amazing career; I hope our community continually grows to be a place where kindness, openness, generosity, and collaboration are at the forefront of all of our interactions.

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703 Herpetology Physiology, Ballroom 3 – Cliff Lodge, Saturday 27 July 2019

Rory Telemeco[1], Eric Gangloff[2,3]

[1]California State University, Fresno, Fresno, CA, USA, [2]Ohio Wesleyan University, Delaware, OH, USA, [3]CNRS-Moulis, Moulis, France

Hierarchical Mechanisms of Thermal Limitation: A Mechanistic Framework for Understanding Performance Loss at High Temperature in Reptiles and Amphibians

Much recent theoretical and empirical work has sought to describe the physiological mechanisms underlying thermal tolerance in animals. Leading hypotheses can be summarized as either subcellular components (i.e. proteins or membranes) or organ systems (i.e. oxygen and capacity limited thermal tolerance) failing at high temperatures. Nonetheless, a general framework has remained elusive. We first leveraged decades of research on the physiology of amphibians and non-avian reptiles to address these hypotheses. Available data suggest both mechanisms are important with hierarchical effects. Thus, we propose an integrated framework, which we call Hierarchical Mechanisms of Thermal Limitation (HMTL), to explain how subcellular and organ system failures interact to limit performance and set tolerance limits at high temperatures. We next present results from an experiment where we quantified the thermal performance curve for aerobic scope in *Podarcis muralis* at opposite ends of a natural oxygen-partial pressure gradient (i.e. high and low elevation) to test a novel prediction of the HMTL framework. We hope that the HMTL framework spurs further research in diverse taxa and facilitates mechanistic forecasts of biological responses to climate change.

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131 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Jennifer Terry, Tristan Bulice, Lorin A. Neuman-Lee

Arkansas State University, Jonesboro, AR, USA

Monitoring Illinois Chorus Frog (*Pseudacris illinoensis*) in Northeast Arkansas

Considered rare and threatened across their range, Illinois chorus frogs (*Pseudacris illinoensis*) are poorly understood and likely need further protections at the state and federal levels to maintain existing populations and avoid extirpation. Surveys conducted over a decade ago indicate that populations inhabit limited portions of Clay County in Northeast Arkansas, though increasing agricultural pressures may jeopardize existing populations. We conducted call surveys and habitat assessments (water body size and depth, substrate, and dominant plants) at sites with confirmed populations between 2000-2002, new sites with calling individuals, and randomly selected sites with no calling. Call surveys were conducted beginning in late January through April 2019, which coincides with the breeding season. Calling individuals were scored on a 0-3 index used by the North American Amphibian Monitoring Program (NAAMP). Ambient temperature, time of survey, weather, moon patterns, and traffic conditions were recorded at each site. In focal populations, captured individuals were measured and marked using visible implant elastomer (VIE) for mark-recapture. Frogs were heard at > 40 sites throughout the survey period. These surveys, habitat analyses, and basic population characteristics provide crucial insight to conservation decisions regarding Illinois chorus frogs at the southwestern edge of their range.

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316 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Jason Testin[1], Domenic D'Amore[2]

[1]Iowa Western Community College, Council Bluffs, IA, USA, [2]Daemen College, Amherst, NY, USA

Tooth morphology and biomechanics in Crocodylia: linking beam-theory and functional ecology

The nature of the crocodylian feeding apparatus has been linked to dietary preference and ecological niche, but few studies have quantified morphological and biomechanical properties of the teeth. We apply beam theory to crocodylian teeth to determine functional significance. Data were collected for all teeth from 53 dry skeletons spanning 20 species. Four Euclidean measurements were taken of each tooth using calipers and photographs, and compared in ratios and regression analysis. Bending strengths about both the labio-lingual and mesial-distal axes were calculated from these measurements. Residual bending strengths were derived from allometric regressions, which were then compared between both tooth positions and species. Lateral compression decreased with tooth size, and coupled with an increase in relative tooth height. Significant changes occurred along the tooth row in the mesial-to-distal direction, including increased lateral compression, decreased relative height, and increased residual bending strengths. This condition is a result of increased forces generated closer to the jaw hinge. Slender-snouted taxa, including *Gavialis*, *Tomistoma*, and *Crocodylus johnstonii* had the "tallest" teeth with the lowest bending strengths, appropriate for focusing on small, aquatic prey. *Melanosuchus niger* and *Paleosuchus trigonatus* had low mesial-distal bending strengths due to a high degree of lateral compression, which may limit their rolling behavior. Crocodylians with a high degree of durophagy, such as *Alligator* and *Osteolaemus* had the greatest bending strengths, especially the enlarged distal crowns. Ecomorphological categories of crocodylians

may be formed by linking these biomechanical properties with gut content studies, and may be applied to analogous fossil taxa.

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189 Turtle Conservation/Amphibian Conservation, Ballroom 3 – Cliff Lodge, Friday 26 July 2019

Sasha Tetzlaff[1,2], Alondra Estrada[2], Brett DeGregorio[1,3], Jinelle Sperry[1,2]

[1]US Army ERDC-CERL, Champaign, Illinois, USA, [2]University of Illinois, Urbana, Illinois, USA, [3]University of Arkansas, Fayetteville, Arkansas, USA

3D Printed Models Aid in Identifying Factors Affecting Predation Risk for Juvenile Box Turtles

Juvenile turtles suffer substantial predation rates, yet little is known about what biotic and abiotic factors affect predation risk for these small, cryptic animals. We placed 3D printed models resembling juvenile eastern box turtles (*Terrapene carolina*) across habitats commonly utilized by the species at three sites within their geographical range and monitored models with motion-triggered cameras. To explore how the presence or absence of visual and olfactory cues affected attacks by predators, we employed a factorial design where models were either exposed or concealed and did or did not have juvenile box turtle scent applied to them. Small- to medium-sized mammals predominantly attacked models (96% of attacks), with raccoons (*Procyon lotor*) being the most dominant predator (73% of attacks). Exposed models were attacked more than concealed models by all predators, but scented models were no more likely to be attacked than unscented models. Attack probabilities were similar in forest, wetland, and edge habitats but attacks were nearly non-existent in grasslands. Attack probability decreased as models were located farther from woody structure. At the smallest site, where box turtles are not known to occur, attack probability was twice that of the other sites, where the species is frequently detected. Our results corroborate the widespread presumption that raccoons pose high predation risk for juvenile turtles. Our findings further suggest that although remaining hidden and selecting macrohabitats with uniformly dense ground vegetation might reduce predation risk, selecting woody structure could be risky if predators frequently forage near such microhabitat features.

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41 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Lyranda Thiem, Chris Gienger

Austin Peay State University, Clarksville, Tennessee, USA

Energetic Investment into Egg Retention in the Eastern Musk Turtle

Turtles are thought to have no parental care after oviposition, and instead females primarily invest energy into the formation of eggs prior to oviposition. Individuals allocate their reproductive resources to increasing body lipids, vitellogenesis, developing the embryo, and egg retention (retaining eggs within the oviduct while development is temporally arrested). Egg retention in turtles presents a potential tradeoff. Retaining eggs for an extended period after fertilization benefits turtles in allowing flexibility in timing of reproduction and in nest site selection. At the population level, egg retention can lead to synchronized hatching among nests, which increases survival rates of offspring due to predator dilution. Conversely, females risk becoming egg-bound if eggs are retained too long. Additionally, prolonged egg retention may also be energetically expensive for the female. This seems unlikely due to many species retaining their eggs for prolonged periods of time. Our objective in this study was to test the energetic costs of egg retention in the freshwater Eastern Musk Turtle (*Sternotherus odoratus*) to determine the potential energetic tradeoff associated with limited parental care. We measured the metabolic rates of gravid and non-gravid females throughout their reproductive cycle using open flow respirometry. Metabolic rates were higher in gravid females than in non-gravid females, but the energy invested to maintenance of embryonic tissue was small. Energy investment was related to clutch size and egg size. These findings support the hypothesis that egg retention is not an energetically expensive strategy for musk turtles.

CANCELLED

~~733 SSAR SEIBERT SYSTEMATICS AND EVOLUTION AWARD I, Ballroom 2 – Cliff Lodge, Friday 26 July 2019~~

~~Vicki Thill, Mike Teglas, Haley Moniz, Chris Feldman~~

~~University of Nevada, Reno, NV, USA~~

~~Variation in Resistance to Black Widow Spider Venom across Lizards: Ecology overrides Phylogeny~~

~~Black widow spiders (*Latrodectus*) have evolved a potent venom that is effective against a variety of prey, including small vertebrates, and may also be an effective defensive weapon. While the effects of black widow spider venom (BWSV) on mammals are well understood, effects on reptiles have never been investigated despite the important role that lizards play as major predators of spiders. In the Western U.S., at least two lizard species (*Elgaria multicarinata* and *Sceloporus occidentalis*) are syntopic with, and prey on, Western Black Widows (*L. hesperus*). We sought to determine resistance to BWSV in these two species as well as four other species that represent five major lizard families. We selected taxa from across the lizard phylogeny that represent both insectivorous and herbivorous species (*Iguana iguana*), as well as species that do not co-occur with *L. hesperus* (*Takydromus sexlineatus*: *I. iguana*). We evaluated resistance to low and high concentrations of BWSV using whole-animal performance trials and comparative tissue histology. We detected a decrease in maximum performance for *I. iguana*, *T. sexlineatus*, and *Uta stansburiana* in the high dose treatment, while *E. multicarinata* and *S. occidentalis* were not affected at any treatment level. Percent area of muscle tissue damage was variable, with *E. multicarinata* and *S. occidentalis* having lower percent area damaged compared to other species. These data suggest that predator-prey relationships between lizards and spiders~~

~~are more complex than previously imagined, potentially involving several physiological and molecular adaptations that allow lizards to tolerate the effects of arachnid venoms.~~

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483 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Sean X. Thimons[1], Kenwyn R. Cradock[2], Marvin M. F. Lutnesky[1]

[1]Department of Science and Mathematics, Texas A&M University - San Antonio, San Antonio, TX, USA, [2]Department of Biology, Eastern New Mexico University, Portales, NM, USA

A Preliminary Characterization of Fish Survivorship in Backwater Pools on the Pecos River, New Mexico, USA

Backwater pools (isolated pools) form in depressions when rivers recede after a flooding event. We characterize the dimensions of all pools with a long axis of about one m or greater along a ~2.0 km reach of the Pecos River, NM (34º24’08.2”N 104º12’09.4”W). We sampled 20 pools eight times over 448 days (Aug. 2014 – Dec. 2015) to provide a description of the average pool in cm (503 ± 37 L x 170 ± 11 W x 12 ± 1 D), average volume in L (1,106 ± 189), and standard water quality metrics. We test the hypothesis that fish survivorship is significantly different than water volume decay, i.e. if fish survivorship is significantly less than that of pools. Setting the initial sum of the pool volumes, and the proportion of pools with fish, each to unity, proportion volume and proportion with fish were each regressed over the 448 day period. The proportion of pools with fishes started at 0.65, but did not significantly decline over the time period. Furthermore, the proportion of pools with fishes was not significantly different from the proportional water change over the same period (common regression equation: proportion fish or proportion water = - 0.0019x + 0.7573). At the last sampling event, all pools had been eradicated by another flooding event. That the fish persisted at the same rate as water over the sampling period suggests that the pools, despite water losses and evidence of predator activity, provided some refuge until the re-flooding for this event.

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522 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Courtney Thomas, Jessica Ryan, Cari-Ann Hickerson, Carl Anthony

John Carroll University, University Heights, OH, USA

Behavioral Interactions between Striped and Erythristic Color Morphs of Eastern Red-backed Salamanders, *Plethodon cinereus*

Color polymorphic species provide model systems with which to examine the conditions under which divergent selection may occur. Previous research on the most common color morphs of red-backed salamanders (striped and unstriped) indicate that some populations exhibit ecological divergence by morph. Color morph differences in diet, surface activity related to temperature,

and differences in agonistic behavior may work in concert to influence mate choice is this species. For example, in an Ohio population the striped morph is found in more prey rich territories and is more aggressive in defending space from intruders, two factors that may contribute to assortative mating by color in this population. Much of our current understanding of ecological separation between morphs of red-backed salamanders comes from studies on striped and unstriped morphs. We know much less about how the rare erythristic morph interacts with striped individuals in sympatry. We used a laboratory approach to explore differences in territorial behavior between striped and erythristic morphs collected from a sympatric locality in western Pennsylvania. Both morphs exhibited species-typical behaviors, and we did not detect differences in behavior between morphs. Intruders of both morphs exhibited increased investigatory behavior (i.e. nose taps) compared to residents. Aggressive behaviors (look toward and biting) and submissive behaviors (look away, move away, and escape) differed between residents and intruding salamanders, suggesting a similar territorial residency effect for both morphs. Our study is the first to document aggressive and territorial behavior in the erythristic morph, but additional research on homing and territorial advertisement is needed.

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555 SSAR HUTCHISON ECOLOGY, NATURAL HISTORY, DISTRIBUTION, & BEHAVIOR AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Cassandra Thompson, Viorel Popescu

Ohio University, Athens, OH, USA

Of Pools & Predators: How predator exposure and hydro-period length drive larval development and thermal preference

Environmental variation during ontogeny can have profound, variable effects on an organism’s phenotype, fitness, morphology, and physiological attributes. Abiotic factors such as temperature regimes and pool drying rates often have negative impacts on the developmental environments of larval amphibians. Additionally, biotic pressures from competitors, food availability, and predation risk can interact to create synergistic, additive, or antagonistic effects on larval development. The presence of predators can alter tadpole morphology, causing indirect trait-mediated effects in amphibians. As both hydro-period length and predation risk can alter time to metamorphosis and larval development, we wanted to understand how the two stressors may interact and what potential carryover effects into the terrestrial stage they may create. As temperature is a driving force in amphibian larval development, we also wanted to understand how thermal preference may vary among tadpoles from each aquatic treatment, with and without predation risk. We manipulated hydro-period lengths in cattle tank mesocosms with and without predator cues (caged odonate larvae). During the larval stage we assessed the effects of the aquatic treatments on larval growth and development, temperature preference at 3 distinct developmental stages, and overall survival to metamorphosis. While shortened hydro-periods decreased larval survival and increased developmental rates, shortened hydro-periods with predation risk had variable effects on the time to metamorphosis. Tadpoles from predator cue treatments also shifted their thermal preference towards overall warmer temperatures. The biological and physiological insights from this work can be used to better understand the impacts multiple aquatic stressors have on amphibian larval development.

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219 General Ichthyology II, Cottonwood A-D – The Snowbird Center, Saturday 27 July 2019

Ken Thompson[1], Clark Hubbs[2]

[1]Lock Haven University of Pennsylvania, Lock Haven, PA, USA, [2]The University of Texas at Austin, Austin, TX, USA

Artificially Produced Intergeneric Hybrids Among Three Genera of Neotropical Cichlidae

Hybrids were artificially produced by stripping and mixing gametes from three species of Neotropical Cichlidae. Female *Herichthys cyanoguttatus* were crossed with conspecific males and males of both *Rocio octofasciata and Cichlasoma trimaculatum*. All crosses produced viable hybrids. Hybrid compatibility at hatching was calculated as the ratio of heterospecific /homospecific survival and was compared with the controls. Compatibility values of 36.9 (*Heichthys x Cichlasoma*) and 149.2 for (*Herichthys x Rocio*) were found. Meristic data confirm that hybrids are physically intermediate between the parental species. Color patterns for F_1 hybrids as determined by analysis of color photos of living specimens were found to be intermediate as well. C-metaphase karyotypes from gill epithelium were produced for both hybrids and parental species. These data indicate the intermediate nature of the karyotypes. The hybrid karyotypes were also used to compare chromosome size between the various species included in this study.

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528 Amphibian Conservation, Ballroom 2 – Cliff Lodge, Saturday 27 July 2019

Michelle E. Thompson[1], Rudolf von May[2], Germán Chávez[3], Giussepe Gagliardi-Urrutia[4], Guillermo Knell[5], Jonh Jairo Mueses-Cisneros[6], Lily O. Rodríguez[7], Pablo J. Venegas[3], Mario H. Yánez-Muñoz[8]

[1]Field Museum of Natural History, Chicago, Illinois, USA, [2]University of Michigan, Ann Arbor, Michigan, USA, [3]Centro de Ornitología y Biodiversidad (CORBIDI), Lima, Peru, [4]Pontifícia Universidade Católica do Rio Grande do Sul, Puerto Alegre, Brazil, [5]Ecologistica Perú, Lima, Peru, [6]Corporación para el Desarrollo Sostenible del Sur de la Amazonia (CORPOAMAZONIA), Bogotá, Colombia, [7]Centro de Conservación, Investigación y Manejo de Áreas Naturales – Cordillera Azul, Lima, Peru, [8]Instituto Nacional de Biodiversidad (INABIO), Quito, Ecuador

Anuran Species Richness and Composition in the Amazonian Lowlands of the Putumayo Watershed: Implications for Conservation

The Putumayo River is one of the principal tributaries of the Amazon River and harbors one of the last great intact forests in the world, with more than 75% of the basin in indigenous territories, conservation lands, or new conservation proposals. We used field survey data from 23 rapid inventory sites and compiled data from the literature to determine anuran species richness and composition in lowland forests of the Putumayo watershed at local and regional scales and highlight conservation implications for amphibians in this region. We found that lowland forests of the Putumayo watershed boast high species richness for anurans at both the local scale and regional scale, containing more than one quarter of the described anuran species in Peru. Species dissimilarity was high among sites and was more highly correlated with geographic distance at the regional scale than the local scale. High beta diversity is likely driven by limited dispersal capability of anurans and high habitat heterogeneity in geology and vegetation types in the region. Our results indicate the relative importance of factors affecting community structure of anurans depends on the spatial scale. High species richness and beta diversity coupled with the large number of undescribed species observed during field surveys highlight the Putumayo watershed as an area of high conservation value for amphibians.

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103 SSAR HUTCHISON EVOLUTION, GENETICS, & SYSTEMATICS AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Jessica Tingle

University of California, Riverside, CA, USA

Correlated Evolution of Snake Body Size and Vertebral Count with Habitat and Biome

An animal's body plan constrains its locomotor behavior. At the same time, the requirements of moving through particular habitat types may lead to considerable natural selection on morphology. This project tests for correlated evolution of environment, behavior, and morphology in snakes, which have evolved many distinct types of locomotion in many habitat types, despite their superficially simple body plans. I assembled literature data on total length, body and tail vertebral counts, habitat, biome, and geographic range of over 1,000 snake species representing all major clades. I used a time-calibrated phylogeny to explore the evolution of these traits, as well as their relationship with diversification rates. Preliminary analyses show that body length and number of vertebrae have evolved in relation to both habitat and biome. Aquatic, arboreal, and semi-arboreal species are all relatively long compared to terrestrial species, whereas fossorial, semi-fossorial, leaf-litter, and sand-swimming species are all relatively short-bodied. Species from wetter, more vegetated biomes (e.g. rainforest) are longer on average than those from drier, less vegetated biomes (e.g. desert). Adjusting for body length, both arboreal and semi-arboreal snakes have more body and tail vertebrae than terrestrial ones, whereas fossorial and semi-fossorial snakes have fewer tail vertebrae. These results increase our understanding of biological diversity and evolutionary adaptation in a vertebrate body plan without limbs.

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150 ASIH/HL/SSAR Symposium: Citizen Science in Herpetology: Productive Past and Promising Future, Ballroom 2 – Cliff Lodge, Sunday 28 July 2019

Brian Todd[1], Justin Nowakowski[1], Jonathan Rose[1], Steven Price[2]

[1]UC Davis, Davis, CA, USA, [2]University of Kentucky, Lexington, KY, USA

Traits Linked to Contemporary Snake Distributions and Their Sensitivity to Human Land Use as Revealed by Citizen Science Data

Citizen scientists can provide timely and expansive information about contemporary species distributions that can aid biodiversity management. For example, opportunistically reported citizen science data can reveal which species are found less often in human-dominated landscapes than in natural landscapes, and thus which species may be more sensitive to habitat loss or alteration. Here, we used randomization tests to account for possible sampling biases to analyze occurrences of 33 snake species in North and South Carolina, USA. Our analysis resulted in a quantitative ranking of species from most sensitive, like *Seminatrix pygaea* and *Nerodia floridana* found mostly in unmodified natural areas, to least sensitive, like *Storeria dekayi* and *Carphophis amoenus* found mostly in altered landscapes. We next examined which traits of these 33 snake species were most correlated with their sensitivity to human land use. We found that species that feed primarily on vertebrates, that use a high proportion of aquatic habitats, and that have small geographic ranges occurred in more natural and less human-dominated landscapes. Body size, clutch size, exposure to human-dominated landscapes, reproductive mode, habitat specialization, and whether a species is venomous had less effect on their sensitivity to human land use. Our results accord with studies from other taxa that show high trophic position and narrow distributions are often correlated with heightened extinction risk. Our results also suggest that conservation practitioners should prioritize preserving intact natural habitat with extensive aquatic areas to support sensitive species that may decline in the face of habitat alteration.

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434 Ichthyology Systematics I, Cottonwood A-D – The Snowbird Center, Sunday 28 July 2019

Luke Tornabene[1,2], David Greenfield[3], Mark Erdmann[4]

[1]University of Washington, Seattle, WA, USA, [2]Burke Museum of Natural History and Culture, Seattle, WA, USA, [3]California Academy of Sciences, San Francisco, CA, USA, [4]Conservation International, Arlington, VA, USA

Taxonomic explosion in the most diverse genus of marine fishes (Gobiidae: *Eviota*): is there an end in sight?

The gobiid genus *Eviota*, commonly known as dwarfgobies, is the most species-rich genus of marine fishes in the world. As of March 2019 there are more than 110 valid species. Recent taxonomic efforts combining underwater photography and multi-locus DNA sequencing have revealed a tremendous cache of undescribed diversity in the genus. Here we provide a synopsis of the recent taxonomic developments in *Eviota*, and discuss the observed patterns of biodiversity. Several of the recently discovered new species represent 'cryptic species', i.e. splitting of previously widespread taxa into more restricted species based on subtle differences in live coloration and variation in DNA sequences, however, many other new species are strikingly distinct from any named species and are not simply the consequence of taxonomic spitting. Biogeography of species groups across the genus show a variety of distributional patterns, ranging from widespread, broadly overlapping groups of sister species, to clusters of geographically-restricted (island endemic) species with allopatric distributions. In addition, we present data that suggests the possibility that the genus *Eviota* may not be monophyletic, and discuss the taxonomic implications of this.

CANCELLED

532 SSAR SEIBERT PHYSIOLOGY & MORPHOLOGY AWARD, Ballroom 3 – Cliff Lodge, Thursday 25 July 2019

Claire Tracy[1], David Blackburn[2], Edward Stanley[2], Todd Jackman[1], Aaron Bauer[1]

[1]Villanova University, Villanova, PA, USA, [2]University of Florida, Gainesville, FL, USA

Evolutionary history of African dwarf toads and the implication on loss of the tympanic middle ear

The sub-Saharan African dwarf toads of the genera *Poyntonophrynus, Mertensophryne,* and *Capensibufo* form a putative monophyletic group of relatively understudied anurans. Each genus has at least one species exhibiting the loss of the columella or the tympanic middle ear (TME). Loss of the TME has occurred in many different clades across Anura as a whole. This phenomenon is well documented but is still not completely understood. Previous hypotheses relate these losses to paedomorphosis or miniaturization, however a recent study has shown that columellar loss is a highly labile trait across frogs, independent of these trends. We test these hypotheses on a much smaller scale within the clade of *Poyntonophrynus, Mertensophryne,* and *Capensibufo* which have not yet been examined in depth for the nature of TME loss. This study expands on the current phylogenetic hypothesis of the relationships within and among these three genera, and characterizes the loss of the columella within the clade using computed tomography (CT) scans.

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662 ASIH STORER ICHTHYOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Aline Trejo[1], Shannon O'Leary[1], Charles Cotton[2], Steve Murawski[3], David Portnoy[1]

[1]Texas A&M University-Corpus Christi, Corpus Christi, TX, USA, [2]Florida State University, Cobleskill, NY, USA, [3]University of Southern Florida, St. Petersburg, FL, USA

Populations structure of King Snake Eel (*Ophichthus rex*) throughout the Gulf of Mexico

King snake eel (*Ophichthus rex*) is a large, long-lived demersal predator in the family Ophichthidae that is restricted to the Gulf of Mexico (Gulf) along the continental shelf. King snake eels are a data deficient species affected by limited commercial and recreational fisheries, and little is known about the species' biology. In this study, SNP-containing loci were characterized using next-generation sequencing of king snake eels tissue samples taken from the northern Gulf (east and west of Desoto Canyon) and the southern Gulf and subsequently used to assess population structure. Previous studies of genetic connectivity in the Gulf of Mexico have been limited to a few commercially important species and are often geographically limited to northern Gulf waters. Understanding gene flow across international boundaries in a variety of species will increase our understanding of Gulf-wide connectivity, thus facilitating fisheries management.

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805 AES Symposium: The Sensory Biology of Elasmobranch Fishes, Rendezvous A&B – The Snowbird Center, Saturday 27 July 2019

Timothy Tricas

Department of Biology (Zoology), University of Hawai'i at Mānoa, Honolulu, HI, USA

The mechanosensory lateral line and ear of sharks and rays: Still far from the source

Most elasmobranch fishes have a well-developed mechanosensory lateral line and an inner ear that share many functions with other extant vertebrates. Recent physiological studies have confirmed that the superficial and canal lateral line systems are detectors of water velocity and acceleration, respectively. Behavioral studies demonstrate their use for hydrodynamic imaging, rheotaxis, prey tracking and prey capture. In addition, a novel mechanotactile function for the detection of prey was physiologically demonstrated for the non-pored, subdermal lateral line on the ventral surface of batoids but a role in sharks remains unknown. The shark ear includes three otolithic organs that are sensitive to the inertial forces of acoustic particle motion that produce a relative movement between the dense otoconia and the underlying sensory hair cells. The ear functions in elasmobranch hearing, as in other fishes, and is especially keen for sharks in the low frequency range of sounds produced by their prey. Sharks and rays lack a gas-filled swim bladder or accessory structure that can promote the indirect detection of sound pressure by the ear, and the underlying sensory mechanisms used to locate the sources of sounds still remain to be experimentally demonstrated. Recent physiological studies on the well-developed but enigmatic shark macula neglecta, which lacks otoconia and cannot experience otolithic shear forces, confirms that it is most sensitive to dipole stimuli presented above the head. Several models for sound source localization by sharks, including the possible integration of stimuli from the ear and lateral line at close distances, are discussed.

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671 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Timothy Tricas[1], Kelly Boyle[2]

[1]Department of Biology (Zoology), University of Hawai'i at Mānoa, Honolulu, HI, USA,
[2]Department of Biological Sciences, University of New Orleans, New Orleans, LA, USA

Eavesdropping on the parrotfish crunch: Implications for coral reef monitoring and management

Parrotfish (Labridae: Scarinae) are conspicuous members of the coral reef herbivore-detritivore feeding guild. Scraper and excavator species have a beak-like jaw used to remove the epilithic algal matrix common on hard reef substrates, and also modified pharyngeal jaws that facilitate the grinding of the post-ingestion diet. Thus, parrotfish are major agents of algae/epilithic matrix removal, exposure of new settlement sites for coral larvae, bioerosion, coral sand redistribution and coral rock concretion on the coral reef. Assessment of their feeding patterns is critical for efficient monitoring and management of coral reef systems, yet most past studies used direct observations of feeding made by divers that were constrained by time, space or personnel. Feeding bites of scraper and excavator species produce brief acoustic pulses from intermittent contact of the jaws with the hard substrate. We used passive acoustic monitors to collect hourly samples of ambient parrotfish feeding sounds over a three-year period on two Hawaiian reefs, and an automated detection routine to test for environmental correlates and temporal patterns. Parrotfish feeding activity was correlated with sea surface temperature, day length and daily tide range. Bite activity peaked in the summer months in conjunction with the annual rise in sea surface temperature, but was more closely associated with day length. Their daytime feeding activity showed a strong mid-morning peak and a secondary late afternoon peak across the study period. This study confirms the utility of bioacoustic monitoring of parrotfish feeding, and its long-term potential for monitoring of healthy or stressed coral reefs.

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291 Amphibian Disease, Ballroom 3 – Cliff Lodge, Sunday 28 July 2019

Alexa Trujillo[1], Eric Hoffman[1], Guilherme Becker[2], Anna Savage[1]

[1]University of Central Florida, Orlando, FL, USA, [2]University of Alabama, Tuscaloosa, AL, USA

Spatiotemporal Adaptive Evolution of Immune Genes in a Frog-fungus Disease System

Immune gene diversity is linked to disease susceptibility in many animal taxa, particularly relationships between Major Histocompatibility Complex (MHC) polymorphism in vertebrates and resistance to specific pathogens. While MHC polymorphism is a significant predictor of disease susceptibility across vertebrate taxa, we lack a spatiotemporal understanding of how immune gene diversity and disease pressure interacted to shape population persistence. Chytridiomycosis has caused the decline or extinction of hundreds of amphibian species, prompting genetic and immunogenetic investigations into disease susceptibility. Here, we used the widespread northern leopard frog, *Rana pipiens*, to characterize evolutionary history, population genetic diversity, and population differentiation of an expressed MHC class IIß gene. We investigated natural populations spanning the species range across four decades to evaluate neutral, selective, and disease-driven processes shaping immune gene diversity. We compared MHC-derived genetic parameters to neutral genetic loci to assess the role of demography compared to selection in driving MHC evolution. We also directly tested for adaptive evolution by examining site-specific patterns of molecular evolution at each codon within the MHC peptide-binding region. Finally, we tested the relative importance of neutral genetic diversity, functional immunogenetic diversity, and environmental factors in explaining spatial and temporal patterns of disease using a generalized linear modeling approach to identify variables best explaining *Bd* prevalence and intensity. Our study improves the understanding of how frogs respond to disease on a broad spatial scale by resolving whether immunogenetic adaptation is a central driver of population persistence or if neutral demography dictates evolutionary trajectories.

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758 ASIH STORER HERPETOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Mary Tucker[1,2], Stephen Mirkin[1], Dean Williams[1]

[1]TCU, Fort Worth, TX, USA, [2]Auburn University, Auburn, AL, USA

Ectoparasite loads of Texas horned lizards (*Phrynosoma cornutum*) living in small Texas towns

Ectoparasites are a vital but often overlooked part of ecosystem dynamics, which have been shown to be negatively correlated with growth and decreased body condition in various vertebrate species. Texas horned lizards living in natural environments are known to harbor red mites (*Trombiculidae*), but the impact and density of these mites on lizards living in urban environments is not well known. Using weekly surveys during the summer of 2018, we examined the ectoparasite loads on Texas horned lizards (*Phrynosoma cornutum)*(n = 87) from 11 different sites in Kenedy and Karnes City, Texas. We counted mites present and recorded where they were found on the lizard's body. We also determined the sex, age (juvenile versus adult), and body condition (body weight/snout-to-vent length) of each captured lizard. Males had significantly higher parasite loads than females. The number of ectoparasites did not differ by age, and parasite loads were not correlated with body condition or lizard density (lizards/hectare). We present the first known research of ectoparasite loads of Texas horned lizards from an urban environment. Although the sample size is small, we found no ectoparasites on Texas horned lizards (n = 6) from a nearby natural area, suggesting Texas horned lizards from natural environments may have lower ectoparasite loads than lizards found in an urban environment. These findings deserve further exploration to see if urban environments play a role in increased parasitism.

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770 Ichthyology Ecology, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Thomas Turner[1], Tyler Pilger[2], Alexander Cameron[1], Keith Gido[3], James Whitney[4], David Propst[1]

[1]University of New Mexico, Albuquerque, NM, USA, [2]FISHBIO, Chico, CA, USA, [3]Kansas State University, Manhattan, KS, USA, [4]Pittsburgh State University, Pittsburg, KS, USA

Genetic and demographic data predict fish meta-community response to catastrophic wildfire

Stream networks experience extreme disturbances that alter fish community structure. For example, mega-wildfires cause remarkable changes in distribution and abundance of fishes of the Gila River in the southwestern US. Properties of both the stream network and species that reside there are thought to influence fish community response. Demographic and genetic monitoring approaches were used together to characterize responses of a fish community to disturbance resulting from a series of three catastrophic wildfires in the Gila. Three of eight species exhibited declines in genetic diversity and lowered effective population sizes (N_e) in response to wildfires, whereas other species exhibited no change. Temporal genetic sampling revealed synergy between changes in allele frequencies and species-specific demographic parameters. By comparing temporal changes in genetic diversity and structure spanning pre-disturbance through recovery phases, we developed a conceptual framework that makes explicit predictions about the trajectory of genetic response to disturbance. Applying this framework across species helped distinguish how dispersal and local compensatory reproduction contributed to resilience and recovery of individual species following wildfire-related disturbance. Integration or results across species helped predict post-disturbance community structure.

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250 ASIH STOYE PHYSIOLOGY & PHYSIOLOGICAL ECOLOGY AWARD, Primrose A&B – Cliff Lodge, Friday 26 July 2019

Catherine Tylan, Tracy Langkilde

The Pennsylvania State University, University Park, PA, USA

Surviving the Invader: What Branches of the Immune System are Altered by Multigenerational Exposure to a Novel Predator?

Anthropogenic ecosystem alterations, such as the introduction of invasive species, are a common perturbation affecting many animals. Such stressors can have fitness-relevant consequences, including for immune function. The eastern fence lizard (*Sceloporus undulatus*) has been dealing with invasive stinging fire ants (*Solenopsis invicta*) for over 70 years and exhibit associated morphological, behavioral, and physiological adaptations. We conducted a suite of immune assays on lizards caught from sites with long histories of fire ant invasion and lizards from fire ant free sites. Our results build on earlier findings of suppressed immune function of lizards within fire ant invaded populations to show that some portions of the immune system are affected by a history of fire ant invasion (e.g. cell-mediated immunity, antibodies to fire ants), whereas others remain unaltered (e.g. superoxide production by phagocytes; natural antibodies). For several immune variables females were found to have reduced immune function compared to males, particularly early in gestation when actively producing follicles. This may indicate that reproductively active females are more susceptible to the negative effects of immunosuppression from stressful interactions with fire ants. Variability in the responses of different aspects of the immune system to invader-induced stress may reveal which portions of the immune system are most vital to survival, and those which may be sacrificed in times of elevated stress.

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463 Herpetology Morphology and Systematics, Ballroom 1 – Cliff Lodge, Friday 26 July 2019

Veronica Urgiles[1,2], Anna Savage[1]

[1]University of Central Florida, Orlando, Florida, USA, [2]Instituto Nacional de Biodiversidad del Ecuador, Quito, Pichincha, Ecuador

Diversification of Terrestrial Frogs in a High Altitude Tropical Hotspot

The Ecuadorean Andes sustains one of the most remarkable frog diversifications. In this region, nearly one in three known species of amphibians belong to the *Pristimantis* genus, which contains the majority of the direct-developing terrestrial frog species. Although efforts are ongoing to understand the diversity of *Pristimantis* in the Ecuadorean Andes, large regions, particularly in high altitude ecosystems, remain poorly documented and speciation and diversity of this genus remain widely misunderstood. Within this context, an interesting taxon with many unresolved questions regarding the pattern and process of diversification is the *Pristimantis orestes* species complex, which is distributed across Páramo landscape and montane forest in the eastern and western slopes of southern Ecuador. Although several new species have been recently placed within this group, the small number of samples, geographic regions and loci included in these previous studies have prevented any definitive conclusions from being drawn. Moreover, delimiting and identifying species within this group is problematic because of the lack of molecular data, most notably from holotypes. Here, we present a new molecular phylogeny for the *P. orestes* complex reflecting the complex evolutionary relationships and diversification of the group. We use morphological, ecological, biogeographical and molecular evidence to support several new terrestrial frog species, resulting from a three-year series of expeditions conducted in the high elevation ecosystems of southern Ecuador between 2500 and 4500m of elevation. Our results identify previously unrecognized species diversity and suggest that these species exhibit restricted distributions, driven by particular elevational and habitat associations.

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80 ASIH/HL/SSAR Symposium: Professional Women in Herpetology: Lessons and Insights, Ballroom 1 – Cliff Lodge, Saturday 27 July 2019

Nicole Valenzuela

Iowa State University, Ames, IA, USA

The Fascinating Biology and Challenges of Studying Turtles

I was enamored by the endangered giant Amazonian river turtle the first time I saw females nesting in the sandbars of the Caquetá river. I was fascinated by their temperature-dependent sex determination (TSD) and concerned for their conservation in the face of climate change. Understanding TSD became a central focus of my research (how it works, why it evolves, how it differs from genotypic sex determination - GSD). Those questions lead me in an unusual trajectory. First, I worked on thermal ecology, population genetics, and reproductive behavior. Years later, I re-trained myself in evo-devo and genomics to decipher the regulation of TSD and GSD during embryonic development, using new models like painted and soft-shell turtles. While difficult, diving into new disciplines allowed me to study the evolution of genomes, sex chromosomes and their dosage compensation in a variety of turtles. Some questions have been answered, new ones continue to emerge, and I will discuss both in this talk. I also learned that professional and personal decisions are not always easy when navigating the challenges of academia, and that some hurdles are real, some self-imposed, and some derived from the very well-intentioned institutional efforts that attempt to prevent them. For instance, dedicating excessive time to over-diagnosing hurdles takes people away from devoting the precious limited time we have to excel in our research. For me, a strong support system and team decision-making were essential to balance the demands from my profession and my personal life. Others may have their unique solutions.

CANCELLED

~~683 AES Conservation & Management IV/Behavior, Rendezvous A&B – The Snowbird Center, Sunday 28 July 2019~~

~~Maurits van Zinnicq Bergmann[1,2], Tristan Guttridge[2,3], Mariana Fuentes[4], Matthew Smukall[2,5], Mark Bond[1], Patrick Burke[6], Samuel Gruber[2], Yannis Papastamatiou[1]~~

~~*[1]Florida International University, North Miami, FL, USA, [2]Bimini Biological Field Station Foundation, Bimini, Bahamas, [3]Saving the Blue, Inc., Miami, FL, USA, [4]Florida State University, Tallahassee, FL, USA, [5]University of Alaska Fairbanks, Fairbanks, AK, USA, [6]Macquarie University, Sydney, Australia*~~

~~Using a Multi-Species Conservation Planning Approach to Identify Hotspots for Protection of Marine Predators Through Acoustic Monitoring and Marxan~~

~~Identifying spatial hotspots of elasmobranchs is paramount to the persistence of populations and concomitant trophic interactions that have the potential to shape ecological communities. Without accounting for elasmobranch spatial distributions, marine protected areas (MPAs) and sanctuaries may not adequately protect the vital habitats essential for the prevention of further population declines. The Bahamas harbors thriving elasmobranch populations. This is largely due to bans on longline and gillnet fishing enacted in 1993, and the country's establishment as a shark sanctuary in 2011. However, essential habitats that many species rely on are not protected. While Bimini Bahamas is a marine biodiversity hotspot, its habitats are continuously being degraded as a result of mega-complex constructions, likely causing time-lagged population declines. This study uses acoustic monitoring data (59 receivers) from 139 individuals from eight elasmobranch species (southern stingray, great hammerhead, bull, tiger, lemon, nurse, Caribbean reef and blacktip shark) detected between October 2016-July 2018. The conservation planning software Marxan was used to highlight spatial elasmobranch hotspots and candidate priority areas for conservation, allowing for the evaluation of the efficacy of the proposed North Bimini Marine Reserve. The identification of essential marine habitats facilitates an improvement of MPA design in Bimini. Consequently, this may not only aid population persistence of residential species but also transboundary species during periods of seasonal residency.~~

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205 ASIH/HL/SSAR Symposium: Citizen Science in Herpetology: Productive Past and Promising Future, Ballroom 2 – Cliff Lodge, Sunday 28 July 2019

Andrew Durso[2], Kevin Messenger[3], Christopher Smith[4], James Van Dyke[5], Michael Thalman[6]

[2]*University of Geneva Institute of Global Health, Geneva, Switzerland,* [3]*Nanjing Forestry University, Nanjing, China,* [4]*HerpMappper, Saint Paul, USA,* [5]*La Trobe University, Melbourne, Australia,* [6]*Unaffiliated, Earlham, USA*

The Only Good Snake is an Identified Snake: The Power of Collective Knowledge

Many people fear snakes but are interested in learning to identify them. Our social media outreach and education tool, the "Snake Identification" Facebook group (www.facebook.com/groups/22137638452, www.snakeIdentification.org) allows users to post photos of snakes for rapid identification (response time as low as < 1 minute). Snake Identification currently has over 100,000 members (representing 101 countries), and as a public group, people can watch or participate at their discretion. Daily requests vary from ~10/day in the winter in the Northern Hemisphere , where most members live (>82%), to nearly 300/day during the spring. Our ability to reach a massive audience has resulted in >10 years of 1) insights into snake biology, including geographic distribution, phenology, and natural history, 2) insights into human-snake interactions (e.g. only 11% of snakes encountered were killed), and 3) education and behavioral change, with many positive testimonials by members who used to kill snakes but now educate others about their benefits. We suggest that this group has great potential to create lasting behavioral change and benefit snake conservation. We discuss the demographics, logistics, and challenges of our group, comment on how effective outreach leads to better conservation, and discuss ways to integrate community collected data with science (e.g. HerpMapper, Snake ID Challenge).

CANCELLED

230 SSAR HUTCHISON CONSERVATION & MANAGEMENT AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

John Vanek[1], Richard King[1], Gary Glowacki[2]

[1]Northern Illinois University, DeKalb, IL, USA, [2]Lake County Forest Preserve District, Libertyville, IL, USA

Landscape and Management Factors Influence the Occupancy Dynamics of Sympatric Salamanders in an Urban Preserve System

The conservation of amphibians living in urban areas is challenged by a lack of information about their natural history, ecology, and responses to habitat management. To address these knowledge gaps, we used 10 years of monitoring data to investigate patterns of occupancy, detectability, and population turnover for sympatric *Ambystoma laterale* (Blue-spotted Salamanders) and *A. tigrinum* (Eastern Tiger Salamanders; hereafter Tiger Salamanders) inhabiting preserves in the Chicago Metroregion (third largest metropolitan area in the United States). We constructed dynamic occupancy models and used AIC_c to rank *a priori* candidate models containing landscape, survey, and management covariates. From 2009-2018 we conducted 2181 artificial cover object surveys (4 boards/survey) and detected Blue-spotted Salamanders during 375 surveys and Tiger Salamanders during 85 surveys. Top ranked occupancy models for both species included percent tree cover and the presence of a breeding wetland within 164.3 m. Detection probability for both species was substantially < 1 and was influenced by survey and landscape covariates. Prescribed fire was an important predictor of colonization for *A. laterale* and an important predictor of extinction for *A. tigrinum*. However, overall rates of turnover were low for both species. Our results reveal that salamander populations can persist in highly fragmented urban preserve systems and that forested habitat is important for the regional conservation of ambystomatid salamanders. We recommend that urban land managers be cognizant of the impacts of habitat management on non-target species and call for experimental studies into the direct effects of prescribed fire on ambystomatids.

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660 Ichthyology Ecology, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Jesús Vargas-González[1], Ángel L. Martínez-González[1], Fredys F. Segura-Guevara[1], Glenys Tordecilla-Petro[2], Charles W. Olaya-Nieto[1]

[1]*Fishery Biology Research Laboratory-FBRL, Department of Aquatic Sciences. University of Cordoba, Lorica, Cordoba, Colombia,* [2]*Institución Educativa Lácides C. Bersal. Alcaldía de Lorica,, Lorica, Cordoba, Colombia*

Length–Weight relationship of Liso *Rhamdia quelen* in the Sinú River, Colombia

The length–weight relationship of Liso *Rhamdia quelen* (Quoy & Gaimard, 1824) collected in the low Sinú River, Colombia, was estimated. The length-weight relationship and condition factor were estimated with the equation $TW = a\ TL^b$ and $K = TW/TL^b$, respectively. The size ranged between 15.5 and 37.0 (23.6 ± 3.3) cm TL, the total weight between 28.0 and 486.0 (138.6 ± 69.4) grams, and the mean length in the catch estimated was 23.7 cm TL. Length-weight relationship estimated for combined sexes was $TW = 0.010\ (\pm\ 0.11)\ TL^{2.99\ (\pm\ 0.08)}$, r =0.96, n =419, where the monthly growth coefficient ranged between 2.65 (July) and 3.33 (November), being isometric for the study year, with statistically significant differences; while the condition factor ranged from 0.004 (November) and 0.029 (July), without statistically significant differences. Direct correlation between the condition factor, the gonadosomatic index and the hydrological cycle of low Sinú River in upward waters was observed.

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535 Ichthyology Reproduction, Development, and Morphology, Cottonwood A-D – The Snowbird Center, Sunday 28 July 2019

Diego Vaz, Eric Hilton

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

Ontogeny of the Plainfin Midshipmen, *Porichthys notatus* (Batrachoididade: Batrachoidiformes)

Batrachoidiformes is a monophyletic group of mostly benthic, ambush-predatory fishes. Species of the genus *Porichthys*, the midshipmen, are unique in this order for having photophores and being relatively pelagic. Despite inhabiting deeper habitats than other Toadfishes, species of *Porichthys* build nests in intertidal rocky habitats, similar to other Batrachoidiformes. Previous ontogenetic studies have described only the external larval morphology of few species of Toadfishes, and data on internal morphology is lacking. An ontogenetic series of the early life stages of Plainfin Midshipmen, *P. notatus* (5 to 28 mm TL), was collected during the summers of 2017 and 2018, and skeletal ontogeny was investigated using cleared-and-stained specimens. Changes in the neural and muscular system were examined by staining whole specimens with Phophomolybdic Acid and CT-scanning them at resolution of 5.7 microns. The development of the vertebral column occurs in an anterior to posterior direction, as in other percomorph fishes. When larvae hatch from the corion, the basidorsal elements of the first vertebrae are already present. The third dorsal-fin spine, previously proposed to be absent in *Porichthys*, was observed in early stages (7 mm TL), but is reabsorbed before larvae become free swimming (25 mm TL). The brain displays allometric growth, having an optic lobe that is almost one-half of the length of the brain in early stages (5-8 mm TL); it becomes less than one-quarter of brain length in free-swimming juveniles (>30 mm TL). Individual portions of the adductor mandibulae complex are completely distinct in all observed stages.

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440 General Herpetology I, Primrose A&B – Cliff Lodge, Sunday 28 July 2019

Cameron Venable, Tracy Langkilde

The Pennsylvania State University, State College, PA, USA

Lizard's Exposure to Invasive Ants Affects the Subsequent Consumption of Native Ants

Interactions between invasive species and their native predators or prey provide an opportunity to examine the consequences of learned avoidance. In cases where invasive species are similar to harmless native species, or the native species uses broad cues to identify a threat, learned avoidance of invasive species can carry over to native predators of prey. The red imported fire ant, *Solenopsis invicta,* acts as an invasive predator and prey source of the eastern fence lizard, *Sceloporus undulatus*. Lizards that have elevated antipredator responses to attack by these invasive ants also exhibit behavioral avoidance of harmless native ants. Juvenile fence lizards also eat fire ants, but this can prove lethal and lizards quickly learn to avoid eating them. We tested whether prior consumption (and subsequent avoidance) of invasive fire ants will reduce the subsequent consumption of a palatable native ant species. We found that lizards that ate fire ants were subsequently less likely to consume palatable native ants. Ants comprise a large portion of the fence lizard diet, and this shift away from consuming ants could have broad consequences. These results suggest that learned avoidance of eating noxious invasive prey can alter broader native species diets, which could have important effects that may cascade through the ecosystem.

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145 AES Reproduction & Life History, Alpine A,B,C – The Snowbird Center, Friday 26 July 2019

Hannah Verkamp[1], Gregory Skomal[2], Megan Winton[3], James Sulikowski[1]

[1]University of New England, Department of Marine Science, Biddeford, ME, USA, [2]Massachusetts Division of Marine Fisheries, Boston, MA, USA, [3]University of Massachusetts Dartmouth, School for Marine Science and Technology, New Bedford, MA, USA

First observations of reproductive hormone concentrations in white shark (*Carcharodon carcharias*) skeletal muscle tissue

The need to establish basic reproductive information for white sharks (*Carcharodon carcharias*) is well established, however the stock status of this species precludes the collection of information via traditional lethal means. Quantifying reproductive hormones in muscle tissue, which can be collected without restraining individuals, is a nonlethal alternative to such studies that has not been previously evaluated in this species. Here, we biopsied free-swimming white sharks and determined concentrations of reproductive hormones within their skeletal muscle tissue. Testosterone and estradiol were successfully isolated from muscle tissue collected from 7 male and 6 female white sharks, respectively. Isolated hormones in 87.5% of male and 16.7% of female samples were present in a sufficient amount to be quantified via radioimmunoassay. Although most individuals in this study had low hormone levels, this data provides an important first step in establishing this method as a feasible approach for white shark reproductive studies. Additional samples from individuals of different life history stages throughout the year are needed to evaluate potential trends in these hormones.

CANCELLED

725 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Miranda Vesy[1], Ray Moody[2], Jen Mook[1]

[1]University of Oklahoma, Norman, OK, USA, [2]Tinker Air Force Base, Midwest City, OK, USA

Monitoring and Management of a Closed Population of Texas Horned Lizards (*Phrynosoma cornutum*) in Oklahoma City using Harmonic Radar Technology

The Texas horned lizard (*Phrynosoma cornutum*), commonly known as the horny toad, is a species of special conservation concern throughout the Southwest, facing population declines and localized extirpations throughout its range. Since 2003, a small, closed population of horned lizards on Tinker Air Force Base in Oklahoma has been actively studied. To date, studies on this population have used VHF radio-transmitters on adult lizards to investigate localized population demographics, habitat preferences and requirements, as well as general behavioral traits. As with many small species of reptiles, hatchling and juvenile horned lizards have been understudied due to their small body size and weight preventing the attachment of traditional VHF transmitters. Despite a lack of field-based information, population modeling has shown the importance of hatchling survival to overall population growth. The implementation of a new tracking technology known as harmonic radar has proven to be an effective method of monitoring these young age classes. The methodology of this new monitoring system is presented here, as well as preliminary results of hatchling survival for two field seasons of field tracking. The annual survivorship for hatchlings of this species was calculated at a minimum of 27%, with the majority of survey censoring events occurring within the first two weeks of life. Developing this baseline understanding of the survivorship and microhabitat preferences of wild-born hatchling horned lizards will help to shape better management practices for this sensitive species, including when and where to best release lizards from head-start programs.

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784 SSAR HUTCHISON PHYSIOLOGY & MORPHOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Calvin Vick, Matthew Gifford

University of Central Arkansas, Conway, AR, USA

Physiological plasticity in an ambystomatid predator-prey relationship

Across the Eastern half of the United States, two species of ambystomatid salamanders the Marbled Salamander (*Ambystoma opacum*) and the Spotted Salamander (*Ambystoma maculatum*) live within direct contact with one another (Powell, 2016) (Petranka, 1998). Both species lay eggs in ephemeral woodland ponds, but lay eggs during different times of the year, causing a predator-prey relationship between the two species (Petranka, 1998) (Raffaelli, 2014). Marbled salamander (*A. opacum*) eggs are laid and hatched in the fall, allowing the species to reach a size capable of consuming the larval spotted salamanders (*A. maculatum*) which are laid and hatched in the spring and winter. This relationship offers a unique look at the levels of plasticity predators can induce on their prey's morphology, physiology, and behavior. Previous work has shown the presence of marbled salamander larvae cause microevolution and can change the behavior and morphology of larval spotted salamanders (Urban, 2007) (Urban, 2008) (Urban & Richardson, 2015). We intend to look further into the effects that marbled salamanders larvae have on spotted salamander larvae by measuring if there is a change in metabolic rate and if there is a change in swim speed for the spotted salamanders exposed to marbled salamanders.

CANCELLED

700 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Katrin Villinger, Bryan Franks

Jacksonville University, Jacksonville, Florida, USA

Resident and Migratory Sharks Utilizing Jacksonville's Coastal Waters: Examining Their Role in NE Florida's Ecosystems

While the use of telemetry technology for monitoring sharks has rapidly increased in recent decades, there is a paucity of data on movement and space use in particular regions along the US East Coast. Northeast Florida, while supporting a robust seasonal shark community, is one of these regions as a long-term tracking study has not been undertaken. More specifically, fine-scale data on residency, habitat use, and migratory patterns are lacking in the area. Objectives of this project are to utilize passive acoustic telemetry to quantify the spatial ecology of sharks in NE Florida. Potential target species include sandbar sharks (*Carcharhinus plumbeus*), lemon (*Negaprion brevirostris*), and finetooth sharks (*Carcharhinus isodon*), as these are not only coastal species known to utilize the area but may also use these waters as nursery habitat. Sharks are being outfitted with long-term (3-10 year) acoustic transmitters to better capture inter-annual variability in movements and migration. An acoustic array is being developed with a combination of buoy-mounted and seafloor-attached receivers and we will leverage established collaborative receiver networks along the U.S. Atlantic coast to expand our datasets. Movement data will be analyzed to describe spatial usage, habitat preferences, and migratory behavior of these species with a focus on linkages between NE Florida and other areas along the eastern seaboard. The data collected will be invaluable to gaining a full understanding of these species' ecology and will be beneficial in creating effective management strategies in the region.

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608 ASIH STORER ICHTHYOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Bridget Vincent[1], Adam Searles[1], Alexa Trujillo[1], Richard Paperno[2], Douglas Adams[2], Geoffrey Cook[1], Eric Hoffman[1]

[1]University of Central Florida, Orlando, Fl, USA, [2]Florida Fish and Wildlife Conservation Commission, Melbourne, FL, USA

Determining the Relationship of *Micropogonias* Species in the Indian River Lagoon

There is an inherent issue with taxonomic designations when using only one line of evidence (e.g. morphology) and not verifying whether the nomenclature reflects evolutionary history. This is especially important in taxa that display evidence of hybridization based on morphology because without genetic information, species identification can be challenging. Here, we used the mitochondrial COI gene to investigate population structure of the Atlantic Croaker (Micropogonias undulatus) and the Whitemouth Croaker (Micropogonias furnieri) along the east coast of Florida, as individuals cannot be unequivocally identified using morphometrics. The Atlantic Croaker is found in western Atlantic waters ranging from Massachusetts to Louisiana and the Whitemouth Croaker is commonly found in the coastal waters of the Caribbean and South America. Both species coexist in the Indian River Lagoon (IRL), a biodiverse estuary on the east coast of Florida. We sampled throughout the IRL and areas known to contain only one of the two species. To determine relationships between populations, we constructed a phylogenetic tree and haplotype network. Our preliminary data suggest that both species overlap in the northern IRL, providing an opportunity for hybridization. Additionally, there is evidence of a Micropogonias population in the IRL that is genetically distinct from other characterized Micropogonias species.

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600 Herpetology Physiology, Ballroom 3 – Cliff Lodge, Saturday 27 July 2019

Emily Virgin, Susannah French

Utah State University, Logan, UT, USA

Physiological responses to an immune challenge vary by reproductive stage in female Side-blotched lizards (*Uta stansburiana*)

Reproduction is costly and utilizes finite energetic resources that could be allocated toward other physiological functions. Energetic investment during reproduction can vary across different stages (e.g., vitellogenesis) and may exacerbate physiological costs if coupled with other

energetically expensive events, such as fighting off sickness or infection. Here, we subjected 77 wild-caught female Side-blotched lizards (*Uta stansburiana*) varying in reproductive stage to an immune challenge using lipopolysaccharide (LPS), an endotoxin that induces an acute immune response. We measured the effects of LPS or control injection on metabolic rate, antioxidant levels, and reactive oxygen metabolite levels. LPS-injected lizards had higher bactericidal capacity than control-injected lizards and also mounted stage-dependent responses to LPS in both metabolic and oxidative measures. Understanding the metabolic and oxidative costs of immunity and how they may vary depending on reproductive status is crucial to understanding how life history traits evolve in animal populations.

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248 HL GRADUATE RESEARCH AWARD, Ballroom 1 – Cliff Lodge, Thursday 25 July 2019

Anthony Waddle[1,2], Jef Jaeger[2]

[1]University of Melbourne, Melbourne, Victoria, Australia, [2]University of Nevada, Las Vegas, Las Vegas, Nevada, USA

Prior Pathogen Exposure and a Preliminary Vaccine Increase Amphibian Resistance to Chytridiomycosis

The amphibian disease chytridiomycosis, caused by *Batrachochytrium dendrobatidis* (*Bd*), presents a complicated challenge for captive breeding and headstarting programs that aim to introduce amphibians to sites where *Bd* is present. One possible solution for increasing the success of these efforts is to immunize animals before release. Immunizations against chytridiomycosis have been tested with limited enduring success in a few species, but the utility of vaccines to broadly mitigate chytridiomycosis in the wild is not known. For our experiments we used two species of ranids, the northern leopard frog (*Rana pipiens*) and the relict leopard frog (*Rana onca*), both of which have experienced drastic declines in southwestern North America. For both species, the potential of successful reintroductions are likely limited by the presence of *Bd*. Therefore, we aimed to increase resistance of these species to chytridiomycosis using two approaches: (1) exposing frogs to a live *Bd* isolate that has previously demonstrated hypovirulence towards one of our study species; and (2) exposing frogs to a virulent *Bd* isolate followed by clearance with itraconazole. We found that both approaches led to drastically reduced *Bd* infections in previously exposed frogs as compared to naïve controls; (mean maximum infection intensities were 84-92% lower). Importantly, both approaches led to significantly greater survivorship. At this time our approach has not yet been field tested, but a proof-of-concept field experiment is currently being conducted to evaluate the potential importance of this conservation tool.

CANCELLED

476 Ichthyology Life History/NIA, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Graham Wagner[1], William Roumillat[1], Wally Bubley[2], Virginia Shervette[3]

[1]*College of Charleston, Charleston, SC, USA,* [2]*South Carolina Department of Natural Resources, Charleston, SC, USA,* [3]*University of South Carolina Aiken, Aiken, SC, USA*

Age, Growth, and Reproductive Biology of a Data-Deficient Parrotfish Species (*Sparisoma viride*) in the US Caribbean

Coral reef ecosystems are declining globally, and anthropogenic influences have caused a shift from coral dominated reefs to algal dominated reefs. Reef grazers, like parrotfish, feed on algae growing in and on corals and prevent algal domination. In the US Caribbean, Stoplight Parrotfish (*Sparisoma viride*) are the most landed parrotfish species, and have experienced dramatic increases in fishing pressures in recent years; however, recent stock assessments have been unsuccessful, citing a lack of basic life history information. This study addressed these data gaps, using a combination of fishery-dependent and -independent samples to compare age, growth, and reproductive biology of Stoplight Parrotfish in Puerto Rico (PR), St Thomas (STT), and St Croix (STX). In all three islands, Stoplight Parrotfish showed year-round spawning seasonality with the potential for daily spawning. A small proportion of males appear to utilize an alternative mating strategy to avoid competition with haremic males. Size and age structure differed significantly between the three islands, with more small fish in PR compared to STT and STX, and a smaller range of ages in STT. Fish from STT also grew more quickly and reached sexual maturity at a larger size than fish from PR and STX. Differences between the sampling locations may reflect differences in the gear and practices of the fisheries of the islands themselves, which supports the notion of island-specific management and regulations. The results of this study can be used for more successful stock assessments, and for creation of fishing regulations to protect these vital reef grazers.

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114 Amphibian Ecology, Ballroom 2 – Cliff Lodge, Friday 26 July 2019

Eli Walker[1], Kristen Cecala[1], Shawna Mitchell[2], Josh Ennen[2], Jon Davenport[3]

[1]*University of the South, Sewanee, TN, USA,* [2]*Tennesee Aquarium Conservation Institute, Chattanooga, TN, USA,* [3]*Appalachian State University, Boone, NC, USA*

Exploring mechanisms regulating interspecific interactions in headwater vertebrate communities

Vertebrate communities in headwater streams are assumed to be regulated through competitive and predatory interactions. While documented predation is rare, studies regularly report competitive dominance by fish as larger competitors reliant on aquatic habitat that exclude semi-aquatic salamanders to use marginal stream habitat. However, it is unclear whether fish outcompete salamanders for food, cover, or through the threat of predation. This study sought to determine if competitive outcomes between a headwater fish and headwater salamander were regulated through resource depletion (exploitative competition) or behavioral avoidance (interference competition). We reared mottled sculpin (*Cottus bairdii)* and larval red salamanders (*Pseudotriton ruber*) for 6 weeks in independent flow-through mesocosms with intra- and inter-specific pairs allowed to interact or physically blocked from interacting with one another or influencing the available food and cover availability. Mottled sculpin negatively influenced growth of red salamanders regardless of whether they were allowed to physically interact suggesting that this community is regulated through interference competition and behavioral avoidance. The presence of fish also appeared to increase the probability of metamorphosis by larval red salamanders suggesting potential life history implications of co-occurrence with fish.

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265 SSAR HUTCHISON PHYSIOLOGY & MORPHOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Whitney Walkowski, William Gordon, Nicolas Bazan, Hamilton Farris

LSUHSC, New Orleans, LA, USA

Endocrine Control of Retinal Sensitivity in *Hyla cinerea*

Many behavior patterns that are strongly modulated by hormones, such as mate choice are mediated by visual processing. Yet, little is known about the effect of reproductive hormones on the retina, in particular, which is critical to understanding how visual signals are processed during these behaviors. This project focuses on the retina itself by examining the effects of sex steroids on spectral sensitivity, or the ability to detect differences in color signals. **Our hypothesis is that hormones modulate stimulus sensitivity in the retina during reproductively receptive phases and influence mate choice behavior through modulation of color vision**. We tested the effect that hormones have on color vision using the green treefrog (*Hyla cinerea*), which detect and respond to wavelengths spanning (and beyond) the visible light spectrum. Experiments used electroretinograms (ERGs) to compare stimulus threshold and response amplitude in retinas before and after injections of human chorionic gonadotropin (hCG), which causes secretion of estrogen and progesterone in females and testosterone in males. Our findings indicated that hormone injections cause an increase in spectral sensitivity to specific wavelengths of light in female frogs. To determine the functional consequences of endocrine modulation behavioral mate choice experiments under different wavelengths of light will be conducted.

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497 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Danielle Walkup[1], Wade Ryberg[1], Jarret Kachel[1], Connor Adams[2], Shelby Frizzell[1], Timothy Johnson[1], Dalton Neuharth[3], Toby Hibbitts[1]

[1]Texas A&M University, College Station, TX, USA, [2]Stephen F. Austin State University, Nacogdoches, TX, USA, [3]Texas State University, San Marcos, TX, USA

Out in the Open: Habitat Use, Movements, and Home Ranges in the Spot-tailed Earless Lizard

Holbrookia lacerata is a small phrynosomatid lizard endemic to the Central Texas semi-desert grasslands of the Edwards Plateau. Their populations are thought to be declining, although little is known about this species. Our goals were to characterize habitat use, movements, and home range for *H. lacerata*. During May-July 2017 and May-June 2018, we surveyed for *H. lacerata* in Crockett County, Texas. Walking and driving visual encounter surveys were conducted for lizards in habitat and along roads and well pads. Each adult lizard captured was fitted with a radio-transmitter and tracked three times each day. During each relocation we located the lizard, recorded its behavior, and collected microhabitat data. We also quantified microhabitats available to lizards along transects across the study area. *Holbrookia lacerata* had relatively large, non-overlapping home ranges compared to other lizards with similar life history characteristics. Lizard relocation sites were more open, contained highly compact natural substrates with low grassy cover, and were closer to roads compared to other sites available in the study area. The larger home ranges observed are most likely due to the sparse distribution of early successional, open natural habitats in this grassland, which the species appears to prefer. Because *H. lacerata* prefers a more open grassland, disturbances like mowing, disking, or grazing may open (at least temporarily) more grassland patches and be a viable option for restoring lizard populations. However, since *H. lacerata* are possibly attracted to roadsides, additional conservation issues from road mortality risk may create roadside population sinks.

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661 ASIH STORER ICHTHYOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Julia Wallen, Shannon O'Leary, David Portnoy

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

Population Structure of *Bagre marinus* in the Gulf of Mexico

Gafftopsail catfish (*Bagre marinus)*, named for their large sail-like dorsal fin, are abundant, widely-distributed marine catfish found throughout the Gulf of Mexico and along the southern Atlantic coast of the United States. The species migrates into estuaries seasonally for reproduction, where males brood fry in their mouths, and are often found in water conditions uninhabitable by other fishes. Seen as a nuisance by many anglers, *B. marinus* plays an important role in the Gulf ecosystem as a ubiquitous top mid-water predator. However, despite their abundance, little is known about the population structure of *B. marinus* in the Gulf. This species has specific attributes and life history traits that suggest a susceptibility to overfishing as well as potential future marketability. Here, the mitochondrial control region was amplified in approximately 500 individuals to assess patterns of population structure and connectivity throughout the Gulf of Mexico and the Atlantic Coast of Florida.

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93 Herpetology Conservation and Disease, Ballroom 3 – Cliff Lodge, Saturday 27 July 2019

Susan Walls

US Geological Survey, Gainesville, Florida, USA

Need for Climate Adaptation Strategies for Imperiled Amphibians and Reptiles in Coastal Regions

Species' declines and extinctions are predicted to escalate as changes in land-use, climate, and other stressors intensify. Effective conservation and management in the face of climatic uncertainty requires a proactive framework to reduce risk of future catastrophic storm impacts to vulnerable populations of imperiled species. Yet, compared to climate change mitigation and adaptation plans developed for human communities, few management strategies have been developed specifically for biodiversity, and ones targeting amphibians and reptiles are especially rare. Using the U.S. Fish & Wildlife Service (USFWS) Environmental Conservation Online System, I inspected recovery plans for 65 vertebrate species whose ranges include coastal regions that are vulnerable to the impacts of hurricanes. I determined whether recovery plans outlined a strategy for enabling a species to adapt to the threat of hurricanes and associated impacts such as storm surge. I found that only 33 vertebrate species have recovery plans that mention hurricanes and, of those, the need for management actions in response to the threat of hurricanes is discussed for only five. Given that 30% of 1,660 currently listed species are still in need of a recovery plan, and the USFWS National Listing Workplan prioritizes > 550 other species that are awaiting status reviews and listing determinations, it is unclear when recovery plans for coastal species may be reviewed for possible updating. Building resilience is fundamental to future conservation of populations in coastal environments, but more active planning and management will likely be needed to protect the most vulnerable coastal environments.

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442 AES Conservation & Management III, Rendezvous A&B – The Snowbird Center, Sunday 28 July 2019

Yen-Jun Wang

National Kaohsiung University of Science and Technology, Kaohsiung, Taiwan, Tokal University, Shizuoka, Japan, Nagasaki University, Nagasaki , Japan

Using two-sex stage-based matrix model for assessing eagle ray in Ariake Bay, Japan

The feature of the elasmobranch (e.g. rays, sharks, and skates) are including longevity, large body size, late maturity and less offspring, then make them particularly vulnerable to over-fishing. The eagle ray, *Aetobatus narutobiei*, is the endemic species in Ariake Bay but recently

has dramatically declined. Therefore, urgent conservation and management action for this species is needed. However, accurate assessment of ray population status is often constrained by limited and unreliable data. To provide a basis stock assessment and fishery management of ray population, a two-sex stage-based matrix model coupled with Monte Carlo simulations was developed in this study. The simulations indicated that without mortality from fishing, the estimated sex combined mean population growth rate (λ) was 1.075 yr^{-1} (1.019 and 1.101 yr^{-1} for male and female, respectively). However, the fishery management scenarios showed that even under low levels of fishing mortality, the eagle ray population may be on the edge of collapse. Therefore, better estimates of current fishing levels are needed to obtain a more accurate estimate of the impact of fishing on the population. Additionally, this study also indicates that protection of immature stage is the most efficient conservation for this species, because of the higher population growth rates than the protection of mature stages only. Given the increasing catches and landings, the eagle ray populations should be constantly monitored to ensure their sustainability in Ariake Bay.

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96 ASIH STORER ICHTHYOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Sarah Ward, Kyle Piller

Southeastern Louisiana University, Hammond, Louisiana, USA

Assessing molecular variation of the Largespot Livebearer (*Poeciliopsis pleurospilus*): A comparison of Pacific and Atlantic basin populations

Both biotic and abiotic features can influence biogeographical patterns. An important abiotic factor affecting the structure of fish populations in Middle America is the Isthmus of Tehuantepec, which represents one of the lowest elevational points between the Pacific and Atlantic basins. This area represents a prime location to study the divergence of evolutionarily independent lineages of fish populations. A species of interest is *Poeciliopsis pleurospilus* (Cyprinodontiformes: Poeciliidae), a group of small-bodied livebearers that occurs in both Pacific and Atlantic basins in Middle America. This study aims to examine genetic variation and shed light on the evolutionary relationships of *P. pleurospilus* across the basins using a combination of molecular methods. First, we created a mitochondrial haplotype network (cytb) and phylogeny to demonstrate the amount of molecular variation present within and between populations of *P. pleurospilus*. Next, we gathered SNPs using ddRADseq to determine the phylogenetic relationships and directionality of gene flow among populations of *P. pleurospilus*. Together these methods show the amount of intraspecific DNA sequence variation present within and between Atlantic and Pacific basin populations of *P. pleurospilus* and provides a historical framework to better understand the evolutionary history of this species.

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339 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Bryanna Wargat, James Gelsleichter

University of North Florida, Jacksonville, Florida, USA

Characterization of a Scalloped Hammerhead (*Sphyrna lewini*) Nursery Habitat in Portions of the Atlantic Intercoastal Waterway

The scalloped hammerhead shark (*Sphyrna lewini*) population has been in sharp decline and is currently listed as endangered by the IUCN. This warrants a need to identify and protect critical habitats of the species, which promote stable populations. A portion of the Tolomato River, in northern Florida, has been shown to serve as a nursery for the scalloped hammerhead shark. Based on an eight-year bottom long-line survey, of the 13 elasmobranch species recorded in the area, the scalloped hammerhead shark makes up the largest proportion of the catch. 80% of the scalloped hammerhead sharks captured were neonates, indicating the importance of this area as a nursery habitat. In order to characterize this habitat more fully, catch per unit effort of scalloped hammerhead neonates was compared to a suite of environmental factors, so that the abiotic factors that had the greatest effect on abundance could be determined. This work prefaces a tagging study that will be initiated during the summer of 2019.

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289 SSAR HUTCHISON CONSERVATION & MANAGEMENT AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

McKenzie J. Wasley, Stephen J. Mullin

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

Piles of *Osteopilus*: Competition at the Larval Stage Backs Native Anurans into a Corner

The sustained frequency of transporting humans and commodities creates opportunities for species introductions around the world. Establishment of invasive species is often associated with a reduction in population sizes of native species. Larval competition is a negative effect that invasive species can impart on early life-history stages of native anurans. Potential cascading effects can include reduced body condition and decreased recruitment rates of native species. Following their establishment in Florida, Cuban Treefrogs (*Osteopilus septentrionalis*) have been found in Louisiana, and there is concern that this invasive species will spread further west along the Gulf Coast. We are investigating the larval interactions between Cuban Treefrogs and two anuran species: Green Treefrogs (*Hyla cinerea*) and Gulf Coast Toads (*Incilius nebulifer*). Our experimental design presents treatments where the post-hatching larvae are reared in isolation (control), or with one or both of the other two species. We are recording measurements of body mass, tail length, and total length for subsets of individuals from each treatment to detect differences among groups. We predict that *H. cinerea* is the more susceptible of the two native species to the effects of syntopic larval *O. septentrionalis*. This research provides insight on a mechanism that contributes to successful establishment of Cuban Treefrogs

beyond their current range, and serves as a baseline from which to predict how native frog species will respond.

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413 AES Symposium: The Sensory Biology of Elasmobranch Fishes, Rendezvous A&B – The Snowbird Center, Saturday 27 July 2019

Yuuki Watanabe

National Institute of Polar Research, Tokyo, Japan

Using accelerometers to understand the behavioral ecology and energetics of elasmobranchs

Behavioral ecology of elasmobranchs under natural conditions are primarily studied by acoustic or satellite telemetry. Acoustic telemetry provides information on the horizontal and vertical movements of the animals at specific study sites, whereas satellite telemetry allows us to track large-scale, migratory movements. However, the third method using accelerometers are increasingly used in the ecological studies of elasmobranchs. In the method, body acceleration of the animals, along with depth, swim speed, and ambient temperature, are recorded by animal-borne loggers at a high sampling frequency (typically 20-40 Hz for accelerations). It provides more detailed information on the animals' swimming behavior and energetics than acoustic or satellite telemetry does, although recording durations are shorter (typically 2-5 days). In this presentation, I will talk about the history, utilities, and limitations of accelerometers as a tool of studying elasmobranch ecology.

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25 ASIH/HL/SSAR Symposium: The Expanding Role of Natural History Collections, Ballroom 1 – Cliff Lodge, Sunday 28 July 2019

Gregory Watkins-Colwell

Yale Peabody Museum of Natural History, New Haven, CT, USA

Predicting the future of natural history collections and specimen usage

Technological advances are difficult to predict and often occur much faster than anticipated. Routine techniques used in research today would have seemed like science fiction a few decades ago. Natural history collections are regularly utilized in studies that would not have been dreamt of, nor even possible, at the time the specimens were collected. Building and maintaining a collection for currently unimaginable future uses is increasingly difficult. Additionally, funding sources for museums and administrative priorities frequently change and are equally difficult to predict. An important tool to defend against administration-induced extinction is to remain

relevant. What can natural history collections do now to be relevant and necessary to future researchers?

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778 Ichthyology Life History/NIA, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

L. Cynthia Watson[1], Donald Stewart[2], Kean Clifford[2], Leandro Castello[3], Deirdre Jafferally[4], Samantha James[4], Graham Watkins [5], Zacharias Norman[6]

[1]Watershed Hydrology and Ecology Research Division, Environment and Climate Canada, Burlington, Ontario, Canada, [2]State University of New York-College of Environmental Science and Forestry, Syracuse, New York, USA, [3]Virginia Polytechnic Institute and State University, Blacksburg, Virginia, USA, [4]Iwokrama Centre, Georgetown, Guyana, [5]Inter-American Development Bank, Northwest Washington, D.C., USA, [6]North Rupununi District Development Board, Annai, Guyana

State of Recovery and Environmental Influences on Arapaima Populations in Guyana

Using population estimates that were made regularly from 2001 to 2013, we assessed the state of recovery of *Arapaima* populations after they were almost extirpated from the Essequibo basin, Guyana. Recovery rates were compared across multiple areas with different degrees of access by fishers to evaluate effectiveness of conservation efforts. Population estimates were also used to investigate the influence of environmental factors on *Arapaima* abundances in lakes with different water types and to determine the relationship between the numbers of spawners and subsequent recruits (at about age two). The most recent census conducted in November–December of 2013 indicated a 5.6-fold increase in overall abundance compared to 2001, with a total of 4591 individuals, of which 1932 were juveniles (<1.5 m total length) and 2659 were adults (>1.5 m TL). Areas that are accessible by road and with ramps for launching boats showed lower rates of recovery than areas that were less accessible. *Arapaima* in the Essequibo basin appear to favor larger lakes with abundant aquatic macrophytes. Stock-recruitment relationships suggest that the entire Essequibo basin population is still growing and that there is approximately a 1:1 juvenile to adult ratio. This ratio of juveniles to adults across the basin indicates a paucity of young fishes to sustain overall population growth. That suggests that illegal removal of young fishes still may be widespread in the basin. Compared to recent population density estimates from the Amazon basin, the Essequibo population has an intermediate density of 2.2 fish/ha dry season lake area.

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111 Herpetology Conservation and Disease, Ballroom 3 – Cliff Lodge, Saturday 27 July 2019

Jessa Watters[1], Tamaki Yuri[2], Lara Souza[3,4], Cameron Siler[1,5]

[1]Sam Noble Museum, University of Oklahoma, Norman, OK, USA, [2]Museum of Biological Diversity, Ohio State University, Columbus, OH, USA, [3]Oklahoma Biological Survey, University of Oklahoma, Norman, OK, USA, [4]Department of Microbiology & Plant Biology, University of Oklahoma, Norman, OK, USA, [5]Department of Biology, University of Oklahoma, Norman, OK, USA

Environmental DNA: an Innovative Technique to Monitor Herpetological Species of Conservation Concern in Oklahoma

Our planet is experiencing continuous decline in biodiversity, which is accelerating due to human-mediated disturbances. Currently, most conservation strategies depend on time- and labor-intensive monitoring programs to collect data on local-level population sizes and landscape-level species' distributions. However, there is a need for more efficient alternative methods for monitoring biodiversity across spatial scales. Environmental DNA (eDNA), one promising sampling technique, involves genetic material left behind in many forms as individuals interact with their environment. Sampling eDNA is an innovative, non-invasive approach for biodiversity monitoring that can be applied broadly across aquatic systems, allowing researchers to screen for the presence of rare or enigmatic species that are hard to find through traditional survey methods. We sampled a total of 79 water bodies across 11 counties in eastern Oklahoma for detecting the following species' eDNA: Blanchard's Cricket Frog (*Acris blanchardi*; positive control), Crawfish Frog (*Lithobates areolatus*), Ringed Salamander (*Ambystoma annulatum*), Three-Toed Amphiuma (*Amphiuma tridactylum*), and Chicken Turtle (*Deirochelys reticularia*). Within each water body, we sampled at 4–8 points, resulting in 647 eDNA samples from 2017–2018. Positive observations (species presence) were recorded for all taxa but *A. tridactylum*, although in very small percentages for the species of conservation concern. Despite the observed presence of the positive control species at all sampled sites, its eDNA was detected in only 60% of the sites. However, since eDNA successfully identified four species within the state of Oklahoma, these methodologies may be useful for rapid monitoring of protected species to make local management decisions.

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602 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Heather Waye, Peter Dolan, Alexis Hernandez

University of Minnesota Morris, Morris, MN, USA

White Blood Cell Profiles in Long-Term Captive and Recently Captured Eastern Tiger Salamanders (*Ambystoma tigrinum*)

Physiological responses to stress are important indicators of the effects of environmental disruption on individuals and, therefore, a way to determine the health of populations. These responses can be measured in a variety of ways, including the survey of differential counts of white blood cells. Baseline cell numbers and neutrophil to lymphocyte ratios have been determined for a number of species in the genus *Ambystoma*, but not for *A. tigrinum*, and baseline values are necessary for assessments of stress in natural and captive populations. We counted white blood cells in blood smears from long-term captive and recently captured Eastern Tiger Salamanders (*A. tigrinum*) and compared the proportions of each cell type between these two samples. We also compared our results to the published values for other post-metamorphic or paedomorphic ambystomatids. Mean neutrophil to lymphocyte ratios, a measure of stress, were higher in our captive salamanders (0.81) than in the wild sample (0.41), as were the mean number of basophils (36.0 for captive and 10.3 for wild). The cell counts for our wild salamanders were comparable to those for other unstressed ambystomatids. Our results suggest that our long-term captive salamanders are under a small degree of stress and are not a good source of baseline values for this species.

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611 Session Honoring Contributions and Retirement of Pat Gregory, Ballroom 3 – Cliff Lodge, Sunday 28 July 2019

Heather Waye[1], Karl Larsen[2]

[1]University of Minnesota Morris, Morris, Minnesota, USA, [2]Thompson Rivers University, Kamloops, British Columbia, Canada

A Retrospective Through the Eyes of His Students

There once was a man named Pat Gregory,

Whose snake-catching skills were quite legend’ry.

He gave us our start,

He’s now a large part

Of herpetological history.

Canada’s Most Interesting Herpetologist has retired, although he is still actively involved in research. We present Pat's contribution to the field through his academic progeny - his students share their stories and appreciation of his support and mentorship.

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261 ASIH STORER HERPETOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Alison Webb, Nicholas Lilly, Juliane Wood, Susannah French

Utah State University, Logan, Utah, USA

Behavioral and physiological response to an immune challenge in side blotched lizards, *Uta stansburiana*

In the present study we sought to disentangle the behavioral thermal response to a well-known mitogen and understand how behavioral changes may affect immune performance. Specifically, the goals of this study were to **1)** understand how a measure of innate immune function, bacterial killing ability (BKA), responded to different immune challenges and temperature, **2)** examine lizard thermoregulatory behavior in response to an immune challenge, and finally, **3)** to test how environmental temperature and an immune challenge interact to affect immune performance. To accomplish this, three separate experiments were performed. In experiment 1, lizard BKA was measured following a cutaneous wound, lipopolysaccharide (LPS), or phytohemagglutinin (PHA) challenge while lizards were allowed to thermoregulate. We found that only the LPS challenge significantly increased BKA and that all lizard plasma, regardless of treatment, performed better at higher assay incubation temperatures. In experiment 2, thermoregulatory behavior in response to an LPS challenge was monitored and quantified. We found that LPS challenged lizards spent more time in warm zones of the thermal gradients and more time buried in the sand when compared to the control treatment. Finally, in experiment 3, we measured immune function in response to LPS when lizards were held at either a warm or cool temperature and not allowed to thermoregulate. In this experiment, we found that BKA was higher for lizards held at the warm temperature compared to the cool temperature. Together, these results demonstrate the importance of assessing the environmental context and individual variation when interpreting immune measures.

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479 AES GRUBER AWARD I, Rendezvous A&B – The Snowbird Center, Thursday 25 July 2019

Nick Weber[1,2], Bryan Frazier[1], Nick Whitney[3], Mike Janech[2], Lou Burnett[2], Gorka Sancho[2]

[1]South Carolina Dept. of Natural Resources, Charleston, SC, USA, [2]College of Charleston, Charleston, SC, USA, [3]New England Aquarium, Boston, MA, USA

Stress Response and Post-Release Mortality of Blacktip Sharks, *Carcharhinus limbatus*, Captured in Shore-Based and Charter Recreational Fisheries

The number of recreational anglers, including those participating in a specialized method of recreational fishing targeting large coastal sharks from beaches (i.e. shore-based fishing), has increased in recent decades. While recreational fishing pressure has increased, the physiological stress and associated mortality experienced by captured sharks remain poorly understood. Estimates of post-release mortality (PRM) can have significant impacts on total fishery mortality estimates, and are thus critical to effective management plans. In the coastal waters of the southeastern U.S., the blacktip shark (*Carcharhinus limbatus*) is targeted by recreational anglers, and is currently the most commonly captured large coastal shark species. We estimated PRM rates for blacktip sharks captured on rod-and-reel by shore-based and charter boat-based fishermen using acoustic transmitters (n = 81). Additionally, 24 individuals were double-tagged with pop-off satellite archival tags (PSATs) to verify the survivorship results obtained from the

acoustic transmitters. The stress response associated with both recreational capture methods was quantified using numerous blood chemistry parameters. PRM rates were relatively low (< 15%) and were similar between capture methods. The survivorship results inferred from acoustic transmitters were consistent with results inferred from PSATs, suggesting that acoustic transmitters can be effectively used to assess PRM in migratory, coastal shark species. Blood lactate, potassium, and glucose increased with disturbance time, and the effect of disturbance time on lactate and potassium differed significantly between capture methods. Hook location was the best predictor of PRM, and 50% of foul-hooked sharks (i.e. sharks hooked anywhere but the jaw) died post-release.

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510 SSAR RABB UNDERGRADUATE AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Rebecca Weber[1], Alexandra Karwowska[1], Armand A. Cann[2], Joseph R. Milanovich[2], Leigh Anne Harden[1]

[1]Benedictine University, Lisle, IL, USA, [2]Loyola University Chicago, Chicago, IL, USA

A Collaborative Effort to Assess the Hematological Health of Augmented Blanding's Turtle (*Emydoidea blandingii*) Populations

Blanding's turtles (*Emydoidea blandingii*) are an IUCN-listed wetland-dependent species that have experienced population declines due to habitat loss and fragmentation, road mortality, and increased depredation rates. To mitigate these declines in the greater Chicago area, captive-rearing programs have been implemented to augment wild Blanding's populations, however; program effectiveness (e.g. juvenile health and survivorship) is largely unknown. During May-Oct 2016-17, we assessed the hematological health of captive-reared and released juvenile Blanding's via leukocyte profiles (e.g. heterophil/lymphocyte [H:L] ratios), which can provide a measure of immune health and stress in vertebrates. Our aim was three-fold: 1) to compare leukocyte profiles of juveniles pre- and post- release from captivity, 2) to compare leukocyte profiles of recently-released to formerly-released juveniles, and 3) to explore seasonal trends in leukocyte profiles. We also recorded monthly body condition and survivorship rates post-release, which when combined with leukocyte profiles, can provide a more comprehensive measure of health. Preliminarily, H:L ratios did not differ significantly between pre- and post-release juveniles or between recently- and formerly-released juveniles, however; H:L ratios for recently-released juveniles varied across the active season. We plan to develop a Summarized Health Index using blood and body condition data to predict juvenile health and survivorship. This study is the first to measure leukocyte profiles for juvenile Blanding's turtles, and our results can inform Blanding's conservation efforts as they can provide a basis for fine-tuning augmentation programs (e.g. captive-rearing environment and release site selection) to mitigate stress and increase survivorship.

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408 ASIH/HL/SSAR Symposium: The Expanding Role of Natural History Collections, Ballroom 1 – Cliff Lodge, Sunday 28 July 2019

Michael Webster

Cornell University, Ithaca, NY, USA

What is the 'Extended Specimen'?

Specimen-based research has long been the backbone of biological research, leading to considerable insight into the natural history, evolution, ecology, functional anatomy, and life histories of reptiles, amphibians, fish and other taxa. Most of this research has utilized traditional physical specimens, which capture many dimensions of the phenotype of individual organisms and continue to hold enormous research potential for studying variation over taxa, space and time. Recent technological and databasing advances, though, now make it possible to collect additional ancillary data, such as audio and video recordings, that capture additional dimensions of the individual phenotype, such as behavioral traits. These data can be associated with physical specimens to create an "extended specimen" that opens new doors for research. The tradition of collecting data, such as audio recordings, along with physical specimens is common in research on some taxa, such as frogs, but relatively uncommon for research on other taxa, such as fish. In this talk I will illustrate the concept of the extended specimen, and discuss both past research and future research potential for various taxonomic groups.

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426 AES GRUBER AWARD I, Rendezvous A&B – The Snowbird Center, Thursday 25 July 2019

Ornella C. Weideli[1,2], Ian A. Bouyoucos[3,1], Yannis P. Papastamatiou[4], Gauthier Mescam[5], Serge Planes[1,6], Jodie L. Rummer[3]

[1]PSL Research University: EPHE-UPVD-CNRS, USR 3278 CRIOBE, University of Perpignan, Perpignan, France, [2]SOSF - D'Arros Research Centre (SOSF-DRC), c/o Save Our Seas Foundation (SOSF), Geneva, Switzerland, [3]Australian Research Council Centre of Excellence for Coral Reef Studies, James Cook University, Townsville, Australia, [4]Department of Biological Sciences, Marine Sciences Program, Florida International University, Miami, USA, [5]Project Abroad, Shark Conservation Project Fiji, West Sussex, United Kingdom, [6]Laboratorie d'Excellence CORAIL – LABEX CORAIL, Perpignan, France

Intraspecific Variability in Maternal Investment, Body Condition, and Foraging Rates of Young Reef Sharks Between an Atoll and Island System

Acquiring and storing energy to maintain body functions is vital to sharks of all age-classes. Prior to birth, neonatal viviparous sharks receive endogenous maternal energy reserves to sustain them during their first days or weeks. Then, in order to maintain body condition, sharks must start foraging. Our goal was to understand whether maternal energy investments vary between blacktip reef sharks (*Carcharhinus melanopterus*) from two genetically and geographically isolated populations in the Indo-Pacific, and to what extent body condition and the initiation of foraging might be affected by presumably variable maternal energy investments. A total of 546 young sharks were captured from an atoll (St. Joseph, Seychelles) and island (Moorea, French Polynesia) population during the parturition months (September – March) between 2016 and 2018, and different indices of body condition as well as stomach contents (i.e., percentage of prey occurrence) were measured in pups at different neonatal and juvenile life-stages. Maternal investment was found to be site-specific, with significantly larger, heavier, and better conditioned pups in Moorea. Despite this advantage, the Moorea population exhibited significant decreases in body condition during their first months of development, and sharks were slower to initiate foraging. We suggest that maternal investments, although invaluable immediately upon birth, only partially contribute to the condition of young sharks. Other factors, like prey availability, anthropogenic stressors, environmental conditions etc., are likely responsible for the observed differences across sites. Insights into intraspecific variations in early life-stages may further support site-specific management strategies for genetically isolated shark populations from remote nearshore habitats.

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184 ASIH STORER HERPETOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Amelia Weixler

Utah Valley University, Orem, UT, USA

Genetic Divergence within *Iguana iguana*

Current and historical geologic barriers across the Neotropics have resulted in species diversification as detected in many species, including green iguanas (*Iguana iguana*). In a prior study, genetic data collected from across the range of this species identified multiple distinct clades. We add to the existing dataset by including finer scaled sampling on either side of the Panamanian Isthmus and DNA sequences from 4 polymorphic loci (mtDNA: ND4 and nuclear DNA: MLH3, PAC, and NT3). These data were analyzed in gene networks within a phylogeographic framework. Our results support the earlier finding of species diversification between Central and South America, Curacao, and within South America on either side of the northern Andes mountain range. Additionally, two South American clades converge at the base of the Santa Marta Mountains in Colombia. The South American clade on the north-west of the northern Andes extends into Central America along the Pacific coast into southern Costa Rica: a similar pattern that is seen in other taxa. These data give a more comprehensive view of how historical geological barriers gave rise to evolutionary events in the Neotropics and will aid in assessing taxonomy and informing conservation efforts.

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241 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Brooke Welch[1], Kim Bassos-Hull[2], Krystan Wilkinson[2,3]

[1]University of South Florida Sarasota Manatee, Sarasota, FL, USA, [2]Center for Shark Research, Mote Marine Lab, Sarasota, FL, USA, [3]Chicago Zoological Society's Sarasota Dolphin Research Program, Sarasota, FL, USA

Once a Spot always a Spot? Investigating Natural Marking Stability in Recaptured Whitespotted Eagle Rays off West Coast of Florida

Distinctive natural markings are often used to identify individual animals to help define population size and trends as well as movement patterns. The dorsal surface of the whitespotted eagle ray (*Aetobatus narinari*) presents with a variety of these natural markings in the form of spots, "donuts", "peanuts" and ragged lines. The objective of this study was to assess the stability of these markings over time. Between 2009 and 2018, 574 eagle rays were caught, measured, photographed, PIT tagged, and released near Sarasota, Florida as part of a long-term study. Some of these rays (n=34) were recaptured between 5 and 1413 days at liberty (verified by PIT ID). Natural markings on these individuals were classified from photographs taken upon initial capture and compared with photographs taken at time of recapture. Size at initial capture was an important factor in stability of marks over time with smaller animals showing the greatest amount of change. Most commonly, spot shaped markings remained stable over time; however, occasionally, prominent spots would change shape (into a "donut") or split into two separate markings. As the animal grew in size, new markings would sometimes emerge, but established markings did not disappear. Once new markings emerged, the distribution of the markings relative to each other stayed fairly consistent, lending evidence to the applicability of using photo-identification methodology to distinguish eagle ray individuals. This verification is especially important as more research projects use photographs of free-ranging animals (often contributed by citizen scientists) to track animal movements and population trends.

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308 ASIH/HL/SSAR Symposium: The Expanding Role of Natural History Collections, Ballroom 1 – Cliff Lodge, Sunday 28 July 2019

Rachel Welicky, Katie Leslie, Evan Fiorenza, Natalie Mastick, Katherine Maslenikov, Luke Tornabene, Chelsea Wood

University of Washington, Seattle, WA, USA

Natural history collections as time capsules: Assessing a century of change in disease burden and trophic level of marine fishes

In recent decades, marine ecosystems have been reshaped by fishing, pollution, and climate change, but ecologists' ability to assess the impact of these changes has been hobbled by a dearth of historical data. Two important knowledge gaps concern fish health: how have the parasite

burden and trophic level of marine fishes changed over the past century in response to the anthropogenic pressures experienced by ocean ecosystems? Understanding parasitism of fishes is particularly important, because parasites can reduce host fitness and influence host population dynamics. Assessing whether fish are feeding lower on the food web (as a result of overfishing) can allow us to infer whether fish are meeting the energetic demands associated with maintenance and reproduction. Our group has worked to fill these knowledge gaps by extracting information from liquid-preserved fish specimens held in natural history collections. These fish serve as "time capsules" of information on parasite burden and fish trophic level. Using the University of Washington Fish Collection, we conducted two studies that span a century-long time scale. First, we identified and quantified the parasites infecting 10 fish species (n = 1025 individuals) of Puget Sound, Washington collected between 1910 and 2015. Second, using five of the 10 aforementioned species (n = 250 individuals), we employed compound-specific stable isotope analysis to quantify temporal change in trophic level. With our temporally resolved data, we can assess parasite burden and trophic level of fishes across the 20th century, testing whether increasing anthropogenic pressures have driven temporal change in fish health.

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335 HL GRADUATE RESEARCH AWARD, Ballroom 1 – Cliff Lodge, Thursday 25 July 2019

Florence Wen

Southeastern Louisiana University, Hammond, LA, USA

Determining Olive Ridley Sea Turtle Hatchling Sex Ratios at an Arribada Nesting Beach in Costa Rica

Sea turtle sex ratios and hatching success are greatly influenced by incubation temperature. With current predictions for global climate changes, species with temperature dependent sex determination (TSD), such as sea turtles, may be in danger due to increasing temperatures. Sea turtle populations may be threatened if sex ratios completely skew towards the production of females and if embryo mortality increases. Ostional, Costa Rica hosts one of the most important nesting beaches for the Olive Ridley Sea Turtle (*Lepidochelys olivacea*). Up to hundreds of thousands of females may arrive to nest in mass nesting events, known as an *arribada*, throughout the year. In May to August 2017, I constructed a hatchery at Ostional Beach with five different thermal zones to study the effects of shading, watering, and nest depth on hatching success and sex ratios. Nest temperatures in the hatchery were recorded throughout the incubation duration with temperature loggers. The associated sex ratios at these thermal zones were determined using histological examination of hatchling gonads. Temperature loggers were placed throughout the 4km of the beach to determine sand temperatures throughout the study period. Sex ratio information from the hatchery was extrapolated to estimate sex ratios of hatchlings throughout the beach. Gaining a better understanding of current sand temperatures and associated sex ratios in different beach zones will serve as a baseline for the long-term study and management of this protected sea turtle population.

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735 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Sarah M Wenner[1], Katy S Delaney[2], Melanie A Murphy[3], Jeanne M Robertson[1]

[1]California State University, Northridge, Northridge, CA, USA, [2]National Park Service, Thousand Oaks, CA, USA, [3]University of Wyoming, Laramie, WY, USA

Estimating spatial patterns of gene flow in the Blainville's horned lizard (*Phrynosoma blainvillii*) in an urbanized landscape

The Blainville's horned lizard (*Phrynosoma blainvillii*) has experienced an immense reduction in range due to urbanization throughout the Los Angeles region of southern California. This study uses principles of conservation genetics to infer patterns of gene flow among remaining populations in this area. We will perform these analyses with a landscape perspective to determine the effects of environmental variables, due to natural heterogeneity as well as anthropogenic disturbance, on genetic structure. To address my aims, we collected 132 non-lethal tissue samples from individual horned lizards throughout the Santa Monica Mountains and the adjacent Transverse Ranges. We will use RAD-sequencing to generate a dataset of neutral loci to calculate genetic diversity and effective population sizes and infer patterns of gene flow. We will examine the influence of biotic and abiotic factors on spatial patterns of gene flow by testing for isolation by resistance and modeling estimated effective migration surfaces. These data can be used to determine the most important routes of genetic connectivity for maintaining populations of Blainville's horned lizards in this urban region.

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772 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Taylor R. West[1], Yatin Kalki[1], Tristan D. Schramer[1], Kevin D. Wiseman[2,3], Douglas J. Long[4,5], Daniel B. Wylie[1]

1Illinois Natural History Survey, Urbana, Illinois, USA, 2Garcia and Associates, San Francisco, California, USA, 3Department of Herpetology, California Academy of Sciences, San Francisco, California, USA, 4Riverside Metropolitan Museum, Riverside, California, USA, 5Department of Vertebrate Zoology and Anthropology, California Academy of Sciences, San Francisco, California, USA

Feeding Ecology of the Prairie Kingsnake (*Lampropeltis calligaster*)

Studies of predator-prey relationships are crucial for deciphering the trophic position and niche of various organisms as well as individual, population, and community interactions within an ecosystem. Understanding dietary preferences can serve as a foundation for future studies examining species coexistence patterns and other community processes. In this study, we examined the diet of the prairie kingsnake (Lampropeltis calligaster) across its range by dissecting museum specimens for stomach contents. Prey items were found in 169 specimens and successfully identified in 161. Our museum specimen data reveal that L. calligaster feeds predominately on mammals (73.3%), squamates (25.4%), and birds (1.3%). The vast majority of prey items are acquired by active foraging and swallowed head-first (98%). On average, the adult L. calligaster diet consists mainly of small-to-moderately size mammals, while juveniles consume more squamate prey than their adult counterparts. This study features the largest sample size to-date (n = 1,337) for a comprehensive look into the diet of L. calligaster.

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659 Amphibian Ecology, Ballroom 2 – Cliff Lodge, Friday 26 July 2019

Michael Westphal[1], Karen Kiemnec-Tyburczy[2], Emme Nix[1], Maxwell Westphal[3], Eva Gruber[1]

[1]US Bureau of Land Management, Marina, CA, USA, [2]Humboldt State University, Arcata, CA, USA, [3]Hollister, CA, USA

Timing of Larval Development in a Sympatric Population of *Taricha torosa* and *T. granulosa*

Direct and indirect interactions among amphibians can be important drivers of survival of individual species. In March 2016 we observed large, unidentified salamander larvae devouring eggs of the US Federally listed California red-legged frog, *Rana draytonii* in an artificial pond. We used mtDNA to identify the larvae as *Taricha granulosa*, the rough-skinned newt. Larvae of a sister species, the California newt, *T. torosa*, had already been phenotypically identified in the same pond. We further tested larvae of both species to see if hybrid individuals were present. Typical phenotypes for both species aligned with published mtDNA genotypes. We sampled the pond at monthly intervals, obtaining relative frequencies and size of individual larvae for both species. *Taricha torosa* breeds once in early spring and larvae undergo metamorphosis June-September. *Taricha granulosa* larvae first appear in May, and two or more successive waves of reproduction may occur. The final cohort overwinter, during which time larval growth slows. We conclude that overwintering *T. granulosa* may present a significant, albeit natural, risk to *R. draytonii* that could be exacerbated by climate change.

CANCELLED

346 Ichthyology Lightning Talks, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Jim Wharton[1], Hap Fatzinger[2], Beth Firchau[3]

[1]Seattle Aquarium, Seattle, WA, USA, [2]North Carolina Aquarium at Fort Fisher, Fort Fisher, NC, USA, [3]Information Curation, Virginia Beach, VA, USA

Aquariums and Zoos Working with Conservation Partners for the Conservation of Sharks and Rays: AZA SAFE Update

The Association of Zoos and Aquariums is 230+ national and international accredited zoological institutions working together towards the conservation of species through the SAFE initiative (Saving Animals from Extinction). Institutional members and their conservation partners are currently collaborating on Conservation Action Plans (CAPs) for 19 identified species (or species complexes). The AZA SAFE: Sharks and Rays program is wrapping up its first three-year plan and transitioning to a new plan with expanding partners and leadership. This lighting talk will update AES members on the state of three ongoing projects from the first plan, with emphasis on continuing efforts to foster a unified conservation messaging framework. With 1,200 species of sharks and rays distributed through 200 range countries (and international waters), a single set of conservation messages may be unrealistic. This messaging framework aims to develop a suite of messaging themes (categories) within which institutions and communicators can craft species- and community-specific messages that will be appropriate for their context. Messaging themes/categories will also serve as an organizing framework for additional resources (expert contacts, academic literature, social media templates, exhibit signage, curriculum, etc.). In addition, we will update members on the status of projects related to collections sustainability, and *in situ*/*ex situ* research, as well as progress on the development of the new CAP for sharks and rays. Opportunities for collaboration will be presented.

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195 AES Ecology, Rendezvous A&B – The Snowbird Center, Friday 26 July 2019

Clemency E. White[1,2], Maurits van Zinnicq Bergmann[3,1], Tristan L. Guttridge[1], Bryan R. Franks[4], Kristine L. Stump[5], Samuel H. Gruber[1]

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Using Biotelemetry to Infer Ontogenetic Shift and Assess the Impact of Anthropogenic Development in the Lemon Shark, *Negaprion brevirostris*

Biotelemetry serves as a tool for elucidating movement and behavior indirectly, which is particularly useful for animals that are hard to observe, including large marine predators. Tracking methods can be used to produce detailed baselines of space use, identify ontogenetic shifts and inform conservation management. This study compiled active and passive acoustic tracking data from 141 lemon sharks (*Negaprion brevirostris)* around Bimini, the Bahamas, from 1992-2018, providing information on space use across a broad timescale. Differences in space use were compared between sex, life stage (newborn to adult) and stages of industrial development using dynamic Brownian-bridge movement models. Different life stages consistently showed clear partitioning in space use across the 26-year period, with increases in home range size through ontogeny. Partitioning was pronounced in newborn sharks who used significantly smaller activity spaces close to the island's fringing mangroves, likely for protection from predators. Differences in space use before and after industrial development suggest anthropogenic impacts are reducing size of activity space in neonate and juvenile sharks. In the context of life history research on this species, this study provides a comprehensive overview of how populations of *N. brevirostris* use habitat, and specifically how they use Bimini, providing us with an example of how biotelemetry projects can inform conservation. Considering our finding that all life stages are regularly using limited space around Bimini, for adequate protection of the population more robust spatiotemporal regulations may be required.

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629 AES Symposium: The Sensory Biology of Elasmobranch Fishes, Rendezvous A&B – The Snowbird Center, Saturday 27 July 2019

Connor White[1,2], Chris Clark[3], Chris Lowe[2]

[1]New England Aquarium, Cambridge, Massachusetts, USA, [2]California State University Long Beach, Long Beach, California, USA, [3]Harvey Mudd College, Claremont, California, USA

Shark Tracking Robots: Development of Autonomous Vehicles for Tracking Animals

Over the past 60 years, electronic tags have been increasingly used to study animal movement. For elasmobranchs, this has primarily been conducted using acoustic tags. Originally this practice required humans in small vessels to actively follow individuals. However, this process of active tracking is labor intensive, thus the field has moved toward autonomous passive acoustic tracking. However, passive tracking sacrifices spatial accuracy and scale for reduced effort and increased monitoring duration. Over the past 10 years, autonomous underwater vehicles have been developed for a variety of marine research purposes. Advances in underwater robotics and autonomous control systems have greatly enhanced our ability to measure a wide array of oceanographic variables via autonomous mobile underwater or surface vehicles. By outfitting these platforms with acoustic receivers, researchers have been able to survey for acoustically tagged fish over large swaths of the ocean. Additionally, over the past 5 years, these platforms have been pushed in their design to respond in real-time to shark movements, allowing them to course-correct and actively track animals as once was done by humans. This autonomous tracking has the potential to increase the spatial scale and temporal resolution of animal tracks with less human effort.

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816 Herpetology Physiology, Ballroom 3 – Cliff Lodge, Saturday 27 July 2019

Mary White[1], Mark Merchant[2]

[1]Southeastern Louisiana University, Hammond, LA, USA, [2]McNeese State University, Lake Charles, LA, USA

Expression of Innate Immune System Genes and Antimicrobial Proteins in Infected and Uninfected Alligators

Crocodilians have potent antimicrobial activity in their tissues and blood, and they have been suggested to have a particularly active innate immune system. Proteins involved in this immune response are produced in the liver and secreted into the blood serum. We constructed transcriptomes from liver tissue of alligators that had been subject to infection to compare them to liver transcriptomes from uninfected alligators. Expression of some antimicrobial and innate immune system genes will be discussed and compared between infected and uninfected animals.

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419 Turtle Conservation/Amphibian Conservation, Ballroom 3 – Cliff Lodge, Friday 26 July 2019

Steven Whitfield[1,2], Daniel Valle[3], Adrian Figueroa[3], Brianna Chin[4]

[1]Zoo Miami, Conservation and Research Department, Miami, FL, USA, [2]Florida International University, School of Environment, Arts, and Society, Miami, FL, USA, [3]Florida International University, Department of Earth and Environment, Miami, FL, USA, [4]Florida International University, Department of Biological Sciences, Miami, FL, USA

Habitat Associations of Gopher Tortoises in Miami's Urban Natural Areas

Gopher Tortoises (*Gopherus polyphemus*) are the only tortoises native to the eastern United States, and are listed by Florida as a threatened species and a species of greatest conservation need. In extreme southern Florida, gopher tortoise habitat is uniquely limited - by urbanization, by unique geology (including seasonally flooded and/or shallow rocky soils), and by fire suppression (resulting in dense canopies and limited grassy vegetation). Here, we present the results of a habitat preference study of two gopher tortoises populations in two urban pine rockland preserves in Miami-Dade County: Zoo Miami's Ecological Preserve and the Deering Estate. We compare a suite of habitat features (including soils, geology, vegetation characteristics, and anthropogenic features) at gopher tortoise burrow locations with similar habitat features at random points within each of the two preserves. We discuss habitat limitation in relation to factors that cannot be easily mitigated (i.e., urban development, shallow or seasonally flooded soils) and discuss how management actions (i.e., prescribed fire or mechanical treatment of vegetation) can maximize habitat improvement for gopher tortoises.

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779 ASIH STOYE GENERAL ICHTHYOLOGY AWARD II, Cottonwood A-D – The Snowbird Center, Friday 26 July 2019

Dylan Wichman, Raelynn Deaton Haynes, Samuel Cornelius, Sunny Scobell

Saint Edward's University, Austin, Texas, USA

The Effects of Prozac on Feeding Behaviors and Reproductive Success in a Sex Role-Reversed Saltwater Fish

Fluoxetine, commonly known as Prozac, is a pharmaceutical found in human waste and in freshwater bodies as a result of sewage outflows. It is known to impact various behaviors and embryonic development of freshwater vertebrates; however, it has been poorly studied in saltwater systems. The male Gulf Pipefish, *Syngnathus scovelli*, presents an ideal model for the study of fluoxetine on saltwater vertebrates. This species has an easily identifiable mode of reproduction, male pregnancy in which eggs develop in a regulated brood pouch, and well-described feeding behaviors commonly called "snicks." We hypothesized that *chronic exposure of male Gulf pipefish in a laboratory setting to fluoxetine at environmental levels*

would decrease paternal feeding, and subsequent reproductive success and brood survivorship. To analyze this, we exposed individual males to one of three concentrations of fluoxetine: 0 µg/L (Control), 1 µg/L (Low), and 10 µg/L (High) in a double-blind between-subjects design. Feeding behaviors, liver mass, body mass, brood weight, brood number, and brood development were measured to indicate the effects of fluoxetine. If behavior and physiology in pipefish are affected, it is likely that a number of saltwater and brackish water vertebrates may also be affected by fluoxetine exposure. Because seagrass beds are a spawning ground for a number of species and are already threatened by a number of other anthropological disturbances, effects of fluoxetine could impact population dynamics and biodiversity.

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583 Ichthyology Conservation, Cottonwood A-D – The Snowbird Center, Saturday 27 July 2019

Abby Wicks[1], Trevor Krabbenhoft[2], Thomas Dowling[1]

[1]Wayne State University, Detroit, MI, USA, [2]University at Buffalo, Buffalo, NY, USA

Exploring Variable Growth Rates in Captive Reared Razorback Suckers (*Xyrauchen texanus*) with Differential Gene Expression Analysis

The Razorback sucker (*Xyrauchen texanus*) is a long lived, large bodied fish endemic to the Colorado River system. Historically abundant, the species has experienced significant declines and is now a federally endangered species managed through various captive rearing programs in which larvae are collected in the wild, reared in captivity and restocked once large enough to avoid predation by non-native species (a major factor in the ability of the species to sustain a naturally recruiting population). *Xyrauchen texanus* has highly variable growth rates, thus some fish reach sufficient size for stocking at a much younger age and are stocked first. We sought to explore the mechanisms contributing to variable growth rates by quantifying differential expression of genes in liver and brain tissue of fast and slow growing individuals. Using principal component analysis, we found that in brain tissue, growth rate explained the greatest proportion of the variance (16%) and 17,968 genes were differentially expressed between fast and slow growers. In liver tissue, growth differences corresponded to principal component 2, explaining 9% of the variance with 1,681 genes differentially expressed. Of the differentially expressed genes, 294 were shared between the two tissues. For genes differentially expressed between the fast and slow growers, Gene Ontology enrichment analysis identified enrichment of several pathways involved in growth regulation including Ras-mitogen-activated protein kinase signaling cascade, fibroblast growth factor and epidermal growth factor signaling pathways.

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144 AES Conservation & Management I, Rendezvous A&B – The Snowbird Center, Sunday 28 July 2019

Tonya Wiley[1], Sonja Fordham[2], Adam Brame[3]

[1]*Havenworth Coastal Conservation, Palmetto, Florida, USA,* [2]*Shark Advocates International, Washington , DC, USA,* [3]*NOAA Fisheries Service, St. Petersburg, Florida, USA*

U.S. Restrictions on Sale and Trade of Sawfish Rostra: Room for Improvement

The fate of sawfishes, now among the most threatened marine species, has long been tied to their characteristic elongated, tooth-studded snouts. These rostra are easily entangled in fishing gear and have been valued around the world for centuries as souvenirs, decorations, weapons, and medicines. Largely incidental fishing mortality has been the primary factor in global sawfish depletion. All five species (*Anoxypristis cuspidata*, *Pristis clavata*, *P. pectinata*, *P. pristis*, and *P. zijsron*) are now classified as Endangered or Critically Endangered on the IUCN Red List of Threatened Species, and Endangered under the United States (U.S.) Endangered Species Act. Although sawfish are legally protected in the U.S., they are still subject to incidental capture and illegal harm. Ending demand for rostra is key to minimizing the incentive to kill sawfish or remove rostra prior to release. Numerous state, federal, and international policies aim to ban or severely restrict sawfish rostra commerce in the U.S. Inter-jurisdictional inconsistencies and confusion surrounding applicable regulations; however, hinder enforcement and allow rostra sales to continue. Current regulations affecting U.S. sale and trade of rostra will be discussed along with recommendations for enhancing sawfish recovery though improved legal guidance and public awareness.

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414 General Ichthyology I, Cottonwood A-D – The Snowbird Center, Saturday 27 July 2019

Clare Wilkinson[1], Kenny Wei Jie Chua[1], Roswitha Fiala[2], Jia Huan Liew[3,4], Victoria Kemp[2], Darren C J Yeo [4], Pavel Kratina[5]

[1]*National University Singapore, Singapore, Singapore,* [2]*Queen Mary University London, London, United Kingdom,* [3]*Hong Kong University, Hong Kong, Hong Kong,* [4]*National University Singapore, Singapore, Singapore,* [5]*Queen Mary University London, London, Singapore*

Impacts of land use change on fish trophic ecology in Borneo

Tropical freshwater ecosystems are increasingly threatened by anthropogenic land use change. The impacts these anthropogenic disturbances have on trophic ecology of freshwater fish remain largely unknown. We determined the difference in isotopic niche size and trophic position of three highly abundant species of freshwater fish using bulk stable isotope analysis (SIA), and the maximum trophic position and level of autochthony of apex predators using compound-specific stable isotope analysis, along a gradient of disturbance (from primary forest, to logged forest, to oil palm plantations) at the Stability of Altered Forest Ecosystems Project in Sabah, Malaysia. While traditional theories suggest a decrease in trophic position and niche contraction in response to habitat degradation, we show an increase in trophic position of common species, and

apex predators in more disturbed streams. There was no impact of land use change on isotopic niche size or level of autochthony. Furthermore, several environmental variables (pH, sedimentation and dissolved oxygen) were found to impact trophic position of fish, whilst there was no effect on isotopic niche size. These findings suggest that anthropogenic land use change influences the complexity of freshwater food webs and resilience to further disturbances. To guarantee future stability of freshwater food webs in Southeast Asia it is therefore necessary to continue protecting primary forest from conversion and consider these findings in future conversion as well as current oil palm plantation management.

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415 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Clare Wilkinson[1], Jia Huan Liew[2,1], Darren C J Yeo[1]

[1]National University Singapore, Singapore, Singapore, [2]Honk Kong University, Hong Kong, Hong Kong

Impacts of catchment land use on freshwater trophic ecology

Land use change and associated habitat loss and degradation is the single greatest threat to aquatic biodiversity. Freshwater ecosystems are fuelled by allochthonous inputs from surrounding lands and internal lake/stream primary production (autochthony). Helpfully, allochthony, or the incorporation of terrestrial organic matter into aquatic food webs is one of the more well studied ecosystem functions. While the exact role of terrestrial carbon in aquatic ecosystems remains unresolved, changes in the levels and types of allochthonous material are generally thought to have bottom-up influences on aquatic trophic ecology. We conducted a global meta-analysis to characterize the changes in maximum food chain length and/or levels of allochthony (from stable isotope or gut content analysis) in freshwater food webs across anthropogenic disturbance gradients, e.g., comparisons between rivers with intact riparian forests vs. rivers bordering agricultural land. We hypothesize that riparian vegetation and increasing forest cover within catchments increases food chain length within stream ecosystems, but remains more mixed in lakes and reservoirs. Combining these measures of ecosystem structure and function can help to make better informed management decisions and to develop more focused priorities for mediating the negative effects of anthropogenic impacts on freshwater ecosystems.

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334 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Krystan A. Wilkinson[1,2,3], Randall S. Wells[1], William E. Pine, III[2,4], Rena R. Borkhataria[4], Robert E. Hueter[3]

[1]Chicago Zoological Society's Sarasota Dolphin Research Program, Sarasota, Florida, USA, [2]University of Florida, School of Natural Resources and Environment, Gainesville, Florida,

USA, [3]Center for Shark Research, Mote Marine Laboratory, Sarasota, Florida, USA, [4]University of Florida, Wildlife Ecology and Conservation, Gainesville, Florida, USA

When the shark bites: Evaluating predator-prey interactions between sharks and resident bottlenose dolphins (*Tursiops truncatus*) in Sarasota Bay, FL

In Sarasota Bay, Florida, predation from large sharks (primarily bull sharks, *Carcharhinus leucas*) has been suggested to be an important factor influencing habitat use and group size in the resident community of common bottlenose dolphins (*Tursiops truncatus*). The objectives of this research were to (1) characterize the minimum frequency of shark-dolphin interactions; (2) determine if dolphins with shark bite scars use different habitats as compared to dolphins without shark bite scars; and (3) examine whether dolphins undergo social and habitat shifts following a failed predation attempt by a shark. Approximately 35.5% of dolphins in Sarasota Bay have at least one shark bite scar and most fresh shark wounds occurred during July – October. Individual dolphins with home ranges having increased water depth, and higher proportions of mangrove or open bay habitat were more likely to have a shark bite. Individual dolphins with home ranges having higher proportions of seagrass habitat were less likely to have a shark bite. We did not find that the dolphins exhibited a strong directional change in group size or habitat use or selection following a negative interaction with a shark. Future work will address movement patterns and habitat use of large sharks within the Sarasota Bay area as well as the dietary overlap of these species. Integration of this new information will improve understanding of the niche overlap between these apex predators.

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488 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Jeffery Wilkinson[1,2], Anna Sellas[3], Matt Pollock[1], Daniel Mulcahy[4]

[1]H. T, Harvey & Associates, Los Gatos, CA, USA, [2]California Academy of Sciences, San Francisco, CA, USA, [3]Biohub, San Francisco, CA, USA, [4]National Museum of Natural History, Washington D.C., USA

The *Polypedates leucomystax* Species Complex How Many Species Are There?

Though the majority of the 24 species within *Polypedates* are narrowly distributed, six (*P. bruaeri*, *P. leucomystax*, *P. maculatus*, *P. macrotis*, *P. megacephalus*, and *P. mutus*) are widely distributed and have been fraught with much taxonomic and distributional confusion. In this state of taxonomic uncertainty, we attempted to understand the distributional patterns of species of *Polypedates* within Myanmar, as Myanmar is situated within the potential geographic confluence of these six widespread species. We examined specimens of *Polypedates* collected from throughout Myanmar and compared these specimens with other putative species of *Polypedates* from throughout Asia. Based on these morphological comparisons and molecular analyses, we describe the taxonomic, phylogenetic, and distributional relationships of the species of the *Polypedates leucomystax* complex in Myanmar and throughout Asia, and evaluate the taxonomic and distributional conclusions of species within this complex by previous studies.

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325 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Becky Williams, Jake Richardson

Utah State University Uintah Basin, Vernal, UT, USA

Epithelial Microbiomes of the Tetrodotoxin-bearing Rough-skinned Newt and the Tetrodotoxin-free Pacific Tree Frog in the Same Microhabitat

We sequenced microbiomes in dorsal epithelial samples from two sympatric amphibians in the same pond and microhabitat in Western Oregon, USA, the Rough-skinned Newt (*Taricha granulosa*) and the Pacific Tree Frog (*Pseudacris regilla*). The Rough-skinned Newt contains a powerful neurotoxin, tetrodotoxin (TTX). While TTX may be produced by symbiotic bacteria or bioaccumulated in marine organisms, some contend that there is no evidence for bacterial production of TTX in Rough-skinned Newts. Epithelial bacterial communities of TTX-bearing and TTX-free amphibians from the same microhabitat are similar and cannot be differentiated via principle components analysis. This is consistent with other research that finds a strong environmental component in amphibian epithelial microbiomes. Our findings reiterate that microhabitats must be considered as a factor in comparison of microbiomes such that environmental differences in microbiomes are not mistakenly attributed to species-level differences. We also found that TTX levels in Rough-skinned Newts are positively correlated with PC 2 (df = 7, F = 5.88, p = 0.05). Whether microbial communities influence TTX levels or vice versa in Rough-skinned Newts is unknown.

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472 Reptile Conservation, Ballroom 2 – Cliff Lodge, Saturday 27 July 2019

Dean Williams

Texas Christian University, Fort Worth, TX, USA

Genetic Considerations for Reintroducing Captive-bred Texas Horned Lizards (*Phrynosoma cornutum*)

Texas horned lizards (*Phrynosoma cornutum*) have experienced significant declines in the past 50 years. Texas Parks and Wildlife has teamed up with the Fort Worth, Dallas, and San Antonio Zoos to reintroduce captive-bred lizards into formally occupied areas that contain suitable habitat. Reintroduction efforts should utilize individuals that are matched ecologically and genetically to the introduction region and should comprise a sufficient number of individuals to maintain allelic diversity. This strategy should increase the capacity of the population to adapt to changing conditions and increase long-term viability. I conducted a genetic analysis of all captive Texas horned lizards (N = 115) housed at these zoos in 2017-2018 to determine the regional origin of captive populations and to estimate the current captive populations' genetic diversity. The zoos had mixed ancestry from different regional genetic units in Texas and relatively low genetic diversity. The zoos will need to partition their breeding animals by genetic region and supplement their stock with more wild caught individuals. I then used *AlleleRetain* to simulate demography and estimate the number of individuals that need to be released at a site to retain low frequency (0.05) alleles. Large numbers of captive-bred hatchlings (~300) will need to be released at a site and then supplemented with a minimum of 25 hatchlings every two years to maintain genetic diversity. Additionally, several parameters need to be characterized for this species including mating system and hatchling survival since these can have large effects on allele retention.

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605 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Emily Williams, Jim Gelsleichter

University of North Florida, Jacksonville, Florida, USA

Total Mercury Concentrations in Egg Yolk from Sharks and Rays

Previous studies have found that mercury, a persistent environmental toxicant, can accumulate in aquatic organisms, especially those that occupy high positions in aquatic food webs. This is particularly true for elasmobranchs (sharks and rays), which have been shown to exhibit perhaps the highest concentrations of mercury observed in any of the marine fishes. The purpose of this study was to examine if the high concentrations of mercury often observed in sharks and rays result in similarly high and potentially embryotoxic levels of mercury in egg yolk through the process of maternal transfer. To address this question, we examined total mercury concentrations in yolk collected from females of 5 elasmobranch species: the bonnethead shark (*Sphyrna tiburo*), blacknose shark (*Carcharhinus acronotus*), Atlantic stingray (*Hypanus sabina*), sandbar shark (*Carcharhinus plumbeus*), and blacktip shark (*Carcharhinus limbatus*). Mercury analysis was conducted on dried yolk samples using a Direct Mercury Analyzer (Milestone DMA-80) following EPA Protocol 7473. To date, the results of this study have demonstrated that egg yolk of sharks and rays generally contains low concentrations of total mercury (<0.09 mg/kg dry weight); levels below thresholds for embryotoxic effects in other vertebrates (e.g., birds: 0.25-1.0 mg/kg).

CANCELLED

416 General Herpetology II, Primrose A&B – Cliff Lodge, Sunday 28 July 2019

J.D. Willson[1], Shannon Pittman[2], Brett DeGregorio[1], Jennifer Mortensen[1], Jinelle Sperry[3]

[1]University of Arkansas, Fayetteville, AR, USA, [2]Athens State University, Athens, AL, USA, [3]3ERDC-CERL; University of Illinois-Urbana/Champaign, Urbana, IL, USA

Influence of behavioral responses to roads on snake density estimation

Accurate estimates of population density and individual detection probability are critical components of effective wildlife conservation and management. However, the detectability of many snake species is so low that density cannot be feasibly determined using traditional methods such as capture-mark-recapture. Coincidentally, many of the most secretive snake species are most effectively sampled using road surveys. We have developed a novel method for estimating density of secretive snakes, that uses simulations of snake spatial movements and an understanding of snake road crossing behavior to estimate detectability during systematic road surveys. Although we have applied this method to several species, we have not yet applied the method to a system with robust enough movement data to assess the influence of behavioral responses to the road (avoidance or attraction) on the density estimation process. Here, we take advantage of an extensive existing road survey and radio telemetry dataset for western rat snakes (*Pantherophis obsoletus*) at Ft. Hood, Texas, to test for bias in spatial movements relative to roads and explore the implications of these effects on density estimates. We find evidence for road attraction in a substantial proportion of individual *P. obsoletus*, possibly resulting from a preference for edge habitats along roads. Failing to account for this effect would result in overestimation of rat snake density.

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253 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Hannah Wilson, Alan Savitzky

Utah State University, Logan, Utah, USA

An Arduino Electrocardiography Unit for Snakes

Obtaining a clear electrocardiogram (ECG) of an unrestrained snake can be difficult. Their highly keratinized and elastic skin precludes the use of external electrodes, so electrodes must be inserted subcutaneously. The electrodes also must be prevented from dislodging or shifting position in order to obtain a good signal. The small size of some species also results in a weak signal, requiring sensitive electrodes and stronger amplification. We have been working to develop an ECG unit that can be attached to the back of a relatively small snake, to obtain clear ECGs from unrestrained individuals. Arduino is an electronics development environment that allows non-expert users to design small, low-cost sensors and controllers. Using Arduino components, we have been designing an electrocardiography unit that is small enough to be attached to the back of an adult male *Thamnophis*. Refinement of the unit is ongoing. The latest iteration produces a clear ECG signal, but the unit is still too large to attach to even a female *Thamnophis*. Future work will focus on further miniaturizing the unit, as well as refining the electrode design. The basic instrumentation could be used, with minor modifications of shape and attachment, on many species of reptiles and amphibians.

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708 ASIH/HL/SSAR Symposium: The Expanding Role of Natural History Collections, Ballroom 1 – Cliff Lodge, Sunday 28 July 2019

Julie Winchester[1], Doug Boyer[1], Tim Ryan[2], Tim McGeary[1]

[1]Duke University, Durham, NC, USA, [2]Pennsylvania State University, University Park, PA, USA

How MorphoSource is Helping Museum Collections to Connect Specimens to 3D and 2D Media and to the Broader World

MorphoSource (www.morphosource.org) is a publicly accessible web repository where museum curators, researchers, and the public can upload, search, view, and download 3D and 2D media representing physical objects, primarily biological specimens. Global specimen collections are currently leveraging MorphoSource in multiple ways to enhance research and outreach utility of their specimens. In this talk, we outline how collections are using MorphoSource to archive and share digital assets representing their specimens while obtaining use/impact statistics. Specifically, features supporting archiving and discovery include a digital asset management system tailored for the needs of 3D and 2D media. In particular, unlike any other platform we know of, MorphoSource maintains a series of imaging modality specific metadata profiles and supports complex data creation protocols with many processing steps and intermediate files. Automated systems provide usage tracking reports per collection, curator-defined project, specimen, and media. An API also allows curators to individually tailor data query and reporting in a highly customized fashion. Our plans for future improvements on these systems include deep automated integrations between the MorphoSource repository software and already-existing institutional collections management software, as well as ways to allow collections without already-existing management software to roll out a local MorphoSource "container" solution. This latter solution potentially provides a path for museums to implement 3D-aware infrastructure with minimal technical investment. We are actively seeking feedback on these future features in order to better serve the needs of museums and collections as 3D media continues to become more common and more relevant over time.

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569 Turtle Conservation/Amphibian Conservation, Ballroom 3 – Cliff Lodge, Friday 26 July 2019

Bryan Windmiller, Cara McElroy

Zoo New England, Boston, MA, USA

Growth Rates of Headstarted Blanding's Turtles in Captivity and Survival Rates Post-Release

In recent years, many turtle conservationists have initiated headstarting programs to improve the survival probabilities of young individuals of chelonian species of conservation concern. The presumption underlying this conservation intervention is that, by raising hatchling turtles in captivity to a considerably larger size than at hatching, managers can reduce size-related mortality rates incumbent upon small turtles. Since 2007, we have raised more than 600

Emydoidea blandingii (Blanding's Turtles) in captivity prior to their release at five different natal sites in eastern Massachusetts. Collectively, we have radio-tracked more than 100 headstarted Blanding's turtles for up to six years following their release, documenting survival rates. At our primary site, telemetry data demonstrate annual survival rates among released headstarted Blanding's turtles that appear at least 10-fold greater than those experienced by unmanipulated conspecifics of similar age. Most observed post-release mortality has been the result of predation and predation rates vary substantially between release sites. We have also examined factors influencing the size at release and rates of growth experienced by the hatchlings that we have headstarted in more than 30 schools and institutions. Our analyses document that hatching year, hatching gender, size at hatching , maternal identity, and headstarting institution all affect at least some measures of hatchling growth. We also document the results of our efforts to encourage greater growth rates in headstarted turtles by altering our communications with the headstarting supervisors at participating schools.

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356 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Jessica Wingar[1], Daniel Abel[1], George Boneillo[1], Paul Yancey[2]

[1]Coastal Carolina University, Conway, SC, USA, [2]Whitman College, Walla Walla, WA, USA

Osmoregulation and Salinity Preference in Juvenile Sandbar Sharks (*Carcharhinus plumbeus*) in Winyah Bay, SC

Juvenile sandbar sharks (*Carcharhinus plumbeus*) have been caught in salinities from 7- 40 along the eastern US. In Winyah Bay, SC, they tidally alternate between lower salinities in middle bay and higher salinities in lower bay. To assess duration in low salinities, we caught juveniles on longlines from May-August, 2018 and used active and passive acoustic telemetry. To determine osmoregulatory changes, we measured plasma sodium, chloride, urea, and trimethylamine oxide (TMAO) concentrations and total osmolality. All plasma variables differed significantly ($p < 0.001$; ANOVA) between salinity groups (15 – 19.9, 20 – 24.9, 25 – 29.9, and 30 – 35). Sodium and chloride concentrations decreased by 31.4 and 41 mM, respectively, from the highest salinity group (HSG) to the lowest salinity group (LSG). Between the HSG and LSG, urea decreased by 78.1 mM, and TMAO by 29.6 mM. Total osmolality in the HSG was 987.3 ± 11.4 mOsm/kg and 802.8 ± 3.4 mOsm/kg in the LSG. Post hoc Tukey tests of all variables revealed that the HSG was significantly different than the other three salinity groups ($p < 0.05$). Two active acoustically tagged juvenile sharks remained in middle bay until ebb tide before moving seaward. Preliminary passive acoustic telemetry (n=3) showed that juveniles remain in middle bay until low tide, in salinities as low as 5.88, and then move seaward. These results suggest that juvenile sandbar sharks reside in lower salinities in Winyah Bay for extended time periods and reduce their internal inorganic and organic osmolytes at lower salinities, which was heretofore unknown.

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620 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Christine Wisell, Shana Geffeney, Charles Hanifin

Utah State University Uintah Basin, Vernal, Utah, USA

Cause or Consequence: The Evolution of TTX-resistance in Cardiac Tissue of *Taricha* newts

Multiple amphibian species use toxins that target important proteins in the nervous system to defend themselves against predation. These species are often resistant to their own toxin. Resistance to neurotoxins that target ion channels has evolved in several toxic amphibian species including multiple poison frog lineages as well as tetrodotoxin-defended salamanders. Identifying the processes that generate resistance phenotypes is central to understanding the evolutionary history of amphibians. Multiple species, including salamanders, have evolved the ability to resist tetrodotoxin (TTX) block of voltage-gated sodium ion channels (VGSCs). We used comparative analyses to reveal the history of TTX resistance in TTX-bearing salamanders. We know from earlier work that TTX resistance in the Salamandridae results, in part, from the expression of TTX-resistant VGSC variants in skeletal muscle salNa$_V$ 1.4 (SCN4a). The project reported here focuses on the VGSCs expressed in heart muscle tissue of multiple salamander species. Our results indicate that evolution of TTX resistance in salamanders includes multiple pathways to resistance of the VGSCs expressed in heart muscle tissue salNa$_V$ 1.5 (SCN5a). TTX-resistance of salNa$_V$ 1.5 has evolved in multiple species, some possess TTX and some do not. These results document multiple mutational mechanisms for TTX-resistance in salNa$_V$ 1.5. Our results agree with previous work that suggest that organismal TTX-resistance in *Taricha* evolved before the TTX-bearing phenotype but strongly suggest that TTX-resistance in salNa$_V$ 1.5 may be driven by other selective pressures possibly including selection for altered core biophysical properties of these channels.

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130 Herpetology Ecology, Primrose A&B – Cliff Lodge, Saturday 27 July 2019

Van Wishingrad, Robert Thomson

University of Hawaiʻi at Mānoa, Honolulu, HI, USA

Sceloporus occidentalis lizard landscape genetics in the Sierra Nevada mountain range

The field of landscape genetics aims to understand the effect of landscape structure on evolutionary processes. Research in this field has contributed greatly to our understanding of the relative strength of geographic distance, topography, and environmental heterogeneity in shaping population connectivity, and how adaptive genetic variation is linked to environmental variation across geographic space. However, while several studies have described landscape effects on genetic divergence, the degree to which landscape genetics processes are generalizable in different locations or at different spatial scales is not well understood. I measured gene-flow in

several study areas and calculated the effect of environmental variation and habitat types on gene-flow to understand how consistent or idiosyncratic the effect of habitat and environmental variation on gene-flow between populations of a species may be. Specifically, this study tests the generalizability of inferences in landscape genetics using the Western Fence Lizard (*Sceloporus occidentalis*), which is widely distributed over a diverse range of habitat types to answer the following questions: (1) How consistent are landscape genetics results across space? (2) Are species interacting differently with their landscape at different scales? This study aims to resolve some of the important problems facing landscape geneticists by drawing inferences about the reproducibility and generalizability of the field's findings, bringing about greater understanding of concordance and conflict in landscape genetics studies at multiple scales, and contributing to the development of landscape genetic theory.

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512 Ichthyology Ecology, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Kirsten Work

Stetson University Biology Department, DeLand, FL, USA

The Integrity of Coldwater Spring Resources for Fish and Invertebrates

Springs are the intersection of ground and surface water and so they represent both a window into our groundwater supplies and a unique set of ecosystems. Many states rely on groundwater for drinking and agricultural water supply, so increases in use can threaten groundwater-dependent ecosystems. The magnitude of this threat likely depends upon both the demand for groundwater and the hydrology of the landscape. The purpose of this ongoing study is to evaluate the integrity of discharge from springs nationwide with the goal of representing resources for spring-dependent fish and invertebrates. Literature on the magnitude of threat to southwestern US springs and the establishment of minimum flow regulations in Florida point to a large-scale problem in spring discharge maintenance. I collected time series data (50+ years) from the USGS National Water Information System as well as from individual state parks across the country to analyze trends in discharge over time. I also evaluated the literature on endemic species and on regional rainfall for relationships between regional spring isolation and degree of endemism of spring residents. Of the springs evaluated to date, the maintenance of discharge was highly variable. The largest declines in discharge have occurred for the Snake River springs in Idaho; in contrast, springs in Missouri have the most consistent maintenance of discharge. Endemic fish and invertebrates occur in springs throughout the country, although a large number occur in the arid southwestern US. Together, these discharge declines and occurrences of endemics point to a need for targeted spring conservation.

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32 Turtle Conservation/Amphibian Conservation, Ballroom 3 – Cliff Lodge, Friday 26 July 2019

F. Boyd Wright[1], Erin Muths[2], Larissa Bailey[3]

[1]Colorado Parks and Wildlife, Fort Collins, CO, USA, [2]U.S. Geological Survey, Fort Collins, CO, USA, [3]Colorado State University, Fort Collins, CO, USA

Two decades of reintroductions of toads in the Rockies: Results and ruminations

There is inherent risk in moving animals around, particularly when disease is part of the landscape. We present an overview of reintroductions of boreal toads in the southern Rocky Mountains through the lens of risk tolerance and illustrate that the success of current conservation measures may not be a result of specific methods, but of certain biotic constraints. We focus on two recent efforts summarizing data from one reintroduction where we gained an understanding of egg to metamorph survival and showed that egg survival depends on source; and from another, where the effort yielded the first estimates of survival (0.87, SE = 0.06) from a population of reintroduced boreal toads.

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593 AES Reproduction & Life History, Alpine A,B,C – The Snowbird Center, Friday 26 July 2019

Jennifer Wyffels[1], Lisa Hoopes[2], Cayman Adams[1], Tim Handsel[3], Michael Hyatt[4], Alisa Newton[4], Linda Penfold[1]

[1]South-East Zoo Alliance for Reproduction & Conservation, Yulee, FL, USA, [2]Georgia Aquarium, Atlanta, GA, USA, [3]Ripley's Aquariums, Myrtle Beach, SC, USA, [4]Wildlife Conservation Society, New York Aquarium, Brooklyn, NY, USA

Endocrine and Nutritional Parameters and Semen Quality for *In Situ* and Aquarium Sand Tiger Sharks (*Carcharias taurus*)

Mature sand tiger sharks *Carcharias taurus* have been maintained in aquaria for nearly a century and despite observations of copulation at many facilities, young have been born at only four aquaria worldwide. Poor gamete quality might be contributing to the lack of observed pregnancies. For example, the percentage of motile sperm in semen collected from *in situ* sharks is higher than aquarium sharks. Gamete quality is affected by diverse environmental and physiological factors and among the most important are endocrine and nutrition. Fatty acid profiles, trace minerals and steroid and thyroid hormones were characterized for mature male sand tigers *in situ* and in aquaria to identify differences in nutritional and endocrine parameters that might impact semen quality. *In situ* sharks had higher testosterone ($p<0.05$) than aquarium sharks indicating differential stimulation of the hypothalamus-pituitary-gonad axis between populations. Triiodothyronine and iodine were higher ($p<0.05$) and thyroxine lower ($p<0.05$) for aquarium sharks compared to *in situ* sharks suggesting thyroid dysfunction. Cobalt ($p<0.01$) and iron ($p= 0.02$) were significantly higher for aquarium sharks compared to *in situ* sharks. Most major fatty acids (61%) were different ($p<0.05$) between *in situ* and aquarium sharks. Notably, the essential fatty acids arachidonic ($p=0.04$) and eicosapentaenoic ($p=0.03$), known to impact semen quality for other animals, were significantly lower for aquarium sharks. Collectively,

these endocrine and nutritional differences may negatively impact semen quality and reduce the chance of successful fertilization and pregnancy for sand tiger and other species of sharks under managed care.

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303 Herpetology Lightning Talks, Ballroom 3 – Cliff Lodge, Saturday 27 July 2019

Amy Yackel Adams[1], Björn Lardner[2], Julie Savidge[2], Robert Reed[1]

[1]U.S. Geological Survey, Fort Collins, CO, USA, [2]Colorado State University, Fort Collins, CO, USA

Maximizing Animal Detection Rate by Optimizing the Walking Pace: A Visual Encounter Survey Experiment Targeting an Invasive Snake

Visual encounter survey efforts can be defined and constrained by duration, distance, or both duration and distance simultaneously. But what is the optimal walking pace to maximize number of animal detections within a limited time frame? We predicted that animal sighting rate per unit of distance would decline with increasing pace, but that maximal sighting rate per unit of time would occur at some intermediate pace because walking faster means covering more ground and passing more animals that could potentially be detected. We conducted a controlled experiment during which we searched for Brown Treesnakes (*Boiga irregularis*) while walking 220-m long transects at either 0.44 km/h, 0.75 km/h, or 1.32 km/h. For narrow transects inside the forest, detection rate per unit distance decreased (non-linearly) with increasing pace. However, when considering catch per unit time, we found 5% more snakes at the medium pace compared to the slow pace, and 63% more snakes at the fast pace compared to the slow pace. The pattern appeared different for surveys along forest edges with higher vegetation density, in which snakes might be more difficult to spot. Surprisingly, pace had no detectable effect on the body sizes or perch heights of snakes successfully detected. Finding the optimal search pace for one's study organism in a focal habitat has the potential to substantially increase survey cost-efficacy.

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782 AES Genetics/Ecology, Rendezvous A&B – The Snowbird Center, Friday 26 July 2019

Atsuko Yamaguchi, Keisuke Furumitsu

Nagasaki University, Nagasaki, Nagasaki, Japan

Role of estuarine and coastal areas as nursery grounds of elasmobranchs

Elasmobranch populations are declining owing to overfishing including incidental cases and habitat loss or degradation. In Japan, the first red list assessment of elasmobranchs was prepared and published by the Ministry of Environment (2017), although available information was limited. Our study area, Ariake Bay, a part of the East China Sea, is one of the most productive

bays in Japan. The bay has a great tidal range, approximately 6 m, which has resulted in the formation of the largest mudflats in Japan. The bay has high species diversity and a large resident population of elasmobranchs. We have studied the seasonal distribution, migration, and life history of each elasmobranch species in this bay, as well as documented ecosystem functions with prey-predator relationship since 2001. Our study revealed that the estuarine and coastal areas of this bay serve as the nursery ground of at least 11 elasmobranch species including 3 sharks and 8 rays, resident or seasonal resident in 23 species. In contrast, Yatsushiro Bay, connected with the southern part of Ariake Bay, has similar environmental conditions and a great estuary, but it serves as the nursery ground of only a few elasmobranch species. We will present information on habitat use as a nursery ground, reproductive biology, and seasonal migration patterns of elasmobranchs based on data of 13049 specimens for future conservation. In addition, we discuss the role of estuarine and coastal areas as nursery grounds, which contributes to the high biodiversity of elasmobranchs in these areas.

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208 AES Physiology I, Alpine A,B,C – The Snowbird Center, Sunday 28 July 2019

Kazuaki Yamaguchi[1], Mitsumasa Koyanagi[2], Yuichiro Hara[1], Akihisa Terakita[2], Shigehiro Kuraku[1]

[1]RIKEN BDR, Kobe, Japan, [2]Osaka City University, Osaka, Japan

Whale Shark Visual Ecology Revealed by Genomic and Spectroscopic Analysis

As fundamental resources for molecular studies of elasmobranchs, we previously reported a comprehensive genome-wide analysis on three shark species (Hara et al., 2018. *Nat. Ecol. Evol.* 2: 1761-1771) and released associating sequence data at the online archive Squalomix (https://transcriptome.riken.jp/squalomix/). This study provided the first-ever measurement of the genome size of the whale shark by means of flow cytometry (3.75 Gbp) as well as the repertories of genes potentially responsible for homeostatic controls, vision, and olfaction in its genome. We are extending our study on these genes of more elasmobranch species, with exhaustive search of potential homolog and phylogenetic analysis. For visual opsins, we performed spectroscopic analysis using synthetic peptides to obtain their absorption spectra. Our phylogenetic analysis indicated the absence of three visual opsin genes (Rh2, SWS1, and SWS2) from the whale shark genome, while we identified the orthologs of rhodopsin (RHO) and long wavelength-sensitive (LWS) genes. Our spectroscopic analysis of the RHO pigments revealed a blue-shifted spectrum for the whale shark (478 nm), suggesting the adaptation to a deep-sea life. Our result was consistent with occasional migrations of the whale shark down to the bathypelagic zone besides daytime surface feeding habits. Our study portrays the diversity of visual opsin gene repertories among elasmobranchs and illustrates the potential of *in vitro* molecular experiments supported by genome sequencing, in understanding underwater ecology of inaccessible marine species.

CANCELLED

327 ASIH STOYE GENETICS, DEVELOPMENT & MORPHOLOGY AWARD II, Primrose A&B – Cliff Lodge, Friday 26 July 2019

Jessica M. Yamauchi, Robert E. Espinoza, Gilberto E. Flores

California State University, Northridge, Northridge, CA, USA

Characterization of changes in the gut microbiome across ontogenetic development in the American Bullfrog

An organism's gut microbiome changes over the course of its life as a function of age, diet, and environmental factors, but species with complex lifecycles have been scarcely studied in this regard. For example, we would expect dramatic changes in the microbiome of a frog as it undergoes the profound changes associated with metamorphosis. Transforming tadpoles experience not only changes in appearance, but a complete remodeling of their digestive tracts during the shift from an herbivorous to a carnivorous diet. Our project aims to characterize changes in the microbial community living in the guts of American Bullfrogs (*Rana catesbeiana*) as they develop and undergo metamorphosis. We collected wild tadpoles and frogs representing most developmental stages, sampled their dissected guts for microbes, and extracted the DNA from these microbial communities. Next, we purified, amplified, and sequenced the microbial DNA, and identified operational taxonomic units, which will allow us to determine how ontogeny affects changes in the gut microbiome. Preliminary data (n = 4 adults) indicate that *Cetobacterium* is the dominant bacterial genus, suggesting these bacteria play an as-yet unknown role in this community. Our study is the first to characterize changes in the gut microbiome of a wild vertebrate with a complex life cycle over the course of its entire life. As such, it will provide insight into the interactions among development, ontogenetic shifts in diet, and microbial community ecology over the course of the radical transformation experienced by animals with complex lifecycles.

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211 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Sarah Yerrace[1,2], Luke Tornabene[1,2], Carole Baldwin[3], Jordan Casey[3,4], Simon Brandl[5]

[1]University of Washington, Seattle, Washington, USA, [2]Burke Museum of Natural History and Culture, Seattle, Washington, USA, [3]Smithsonian's National Museum of Natural History, Washington, DC, USA, [4]École Pratique des Hautes Études, Perpignan, France, [5]Simon Fraser University, Vancouver, Canada

Using Integrative Taxonomy to Discern Species Boundaries in *Risor ruber* (Gobiidae)

Microhabitat association is a key factor contributing to the diversification of coral reef fishes. For species with specific microhabitat associations, a change in host organism (a coral, sponge, or other organism) on a reef could enable sympatric or parapatric speciation, where a new species evolves in the same or adjacent geographic area as the ancestral species. The tusked

goby, *Risor ruber,* is a poorly studied obligate sponge-dwelling coral-reef fish. Preliminary genetic data on *R. ruber* indicates that there are eight genetically distinguishable lineages based on mitochondrial DNA sequence data. Field data taken during collection of specimens suggest that these lineages often live on specific host sponges, pointing to the possibility of ecologically-driven speciation. The purpose of this study was to determine if there is significant morphological variation that could be used to distinguish genetic lineages and allow for formal taxonomic description. Our results suggest that some pairs of lineages can be distinguished from each other on the basis of scale morphology or coloration, but overall we were unable to unambiguously diagnose all lineages using traditional taxonomic characters (e.g. meristics, coloration, morphometrics, and tooth morphology). The combination of high intraspecific variation in some characters, and morphological conservatism in others, may be an evolutionary byproduct of the highly plastic morphology of the host sponges, coupled with strong selective pressure to conserve certain morphological traits given the specific niche these obligate sponge dwelling gobies occupy.

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558 AES Symposium: The Sensory Biology of Elasmobranch Fishes, Rendezvous A&B – The Snowbird Center, Saturday 27 July 2019

Kara Yopak

University of North Carolina Wilmington, Wilmington, NC, USA

No Scalpel Required: Advancing our Understanding of the Brain in Elasmobranchs using 3D bioimaging

Gross dissection and histological techniques have historically been vital for our understanding of the internal anatomy of elasmobranchs (Class: Chondrichthyes). However, these methodologies are highly invasive, distorting the precise relative positions of tissue structures, and are often impractical for the study of rare and/or valuable specimens. Magnetic resonance imaging (MRI) is a non-invasive technique that uses a magnetic field and radiofrequency waves to create high-resolution images of soft tissue structures. In the last few decades, the use of this technology has been extended from well-established applications in humans and veterinary medicine to the visualization and quantification of internal anatomy in chondrichthyans. This talk will focus on the use of MRI as an investigative tool of the sensory biology and neuroanatomy of cartilaginous fishes. Across three case studies, we will explore (1) the optimization and applicability of MRI on peripheral and central anatomy *in situ* in sharks and batoids; (2) non-invasive data acquisition from rare specimens (e.g. the Greenland shark, *Somniosus microcephalous*; sawfishes, *Pristis spp*.), where dissection is sub-optimal; and (3) using 3D imaging to reconstruct damaged specimens (e.g. the whale shark, *Rhincodon typus*). These “digital dissection” methods greatly extend the capabilities of researchers to incorporate quantitative anatomical measurements of rare samples and museum collections into the study of elasmobcranch biology. Further, digitization of specimens serves a critical role in preserving biological material in perpetuity, enabling worldwide access to specimens and allowing for new questions of the same tissue by future generations of scientists.

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75 AES Conservation & Management II, Rendezvous A&B – The Snowbird Center, Sunday 28 July 2019

Chelsey Young[1], John Carlson[2]

[1]NOAA Fisheries, Office of Protected Resources, Silver Spring, Maryland, USA, [2]NOAA Fisheries, Southeast Fisheries Science Center, Panama City, Florida, USA

The Oceanic Whitetip Shark (*Carcharhinus longimanus*): Status and Future Directions for Conservation and Recovery under the U.S. Endangered Species Act

The oceanic whitetip shark (*Carcharhinus longimanus*) was once described as one of the most abundant and ubiquitous pelagic shark species in tropical seas worldwide. However, numerous lines of evidence, including a recent stock assessment and several other abundance indices, indicate significant historical and ongoing declines of the species due to heavy fishing pressure and demand in the international shark fin trade. After a comprehensive status review, NOAA Fisheries determined that oceanic whitetip shark abundance likely declined significantly over the last several decades (e.g., between 50-88% in the Atlantic and Gulf of Mexico, 80-95% across the Pacific Ocean basin, and variable declines in the Indian Ocean). As a result, NOAA Fisheries concluded that the oceanic whitetip shark met the definition of a "threatened" species and listed it as such under the Endangered Species Act (ESA) in January 2018. NOAA Fisheries is developing a recovery plan for the conservation and survival of the oceanic whitetip shark, and has published a recovery outline to serve as an interim guidance document to direct recovery efforts until a full recovery plan is developed and approved. The recovery outline presents a preliminary strategy for recovery of the species and recommends high priority actions to stabilize and recover the species, including reducing the primary threat of bycatch-related mortality in commercial fisheries. We will provide an overview of the current conservation status of the oceanic whitetip shark and our preliminary strategy for recovering the species under the ESA.

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762 AES Symposium: The Sensory Biology of Elasmobranch Fishes, Rendezvous A&B – The Snowbird Center, Saturday 27 July 2019

Joy Young

FWRI, Tequesta, FL, USA, FACT Network, Tequesta, FL, USA

The role of collaborative networks in advancing the science of movement

Technological advances have fueled the expansion of acoustic telemetry studies across the globe and starting in the early 2000s, regional networks were founded to serve as vehicles for data sharing. The usefulness of these networks is evident in the development and growth of networks across the United States (ACT, FACT, iTAG, POST, SCATN, GLATOS, ATN) and around the

globe (OTN, ATAP, IMOS, ETN). Collaborative networks create a community where collective knowledge is developed and refined and data are shared. The integration of scientists and infrastructure across state and international boundaries allows for collaborative research on larger spatial and time scales. Networks increase the efficiency of research by sharing resources, decreasing redundancy, and increasing the geographical scale of individual studies. The operational structure of regional networks varies between networks and over time. Grassroots collaborative networks, like the FACT and ACT networks, are structured horizontally, where leadership is distributed and shared decision making involves members exploring issues and developing a joint plan of action. Some networks are more horizontally structured, where a board or hierarchal leadership make decisions for the group. Methods of data sharing have evolved from shared tag and receiver lists to cloud-based, aggregated and automated systems with the ability to archive data indefinitely. Organizational networks, like the ATN and OTN, support and coordinate regional telemetry efforts on a national and global level, respectively. Researchers who embrace the challenge and complexity of working alongside scientists in these types of collaborative networks are integral to advancing the science of animal movement.

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46 Herpetology Ecology & Behavior, Primrose A&B – Cliff Lodge, Saturday 27 July 2019

Peter Zani

University of Wisconsin–Stevens Point, Stevens Point, Wisconsin, USA

Overwintering Site Use and Seasonal Activity Extremes by Side-Blotched Lizards as Quantified by Camera Traps Reveals Latent Lives of Lizards

Side-blotched lizards (*Uta stansburiana*) are behaviorally and physiologically plastic, which has enabled them to tolerate a wide range of climatic conditions over their 26° of latitudinal range extent. Greater seasonality at higher latitudes has required that all organisms must withstand longer, harsher winter conditions, which side-blotched lizards avoid by first aggregating around and then overwintering in deep rock crevices in south-facing rimrock. Crevice monitoring across several years of seven replicate natural overwintering sites in eastern Oregon (43 °N, 1320 m elev.) has revealed that, as expected, environmental conditions enable or inhibit lizard activity. Interestingly, lizards are able to select crevices that enable activity all winter long despite these crevices being unused at other times of the year. Weather-enforced inactivity at some crevices can extend for 45 d or more in harsh years, or as little as 7 d in mild years. However, slight differences among crevices, such as in aspect, lead to crevice-specific daily activity in terms of the timing, duration, and abundance of lizards emerging. For each crevice, certain combinations of sun and wind can enable limited lizard activity even when the free-air temperature is well below freezing. Ongoing investigation aims to clarify if there is any adaptive benefit to this seemingly risky behavior.

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493 Herpetology Morphology and Systematics, Ballroom 1 – Cliff Lodge, Friday 26 July 2019

Eugenia Zarza[1], Elizabeth Connors[1], James Maley[1], Whitney Tsai[1], Moises Kaplan[2], Peter Heimes[3], John McCormack[1]

[1]Occidental College, Los Angeles, CA, USA, [2]Ann Arbor, MI, USA, [3]Mexico City, Distrito Federal, Mexico

"Yes, and" is better than "No, but": genomic and barcoding data help uncover cryptic lineages of Mexican highland frogs

Molecular studies have uncovered significant cryptic diversity in the Mexican Highlands. DNA approaches have included both mitochondrial DNA (mtDNA) sequencing (e.g., DNA barcoding) and multilocus genomics. While these approaches have often been pitted against one another, there are benefits to deploying them together. Linked mtDNA data can provide the bridge between uncovering lineages through multilocus genomic analysis and identifying them through comparison to large existing mtDNA databases. Here, we apply ultraconserved elements (UCEs) and linked mtDNA data to a species complex of frogs (*Sarcohyla bistincta*, Hylidae) found in the Mexican Highlands. We sequenced 1,891 UCEs containing 1,742 informative SNPs as well as mtDNA genomes for *S. bistincta*. Genetic analyses agree there are five or six distinct lineages within *S. bistincta*. Genomic data and linked mtDNA data indicate *S. bistincta* is both paraphyletic and includes several already-described species. Phylogenies from UCEs and mtDNA mostly agreed in their topologies; the few differences suggested a more complex evolutionary history of the mtDNA marker, perhaps influenced by gene flow. Our study demonstrates that the Mexican Highlands still hold substantial undescribed diversity, making their conservation a particularly urgent goal. The Transvolcanic Belt stands out as a significant geographic feature in *Sarcohyla* and may have acted as a dispersal corridor for *S. bistincta* to spread north. Combining multilocus genomic data with linked mtDNA data is a useful approach for identifying potential new species and associating them with already described taxa, which will be especially important in groups with undescribed subadult phenotypes and cryptic species.

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112 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Emma Zeitler, Kristen Cecala, Deborah McGrath

University of the South, Sewanee, TN, USA

Larval anuran development in treated wastewater confers an advantage in the terrestrial environment

Constructed wetlands are an important environmental technology because they can serve as a tertiary wastewater treatment among other functions, removing nutrients and pollutants that remain in the water after the primary and secondary treatments. It is hypothesized that tertiary treatment wetlands (TTWs) may function similar to natural wetlands in their ability to support

plant and wildlife communities, but remaining pharmaceuticals have been demonstrated to cause developmental abnormalities in anurans using wastewater treatment wetlands. In a controlled experiment, we evaluated larval anuran development in water from secondary and tertiary treated wastewater versus rain-filled pond water. Tadpoles took 21% longer to metamorphose in pond water and grew to only 70% the size of tadpoles from secondary and tertiary treated wastewater. Survival was 2.2 times higher in wastewater relative to pond water. We also noted that size-corrected leg length was larger in tadpoles from wastewater but size-corrected head size was smaller than individuals from pond water. No malformations were noted in individuals from pond water but 5.5% of individuals from wastewater exhibited minor malformations. Overall, larval anurans developed faster to larger sizes in wastewater relative to pond water with tadpoles from TTWs more closely resembling those from secondarily treated wastewater relative to pond water. Increased growth in wastewater may confer higher long-term survival despite low rates of malformations suggesting that TTWs may serve as high quality habitat for anurans.

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540 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Amanda Zellmer[1], Jeremy Claisse[2,1], Chelsea Williams[1,2], Stuart Schwab[3], Daniel Pondella[1]

[1]Occidental College, Los Angeles, CA, USA, [2]California State Polytechnic University, Pomona, Pomona, CA, USA, [3]University of California, Riverside, Riverside, CA, USA

Predicting Optimal Sites for Ecosystem Restoration Using Stacked-Species Distribution Modeling

Habitat restoration is an important tool for managing degraded ecosystems, yet the success of restoration projects depends in part on adequately identifying preferred sites for restoration. Species distribution modeling provides novel tools for mapping areas of interest for restoration projects. Here we use stacked-species distribution models (s-SDMs) to identify candidate locations for installment of manmade reefs, a useful management tool for restoring structural habitat complexity and the associated biota in marine ecosystems. We created species distribution models for 21 species of commercial, recreational, ecological, or conservation importance within the Southern California Bight based on observations from long-term reef surveys combined with high resolution geospatial environmental data layers. We then combined the individual species models to create a stacked-species habitat suitability map, identifying over 800 km^2 of potential area for reef restoration within the Bight. When considering only the 21 focal species, s-SDM scores were positively associated with observed bootstrap species richness not only on natural reefs, but also this result was supported by two independent test datasets. Additionally, our results demonstrate that the existing manmade reefs included in our study on average are located in regions with habitat suitability that is not only less suitable than natural reefs, but also only slightly significantly better than random, demonstrating a need for more biologically informed placement of manmade reefs. The s-SDM provides insight for marine restoration projects in southern California specifically, but more generally this method can also be widely applied to other types of habitat restoration including both marine and terrestrial.

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324 ASIH/HL/SSAR Symposium: Citizen Science in Herpetology: Productive Past and Promising Future, Ballroom 2 – Cliff Lodge, Sunday 28 July 2019

Amanda Zellmer[1], Gregory Pauly[2]

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

Citizen Science Observations Provide Unique Insight into Salamander Distributions within Urban Environments

Citizen science is rapidly amassing novel observational data with the potential to aid in studying species distributions, especially in urban areas. Yet how these observations change our understanding of species distributions remains to be seen. Here, we test the extent to which citizen science data impacts our understanding of salamander distributions across the highly urbanized Los Angeles Basin, comparing species distribution models (SDMs) using only historical museum records to SDMs using only contemporary citizen science data. Our results show that citizen science based SDMs predict more broad distributions of *Batrachoseps* salamanders that extend further into urban areas than predicted by museum record based SDMs, demonstrating an important difference between historical museum records and citizen science data. We further validate the models using modern citizen-science guided museum collections, with a combined museum and citizen science based SDM as the best supported model. These results suggest that citizen science data provide unique information that expands our understanding of the distribution of *Batrachoseps* salamanders beyond what is known from historical museum collections. The presence of these species throughout the city raises the question of whether these are understudied, isolated remnant populations or if urbanization has instead resulted in an expansion of salamander populations into newly created habitats where irrigation has led to year-round availability of moist soil in a historically seasonally dry landscape. These results highlight the utility of citizen science projects for studying urban species.

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615 AES CARRIER AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Casey Zender[1], James Gelsleichter[1], Nick Whitney[2]

[1]University of North Florida, Jacksonville, Florida, USA, [2]New England Aquarium, Boston, Massachusetts, USA

Evaluation of alternative plasma biomarkers as indicators of post-release mortality in blacktip sharks (*Carcharhinus limbatus*)

The release of sharks caught in recreational fisheries or as bycatch in non-target commercial fisheries is generally regarded as a sustainable fishing approach. However, post-release mortality can occur in these fish due to physiological damage sustained during capture. It is important to

determine the amount of mortality specifically attributed to capture so losses can be accounted for in population management practices. Previous studies have used electronic tagging and/or measurement of secondary stress indicators in plasma (e.g., pH, levels of lactate, glucose, and pCO_2) to estimate rates of post-release mortality. These methods may not always be the best fit, as electronic tagging can be costly, and some secondary stress markers may not consistently correlate with survivorship. Consequently, there has been a call for alternative indicators of post-release mortality in elasmobranchs. To address this, the present study evaluated several possible indicators of post-release mortality in plasma from blacktip sharks, using individuals for which survivorship outcomes were confirmed via electronic tagging in a previous study. These indicators included biomarkers of oxidative stress-induced macromolecule damage such as lipid peroxidation (malondialdehyde), protein (protein carbonyls) and DNA oxidation (8-hydroxy-2'-deoxyguanosine); alternative measures of stress-induced energy mobilization (ketone bodies); indicators of rhabdomyolysis (myoglobin and creatine kinase); and general cell damage (cell-free DNA). Preliminary data suggests that 8-OHG may increase with mortality, but levels of cell-free DNA, MDA and protein carbonyls did not differ with survivorship. Concentrations of ketone bodies appeared to correlate with secondary stress indicators, but not with survivorship. Indicators of rhabdomyolysis are currently under evaluation.

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104 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Kiara Zurow, John Peterson

University of Wisconsin - Platteville, Platteville, WI, USA

Oral abnormalities in Green Frog (*Lithobates clamitans*) tadpoles

Few studies have reported how the tadpole oral disc is influenced by environmental factors. Environmental contaminants, the amphibian chytrid fungus (*Batracochytrium dendrobatidis*), and captive rearing can influence oral disc morphology; however, variation is observed in wetlands independent of the aforementioned factors. We observed the oral discs of Green Frog (*Lithobates clamitans*) tadpoles from two retention ponds and a fen in Platteville, WI as part of a comparative anatomy course. Tadpoles from the large retention pond had significantly more abnormalities and contained half as many teeth compared to the other sites. More authors should investigate oral disc morphology because it is relatively easy to quantify and is variable across habitats. Additionally, professors interested in bringing undergraduate research into the classroom should consider adding a tadpole morphology lab to their curriculum.

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729 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Jonathan Dain, Sam Fellows, Tod Reeder

San Diego State University, San Diego, CA, USA

Morphological and mitochondrial datasets contradict subspecies divisions of *Crotalus cerastes*

Sidewinder Rattlesnakes (*Crotalus cerastes*) are a widespread species currently split into three morphologically-defined subspecies (based on number of scale rows, proximal rattle lobe color, and number of ventral scales) each in one of three North American warm deserts. Previous phylogenetic studies using mitochondrial data support five regional clades (one each in northern and southern areas of the Mohave Desert, northern and southern areas of the Sonoran Desert, and the Colorado Desert) that are not congruent with the current subspecies. Given that the relationships among these mitochondrial clades vary among studies, addressing differences among datasets is a critical component in understanding the species limits, phylogenetic relationships, and diversification history within *C. cerastes.* We analyzed an existing morphological dataset to explore the extent of congruence between the traditional subspecies and mitochondrial clades. This dataset consisted of ~700 individuals, collected across the full range of *C. cerastes,* and eight characters: scale rows counts, ventral scale counts, head length, tail length, body blotch counts, and tail ring counts. Principal component analysis of the morphological data does not support the boundaries between the subspecies, nor does morphology appear to correlate with the mitochondrial clades. The disagreement between these datasets suggests that integrating these datasets for species delimitation and the exclusive use of mitochondrial data may be inappropriate for describing species limits within Sidewinders. Future studies will determine whether the geographic structure in the morphological data is better explained by variation in environmental and/or genomic data.

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690 AES Reproduction & Life History, Alpine A,B,C – The Snowbird Center, Friday 26 July 2019

Toby Daly-Engel[1], Yannis P. Papastamatiou[2]

[1]Florida Institute of Technology, Melbourne, Florida, USA, [2]Florida International University, Miami, Florida, USA

Integrating Genetics and Telemetry to Resolve Discrepancies in Sex-Biased Dispersal in Sharks

In recent years, there has been a discrepancy in our understanding of shark movement patterns between results from studies using telemetry or genetic methods. Molecular studies, including several global and range-wide, have shown high connectivity across long (>1000 km) distances in male-inherited but not female-inherited genes of several species, though such data are often

presented alongside confoundingly fine-scale genetic structure in both sexes. This has led to the conclusion that shark dispersal is male-biased as a rule, with females constrained by philopatry to nursery habitats at the expense of foraging opportunities elsewhere, while males are unconstrained and therefore cosmopolitan. Yet a number of telemetry studies have shown that adults of both sexes consistently make regular long-distance movements, and adult males have been detected near nursery habitats. Here, we integrate findings from genomic and telemetry studies to form a more complete picture of habitat bias and dispersal constraints in sharks. Taken together, these data point to a system where dispersal is less sex-biased than initially thought in wider-ranging species. Instead, both males and females may be constrained by natal philopatry, and may migrate similar distances to optimize foraging and reproductive opportunities, though males may be more cosmopolitan with regards to mating.

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272 SSAR SEIBERT SYSTEMATICS AND EVOLUTION AWARD II, Ballroom 2 – Cliff Lodge, Friday 26 July 2019

Hayden R. Davis[1], Aaron M. Bauer[1], Todd R. Jackman[1], Indraneil Das[2]

[1]Villanova University, Villanova, PA, USA, [2]University of Malaysia Sarawak, Kota Samarahan, Sarawak, Malaysia

Biogeography and Cryptic Diversity Within Bornean *Cyrtodactylus* Species

Investigating cryptic diversity within the gekkonid genus *Cyrtodactylus* has led to a drastic increase in the number of recognized species in the genus. Throughout their expansive range, documented diversity has rapidly increased, yet the Sundanese island of Borneo has remained largely unexplored. We generated the first molecular phylogeny focusing on Bornean *Cyrtodactylus* species, which revealed cryptic species and provided the genetic dataset necessary to investigate the biogeographic role of Borneo in the range expansion of the genus. We discovered that the small bodied forest-dwelling species in Borneo, which bears strong resemblance to other species throughout the range of the genus, is both distinct from those in other regions and is comprised of multiple deeply divergent lineages on the island. Based on more than 60 specimens examined in this complex, no unambiguously diagnostic characteristics could be identified. However, using statistical methods to look for variation, we show that each lineage occupies a distinct region of morphospace. Despite minimal morphological support for delineating the species, both the mitochondrial (ND2) and nuclear (RAG1, MXRA5, PDC) phylogenies support the presence of multiple independent lineages inhabiting the island. Incorporating additional sequences also enabled us to generate a time-calibrated phylogeny focused on the Bornean species and conduct a biogeographic analysis of the group to better assess Borneo's role in the eastward expansion of the genus. The inclusion of new genetic samples has enabled us to establish well-supported phylogenetic trees to uncover Borneo's cryptic diversity and elucidate its critical role in the historical biogeography of *Cyrtodactylus*.

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424 Ichthyology Systematics I, Cottonwood A-D – The Snowbird Center, Sunday 28 July 2019

Matthew Davis[1], W. Leo Smith[2]

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

Evolution of Ray-finned Fishes into the Deep Sea

Over one sixth of all marine fishes live at depths below 200 meters in oceans across the world. These deep-sea fishes have a diversity of fascinating evolutionary traits that have repeatedly evolved in fishes found at these depths. In this study we provide a temporal hypothesis of ray-finned fishes based on molecular data to review and investigate the repeated evolution of adaptations associated with deep-sea fishes and habitat transitions into and out of deep-sea environments. Little is known about the macroevolutionary patterns and processes associated with diversification in the deep sea, and we further investigate macroevolutionary questions regarding the wide-spread dispersal and subsequent diversification of fishes into deep-sea habitats.

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287 ASIH/HL/SSAR Symposium: Professional Women in Herpetology: Lessons and Insights, Ballroom 1 – Cliff Lodge, Saturday 27 July 2019

Alison Davis Rabosky

University of Michigan, Ann Arbor, MI, USA

Building a Tangled Bank: Mimics, Models, and Michigan

The University of Michigan has a long legacy of women in Herpetology, beginning with Helen Gaige (former editor of *Copeia* and co-namesake of ASIH's Gaige Fund Award) who helped found the UM Museum of Zoology Division of Reptiles and Amphibians and served as a curator until 1945. Today, I am one of the curators of this legendary collection and an Assistant Professor in Ecology and Evolutionary Biology. My lab takes integrative approaches to studying the ecology and evolution of reptiles and amphibians, tackling questions from disease ecology and conservation to genomics and behavior. Using predator defense in snakes, I will show how our lab brings together quantitative data on morphology, behavior, and gene expression to study the evolution of coral snake mimicry. By using phylogenetic comparative approaches to reconstruct the timing and trajectories of how each trait evolves across many independent origins of the mimetic phenotype, our work creates an explicit framework for testing hypotheses about how and why mimicry evolves. One reason that we are able to do this research on a large scale is due to the incredible collaborative effort of students across both UM and Latin America, who have worked together on collection expeditions that produce thousands of museum-vouchered "super" specimens that fuel dozens of projects across institutions. This investment in the future of herpetology builds upon the foundation laid by the Gaiges nearly a century ago, demonstrating

how commitment to student-led opportunities is a powerful way for our field to promote diversity and inclusivity.

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765 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Ashley Dawdy, Dean Grubbs, Cheston Peterson, Bryan Keller

Florida State University, Tallahassee, FL, USA

The Effect of Tidal and Diel Cycles on Spatial Use Patterns of Bull Sharks (*Carcharhinus leucas*) and Bonnetheads (*Sphyrna tiburo*)

Apalachicola Bay is a national estuarine research reserve and biodiversity hotspot in the NE Gulf of Mexico, housing many economically and ecologically important species of fishes and invertebrates. Among these species are bull sharks (*Carcharhinus leucas*) and bonnetheads (*Sphyrna tiburo*), top and intermediate predators which are subject to fishing pressure and bycatch mortality from local commercial fisheries. In this study, bull sharks and bonnetheads were tracked using passive and active acoustic telemetry in order to compare spatial use and rate of movement across tidal and diel cycles of each species. This information is critical in the management of these species and may be important in understanding the effects of water management in the Apalachicola River watershed – a significant sociopolitical issue in this region. Additionally, as animal movement studies often utilize passive telemetry as a primary method of spatial use prediction, relatively few studies use both methods on the same individuals. We attempt to compare results of active and passive telemetry for the same animals to provide insight as to whether swimming speed affects detection success at fixed listening stations.

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800 ASIH STORER ICHTHYOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Dominique Dawson[1], Steve Rider[2], Michael Sandel[1]

[1]University of West Alabama, Livingston, Alabama, USA, [2]Alabama Department of Conservation and Natural Sciences, Montgomery, Alabama, USA

Investigating Ancestry and Genomic Diversity of Walleye *(Sander vitreus)* in the Mobile River Basin

The walleye, *Sander vitreus (*Teleostei: Percidae*)*, is a popular sport fish that is widely distributed across eastern North America. Broad scale relationships within Northern walleye show genetic isolation across geographic distances, but within local drainage basins genomic diversity is generally low. Gulf Coastal Plain walleye exhibit high diversity and are distinct from

the Northwest populations. Also it stated that the Mobile river basin sister group is the most genetically distinct, but also the least understood, due to a small sample size of two from the Tombigbee River Drainage (Stepien et al. 2009). The southern walleye of the Mobile Basin population appears to exhibit some vicariance from the northern population. We aim to determine if there is a significant divergence between the northern and southern populations of walleye *(S. vitreus)*. We sequenced and analyzed 18,093 nuclear single nucleotide polymorphisms (SNPs) and 655bp of the mitochondrial Cytochrome Oxidase I (COI) gene to infer nuclear and mitochondrial phylogenetic trees and to estimate gene flow and local population genomic diversity. Results reveal clear evidence of introgression from stocked northern strains, as well as isolated populations of "pure" southern walleye. We also describe the development of an eDNA protocol designed to identify northern and southern mtDNA haplotypes within the Mobile River Basin.

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366 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Christina De Jesús Villanueva[1,2], Kathleen McGinley[2], William Gould[2], Jason Kolbe[1]

[1]University of Rhode Island, South Kingstown, Rhode Island, USA, [2]USFS International Institute of Tropical Forestry, San Juan, Puerto Rico

Impact of the Invasive Green Iguana (*Iguana iguana*) on Puerto Rico's Agricultural Community

Understanding human and invasive wildlife interactions is of major importance in the development and execution of management plans. The invasive green iguana (*Iguana iguana*) has an extensive invasive range in the Caribbean, though its impact is yet to be fully explored. In Puerto Rico, the green iguana has been sparsely reported on by local news sources and by DNER as a problem for agricultural production. In this work, we seek to document current and predict future impact of the green iguana on Puerto Rico's agricultural community. Our goal is to address the following questions 1) How does the green iguana affect the agricultural community in Puerto Rico? and 2) What are the strategies being used to mitigate the possible effects of the species? We explore these questions by using social science and spatial analysis to develop models of risk of iguana damage. We have conducted semi-structured interviews with 20 farmers on the island of Puerto Rico and compiled a preliminary report of affected crops. Among the most reported are the cucurbits, solanum and lettuce plants. Farmers overarchingly reported hunting as their management approach, though it was not a regular activity due to its time consuming and laborious nature. With the insight from these accounts we will design and distribute closed surveys to expand our coverage of the island and build a predictive risk model using spatial analysis in GIS. Once completed, this work will be crucial to the development of action plans in Puerto Rico and the Caribbean.

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496 ASIH STOYE GENERAL ICHTHYOLOGY AWARD I, Cottonwood A-D – The Snowbird Center, Thursday 25 July 2019

Emily DeArmon, Matthew Davis

St. Cloud State University, St. Cloud, MN, USA

Dragons of the Deep: Evolutionary Relationships of the Family Stomiidae (Dragonfishes) and the Evolution of their Bioluminescent Barbels

The order Stomiiformes includes deep-sea fishes (~420 species) that have evolved a variety of bioluminescent organs. The species-rich dragonfishes (Stomiidae) have evolved bioluminescent barbels that are often species-specific and are hypothesized to function for communication and prey attraction. The chin barbels of dragonfishes extend from the urohyal and have incredible anatomical variation of the luminous tissues found on the barbel. In this study we present a hypothesis of evolutionary relationships for Stomiidae based on molecular data. In addition, we investigate the character evolution of anatomical features of the bioluminescent barbels among dragonfishes to further understand the patterns of evolution associated with this fascinating light-producing appendage.

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314 AES Ecology, Rendezvous A&B – The Snowbird Center, Friday 26 July 2019

Breanna DeGroot, Grace Roskar, Matthew Ajemian

Florida Atlantic University- Harbor Branch Oceanographic Institute, Fort Pierce, Florida, USA

Fine-scale Movement and Habitat Use of Whitespotted Eagle Rays, *Aetobatus narinari*, in the Indian River Lagoon

Elasmobranchs inhabit coastal marine ecosystems worldwide, many of which are experiencing rapid degradation. Despite being crucial to their conservation, assessments of fine-scale movements and habitat use of batoids remain relatively unknown, affecting our ability to identify regions of potential concern. Active acoustic tracking technology was used to assess the fine-scale movements and activity space of whitespotted eagle rays (*Aetobatus narinari*) in the Indian River Lagoon, Florida. Geospatial data were analyzed to determine space utilization, habitat selection, and drivers of movement. Rays disproportionately selected the very shallow (<1.0 m) and deep (2.0 – 4.9 m) portions of the lagoon, while under-utilizing widespread areas of 1.0 – 2.0 m depth. Additionally, Brownian Bridge Movement Models showed that whitespotted eagle rays frequently reused portions of the lagoon with high anthropogenic activity such as inlets and channels, as well as habitats parallel to the shore. During the daytime, rate of movement was highest when rays were in waters overlying depths of 0.5 – 2.0 m, but consistently decreased with increasing depth. At night, the rate of movement was highest in waters overlying 1.5 – 2.5 m deep and lowest in waters >3.0 m, which suggests rays are less active in the deep portions of the lagoon and highly active along intermediate depths. To our knowledge, this is the first study of whitespotted eagle rays to examine movement patterns in relation to human-altered habitats.

While more extensive tracking is required to elucidate long-term movement patterns, this study clearly identifies areas of potential interactions between this protected species and anthropogenic activities.

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56 General Herpetology II, Primrose A&B – Cliff Lodge, Sunday 28 July 2019

Jennifer Deitloff[1], Rhiannon McGlone[1], Katie Fitzgerald[1], David Savage[1,2], Landon Allen[1]

[1]Lock Haven University, Lock Haven, PA, USA, [2]USDA APHIS Wildlife Services, Cambridge, MD, USA

Behavioral and Morphological Variation in *Plethodon cinereus* throughout Pennsylvania

Species that have wide geographic ranges can diverge in characteristics such as morphology, resource use, or behavior due to adaptation to local environmental conditions. *Plethodon cinereus* is widely distributed throughout the northeastern United States. For many populations of *P. cinereus*, intraspecific competition for resources may occur, resulting in territorial behavior. In addition, morphology is often associated with behavior and/or competition in this and other closely related species. Furthermore, the extent to which males and females display territoriality can differ among populations. During spring of 2015-2018, we collected *P. cinereus* from 10 populations across Pennsylvania to test the following hypotheses: (1) populations and sexes differ in head-shape and (2) behavior, and that (3) morphology and behavior are correlated. In general, we found support for these hypotheses; however, not all populations differed, and not all sexes within each population differed. We concluded that these characteristics vary with specific conditions within each location, such as food and refuse-site availability or microhabitat conditions. Future research could focus on determining how different locations vary in these characteristics. In addition, *P. cinereus* throughout other areas of its range can be incorporated into this and related studies to better understand the range-wide factors that influence behavior and morphology.

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626 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Hannah deKay[1], Matthew Davis[2], W. Leo Smith[3], Micheal Ghedotti[1]

[1]Regis University, Denver, Colorado, USA, [2]St. Cloud State University , St. Cloud, Minnesota , USA, [3]University of Kansas, Lawrence, Kansas, USA

Morphology and evolution of the luminous roughy bioluminescent organ (Teleostei: Trachichthyidae)

Bioluminescence, the generation of light by living organisms, is widespread in fishes but light organs are often poorly known. The luminous roughies (genera *Aulotrachichthys* and *Paratrachichthys*) have a light organ in the region of the anus that houses bacteria in the

genus *Photobacterium*. In this study we seek to closely determine the anatomic structure of the bioluminescent organ in two species *Aulotrachichthys prosthemius* and *Paratrachichthys fernandezianus* to shed light on the organ's likely evolution. We used histological sectioning and gross dissection to explore the anatomy of the bioluminescent organs and we used a published morphological data in combination with a DNA-sequence based phylogeny for the group. The bacterial bioluminescent organs in the luminous roughies are derived from pouching of the ectodermal proctodeal tissue around the anus and the bacteria-housing components are restricted to this region around the anus. This anatomy in the context of the phylogeny suggests that the bioluminescent organs of the luminous roughies arose via a single evolutionary transition along with a far more anterior position of the anus. The study also suggests that *Sorosichthys,* known from only eight specimens, also likely is bioluminescent.

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61 Ichthyology Genetics, Cottonwood A-D – The Snowbird Center, Sunday 28 July 2019

John Denton, Lei Yang, Shannon Corrigan, Gavin Naylor

Florida Museum of Natural History, Gainesville, FL, USA

The thorny skate project: applying NGS technologies and pipelines to a fisheries-targeted species

The thorny skate (*Amblyraja radiata*) is a boreal and arctic species that is distributed predominantly across the Eastern and Western North Atlantic. The species has historically been fished throughout its range, and has been used both as food and as bait for groundfish fisheries, with regional revenues in the low millions (USD). Current conservation assessments of the species differ significantly—it is identified as a 'species of concern' in U.S. waters, but as a species of 'least concern' in the Eastern North Atlantic. However, phenotypic and ecological data paint a different picture of thorny skate distinct population segments (DPSs) than the genetic data currently used to inform the assessments affecting fisheries. The thorny skate project seeks resolution of the discrepancy between these data types, by leveraging specially-designed target probes, derived from high-resolution whole genome sequence and amplified from specimens densely sampled over the entire species range, to understand the population structure and demography of the thorny skate from comprehensive molecular information. Here, we present the first stage of assessment, based on high-coverage, complete mitochondrial genomes.

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370 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Calum Devaney, Aaron Bauer

Villanova University, Villanova, Pennsylvania, USA

Diet and Reproductive Biology of Angolan Snakes

Although the diets and reproductive cycles of many colubroid snakes of southern Africa are well-studied, such data are less complete for Central and West African taxa. This is especially so for the snakes of Angola, where nearly 40 years of civil war has impeded herpetological research. In this study, we examined specimens of 22 species, representing four families of snakes, derived from recent collections from western and central parts of Angola made during both the warm summer months and cooler winter months. For widespread species (e.g., *Bitis arietans*, *Crotaphopeltis hotamboiea, Dasypeltis scabra' Psammophis* spp.), results are compared with previous studies of these taxa in other portions of their range. The mass, number and identity (to order for arthropods and genus for vertebrates) of prey items are reported. Reproductive data include clutch/litter size as well as male and female gonadal condition. The diverse climate of Angola, combined with its topographic relief (Angolan Plateau versus lowlands) account for much of the variation in reproductive patterns, whereas dietary patterns largely follow those of related taxa elsewhere in sub-Saharan Africa.

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674 GENERAL HERPETOLOGY I, Primrose A&B – Cliff Lodge, Sunday, 28 July 2019

Matthew Dickson[1], Aaron Bauer[2], Robert Espinoza[1]

[1]California State University, Northridge, Northridge, CA, USA, [2]Villanova University, Villanova, PA, USA

Getting Comfortable In Your Own Skin: Variation in Integument Ultrastructure Among Introduced Populations of Mediterranean House Geckos

Invasive species often serve as natural experiments that allow us to observe how species respond to novel environments, leading to a better understanding of the process of adaptation over short timescales. Mediterranean House Geckos (*Hemidactylus turcicus*) first established in southern Florida ~100 years ago. Since then, they have colonized 25 states across a diversity of climates in the US. Our previous studies found that lab-acclimated geckos from distinct climates (desert, Mediterranean, subtropical, and continental) exhibit adaptive differences in physiology. Specifically, at high body temperatures, geckos from hot, dry climates have rates of evaporative water loss (EWL) almost half that of geckos from humid climates. Most EWL occurs cutaneously via diffusion through the integument; however, no one has quantified cellular changes in the epidermis in response to variation in climate. Three distinct layers in the reptile epidermis are hypothesized to reduce EWL: the alpha and beta layers composed of corneous keratin, and the lipid-rich mesos layer. We used electron microscopy to compare the ultrastructure of the epidermis at the surface, and the subsurface cellular layers for populations representing two extreme climates (desert and subtropical) to identify the mechanism of the epidermis that contributes to EWL adjustment in this widespread invasive reptile. We hypothesized that geckos from drier climates would have (1) larger scales to cover more surface area of their epidermis and (2) more cell layers to increase the thickness of their epidermis, particularly between scales where the skin is exposed.

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125 ASIH/HL/SSAR Symposium: The Expanding Role of Natural History Collections, Ballroom 1 – Cliff Lodge, Sunday 28 July 2019

Casey Dillman

Cornell University, Ithaca, NY, USA

Natural history collections as repositories of evolutionary change

Experimental science explicitly implements idealized perturbations in controlled situations and is widely used to understand the response of a specific component for the system under investigation. These studies are observational, albeit observation with measurements for treatments and controls. Natural experiments, i.e. the natural history of the inhabitants of the earth, represent another type of observational study. One that is deeply reliant on specimens deposited in natural history collections. Poss and Collette (1995) noted that 75% of natural history collections surveyed “can be used to document environmental changes”, due to variation the number of extinct, endangered, and/or hybridizing species; textbook examples of change over time due to habitat changes or anthropogenic effects. Another type of change exists: change over time, aka descent with modification, and evidence for this exists in the physical specimens themselves (response) even if we lack the perturbation data that leads to the changed phenotype. These experimental regimes overlap in some long-term data sets; perhaps most famously in the observations of Darwin’s finches in the Galapagos. Natural history collections maintain long term data sets that may lack the abiotic components but do contain then biotic components and can be used to document evolutionary change.

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552 ASIH STORER ICHTHYOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Nastasia Disotell

Austin Peay State University, Clarksville, TN, USA

Are neighbors pillaging nests: detecting spatial complexity of allopaternal care in the imperiled Egg-mimic Darter (Percidae: *Etheostoma pseudovulatum*)

Alloparental care occurs in several clades of animals, including fishes. Despite the increased energy cost of caring for more offspring, this behavior also has potential benefits, including attraction of mates or reduced egg predation by dilution effects. The Egg-mimic Darter, *Etheostoma pseudovulatum*, is an imperiled species restricted to five tributaries of the Duck River, Tennessee. Male Egg-mimic Darters and those of other species of clade *Goneaperca* construct nests under rocks and guard eggs until hatched. Two species from this clade exhibit allopaternal care; whether this is a common strategy to all clade members is not known. Furthermore, the potential benefits of kin-selection and how nest density or male size influences such behaviors have not been tested. We will use genotypic data from the eggs of 15 nests, the guarding male of each nest, and other non-guarding males and females of Egg-mimic Darter from two localities to identify: (1) if allopaternal care occurs, (2) if kin-selection is one benefit of allopaternal care, (3) if male size correlates to the proportion of non-descendant eggs in a nest, and (4) if distance between nests influences allopaternal care frequency. Eggs from 17 nests, the guarding male for each, and 15 other non-guarding males have been collected from one locality. DNA was extracted and used as a template to optimize 18 variable microsatellite locus primers. These loci will be used to generate genotypes for all focal individuals, which will be subjected to parentage analyses using colony (v2.0) to address our objectives.

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387 Ichthyology Lightning Talks, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Terry Donaldson

University of Guam Marine Laboratory, Mangilao, Guam, USA

Global Distribution Patterns of the Hawkfishes (Pisces: Cirrhitidae): What We Know and What We Should Know

Hawkfishes (Cirrhitidae) are small to medium-sized fishes (one species to 60 cm) found in tropical and subtropical/warm temperate insular and coastal waters on relatively shallow coral and rocky reefs; some species to depths of 30-100m. Virtually all species are benthic and utilize thickened lower pectoral rays to perch or wedge themselves in place, either in coral heads, upon rocks, or in wave-swept habitats such as the spur and groove zone of coral reefs or deeper tide pools and reef fronts of rocky reefs. Some are polychromatic and all are presumed to be protogynous hermaphrodites. Thirty-three species are currently recognized and represented in 12 genera of which seven are monotypic. Thirty-one species are distributed in the Indo-Pacific Region, including three in the Eastern Pacific, while three species occur in the Atlantic. At least three species have pronounced disjunct distributions within their respective ranges, two species range from the Red Sea to the Pacific coast of the Americas, and seven species are considered endemic. While knowledge of species distributions is useful for examining patterns of diversity across geographic ranges, how they got that way remains largely unknown. The need for phylogenetic and phylogeographic analyses is emphasized.

CANCELLED

27 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Kate Donlon, William Peterman

The Ohio State University, Columbus, OH, USA

Population Genetics of a Terrestrial Salamander Species Inhabiting Abandoned Mined Lands in Eastern Ohio

A leading contributor to the global decline of amphibians is habitat loss and alteration. It is clear habitat alteration can negatively impact the persistence of an organism on the landscape, but many studies do not offer insight into the long-term genetic impact of disturbance events. Disturbed systems provide the opportunity to investigate the response of populations to habitat alteration. Industrial surface mining is an example of an extreme anthropogenic disturbance. Historically, strip-mined land was often abandoned or only partially restored through the planting of trees on soil banks. Despite extensive habitat destruction caused by the removal of layers of soil and rock to expose seams of coal for extraction, plethodontid salamanders have been found occupying reforested mine land that was abandoned prior to the Surface Mining Control and Reclamation Act of 1977. The goal of this project was to study the population genetics of Northern Ravine Salamander, *Plethodon electropmorphus*, across a landscape impacted by strip mining. Salamanders were sampled on four mined and three unmined forests in Tuscarawas County, Ohio. Population genetic parameters were generated from 11 cross-amplified microsatellite loci. Despite a general trend of decreased genetic diversity within mined sites, a significant difference between genetic diversity, rarefied allelic richness and private alleles, between the two habitat types was not detected. Also, no evidence of genetic bottlenecks was detected at any of the seven sampling sites. These results suggest that once forest succession occurred, Northern Ravine Salamanders were able to recolonize sites without suffering declines in genetic diversity.

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106 ASIH/HL/SSAR Symposium: Professional Women in Herpetology: Lessons and Insights, Ballroom 1 – Cliff Lodge, Saturday 27 July 2019

Maureen Donnelly

Florida International University, Miami, Florida, USA

HERpers as Society Leaders: How Far Have We Come?

I gathered data on society leadership and committee structure for several organismal and thematic societies (e.g., ASIH, SSAR, HL, American Society of Mammalogists, American Ornithological Union, Association for Tropical Biology and Conservation, Society for Conservation Biology, Ecological Society of America) to determine if women occupy leadership positions, and the types of positions they fill. Societies with published records of historical patterns of leadership allow for application of the Wald-Wolfowitz Runs Test for Randomness (for binary data). If women are equally represented as leaders, the “run” should be random. I will describe the results from the Runs tests, I will focus on the women who lead herpetological societies in the United States, and I will reinforce the importance of female mentorship for the large cadre of HERpers who attend the JMIH meetings.

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457 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Dana Drake[1], Sean Giery[1,2]

[1]*University of Connecticut, Storrs, CT, USA,* [2]*University of Arkansas, Fayetteville, AR, USA*

Assessing Drivers of Polymorphism in Egg Masses of Spotted Salamanders (*Ambystoma maculatum*) in Northeastern USA

Egg masses of Spotted Salamanders (*Ambystoma maculatum*) exhibit heritable polymorphism, with clear and opaque, or "white", varieties. Color morph frequency is highly variable within populations as well as throughout the range of Spotted Salamanders (from 100% clear to 100% white). Many factors have been proposed as drivers of variable morph frequencies including nutrient content of breeding ponds, acidity, predation intensity, and protection of developing embryos from damaging ultraviolet (UV) radiation. However, a clear understanding of what drives variation in morph frequency has yet to emerge. Here, we investigated this question with color morph and ecological data collected from 77 Spotted Salamander populations from three different sites in the Northeastern US. Overall, morph frequency varied among sites: very low in southern New Hampshire (2% white), low in northcentral Connecticut (8% white) to moderate in southern Connecticut (41% white). Our preliminary analyses of within-site variation indicate water chemistry (dissolved organic carbon concentration) is a good predictor of interpopulation variation in color morph frequency - indicating a role for UV light in color morph evolution in the Northeastern US. UV light is strongly absorbed by waters high in dissolved organic carbon such that UV is unlikely to penetrate more than a few centimeters below the surface. We believe this functional link between water chemistry and embryo fitness represents an important ecological driver of egg morph frequency evolution in Spotted Salamanders.

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173 AES Ecology, Rendezvous A&B – The Snowbird Center, Friday 26 July 2019

Marcus Drymon[1,2], Kevin Feldheim[3], Auriel Fournier[1], Emily Seubert[1], Amanda Jefferson[1,2], Andrea Kroetz[4], Sean Powers[5]

[1]*Mississippi State University, Biloxi, MS, USA,* [2]*Mississippi-Alabama Sea Grant, Ocean Springs, MS, USA,* [3]*Field Museum, Chicago, IL, USA,* [4]*NOAA Fisheries, Panama City, FL, USA,* [5]*University of South Alabama, Mobile, AL, USA*

Tiger Sharks Eat Songbirds: Scavenging a Windfall of Nutrients from the Sky

As apex predators, some sharks can couple energy pathways from disparate foodwebs. This is particularly true of tiger sharks (*Galeocerdo cuvie*r), notorious for their dietary breadth. In addition to invertebrates, fishes, sea snakes, marine mammals, and seabirds, tiger sharks also consume terrestrial birds. We investigated the prevalence of this unique cross-system subsidy using a combination of monitoring programs, traditional stomach content analysis, and DNA barcoding. Tiger sharks were sampled during bottom longline surveys off the coast of Alabama from 2010-2018. Stomach contents were examined opportunistically and identified to the lowest possible taxon. Avian remains were genetically identified. Avian species composition from tiger

shark stomachs was then compared to bird sighting data from eBird from that same time period. From 2010-2018, 774 bottom longline sets were performed and 292 tiger sharks were encountered. Opportunistic analysis of stomach contents from 105 tiger sharks revealed remains from 11 bird species: 8 true songbirds (barn swallow *Hirundo rustica*, eastern kingbird *Tyrannus tyrannus*, house wren T*roglodytes aedon*, common yellowthroat *Geothlypis trichas*, marsh wren *Cistothorus palustris*, eastern meadowlark *Strunella magna*, swamp sparrow *Melospiza georgiana*, and brown thrasher *Toxostoma rufum)*; 2 near songbirds (white-winged dove *Zenaida asiatica* and yellow-bellied sapsucker *Sphyrapicus variu*s); and 1 waterbird (American coot *Fulica americana*). Peaks in eBird sightings data for the 11 species we identified showed remarkable alignment with individual tiger shark/bird interactions. Using this combination of data, we were able to evaluate the frequency of a cross-system subsidy to a marine predator, thereby furthering our understanding of this unique trophic interaction.

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12 ASIH/HL/SSAR Symposium: Citizen Science in Herpetology: Productive Past and Promising Future, Ballroom 2 – Cliff Lodge, Sunday 28 July 2019

Andrew Durso[1], Rosy Mondardini[2], Jose Luis Fernandez[1], Fanny Jones[2], Marcel Tanner[2], Christopher Gwilliams[2], François Grey[1], Don Becker[3], Michael Pingleton[4], Christopher E. Smith[5], Gabriel Alcoba[6], François Chappuis[6], Nicolas Ray[1], Marcel Salathé[7], Sharada Prasanna Mohanty[7], Camille Montalcini[7], M. Jose Louies[8], Ulrich Kuch[9], Brian Lohse[10], Hanne Epstein[11], Abiy Tamrat[12], David Williams[13], Isabelle Bolon[1], Rafael Ruiz de Castañeda[1]

[1]University of Geneva, Geneva, Switzerland, [2]Citizen Science Center Zürich, Zürich, Switzerland, [3]HerpMapper, Cedar Rapids, Iowa, USA, [4]HerpMapper, Urbana-Champaign, Illinois, USA, [5]HerpMapper, Lakeland, Minnesota, USA, [6]University Hospital of Geneva, Geneva, Switzerland, [7]EPFL, Geneva, Switzerland, [8]Wildlife Trust of India, Kottayam, India, [9]Goethe University, Frankfurt, Germany, [10]University of Copenhagen, Copenhagen, Denmark, [11]Doctors Without Borders, Copenhagen, Denmark, [12]Doctors Without Borders, Geneva, Switzerland, [13]University of Melbourne, Melbourne, Australia

Snapp: Guiding anti-venom selection with snake-identification imagery analysis based on artificial intelligence and remote collaborative expertise

Snakebite is a neglected tropical disease, annually responsible for >100,000 human deaths & >400,000 victims of disability globally. It disproportionately affects poor & rural communities in developing countries, which also have high snake diversity & limited access to antivenom. Antivenom can be life-saving when correctly administered but administration often depends on the correct identification of the biting snake. Snake identification is challenging due to snake diversity & potentially incomplete or misleading information provided to clinicians by snakebite victims or bystanders. Clinicians do not necessarily have enough knowledge or resources in herpetology to identify a snake from a carcass or photo. To reduce potentially erroneous or delayed healthcare actions, we are building the first medical decision-support mobile app for snake identification based on artificial intelligence (AI) & remote collaborative expertise, supporting clinicians, snakebite victims, & laypeople in the identification of snakes. Our ultimate objective is to improve clinical management of snakebite. To do this, we are building a massive global repository of photos of snakes from museum collections (including VertNet & GBIF as well as digitized slides from historical archives), personal & researcher image collections, open online biodiversity platforms (e.g. iNaturalist, HerpMapper), & social media (e.g. Facebook, Twitter, Flickr), updating snake range maps globally, developing a system capable of identifying snakes using photos & geolocation based on machine learning, challenging communities of citizens & experts worldwide to identify snakes, comparing their speed & accuracy with that of machine learning, & establishing an international working group of experts in snake identification to help validate images.

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404 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Richard D. Durtsche[1], Larry Greenberg[2], Karl Fillipson[2], Bror Jonsson[3]

[1]Northern Kentucky University, Highland Heights, KY, USA, [2]Karlstads universitet, Karlstad, Sweden, [3]Norwegian Institute for Nature Research, Oslo, Norway

Altered Metabolism in Brown Trout and the Likely Effects of Climate Change

Under a rapidly changing climate, especially in northern temperate regions, it is not completely known how fish will adapt physiologically to elevated temperatures. Thermal changes in southern Scandinavia over the next 70 years, particularly in winter when salmonid eggs develop, are predicted to increase by about 6˚C. Increased temperatures during embryogenesis have previously been suggested to produce fish with lower metabolic rates (MR). We tested this idea using partial migratory brown trout (*Salmo trutta*), raised from eggs at natural (cold) and elevated (+ 3˚C; warm – climate change) temperatures. Four crosses involving resident (R) and anadromous (A) parents (AA, AR, RA, RR) were raised through hatching under the two embryonic temperature regimes, after which the juveniles were maintained for two months under common ambient thermal conditions before testing. We measured MR with an optical oxygen sensor while fish were in a closed-circuit static flow respirometry system. Our results confirm our hypothesis that standard (resting) metabolic rates are inversely related to incubation temperatures in *S. trutta*. We did not find any significant differences among the migratory and resident crosses. Adaptations to warmer climate change conditions seen in these fish are currently under study to determine if phenotypic plasticity could be the result of epigenetic responses demonstrating adaptability to elevated temperatures. As MR has previously been shown to be positively correlated with aggression and risk-prone (bold) behavior, we predict trout subjected to higher embryogenic temperatures will be less aggressive and less risk-prone than fish raised at normal temperatures.

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423 Amphibian Conservation, Ballroom 2 – Cliff Lodge, Saturday 27 July 2019

Julia Earl

Louisiana Tech University, Ruston, Louisiana, USA

Evaluating Published Amphibian Population Models for Common Assumptions

Population projection models are used increasingly to understand the potential effects of anthropogenic stressors and inform conservation actions. However, the vital rate and life history information needed to create robust population models are often missing or incomplete, making various assumptions about parameters and population processes necessary. Understanding how assumptions affect results is critical, particularly if the study will be used to guide policy or management actions. I reviewed published amphibian population projection models to determine whether models are evaluated with population time series data or patterns, what assumptions are made, and whether sensitivity analyses are performed. I found that only 21% of published models were evaluated with population data, and most models (67%) were explored with sensitivity analyses. Almost all models assumed that females drove population dynamics (90%) and that vital rates were not correlated (89%). Fewer models assumed that vital rates were constant (40%), that they do not depend on population size (28%), and that vital rates from other species can be used (23%). Simulations show that the use of incorrect assumptions can greatly bias model output and the results of sensitivity analyses. Declining populations may be most affected by implementing inappropriate model assumptions due to lack of data. One partial solution is to assess several different assumptions to understand which alters output the most to guide future data collection. Models should be regularly updated with new information to ensure conservation biologists are using the most robust information on potential outcomes of threats and conservation actions.

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754 ASIH STORER ICHTHYOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Anna Eastis[1], Micheal Sandel[1], Zachary Culumber[2]

[1]University of West Alabama, Livingston, Alabama, USA, [2]University of Alabama in Huntsville, Huntsville, Alabama, USA

New Records of the Invasive Green Swordtail (*Xiphophorus hellerii*) in north Florida

Invasive aquatic species are an ongoing issue in North America due to their environmental and economic impacts like threatening biodiversity, ecosystem health, and displacing native fishes. The green swordtail (*Xiphophorus hellerii*) is a tropical ornamental fish native to Central America that is found in ponds, rivers, and swift-flowing streams (Miller 2005). The most important pathways of introduction of the green swordtail include aquarium release and aquaculture escape. The impacts of this introduced species are largely unknown (Leo et al. 2019), so studying the impacts of the green swordtail will provide novel evidence of ecological effects to native fish species. We have collected samples from Florida, Wyoming and Hawaii for invasive populations, and native population samples from Mexico to analyze mitochondrial DNA (mtDNA) relationships for insight into the genetic variation, ancestry, and plasticity of native and invasive populations. We are applying microbiome techniques to study the effects that the green swordtail has on the native fish's biological health and dermal microbial diversity. We are comparing microbiomes from fishes in two streams, one that represents only native species and another stream that has been invaded by the green swordtail. To further investigate how the green swordtail is displacing native fish populations, we are performing stable isotope analysis to elucidate the trophic ecology impacts by analyzing carbon and nitrogen stable isotopes where there are only native fish species and another where native species coexist with the invasive green swordtail.

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763 Ichthyology Lightning Talks, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Anna Eastis[1], Micheal Sandel[1], Zachary Culumber[2]

[1]University of West Alabama, Livingston, Alabama, USA, [2]University of Alabama in Huntsville, Huntsville, Alabama, USA

Applying Genomic Methods to Investigate the Invasive Spread of the Green Swordtail (*Xiphophorus hellerii*)

Invasive aquatic species are an ongoing issue in North America due to their environmental and economic impacts like threatening biodiversity, ecosystem health, and displacing native fishes. The green swordtail (*Xiphophorus hellerii*) is a tropical ornamental fish native to Central America that is found in ponds, rivers, and swift-flowing streams (Miller 2005). The most important pathways of introduction of the green swordtail include aquarium release and aquaculture escape. The impacts of this introduced species are largely unknown (Leo et al. 2019), so studying the impacts of the green swordtail will provide novel evidence of ecological effects to native fish species. We have collected samples from Florida, Wyoming and Hawaii for invasive populations, and native population samples from Mexico to analyze mitochondrial DNA (mtDNA) relationships for insight into the genetic variation, ancestry, and plasticity of native and invasive populations. We are applying microbiome techniques to study the effects that the green swordtail has on the native fish's biological health and dermal microbial diversity. We are comparing microbiomes from fishes in two streams, one that represents only native species and another stream that has been invaded by the green swordtail. To further investigate how the green swordtail is displacing native fish populations, we are performing stable isotope analysis to elucidate the trophic ecology impacts by analyzing carbon and nitrogen stable isotopes where there are only native fish species and another where native species coexist with the invasive green swordtail.

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378 General Ichthyology I, Cottonwood A-D – The Snowbird Center, Saturday 27 July 2019

Kelsie Ebeling-Whited

University of Guam, Mangilao, GU, Guam

Mating success of the six-bar wrasse (T*halassoma hardwicke,* Labridae) utilizing two mating strategies

Thalassoma hardwicke is a widespread reef fish species distributed throughout much of the tropical Indo-West Pacific region. This species utilizes two spawning strategies: paired and group spawning. The former is used by sex-changed terminal-phase (TP) males who establish temporary courtship territories within a lek-like system and attempt to court multiple females in succession. The latter is used by initial-phase (IP) males and females that assemble around a specific site at a specific time and then engage in multiple bouts of group spawning. Both systems operate simultaneously at a resident spawning aggregation site found on Finger Reef, Apra Harbor, Guam. Four questions arise: 1) which spawning type will be most successful? 2) How does the density of *T. hardwicke* affect mating system choice and spawning success rates? 3) Are the spawning rates of *T. hardwicke* affected by lunar cycles and seasons? 4) Do egg predator abundances impact the success rates of the two spawning types? Thus far, I have collected data for 451 group and 9 paired spawning events. Preliminary analysis indicates 95% of group spawns were successful compared to 89% successful pair spawns. Egg predation occurred in 57% of group spawn events and only 50% of pair spawns. Answers to these questions will provide an understanding of the dynamics of spawning aggregations formed by common and easily accessible fish species such as *T. hardwicke* and can be important for use in developing model systems that examine the behavior and ecology of reef fish species.

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155 Reptile Conservation, Ballroom 2 – Cliff Lodge, Saturday 27 July 2019

Sarah Ebert[1], Kasey Jobe[1], Christopher Schalk[1], Daniel Saenz[2], Cory Adams[2], Christopher Comer[1]

[1]Stephen F. Austin State University, Nacogdoches, TX, USA, [2]Southern Research Station USDA Forest Service, Nacogdoches, TX, USA

Correlates of Snake Entanglement in Erosion Control Blankets

In road construction projects across the United States, erosion control methods (e.g., erosion control blankets [ECBs]), are mandated to stimulate seedbed regeneration and prevent soil loss. Anecdotal reports have suggested that snakes are vulnerable to entanglement in ECBs. We conducted a literature review, field surveys, and an entanglement experiment to examine what factors increase a snake's risk of ECB entanglement. Our literature review produced reports of 175 reptiles entangled in mesh products, 89.1% of which were snakes, with 43.6% of snake entanglements occurring in erosion control products. During our field surveys, we found ten entangled snakes (n = 2 alive; n = 8 dead). From our experiment, we found that ECBs that contain fixed-intersection, small-diameter mesh comprised of polypropylene were significantly more likely to entangle snakes compared to ECBs with larger diameter polypropylene mesh or ECBs that have woven mesh made of natural fibers. Snake body size was also associated with entanglement; for every 1 mm increase in body circumference, the probability of entanglement increased 4%. These results can help construct a predictive framework to determine those species and individuals that are most vulnerable to entanglement.

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67 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Karin Ebey

Los Alamos High School, Los Alamos, NM, USA

Modeling the Effects of Invasive Species on Crocodilian Populations

Crocodilians are apex predators that keep ecosystems in balance. Crocodilians have been impacted by many invasive species including pythons and cane toads. Invasive species are organisms established outside of their native range, which can cause many negative effects including disruption to the food chain and extinction. In this experiment, the effects of invasive species on crocodilians were modeled. A model was made using Python code with eight species: crocodilians and prey ranging from birds to reptiles. A novel adaptation of the Lotka-Volterra equation is used that allows for many species, species that are both predator and prey, and a timescale of months with reproduction once a year. Invasive species effects impacting individual and combinations of species were found to cause two ecosystem responses: 1) the crocodilian population increases and other populations decline; 2) the reptile population increases and other populations decline. The response depends on whether the affected species is more important to maintaining the crocodilian or reptile population. The populations most impacted are large predators as they are sensitive to changes in their prey populations. The magnitude of effects only impacted the timescale of the response. Invasive species effects stopping midway through the simulation caused the same responses to occur, but at a slightly later timescale. Following an invasive species establishment, the best first step is to determine which species are impacted as this indicates the ecosystem response and allows for management to protect the ecosystem.

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299 SSAR RABB UNDERGRADUATE AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Colin Eckman, Austin Morder, Teah Evers, Jennifer Deitloff

Lock Haven University, Lock Haven, PA, USA

Assessment of the Density, Spatial Distribution and Movement Patterns of *Plethodon cinereus* (Eastern Red-backed Salamander) Using Spatial Capture-Recapture

Plethodon cinereus (Eastern Red-backed Salamander*)* is a terrestrial salamander commonly found in the Eastern United States. This species is territorial and will defend areas against conspecifics through aggressive behavior. The extent to which males and females defend territories, spatially distribute themselves, and disperse needs to be further explored. We examined the density, spatial distribution and movement patterns of both males and females of *P. cinereus* in their natural habitats using artificial cover boards and spatial capture-recapture methods. We used two locations with 300 cover boards each, which were separated into 6 plots. We tested the following hypotheses: (1) males will have larger foraging areas than females and (2) both males and females will display site fidelity by remaining within the same plot and the same area within a plot. We marked individuals using four colors of Visual Implant Elastomer Tags in order to create a unique color code for each individual. We calculated a home range size and an activity center for each individual based on their movement patterns. Densities varied across plots and between sites. Comparison of mean distance moved showed that gravid females moved slightly more than males and that both males and gravid females, on average, moved more than non-gravid females, but these differences were not significant. Based on the number of recaptures and the individual spatial history, analyses indicated that both males and females of *P. cinereus* display site fidelity. Estimating population density and understanding movement patterns can provide insight into intraspecific interactions among individuals within a population.

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704 Ichthyology Ecology, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Joshua Egan, Andrew Simons

University of Minnesota, Saint Paul, Minnesota, USA

Ecological and evolutionary processes in the origins of the latitudinal diversity gradient in clupeiform fishes (herrings, anchovies, and relatives)

The species diversity of nearly all groups of organisms from fungi and plants to fish and mammals increases from the poles to the equator. This pervasive pattern, called the latitudinal diversity gradient (LDG), has been intensely studied since it was first described in the early 1800s. Incredibly, there is still no accepted explanation for the existence of this pattern. My dissertation examines aspects of a promising, but poorly tested LDG hypothesis that implicates niche evolution and speciation rates as key processes in the origins of the LDG. I am using the economically and ecologically important clupeiform fishes (herrings, anchovies, and relatives) as a study system, phylogenetic comparative methods, and an extensive diet database to examine the validity of this hypothesis. In my presentation I will discuss preliminary findings.

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209 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Jacob Egge, Tess Olsson, Teagan Haden

Pacific Lutheran University, Tacoma, WA, USA

A Preliminary Survey of Extraoral Taste Buds in Fishes

Gustation serves as a major chemosensory system in vertebrates where it plays a discriminatory role during ingestion. As such, taste buds, the primary gustatory sense organs, are generally thought of as being restricted to the oral cavity. However, unlike other vertebrates, many fish lineages have evolved extraoral taste buds on other surfaces including: gill epithelia, lips, barbels, head, fins, and, in some cases, across the entire body surface. While there are scattered reports of extraoral taste buds in the literature, a systematic survey of taste bud distribution across a range of fish lineages has yet to be performed, hindering analyses of their function and evolutionary origin. We surveyed preserved specimens representing 15 actinopterygian orders for extraoral taste buds by sampling tissues from multiple body regions using a combination of light microscopy (LM) and scanning electron microscopy (SEM). Tissues examined under LM were paraffin embedded and stained using hematoxylin and eosin while those used for SEM were dehydrated with hexamethyldisilazane (HMDS) and sputter coated with gold. We then combined these results with reports of extraoral taste buds from the literature and mapped extraoral taste bud distributions onto a phylogeny of actinopterygian fishes. Results suggest that extraoral taste buds are present in at least 10 different actinopterygian orders and have been gained and lost multiple times, raising further questions about their origin and function.

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628 ASIH STOYE GENERAL ICHTHYOLOGY AWARD I, Cottonwood A-D – The Snowbird Center, Thursday 25 July 2019

Diego Elías[1], Fernando Alda[2], Caleb McMahan[3], Prosanta Chakrabarty[1]

[1]Museum of Natural Science, Louisiana State University, Baton Rouge, Louisiana, USA, [2]University of Tennessee at Chattanooga, Chattanooga, Tennessee, USA, [3]Field Museum of Natural History, Chicago , Illinois, USA

Revisiting the Biogeographic History of the Middle American Cichlids (Tribe Heroini)

Middle America is the geographic region encompassing Northern Mexico to the border of Panama and Colombia, and the Greater Antilles. This region is the result of one of the most complex geological histories in the world. One of the major components of the unique ichthyofauna of Middle America is the family Cichlidae (tribe Heroini) containing more than 100 species in 38 genera. Despite efforts to understand the evolutionary history of heroine cichlids some relationships remain controversial, such as the position of South American Caquetaines and the Greater Antillean genus *Nandopsis*. Thus, the lack of confidence in a phylogenetic hypothesis hinders our ability to understand the biogeographic history of heroine cichlids. Four main pathways have been proposed that explain the timing of colonization of Middle America: 1) the Proto-Antillean arc (94-63 mya), 2) the East margin corridor (58- 48 mya), 3) the Greater Antilles Aves ridge (35-32 mya), and 4) marine dispersal. Here, we have inferred a phylogenomic hypothesis for the major groups of Heroini using ultraconserved elements. We identified and filtered loci according to their highest probability of resolving bi-partitions of interest (e.g. *Nandopsis* sister to Amphilophines). We used these loci to generate reduced datasets—of 50 most-informative loci—that were analyzed using *BEAST to generate fossil-calibrated dated hypotheses. We then carried out ancestral area reconstructions based on contrasting phylogenetic hypotheses from complete non-filtered and reduced datasets using BioGeoBEARS. Our work attempts to reconcile gene tree heterogeneity and competing biogeographical scenarios of colonization of Middle America.

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91 SSAR HUTCHISON ECOLOGY, NATURAL HISTORY, DISTRIBUTION, & BEHAVIOR AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Erica Ely[1,2], Chris Feldman[2]

[1]*California Academy of Sciences, San Francisco, California, USA,* [2]*University of Nevada, Reno, Nevada, USA*

Feeding Ecology and Morphometrics Provide Evidence of Resource Partitioning in three sympatric garter snakes (*Thamnophis*)

Understanding how closely related species with similar resource requirements are able to coexist remains a central focus of community ecology. Here, we explore the differences in the feeding ecology of three sympatric garter snake species (*Thamnophis*) in the Sierra Nevada and Lower Cascade Ranges of California: the Sierra Garter Snake: (*T. couchii*); the Western Terrestrial Garter Snake (*T. elegans*); and the Common Garter Snake (*T. sirtalis*). We examined museum specimens for stomach contents and categorized prey into different habitat types. Additionally, we measured morphometric head traits, which can reflect modifications that improve feeding performance on specific types of prey. We found that *T. couchii* feed mostly on aquatic prey, *T. sirtalis* generally feed on amphibious prey, while *T. elegans* display the most varied diet and feed on a majority of terrestrial prey. Our analyses of interspecific variation of head shape signal subtle differences in morphology between species. Thus, *Thamnophis* in this study area appear to partition food resources by preying on species that occupy distinct microhabitats, and these snakes possess variation in head morphology that may reflect these dietary differences. Our study provides insight into niche partitioning of sympatric, ecologically similar snakes, and adds to the growing evidence of ecological flexibility of *Thamnophis* species across North America.

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698 General Herpetology I, Primrose A&B – Cliff Lodge, Sunday 28 July 2019

Eveline Emmenegger[1], Emma Bueren[1], Tamara Schroeder[2], Sharon Clouthier[2]

[1]*USGS, Western Fisheries Research Center, Seattle, WA, USA,* [2]*Department of Fisheries and Oceans, Freshwater Institute, Winnipeg, Manitoba, Canada*

Susceptibility of Native Amphibians from the U.S. Pacific Northwest to an Exotic Fish Rhabdovirus

Spring viremia of carp virus (SVCV) is a rhabdovirus that infects primarily cyprinid finfish with Common Carp (*Cyprinus carpio carpio*) considered to be the most susceptible species. The disease is notifiable to the World Organization for Animal Health which lists fish (and possibly shrimp) as SVCV susceptible host species. In 2015, distressed ornamental Chinese firebelly newts (*Cynops orientalis*) imported into the U.S. were suspected to be infected with chytrid fungus (*Batrachochytrium salamandrivorans*). The newts tested negative for the fungal agent, but SVCV was detected and appeared to be responsible for the observed morbidity. This discovery represented the first isolation of a rhabdovirus in an amphibian species. To better understand the host range of this virus, susceptibility testing of amphibians native to the Pacific Northwest was initiated. Pacific tree frog (*Pseudacris regilla*) tadpoles and larval long-toed salamander (*Ambystoma macrodactylum*) were exposed to the virus by either intra-peritoneal

injection, immersion, or co-habitation with SVCV-infected fish. Cumulative mortality in virus-exposed amphibians ranged from 0 – 100% and many animals that died exhibited clinical signs of disease. SVCV was detected by plaque assay and RT-qPCR assay in both amphibian species regardless of the virus exposure/transmission method. Convalescent amphibians contained measurable levels of viable virus at targeted sampling time-points including 28 days following exposure. These results suggest that SVCV can be transmitted and cause disease culminating in mortality in amphibian species. As such, amphibians may serve as virus carriers in an ecosystem and pose a risk for sympatric fish and amphibian populations vulnerable to SVCV.

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766 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Heather Engler, Braulio Assis, Dustin Owen, Tracy Langkilde

The Pennsylvania State University, University Park, PA, USA

Are Post-anal Scales a Secondary Sex Characteristic in Eastern Fence Lizards?

Most North American iguanid lizard species possess a pair of scales called post-anal scales. These enlarged scales are located below the cloaca near where the hemipenes evert in males. They are widely used to distinguish males (who have these scales) from females (who do not) even at hatching. However, little else is known about this sexually-dimorphic trait. We tested whether post-anal scales of the eastern fence lizard (*Sceloporus undulatus*) exhibited different patterns of growth and asymmetry from hatching to adulthood, when compared to other body scales (chin shields). We also tested for a correlation between the size and asymmetry of post-anal scales and another known secondary sex characteristic - the size and color of badges on the throats of males - and concentrations of testosterone and estradiol which are involved in the development of secondary sex characteristics. We found that post-anal scales began growing relatively larger and more asymmetrical than chin shields as the lizards approached maturity, that males with larger throat badges had more asymmetrical post-anal scales, and males with higher testosterone levels had relatively larger post-anal scales. These results suggest that post-anal scales may function as a male-typical secondary sex characteristic in eastern fence lizards and possibly other species. Further research should examine the potential function of these scales (e.g. in supporting the hemipenes during mating).

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422 Herpetology Physiology, Ballroom 3 – Cliff Lodge, Saturday 27 July 2019

David Ensminger[1], Tracy Langkilde[2]

[1]The Western Kentucky University, Bowling Green, KY, USA, [2]The Pennsylvania State University, State College, PA, USA

Effects of Maternal Glucocorticoids on Offspring Absolute Telomere Length in Wild Lizards

The effect of stress-relevant maternal glucocorticoids (e.g. corticosterone, CORT) on offspring phenotype is of interest to the fields of biology and ecology, particularly in the face of increasing environmental perturbations. However, little is known about the underlying mechanisms or long-term effects of maternal CORT on offspring lifespan. Telomeres, the protective endcaps of chromosomal DNA, could play a role as telomere shortening is associated with disease states and cellular senescence. Few studies have explored this in wild animals, and they used relative telomere length which are difficult to compare across studies. Here, we use a modified RT-qPCR assay protocol to assess absolute telomere length from small amounts of DNA (<60ng). We tested the hypothesis that increased maternal CORT during pregnancy decreases offspring telomere length, as CORT has been shown to increase reactive oxygen species generation which decreases telomere length. We treated wild-caught gravid female eastern fence lizards (*Sceloporus undulatus*) daily with transdermal applications of CORT, at ecologically relevant levels, from capture to oviposition. Mothers and resulting hatchlings were sampled for DNA. Maternal CORT treatment did not alter maternal telomere length but did decrease offspring telomere length of sons but not daughters. There was a strong maternally heritable component to offspring telomere length. These results reveal sex-specific effects of maternal CORT on offspring telomeres. This decrease in offspring telomere length may be costly and could counteract other potentially adaptive phenotypic changes associated with maternally derived CORT. Further research should explore the fitness consequences of this maternal CORT effect.

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673 Turtle Conservation/Amphibian Conservation, Ballroom 3 – Cliff Lodge, Friday 26 July 2019

Wendy Estes-Zumpf[1], Brenna Marsicek[2], Joseph Ceradini[3], Zoe Nelson[4]

[1]Wyoming Game and Fish Department, Laramie, WY, USA, [2]Madison Audubon Society, Madison, WI, USA, [3]Utah Valley University, Fruita, UT, USA, [4]University of Wyoming, Laramie, WY, USA

Rocky Mountain Amphibian Project: A collaborative effort to monitor amphibians in the Rocky Mountain Region

Amphibians are declining globally; however, efforts to manage amphibians are often hindered by a lack of information on population trends as well as inadequate funding for surveys. The Rocky Mountain Amphibian Project (RMAP) is a collaborative effort to monitor amphibians in the region. Standardized surveys in predefined areas (catchments) are conducted each year in the mountains of Wyoming and northern Colorado by citizen scientists, state and federal agency biologists and technicians, and members of local organizations. The monitoring initiative began in 2012 and has expanded to include over 350 wetland sites in 75 catchments across the Medicine Bow-Routt and Bridger-Teton national forests. Since RMAP began involving citizen scientists in 2014, citizen scientists have been integral to ensuring the sustainability of the program, having conducted over 1,050 surveys at over 500 wetland sites. Typically, over 110

participants, including approximately 80 citizen scientists, conduct RMAP surveys annually. Surveyors collectively hike over 500 miles through the mountains each year in search of frogs, toads, and salamanders. Surveyors collect data on the species and number of individuals of each life stage detected during surveys. Coordinating survey efforts and ensuring data integrity is no insignificant task. We provide preliminary results and discuss successes as well as challenges faced by this collaborative amphibian monitoring effort.

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598 ASIH/HL/SSAR Symposium: The Expanding Role of Natural History Collections, Ballroom 1 – Cliff Lodge, Sunday 28 July 2019

Stacy Farina

Howard University, Washington, DC, USA

Reciprocal Value of Museum Vouchers to Collections and to Functional Morphology Research

Biological collections are playing an increasing role in the archiving of specimen-based multimedia data that results from biodiversity expeditions, such as field recordings, videos, and photographs of living organisms. Functional morphology research, especially in the fields of ichthyology and herpetology, often involves data collection in the laboratory or field from wild-caught animals. These studies generate large volumes of multimedia data, including high-speed video, animations of 3D kinematics, physiological recordings such as EMG and intracranial pressure, and behavioral recordings. However, it is relatively uncommon for specimens to be accessioned into collections at the end of functional morphology and biomechanics studies. In the case of wild-caught and/or non-model animals, accessioning these specimens can provide long-term physical storage and vouchering, increasing the longevity and value of the final published study. As multimedia archiving becomes standard practice for publicly funded published research, researchers can coordinate with curatorial staff to link accessioned specimen records to archived data hosted externally. Future researchers then have the opportunity to examine specimens and analyze archived recordings to answer new research questions beyond the taxonomic or functional scope of the original study. In addition to having many benefits, this approach has many logistical challenges that will be discussed in this presentation. Most importantly, it is critical to coordinate with curatorial staff while writing a data management plan before a study begins.

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678 Reptile Conservation, Ballroom 2 – Cliff Lodge, Saturday 27 July 2019

Terence Farrell[1], Joseph Agugliaro[2], Erin Graham[3], Robert Ossiboff[3], Heather Walden[3], James Wellehan[3], Craig Lind[4]

[1]Stetson University, DeLand, FL, USA, [2]Fairleigh Dickinson University, Madison, NJ, USA,

[3]University of Florida, Gainesville, FL, USA, [4]Stockton University, Galloway, NJ, USA

Rapid Geographic Spread of Invasive Pentastome Parasites in Rattlesnakes (*Sistrurus miliarius*) Indicates an Emerging Conservation Threat to North American Snakes.

Parasite spillover, the spread of nonindigenous parasites to native species, can be an important impact of nonnative species. *Raillietiella orientalis*, an Asian pentastome (endoparasitic crustacean), was introduced in south Florida with Burmese Pythons. This parasite has spread to native snakes. In summer 2018, we found *R. orientalis* in three pygmy rattlesnakes (*Sistrurus miliarius*) in central Florida, more than 160 km north of this parasite's published geographic range. In winter 2019, we examined 34 *S. miliarius* either antemortem (endoscopy, lung washes, and/or cloacal washes) or postmortem (necropsy) to determine the prevalence of *R. orientalis* at two central Florida locations that were separated by 34 km. There was a significant difference between the sites in pentastome prevalence, with 76.9% and 18.2% of all *S. miliarius* infected at the two sites. The mean length of the adult female parasites removed from pygmy rattlesnake lungs (59.0 mm) and the mean number of adult females (3.1 individuals/snake) were both greater than that reported in published records for Burmese pythons, a species with which *R. orientalis* shares a coevolutionary history. Infection in *S. miliarius* is associated with emaciation and mortality; heavy pentastome loads appear to be an energy drain. The impact of this invasive parasite on native snake populations will be a function of a variety of unknown aspects of its biology, including its rate of spread, the identity of the intermediate hosts consumed by snakes, and the extent of lethal and sublethal effects of pentastome infection on host fitness.

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756 Ichthyology Lightning Talks, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Kayla Fast[1], Parker Nenstiel[2], Anakela Popp[3], Pat O'Neil[2], Brett Albanese[3], Michael Sandel[1]

[1]University of West Alabama, Livingston, AL, USA, [2]Geological Survey of Alabama, Tuscaloosa, AL, USA, [3]Georgia Department of Natural Resources, Athens, GA, USA

eDNA Surveillance and Genomic Characterization of the Threatened Trispot Darter (*Etheostoma trisella*)

The Trispot Darter (*Etheostoma trisella*) is a small freshwater fish found in the Coosa River watershed in the southeastern United States. In 2018, the trispot darter was listed as a threatened species under the Endangered Species Act (ESA). In an effort to describe population genetic diversity in this newly reclassified species, we have inferred evolutionary relationships and gene flow among extant populations using mitochondrial data from the cytochrome c oxidase I (CO1) gene and restriction-site associated DNA sequencing (RADseq). Population genomic analyses for this species include populations from Alabama, Tennessee, and Georgia. In addition to assessing population genomic variation, we are monitoring the current distribution of the trispot darter at historical and novel sites in coordination with the Georgia Department of Natural Resources (GADNR) and the Geological Survey of Alabama (GSA). We have implemented an alternative to traditional fish sampling methods in the form of environmental DNA (eDNA). This

type of genetic material is DNA extracted from environmental samples (i.e., water) instead of an individual, biological specimen. We extracted eDNA from filtered water samples and detected the presence of trispot darters using loop mediated isothermal amplification (LAMP). LAMP detects small quantities of DNA rapidly by amplifying multimeric DNA at a single temperature in real time. Confirmation of trispot darter presence at historical sites and detection at new localities will provide a platform for conservation efforts and investigation of evolutionary histories.

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467 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Donald Faughnan, Chip Cotton

SUNY Cobleskill, Cobleskill, New York, USA

Age and Growth of Great Lanternshark (*Etmopterus princeps*)

Deepwater sharks make up half of all extant shark species, yet their biology remains poorly described. In order to properly manage these deepwater species in areas where they are subjected to fishing mortality, managers require life history data. The great lanternshark (*Etmopterus princeps*) is a highly abundant, poorly described deepwater shark that was prominent in bycatch of North Atlantic deepwater fisheries prior to area closures. Fisheries interactions remain a concern for this species, thus management consideration is recommended. Using dorsal finspines collected during the MAR-ECO cruise (2004), we conducted the first study of age and growth for this species. In order to model finspine growth, we recorded a series of morphometric measurements on both spines. We then removed tissue from the spines using a hot trypsin bath and dissection tools. Spine tips were embedded in resin and a thin section (130 um) was cut using a low speed saw. We viewed the transverse spine sections on a compound microscope under 25x magnification and transmitted light. Age was assigned based on the total number of visible growth bands, assuming an annual rate of band deposition. A second reader aged the spines in order to estimate precision through reader agreement measures. Sex-specific size-at-age data were fitted with multiple conventional growth models using R software. Results of this ongoing study are preliminary and will eventually be used to estimate age at maturity, longevity, and mortality for this species.

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215 AES Conservation & Management II, Rendezvous A&B – The Snowbird Center, Sunday 28 July 2019

Annmarie Fearing[1], Kelcee Smith[2], Nigel Downing[3], Tonya Wiley[4], Jeff Whitty[5], Barbara Wueringer[6], Kevin Feldheim[7], Peter Kyne[8], Nicole Phillips[1]

[1]Univerisity of Southern Mississippi, Hattiesburg, Mississippi, USA, [2]Louisiana State University, Baton Rouge, Louisiana, USA, [3]University of Cambridge, Cambridge, England, United Kingdom, [4]Havenworth Coastal Conservation, Palmetto, Florida, USA, [5]Florida Fish and

Wildlife Conservation Commission, Milton, Florida, USA, [6]Sharks and Rays Australia, Bungalow, Queensland, United Kingdom, [7]Field Museum of Natural History, Chicago, Illinois, USA, [8]Research Institute for the Environment and Livelihoods, Charles Darwin University, Darwin, Northern Territory, Australia

Sawfish Saws as a Tool to Assess Genetic Diversity in Historic Largetooth Sawfish (*Pristis pristis*) Populations

The Critically Endangered Largetooth Sawfish (*Pristis pristis*) has experienced large declines over the past century due to fisheries bycatch, direct exploitation, and habitat degradation. *Pristis pristis* was historically distributed circumglobally in subtropical and tropical waters, but today, seemingly viable populations are likely limited to northern Australia. Declines in abundance and range are typically accompanied by reductions in levels of genetic diversity, leaving populations more prone to disease and with a reduced ability to adapt to the changing environment. Contemporary *P. pristis* populations have moderate to low levels of genetic diversity that fall within the lower part of the range of those of other elasmobranchs, but it is unknown whether these levels have been maintained over the past century or have been severely reduced from those historically. Temporal changes in genetic diversity can be quantified by comparing levels of genetic diversity between contemporary and historic populations. Sawfish saws (rostra) were commonly taken as fishing trophies in the past; today, these rostra can be found in natural history collections and contain DNA from past populations. We collected tissue samples from ~280 *P. pristis* rostra from collections, ~150 of which have catch data (i.e. date/capture location), including samples from *P. pristis* from West Africa where *P. pristis* are possibly extinct. DNA was extracted from these historic specimens and small DNA fragments in the mitochondrial control region were PCR-amplified and sequenced. These data provide critical baseline information that can be used to assess long-term survival potential of *P. pristis.*

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780 Herpetology Morphology and Systematics, Ballroom 1 – Cliff Lodge, Friday 26 July 2019

Sam Fellows[1], Tod Reeder[1], Bradford Hollingsworth[2]

[1]San Diego State University, San Diego, CA, USA, [2]San Diego Natural History Museum, San Diego, CA, USA

Integrating Genomic and Environmental Data to Delimit Species in Sidewinders (*Crotalus cerastes*) Reveals Cryptic Diversity

Sidewinders (*Crotalus cerastes*) are common rattlesnakes in the deserts in the southwestern United States, northeastern Baja California, and extreme western Sonora, Mexico. Historically, morphological data have been used to recognize three subspecies, each corresponding to different North American warm deserts (*C. c. cerastes* in the Mohave Desert, *C. c. laterorepens* in the Colorado Desert, and *C. c. cercobombus* in the Sonoran Desert). Previous phylogenetic research utilizing mtDNA have found these subspecies to be incongruent with five mitochondrial

clades (“Northern Mohave,” “Southern Mohave,” “Colorado,” “Northern Sonoran,” and “Southern Sonoran”). To address species limits within *C. cerastes,* we integrated genomic RADseq data from 52 individuals from across the range of *C. cerastes* with ecological niche models (ENMs). Phylogenetic analysis of the genomic data supports the existence of three distinct regional lineages (Mohave, Northern Sonoran including Colorado, and Southern Sonoran), while demographic clustering analyses based on 1700 SNPs optimally support two distinct populations (Mohave + Northern Sonoran + Colorado and Southern Sonoran), with limited admixture near their contact zone. None of our analyses support historically defined subspecies within *C. cerastes*. ENM data demonstrate two distinct climatic clusters of *C. cerastes* corresponding to the Mohave + Northern Sonoran and Southern Sonoran groups. Based on the genomic and environmental data, we demonstrate the existence of two evolutionary lineages within *C. cerastes*. Integrating these data into a simultaneous analysis of species limits, and estimation of demographic parameters through simulation and model fit, will validate these species hypotheses.

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317 SSAR HUTCHISON EVOLUTION, GENETICS, & SYSTEMATICS AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Andrew Feltmann, Matthew Gifford, Emily Field

University of Central Arkansas, Conway, AR, USA

Effect of selection and genetic drift on phenotypic diversification in the eastern collared lizard

Organisms display a wide diversity of traits that selection acts upon causing phenotypic change over time. When organisms disperse, however, the resulting small population can experience genetic drift due to decreased genetic diversity within the population. Reintroduction is one of the more common forms of population restoration in conservation management plans. The reintroduced populations face challenges that colonizing populations face (i.e. a reduced population number and possible inbreeding). These issues may lead to genetic drift which can majorly impact fitness in the population, potentially leading to population crash. We examined the effects of selection and drift on a metapopulation of Eastern Collared Lizards (*Crotaphytus collaris*) on Stegall and Thorny mountains in southern Missouri. We measured a suite of morphology and performance traits to assess levels of differentiation between mountains and developed a phenotypic variance-covariance matrix (***P***). Multiple matrix analyses suggest that there is ***P*** does not differ between populations; however, the levels of covariation between traits do differ. Additionally, lizards on Thorny mountain were found to have longer fore limbs, higher bite forces, and had higher respiration rates. Stegall lizards had longer head lengths overall. This supports our prediction that the population on Thorny is experiencing novel selection pressures or genetic drift.

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350 ASIH/HL/SSAR Symposium: The Expanding Role of Natural History Collections, Ballroom 1 – Cliff Lodge, Sunday 28 July 2019

Danté Fenolio[1], Tracey Sutton[2]

[1]Center for Conservation & Research, San Antonio Zoo, San Antonio, TX, USA, [2]Halmos College of Natural Sciences and Oceanography, Nova Southeastern University, Dania Beach, FL, USA

Photographic Documentation of Deep-water Fishes by the DEEPEND Consortium on the Gulf of Mexico

The DEEPEND consortium comprises a group of scientists looking to better understand the damage done to pelagic wildlife communities of the Gulf of Mexico (GoM) by deep-water oil spills. Six deep-water research expeditions were conducted in the GoM between 2015 and 2018; specimens were collected using a large MOCNESS midwater trawl system. The proper documentation of deep-water fishes brought to the surface is incredibly important as records of color in life for deep-water species are scant and high quality images of fresh specimens are equally uncommon. Specimen collection and documentation in poorly understood habitats, such as the mesopelagic/bathypelagic zones of the ocean, are vital because so little is known of these deep-water communities. Many species are known from a small number of individuals and identification/documentation of fresh specimens is essential: future biodiversity surveys, post environmental disaster(s), will rely heavily on records made today. Here we will summarize an imaging project in which dozens of pelagic and deep-water fish species have been photographed prior to preservation, many of which are the first images of their kind for the taxon. We will also detail ongoing research projects in which these specimens, and images of them, are central components - for example, an identification guide to the eel larvae of the Gulf of Mexico.

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383 Herpetology Physiology, Ballroom 3 – Cliff Lodge, Saturday 27 July 2019

Allyson Fenwick, Laura Kimmel, Samah Houmam, Briant Nguyen, Susan McKenna

University of Central Oklahoma, Edmond, OK, USA

Year-Round Temperature Observations of Mediterranean Geckos (*Hemidactylus turcicus*) at the University of Central Oklahoma

The Mediterranean gecko (*Hemidactylus turcicus*) is a small nocturnal lizard that is native to rocky cliffs in the Middle East but has spread worldwide through human introductions. Central Oklahoma is near the northern edge of the known U.S. range and at the northern edge of the predicted range based on climate. Individuals are expected to be dormant throughout the winter. Several years of surveys done by undergraduates in introductory courses, from January through April, have found that geckos are active throughout this time, including at temperatures that would decrease their sprint speeds. A small team of trained student researchers have been collecting gecko observations, perch temperatures, and other data since August 2018.

Preliminary results suggest that geckos are sighted throughout winter and are found at perch temperatures below lab measurements for optimal sprint speeds. Patterns are similar across two buildings – the original site of introduction and one near the outer edge of the UCO range. Individuals are not choosing perches that are warmer than nearby wall areas, supporting previous studies suggesting they are poor behavioral thermoregulators.

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580 AES Genetics/Ecology, Rendezvous A&B – The Snowbird Center, Friday 26 July 2019

Andrew Fields[1], Bryan Frazier[2], Marcus Drymon[3], Dean Grubbs[4], James Gelsleichter[5], Demian Chapman[6], Alexei Ruiz[7], Robert Hueter[8], Jayne Gardiner[9], David Portnoy[1]

[1]Texas A&M Corpus Christi, Corpus Christi, Texas, USA, [2]South Carolina Department of Natural Resources, Charleston, South Carolina, USA, [3]Mississippi State University, Biloxi, Mississippi, USA, [4]Coastal and Marine Laboratory, Florida State University, Tallahassee, Florida, USA, [5]College of Arts & Sciences, University of North Florida, Jacksonville, Florida, USA, [6]College of Arts, Sciences & Education, Florida International University, Miami, Florida, USA, [7]Centro de Investigaciones Marinas, Universidad de la Habana, Havana, Cuba, [8]Center for Shark Research, Mote Marine Laboratory, Sarasota, Florida, USA, [9]Division of Natural Sciences, New College of Florida, Sarasota, Florida, USA

Population Structure of the Bonnethead shark (*Sphyrna tiburo*) in the western North Atlantic

Many species of sharks are capable of large-scale movements but exhibit population structure at surprisingly small spatial scales due to philopatry or limited home ranges. Small coastal sharks have limited movement and differ in aspects of life history that may lead to increased population structure relative to larger sharks. Genetic tools, such as reduced-representation genome sequencing (RRGS), allows researchers to look for population structure by analyzing both drift-mutation and local adaptation signals throughout the entire genome. Using RRGS, we analyzed the population structure of the bonnethead, *Sphyrna tiburo*, along the US coast from North Carolina to Texas and across international boundaries in the western North Atlantic. A preliminary analysis indicates structuring of *S. tiburo* between the Atlantic and Gulf basins as well as within the Gulf basin and across the Florida straits. Future analysis using life history characteristics and a finer geographic scale will assess the importance of local adaptation. This study looks to aid in understanding previous studies which used either far fewer genetic markers or smaller geographical areas.

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94 ASIH STORER ICHTHYOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Kearstin Findley[1], Henry Bart Jr.[2], Kyle Piller[1]

[1]Southeastern Louisiana University, Hammond, Louisiana, USA, [2]Tulane University Biodiversity Research Institute, Belle Chasse, Louisiana, USA

Distributional Assessment of Three Imperiled Fishes in Louisiana: An Ecological Modelling Approach

Louisiana has not produced a comprehensive work dedicated to the diversity, distribution, and conservation status of the fishes that reside within the state's waterways for decades. This is particularly concerning for threatened and endangered species, which have been impacted by a variety of anthropogenic factors over the last thirty years. Therefore, this study aims to assess the distribution of a subset of Louisiana's threatened and endangered freshwater fish species. Distribution maps based on vouchered museum records have been created to depict the distribution of three of Louisiana's imperiled fishes including the Clear Chub (*Hybopsis winchelli*), Bluntface Shiner (*Cyprinella camura),* and Freckled Darter (*Percina lenticula*). Ecological niche models were developed using MAXENT and multiple data layers and were used to establish likely areas where these species may be capable of residing based on environmental conditions. We sampled using seines and a backpack electrofisher to test the accuracy of the ecological niche models in the field, as well as to collect data to determine if species still occur at a select number of known localities. Through the utilization of distribution maps, ecological niche models, and field sampling, this work aims to update the distribution and conservation status of these species and provides another tool to assess the distribution of imperiled species in Louisiana.

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720 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

John Finger[1], Matt Hamilton[2], Meghan Kelley[1], Yufeng Zhang[3], Andreas Kavizis[1], Travis Glenn[4], Tracey Tuberville[4]

[1]Auburn University, Auburn, AL, USA, [2]Purdue University, West Lafayette, IN, USA, [3]University of Memphis, Memphis, TN, USA, [4]University of Georgia, Athens, GA, USA

Selenium exposure and its effects on oxidative status in the American alligator (*Alligator mississippiensis*)

Selenium (Se) is an essential nutrient, which in excess can cause toxicity. Anthropogenic activities, such as the disposal of coal combustion waste products, are increasing the risk of Se exposure worldwide. However, most research investigating the toxic effects of Se have been limited to organisms of lower trophic status or organisms that are shorter lived. To counteract this, we administered juvenile American alligators (*Alligator mississippiensis*) 1000 or 2000 ppm selenomethionine (SeMet) or control water for 7 weeks. After this 7-week period, all alligators were euthanized and tissues were stored -80°C until analysis. Levels of superoxide-dismutase-1 (SOD1), SOD2, and glutathione peroxidase-1 (GPX-1) were measured in whole blood and tail muscle by Western blotting. Save for blood SOD2 levels ($p < 0.01$), SeMet treatment did not affect any other parameter investigated ($p < 0.05$). As this is the first study to investigate Se exposure and its effects on oxidative status in crocodilians, future studies are warranted.

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333 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Thomas Firneno, Alyson Emory, Corey Roelke, Matthew Fujita

The University of Texas at Arlington, Arlington, Texas, USA

Investigation of toxin evolution of the bufonid parotoid gland

Defensive toxins are found in a plethora of vertebrate and invertebrate taxa, and have played a large role in the diversification and co-evolution of many taxa. Within the amphibian world there are a number of taxa that exhibit defensive toxins as part of their natural history. Bufonids, or "true toads," are a group of organisms that have gone relatively understudied in terms of their defensive toxins, which are secreted through the parotoid gland on the back of their head. Here we utilize RNA-Seq techniques to characterize and evaluate the bufonid parotoid gland transcriptome. We aimed to identify candidate genes that are involved in the synthesis of toxin peptides and metabolites, identify if any of these genes are different between species of bufoids found in North America, identify if any of these genes are under selection, and identify peptides or metabolites that may play a role in the delivery of the toxins into the prey.

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330 ASIH STOYE GENERAL HERPETOLOGY AWARD I, Primrose A&B – Cliff Lodge, Thursday 25 July 2019

Thomas Firneno[1], Justin R. O'Neill[2], Daniel M. Portik[3], Alyson Emery[1], Josiah Townsend[2], Matthew Fujita[1]

[1]The University of Texas at Arlington, Arlington, Texas, USA, [2]Indiana University of Pennsylvania, Indiana, Pennsylvania, USA , [3]The University of Arizona, Tucson, Arizona, USA

Mitonuclear discordance reveals cryptic genetic diversity, introgression, and an intricate demographic history in a problematic species complex of Mesoamerican toads

Discordance between nuclear and mitochondrial gene trees, or mito-nuclear/genealogical discordance, can be caused by several evolutionary processes including incomplete lineage sorting, genetic polymorphism, and gene flow (e.g. hybridization/introgression), and is very common in natural systems. Here we utilize the *Incilius coccifer* complex, which is a complex of three species (*I. coccifer*, *I. ibarrai*, and *I. porteri*) found throughout eastern Nuclear Central America that has had a history of taxonomic debate among specialists. By integrating mitochondrial DNA and nuclear loci from ddRADseq, we have uncovered a more resolved population genetic structure amongst the three species in this complex that reflects the complex geography of the region, strong mito-nuclear discordance between the lineages, and gene flow between populations of *I. poteri* within Honduras. We applied Bayesian and maximum likelihood clustering, and phylogenetic inference to test hypotheses of population structure, as well as performing demographic analyses to test hypotheses related to population divergence and gene flow. Our results support the existence of three separate lineages within the *I. coccifer*

complex, reflecting the three current species in the complex; however, the lineage of *I. porteri* does not reflect the current recognized range of the species in Honduras. Our results also indicate the formation of a hybrid zone within populations of the *I. porteri* lineage in central Honduras that are separated from their parental populations by the Honduran Depression to the east and a large unnamed horse-shaped valley that runs from San Pedro Sula south of La Esperanza to the west.

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341 AES Trophic Ecology II/Ecology, Alpine A,B,C – The Snowbird Center, Sunday 28 July 2019

Chris Fischer, Brett McBride, Fernanda Ubatuba, Ami Meite

OCEARCH, Park City, UT, USA

Comprehensive data from live, large sharks at sea: Methods and results of capture, study, release, and funding model by OCEARCH

Beginning in 2007, the nonprofit research and education organization OCEARCH has conducted 34 research expeditions studying large sharks of the Pacific, Indian and Atlantic Oceans, supporting the work of 190 researchers from 98 organizations in 9 countries. OCEARCH research assets include a 130-ft specialized mothership, two smaller support vessels, and a highly experienced fishing crew. Over the past decade, methods of shark capture and handling have been optimized to reduce animal stress while providing safe, complete access of healthy animals to researchers. Fishing methods are hook-and-handline of various types, including a modified break-away drumline rigged to prevent gut-hooking. Captured animals are brought to the mothership, which has a 75,000-pound hydraulic lift and research platform. While on the platform, sharks are provided seawater ventilation, eyes and gill slits are covered with a wet towel, and skin is kept wet with fresh seawater. An aquatic veterinarian specialized in elasmobranchs is present at all times to monitor shark condition. Most large sharks, especially white sharks (*Carcharodon carcharias*), acquiesce to handling with a “learned helplessness” response that reduces stress. The science team is allotted 15-20 minutes to complete a suite of research procedures. Nearly all sharks are fitted with fin-mounted SPOT satellite-linked tags to track post-release movements and behavior. Since 2007, more than 400 sharks of 20 species have been tracked for periods of up to five years or more. OCEARCH’s innovative funding model uses primarily corporate support, with $6 million in expedition assets provided at no cost to collaborating researchers since 2007.

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393 Herpetology Conservation and Disease, Ballroom 3 – Cliff Lodge, Saturday 27 July 2019

Robert Fisher[1], Staci Amburgey[2], Carlton Rochester[1], Cheryl Brehme[1], Stacie Hathaway[1], Katy Delaney[3], Seth Riley[3], JP Montagne[4], Emily Perkins[1], David Miller[2]

[1]*USGS, San Diego, CA, USA,* [2]*Penn State University, University Park, PA, USA,* [3]*NPS, Thousand Oaks, CA, USA,* [4]*San Diego Zoo Global, San Diego, CA, USA*

Patch Dynamics in Southern California Small Vertebrates

Over the past 25 years there has been a major shift in the development process of the biodiversity reserve system in coastal southern California. This Mediterranean ecosystem is one of three hotspots in the United States for endangered species. With data on 45 terrestrial vertebrate species representing 47,156 individuals, we assessed the responses to habitat loss and fragmentation. Data were collected at 698 pitfall arrays across 97 patches ranging in size from 0.42 to 81,402.48 hectares. We determined the relationship between species richness and patch size, and then assessed what this means for the conservation landscape with regards to maintaining biodiversity. Of 9,321 patches (1,388,854 ha) of open space left in southern California, 2,242 patches (524,970 ha) are currently conserved. We found that patches greater than 5,000 ha contained about 80% of the predicted richness within these species based on species distribution models, but that in patches between 30 ha and 5,000 ha there was 27-39% less richness than predicted, and below 30 ha the missing richness was close to 55%. Fortunately, these smallest patches, although the most numerous, represent only about 2-3% of the total land remaining as open space or conserved land. Our results indicate that the percentage of area in conservation is dominated by larger patches which contain greater species diversity. Future conservation could benefit from adding non-conserved open space to existing conserved patches to enlarge them to over 5,000 ha to reduce species loss, versus placing more small "insular" patches into the network.

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367 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Charlotte J. Robinson[1], Austin L. Fitzgerald[1], Jillian M. Josimovich[1], Bryan G. Falk[2], Emma B. Hanslowe[3], Christina M. Romagosa[4], Amy A. Yackel Adams[1], Lea' R. Bonewell[1], Nina Burkardt, Robert N. Reed[1]

[1]*United States Geological Survey (USGS), Fort Collins, CO, USA,* [2]*National Park Service, Homestead, FL, USA,* [3]*Colorado State University, Fort Collins, CO, USA,* [4]*University of Florida, Gainesville, FL, USA*

Invasive Species Internship Program in the Greater Everglades Ecosystem: History, Accomplishments, and Outreach

Since 2013, biologists employed by the U.S. Geological Survey Fort Collins Science Center have been conducting research on southern Florida's invasive reptiles, based out of offices and labs located in Everglades National Park. Our team, a combination of federal staff and interns, works in Everglades National Park, Big Cypress National Preserve, Crocodile Lake National Wildlife Refuge, and other parts of the Greater Everglades Ecosystem. We focus on control and containment of the Burmese python (*Python bivittatus*) and the Argentine black and white tegu (*Salvator merianae*), among other species of concern. Over the past five years we have

developed and maintained a full-time internship program that supplies much of our field and research labor. Our intern program has partnered with the University of Florida and the National Park Service to train interns to conduct field and lab work. This program provides interns opportunities to develop their skills and network for graduate school or careers in the biological sciences. Several interns have contributed to peer-reviewed publications under guidance of USGS staff. Evaluation of the internship program occurs via exit interviews and career path monitoring. Since its inception, the internship program has provided excellent research and career building opportunities to undergraduates and recent graduates from across the United States. We document the history and accomplishments of the program by highlighting some of the publications, graduate opportunities, and careers achieved by program alumni.

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57 SSAR RABB UNDERGRADUATE AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Katie Fitzgerald, Jennifer Deitloff

Lock Haven University, Lock Haven, PA, USA

Head Morphology Variation across Pennsylvanian Populations of *Plethodon cinereus*

Morphology is an important feature that varies between sexes and geographic locations of organisms within the same species. Availability of resources and population density within geographic areas also impact the morphology of organisms. The Eastern Red-backed Salamander, *Plethodon cinereus*, has a wide geographic range across the northeastern United States and is an excellent study organism to test morphological differences based on location. *Plethodon cinereus* displays variation in head-shape due to differences in ecological characteristics and/or behavioral constraints. In this study, we examined lateral and ventral head-shape in *P. cinereus.* We compared sexes (gravid female, nongravid female, and male) and six Pennsylvanian populations using geometric morphometrics. Our hypotheses were that head-shape differed among sexes and populations of *P. cinereus*. We concluded that males differed in lateral and ventral head-shape from gravid females, but not from nongravid females. Nongravid and gravid females did not differ in lateral and ventral head-shape. Nine of 15 pairwise comparisons of populations differed in lateral head-shape, and eleven of 15 population comparisons differed in ventral head-shape (after Bonferroni correction). Difference in head-shape among sexes may be due to differences in behaviors such as territoriality, aggressive displays, or mate defense. From our results, we predict that local habitats include environmental challenges that impact head morphology resulting in salamander populations exhibiting different head-shape. Competition for resources within different populations could favor different morphological characteristics. Future studies could include data on ecological conditions to determine if a correlation exists between head morphology and local resource availability.

CANCELLED

783 ASIH STOYE GENETICS, DEVELOPMENT & MORPHOLOGY AWARD II, Primrose A&B – Cliff Lodge, Friday 26 July 2019

Kelsey Fleming[1], Justin Perrault[2], Nicole Stacy[3], Christina Coppenrath[2], Alison Gainsbury[1]

[1]University of South Florida St. Petersburg, St. Petersburg, FL, USA, [2]Loggerhead Marinelife Center, Juno Beach, FL, USA, [3]College of Veterinary Medicine, University of Florida, Gainesville, FL, USA

Effects of *In Situ* Incubation Temperatures on Hatchling Loggerhead Sea Turtle (*Caretta caretta*) Morphology, Health Indices, and Locomotor Performance

Incubation temperatures, in addition to an embryo's genetic makeup, play a crucial role in development and alter a variety of characteristics in sea turtle embryos. Most sea turtle studies document the effects of "high" and "low" incubation temperatures in laboratory-reared nests. This study's objective was to examine impacts of varying *in situ* incubation temperatures on loggerhead sea turtle (*Caretta caretta*) hatchling morphology, health, and locomotor performance on Juno Beach, Florida during the 2018 nesting season. Results showed mean incubation temperatures were significantly lower in May compared to June and July. Hatchling success decreased when the maximum temperature experienced by a nest for 3 consecutive days was over 35°C. Warmer months resulted in a slower righting time and higher values in umbilicus size, abnormal scutes present, number of unhatched embryos at full-term, and increased levels of several blood health analytes. The results suggest possible lower survival rates in hatchlings from warmer nests due to smaller sizes resulting in increased risk of predation, lowered fitness attributable to increased amount of abnormal scutes, decreased righting times in the ocean, altered hemodynamic balance and potential inflammation due to increased health indices, and decreased hatching success due to nest temperatures exceeding their lethal limit. This study adds novel health reference intervals for loggerhead hatchlings and demonstrates that even sub-lethal increases in sand temperatures due to climate change will likely affect sea turtle hatchling health and have the potential to severely impact hatchling survival.

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47 Ichthyology Lightning Talks, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Adania Flemming[1], Katherine Boole[2]

[1]Florida Museum of Natural History, Gainesville, FL, USA, [2]University of Florida, Gainesville, Fl, USA

Broadening diversity in Ichthyology and Herpetology through experiential learning in Natural History Collections

Museums serve many extremely important roles in society, from research to education. University-based museums function as scientific institutions with the ability to provide undergraduate students with opportunities to not only gain knowledge about the natural world

but develop skills for future careers, like Ichthyology (Ichs). During my tenure as a Master's student in the Biology department at the University of Florida (UF), I created an Introduction to Natural History Course which allowed UF to further harness the power of the Florida Museum of Natural History to enrich students' academic experience. The course is an exploration of careers in museum-based research and a tool to recruit underrepresented students to biodiversity studies. During the course, students are introduced to alternative career paths from pre-professional fields, through observation of and immersion into the roles of museum collections personnel. Students' individual projects within the collections provided them with research and curatorial experience. Two ichthyology undergraduate research projects are now underway as a result of student enrollment in the course, a description of a new species of the genus *Moxostoma* and an analysis of host specificity for different species of remoras. The future plans for the course will attract and potentially increase the retention of undergraduate students from underrepresented backgrounds in Ichs and Herpetology (Herps). Through authentic science experiences, these students will be equipped with skills to help them pursue careers in Ichs or Herps.

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331 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Adania Flemming[1], Katherine Boole[2], Sorilis Ruiz Escobar[2]

[1]Florida Museum, Gainesville, Florida, USA, [2]University of Florida/Florida Museum, Gainesville, Florida, USA

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Museums serve many extremely important roles in society, from research to education. University-based museums function as scientific institutions with the ability to provide undergraduate students with opportunities to not only gain knowledge about the natural world but develop skills for future careers, like Ichthyology (Ichs). During my tenure as a Master's student in the Biology department at the University of Florida (UF), I created an Introduction to Natural History Course which allowed UF to further harness the power of the Florida Museum of Natural History to enrich students' academic experience. The course is an exploration of careers in museum-based research and a tool to recruit underrepresented students to biodiversity studies. During the course, students are introduced to alternative career paths from pre-professional fields, through observation of and immersion into the roles of museum collections personnel. Students' individual projects within the collections provided them with research and curatorial experience. Two ichthyology undergraduate research projects are now underway as a result of student enrollment in the course, a description of a new species of the genus *Moxostoma* and an analysis of host specificity for different species of remoras. The future plans for the course will attract and potentially increase the retention of undergraduate students from underrepresented backgrounds in Ichs and Herpetology (Herps). Through authentic science experiences, these students will be equipped with skills to help them pursue careers in Ichs or Herps.

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51 ASIH STOYE GENERAL ICHTHYOLOGY AWARD II, Cottonwood A-D – The Snowbird Center, Friday 26 July 2019

Joao Pedro Fontenelle, Nathan Lovejoy

University of Toronto Scarborough, Toronto, Ontario, Canada

Matryoshka fishes? Assessing South American continental-scale biogeography using the widespread Neotropical freshwater stingrays (Myliobatiformes: Potamotrygoninae)

Diversification and biogeography of the Neotropical ichthyofauna has been repeatedly shown to be driven by geological changes in the South American continent. Recent studies provide detailed understanding of particular regions of endemism, specific rivers or basins, but continental-scale studies are rare and often lack the necessary sampling for hypothesis-driven inquires. The Neotropical freshwater stingrays (subfamily Potamotrygoninae) include both regional endemics and widely-distributed species, and are found across almost every major river basin in South America. We use a recently generated time-calibrated phylogeny for the family Potamotrygonidae, including 34 out 37 valid species across the entire distribution of the group, to infer diversification and biogeographical dynamics at a species and population level. Our results show evidence of major geological events that shaped the continent over the last 30 million years. We recover area-determined relationships for species and populations, evidence for two independent connections between the Paraná-Paraguay and the Amazon basins, rearrangement of faunal connections through the Rupununi portal (Branco and Essequibo rivers) and Casiquiare channel (Negro and Orinoco rivers), as well as the effects of paleogeographical barriers. We show that upper and lower portions of the Tapajós, Xingu and Tocantins are different biogeographical areas, not closely related to each other. We propose a younger time-frame for diversification of lower Amazon and shield associated faunas, together with an upper to lower Amazon vicariance tendency. Our study provides evidence not only for the evolution of potamotrygonines, but also how large scope phylogenetic studies help to unveil complicated evolutionary scenarios across different time scales.

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288 Herpetology Ecology, Primrose A&B – Cliff Lodge, Saturday 27 July 2019

Jessica Ford

McGill University, Montreal, Quebec, Canada

Evidence for Intraguild Predation amongst Toad Tadpoles

Intraguild predation is when predation occurs within one trophic level, acting to both provide nourishment to the predator and eliminate a potential competitor. While studies on interactions between competitors in larval amphibian communities have reported reduced survival, reduced growth, and reduced weight at metamorphosis when competitors are present, few report predation between tadpole species. When this predation does occur, it tends to be between distantly related species, or when there is a large size difference between species. During

mesocosm experiments involving the tadpoles of the American toad (*Anaxyrus americanus*) and Fowler's toad (*Anaxyrus fowleri*), I unexpectedly found that the American toad tadpoles predated upon the Fowler's toad tadpoles. Not only are these two species closely related, but they were similar in size, age, and appearance in the mesocosms. There was no evidence of predation in single species tanks with the same density as the mixed species tanks. Even when kept at double the density of the mixed species tanks, American toad tadpoles showed no evidence of predation on their own species. This indicates that this predation event was not due to the density of the tadpoles in the mesocosms, and that the American toad tadpoles can distinguish between individuals of their own species and the closely related Fowler's toad. This has implications on how we consider trophic relationships within amphibian guilds, as well as what we consider to be the diet of these tadpoles, as American toad tadpoles were previously thought to be herbivorous.

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278 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Kaya Foster, Subir Shakya, Prosanta Chakrabarty

Louisiana State University, Museum of Natural Science, Baton Rouge, LA, USA

Schooling with Fishes: An Interactive Poster of All Fish Families

In this interactive poster we will illustrate all 500+ known families of fishes. (One species per family was selected as a representative.) This poster will be presented by the authors at JMIH19 in order to get feedback about these full color illustrations and also to request fun and obscure facts about these fishes. We hope to publish the illustrations in a book that will also have brief biographies of each family. We intend for the book to target young readers and to spur or enhance their interests in ichthyology.

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365 ASIH STOYE GENERAL ICHTHYOLOGY AWARD II, Cottonwood A-D – The Snowbird Center, Friday 26 July 2019

Kimberly Foster, Devin Bloom

Western Michigan University, Kalamazoo, MI, USA

Top down diversification: the adaptive landscape of South American Darters (Crenuchidae: Characiformes) across a benthic/pelagic habitat axis

The Simpsonian adaptive landscape posits that species share adaptive peaks when they diversify in response to common selective pressures. Within fishes, transitions across the benthic/pelagic habitat axis may alter the adaptive landscape and create ecological opportunity for phenotypic and lineage diversification. There are classic examples of diversification across this axis in temperate fishes, but few studies have focused on the species rich Neotropical fish fauna. In this study, we investigate the role of benthic/pelagic habitat transitions in the diversification of Crenuchidae, a clade of widespread Neotropical fishes. There are currently 93 species of crenuchids divided among 12 genera. Species vary in habitat preference, with higher species richness (> 70 species) occurring in the benthos. Benthic lineages also display greater morphological diversity, suggesting shifts between benthic and pelagic habitats played an important role in the macroevolutionary dynamics of this clade. We combined morphological trait data with a time-calibrated phylogeny to investigate 1) the adaptive landscape of crenuchids, 2) the trait optima of benthic vs. pelagic crenuchids, and 3) convergent evolution in response to habitat preference. We found that South American darters underwent an early transition from the pelagic to benthic habitats, followed by repeated reversals to pelagic habitats. Multivariate morphometric analyses show significant differences between benthic and pelagic body shape, particularly in positioning of paired and median fins, indicating common adaptive optima associated with habitat preference. Our study provides important insight into the macroevolutionary dynamics of diversification across a critical habitat axis in a clade of Neotropical fishes.

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664 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Benjamin Frable, H.J. Walker, Jr., Philip Hastings

Scripps Institution of Oceanography, University of California San Diego, La Jolla, CA, USA

Integration and curation of the orphaned UCLA Ichthyological Collection into the Scripps Institution of Oceanography Marine Vertebrate Collection

The Scripps Institution of Oceanography (SIO) at the University of California San Diego maintains one of the largest ichthyological collections in the western US. The Marine Vertebrate Collection (MVC) is state-funded and is able to accession and curate vulnerable collections to maintain their availability to the scientific community. Recently, the MVC received institutional support and National Science Foundation funding to acquire, re-curate, digitize and integrate the important at-risk ichthyological collection from the University of California Los Angeles (UCLA). The collection contains around 9000 lots accumulated from 1948-2011 but collected between 1886-2011. The majority of specimens are coastal fishes from California, Baja California and the Gulf of California, and throughout the Tropical Eastern Pacific including remote oceanic islands such as the Galápagos. The UCLA collection also contains selected material from around the globe. Due to the ecological interests of its curators and collectors, there are substantial metadata associated with collection events, such as site descriptions and illustrations. Over the last three years, the MVC Collection Managers and student employees moved and re-cataloged this material including digitization of collection information, geo-referencing, imaging of field notes and replacement of metal lids, gaskets and old alcohol. Upon near-final count, the UCLA material encompasses 1,414 species in 707 genera and 217 families from 2,865 collecting localities in 35 countries. Data associated with the material are now available via the collection's website, iDigBio and VertNet. The addition of this collection further solidifies the SIO MVC as one of the largest repositories for Eastern Pacific ichthyofauna.

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487 AES Ecology, Rendezvous A&B – The Snowbird Center, Friday 26 July 2019

Bryan R. Franks[1], John P. Tyminski[2], Camrin D. Braun[3], G. Christopher Fischer[4], Robert E. Hueter[2]

[1]Dept of Biology and Marine Science, Jacksonville University, Jacksonville, FL, USA, [2]Center for Shark Research, Mote Marine Laboratory, Sarasota, FL, USA, [3]Air-Sea Interaction and Remote Sensing Dept, Applied Physics Laboratory - University of Washington, Seattle, WA, USA, [4]OCEARCH, Park City, UT, USA

Migration and Movements of the White Shark in the Western North Atlantic over Multiple Spatiotemporal Scales

Quantifying the movements and migration of animals is critical for understanding a species' life history and ecology. Combining multiple bio-telemetric methods is a useful approach to studying these parameters in highly mobile marine animals. Using passive acoustic telemetry and two types of satellite-based telemetry, we tracked 44 white sharks (*Carcharodon carcharias*) of multiple age classes in the Western North Atlantic (WNA) during 2012-2019. Results indicate clear differences in space use among age classes and sexes. Latitudinal and longitudinal expansion of movements and migration occur throughout ontogeny with mature animals being found across much of the WNA. Large-scale movements to pelagic, mid-ocean areas were primarily undertaken by adult, female sharks suggesting a reproductive component. Results show subsets of subadult and mature individuals use distinct summer habitats with evidence of seasonal site fidelity. Tagged individuals consistently exhibited directed migration from summer areas at northern latitudes, including Massachusetts and the Canadian Maritimes, to overwintering habitat on the southeastern US continental shelf and Gulf of Mexico, although there was both individual and year-to-year variation in the timing and path of this migration. While our results generally align with previous studies on white sharks in the WNA and other regions, we found distinct differences in space use by sex, age class, and capture location over multiple spatiotemporal scales. Leveraging multi-year datasets across all age classes using a suite of telemetry technologies provides critical information on long-lived, wide-ranging marine animals such as the white shark that is essential for developing sound management strategies for the species.

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652 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Layne Freeman[1], Diego Elías[1], Fernando Alda [2], Prosanta Chakrabarty[1]

[1]Museum of Natural Science, Louisiana State University, Baton Rouge, Louisiana, USA, [2]University of Tennessee at Chattanooga, Chattanooga, Tennessee, USA

Mitogenomic Relationships among Neotropical Cichlids (Heroini: Cichlinae)

The family Cichlidae is a diverse group of freshwater fishes distributed across the tropical regions of the world, including textbook examples of adaptive radiations in the Rift Lakes in Africa. In the Neotropics, the tribe Heroini is a radiation of cichlids comprising 38 genera and more than 100 species mainly distributed across Middle America (the geographic region from Northern Mexico to Panama and the Greater Antilles) with some genera in South America (e.g. *Australoheros, Mesonauta* and *Uaru*). In this study, we investigated the phylogenetic relationships among major groups of Neotropical cichlids of the tribe Heroini using complete mitochondrial genomes: Amphilophines (10 genera), Astatheroines (3 genera), Caquetaines (2 genera), Herichthyines (9 genera) and the Caribbean genus *Nandopsis*. We used the program Geneious to extract mitogenomes as a byproduct of massively parallel sequencing of ultraconserved elements. Mitogenomes were annotated and aligned to infer phylogenetic relationships using Maximum Likelihood methods in the program RAxML. This study is the first time that complete mitochondrial genomes are used to infer phylogenetic relationships among the tribe Heroini. Comparing our results to previous hypotheses will be useful in understanding how different data types result in a variety of evolutionary hypotheses, and their different geographic implications for understanding the relationships among the landmasses of Central America, the Greater Antilles and South America.

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168 Herpetology Ecology, Primrose A&B – Cliff Lodge, Saturday 27 July 2019

Luke Frishkoff[1], Eveling Gabot[2], George Sandler[3], Cristian Marte[2], D. Luke Mahler[3]

[1]University of Texas at Arlington, Arlington, TX, USA, [2]National Museum of Natural History Prof. Eugenio de Jesus Marcano, Santo Domingo, Dominican Republic, [3]University of Toronto, Toronto, ON, Canada

Elevation shapes the reassembly of Anthropocene lizard communities.

Human impacts, especially land-use change, are precipitating biodiversity loss. Yet anthropogenic drivers are layered atop natural biogeographic gradients. We ask whether the effects of anthropogenic habitat conversion depend on climatic context. We studied the structure of *Anolis* lizard communities in intact and human-modified habitats across natural climate gradients in the northern Dominican Republic. Using community-wide mark-resight methods to control for detection bias, we show that the effects of habitat conversion reverse with elevation (*i.e.* macroclimate temperature). Habitat conversion reduces abundance and biomass in lowland communities but has no such effect at high elevations. In contrast, forest loss results in no compositional change in the lowlands, but complete community turnover between habitats in the highlands. These contrasting community-level patterns emerge from consistent responses of individual species based on their thermal niches. Community reorganization in the highlands stems from thermal niche-tracking and habitat-switching by abundant lowland species. We find no support for the hypothesis that climate generalists outperform specialists to succeed in

anthropogenic habitats. Instead, warm-climate specialists dominate anthropogenic habitats, even in cool macroclimates. Human impacts interact with preexisting environmental gradients to reorganize biodiversity. Leveraging a biogeographic perspective will provide insight into the future communities of life on Earth.

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425 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Aaron Fronk, James Albert

University of Louisiana at Lafayette, Lafayette, Louisiana, USA

The Relationship Between Variation and Diversity in *Adontosternarchus* (Apteronotidae, Gymnotiformes)

The extent to which phenotypic diversity among species (macroevolutionary change) arises from variation within species (microevolutionary change) is perennially debated. One way to examine this phenomenon is to compare patterns of phenotypic variance within and among closely related species. Here we use 2D geometric morphometrics and PCA to analyze patterns of variance in head and anterior body shape within and between species of *Adontosternarchus*, a genus of planktivorous electric fishes that inhabit large rivers of tropical lowland South America. *Adontosternarchus* is a suitable target for this study because it has several species well-represented in collections, making statistical comparison between adult congeners possible; small phenotypic differences between and within species, removing any obvious confounding characters, and suggesting a recent evolutionary divergence time; and no large ecological or trophic differences between species to suggest strong adaptive change. What differences there are among the species may be the result of the summation of microevolutionary processes or represent a different suite of processes, depending on the results. A pattern in which the long-axes of variation in a morphospace are aligned would suggest that different species are the result of the accumulation of intraspecific variation over time. By contrast, a pattern in which the axes are orthogonal would indicate different forces operating to shape the variance within and among species. In this way we hope to clarify the relative significance of evolutionary processes above and below the species level, and to provide evidence pertaining to the ontological dichotomy between micro- and macroevolution.

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256 Herpetology Genetic Diversity, Ballroom 1 – Cliff Lodge, Thursday 25 July 2019

Matthew Fujita[1], Sonal Singhal[2], Tony Gamble[3], Robert Fisher[4]

[1]University of Texas at Arlington, Arlington, Texas, USA, [2]California State University, Dominguez Hills, Carson, California, USA, [3]Marquette University, Milwaukee, Wisconsin, USA, [4]US Geological Survey, San Diego, California, USA

Genome evolution in the parthenogenetic lizards

The Mourning gecko, *Lepidodactylus lugubris*, is a complex of parthenogenetic lineages that arose from hybridization between two divergent sexual progenitors. While mutation accumulation is the expected primary consequence of an asexual life history, the hybrid nature of *L. lugubris* establishes an environment with more complex genome dynamics. Here we present the genome of the paternal progenitor of *L. lugubris* along with RNA and RADseq sequencing from parthenogenetic individuals. Alongside results from whiptail lizards (*Aspidoscelis*), we have found that parthenogenetic lineages accumulate mutations, exhibit intergenomic recombination, and differentially express divergent alleles, perhaps due to epigenetic modifications of the genome. These dynamics are more complex than typically assumed for asexual organisms and may play an important role in generating diversity and variation in an otherwise clonal organism.

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352 Ichthyology Systematics I, Cottonwood A-D – The Snowbird Center, Sunday 28 July 2019

Kyoji Fujiwara[1], Hiroyuki Motomura[2]

[1]The United Graduate School of Agricultural Sciences, Kagoshima University, Kagoshima, Japan, [2]The Kagoshima University Museum, Kagoshima, Japan

Two undescribed species of the genus *Lepadichthys* (Gobiesocidae) from southern Japan and the Pitcairn Islands

The clingfish genus *Lepadichthys* (Gobiesocidae: Diademichthyinae) includes 13 nominal species, all of which are currently regarded as valid. Although the diagnosis of the genus should be revised, all species of *Lepadichthys* can be separated from all other gobiesocid genera in having the following characters: pelvic disc "single type" without deep cavity on disc region B; snout not prominently long or narrow; 3 of 5 gill arches with 2 filaments; and gill membranes attached to isthmus. During a revisional study on the genus, two unidentified species of *Lepadichthys* [*Lepadichthys* sp. A (southern Japan) and *Lepadichthys* sp. B (Pitcairn Islands)] were found. *Lepadichthys* sp. A is most similar to *Lepadichthys coccinotaenia* Regan, 1921 and previously misidentified as the latter. However, compared with *L. coccinotaenia*, *L.* sp. A has slightly fewer counts of dorsal- and anal-fin rays (10–12 and 9–11, respectively), significantly fewer counts of gill rakers (6–8 on each arch), and white narrow stripes on the snout tip through the eye to the posterior margin of pectoral fin and the anterior dorsal midline. Although *Lepadichthys* sp. B has previously been regarded as *Lepadichthys frenatus* Waite, 1904, the former is distinct from other congeners in having 13–15 (modally 14) dorsal-fin rays, 11–12 (12) anal-fin rays, 28–29 pectoral-fin rays, 8 gill rakers on each arch, and a very small disc with its length 12.4–15.3 (mean 13.6) % of standard length. *Lepadichthys* sp. A and *L.* sp. B are regarded here as two undescribed species.

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28 ASIH STOYE GENERAL HERPETOLOGY AWARD I, Primrose A&B – Cliff Lodge, Thursday 25 July 2019

Meaghan Gade, Phillip Gould, William Peterman

Ohio State University, Columbus , OH, USA

Habitat mediated responses of terrestrial salamanders to wildfire in the short-term

Wildfire is an important natural disturbance event that promotes landscape heterogeneity and regulates many wildlife communities. The compounding effects of fire suppression and climate change have increased the frequency and severity of wildfire, but the responses of many organisms to wildfire is unknown. Further, microhabitats embedded in the landscape may mediate and buffer the effects of wildfire. Terrestrial plethodontid salamanders are likely disproportionally influenced by wildfire events as a result of their lungless anatomy and reliance on cool and moist habitats; but our knowledge of salamander responses to wildfire in the short-term is limited. We used a combination of mark-recapture data and repeated count surveys to assess the short-term (6 to 18-month post-fire), habitat-mediated responses to the Camp Branch wildfire on Wayah Mountain in North Carolina. We observed precipitous declines of the red-legged salamander, *Plethodon shermaini,* in exposed upland forests but no apparent negative effects in riparian forests 18-months after the wildfire event relative to unburned sites. We also saw a loss of juvenile size-classes in the upland forest with only the largest adult individuals remaining 18-months post-fire. There was no size class differences in the riparian forests. Our results suggest riparian forests may be buffered from the canopy cover, vegetation, and soil duff layer loss and removal following a wildfire event, and salamanders inhabiting riparian forests may be at less risk to declines than those in exposed habitats. Our results underscore the need to assess wildfire effects across a landscape to determine the effects of disturbance to populations.

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210 ASIH STOYE GENERAL HERPETOLOGY AWARD I, Primrose A&B – Cliff Lodge, Thursday 25 July 2019

Bannon Gallaher, Steven Beaupre

University of Arkansas, Fayetteville, AR, USA

Factors That Affect Home Range of Timber Rattlesnakes (*Crotalus horridus*) in Northwest Arkansas

Conservation of animal populations requires knowledge of their habitat and spatial needs. Quantifying spatial requirements involves the analysis of home range. We examined the effects of sex, body size (SVL), body condition (log mass/log SVL), and year on home range in Timber Rattlesnakes (*Crotalus horridus)* in Northwest Arkansas. Data from an ongoing, 22+ year radio-telemetry study in Madison Co., Arkansas were analyzed using both minimum convex polygon

(MCP) and Kernel Density Estimates (KDE). Plots of the number of sequential observations versus home range (MCP and KDE) determined that 25-30 locations per individual per active season (using weekly to bi-weekly sampling) were sufficient to generate a stable home range estimate using MCP and KDE methods. Restriction to samples of ≥25, resulted in 122 snake-years of data, distributed among 55 individuals (26 males and 29 females). Home ranges were estimated using ArcGIS 10.4 with HRT extension. Mixed model ANCOVA revealed a significant SVL by Sex interaction ($p = 0.0033$). Male MCP increased with body size ($p= 0.0169$), whereas, no effect of body size was detected for females. Improved body condition increased MCP and KDE (90% and 95%) in males (regression: $p= 0.0031$, $p= 0.0403$, and $p=0.0418$), but not in females. Differences (MANOVA) in home range centroid were observed in 22 of 24 individuals with a minimum of three years of data. Our results verify that spatial needs of males and females differ, and importantly, suggest that home range frequently shifts in location among years.

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62 AES Trophic Ecology I, Alpine A,B,C – The Snowbird Center, Sunday 28 July 2019

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

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

Trophic Ecology of the Scalloped and Carolina Hammerheads in Coastal Waters of the Southeastern U.S.

The diet of Scalloped Hammerheads has been widely studied in the Pacific as well as the Gulf of Mexico and Brazil, however little is known about the diet of the population in the NW Atlantic. Carolina Hammerheads have only been recently described as a new species, and no research has been conducted to date on their trophic ecology. Stomach content and stable isotope analyses (on muscle, liver, whole blood and plasma tissues) were conducted on genetically identified young-of-year Scalloped and Carolina Hammerheads in the coastal waters of South Carolina, Georgia, and Florida. Preliminary results from stomach content analyses suggest that Scalloped and Carolina Hammerheads have diverse diets with no resource partitioning between species. However, significant differences in stable isotope signatures were detected between species in early (<2 months from parturition) hammerheads. Due to slow tissue turnover rates, these signatures likely reflect maternal isotopic signatures indicating habitat or resource partitioning between adult Scalloped and Carolina Hammerheads. In addition to species differences, we will compare regional and temporal differences in diet and trophic ecology of the two hammerhead species.

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243 AES Conservation & Management III, Rendezvous A&B – The Snowbird Center, Sunday 28 July 2019

Karla Garces-Garcia[1], Javier Tovar-Ávila[2], Dario Chavez-Arrenquin[3], Bibiana Vargas-Trejo[4],Terence Walker[1], Robert Day[1]

[1]University of Melbourne, Melbourne, Victoria, Australia, [2]INAPESCA, Bahia de Banderas, Nayarit, Mexico, [3]INAPESCA, Mazatlan, Sinaloa, Mexico, [4]National Institute of Mexico, campus Bahia de Banderas, Bahia de Banderas, Nayarit, Mexico

Evaluation of Elasmobranchs caught by prawn trawls in the Gulf of California for Vulnerability Analysis (Fishing and Climate change stressors)

This study used fishery independent sampling between 2011 and 2017 in the coastal south-eastern and entrance region of the Gulf of California (GoC). Animals were collected by sampling the catch at each of a series of fixed stations during all seasons, mainly during summer, when prawn trawling is prohibited and information from commercial catches is not available. We analyzed size-frequency composition for six species that frequently appeared in trawls done. For these species, we used beta-binomial logistic regression to explore whether the proportion of trawls in which each species occurred was related to sea surface temperature (SST) and depth strata (shelf-inshore and shelf offshore). We allocated the total of species into ecological groups. A total of 25 species were collected. We found significant differences in the mean size between mature females and mature males for 4 of 6 species tested. For three species, the proportion of trawls in which they occurred was significantly related to SST, whereas for one species, the proportion was related to inshore depths. The three ecological groups were shelf-sand, shelf-inshore and pelagic. We determined that the shelf-inshore ecological group was associated to SST, whereas the other groups were associated to the trawl depth. Although further investigation is required, we have provided insight into how SST and trawl depth influence the bycatch elasmobranchs caught during prawn trawling in the GoC. Biological information will be used to analyze ecological vulnerability to fishing and climate change stressors of these species and help the conservation of elasmobranchs in the GoC.

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638 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Iván García-López[1], Nilson Blanco-López[1], Glenys Tordecilla-Petro[2], Charles W. Olaya-Nieto[3]

[1]University of Cordoba, Monteria, Cordoba, Colombia, [2]Institución Educativa Lácides C. Bersal. Alcaldía de Lorica, Lorica, Cordoba, Colombia, [3]Fishery Biology Research Laboratory-FBRL, Department of Aquatic Sciences. University of Cordoba, Lorica, Cordoba, Colombia

Reproductive biology of Cachana *Cynopotamus atratoensis* in the Cienaga Grande de Lorica, Colombia

To study the reproductive biology of Cachana *Cynopotamus atratoensis* in the Cienaga Grande de Lorica, Colombia, 228 individuals with total length (TL) ranged between 13.8-40.8 (25.7 ±

6.5) cm and total weight (TW) ranged between 28.0- 936.0 (239.4 ± 207.9) grams were collected. The gonads were placed in Gilson solution, the Vazzoler scale was applicated and sexual proportion, maturity index, spawning season, length at first maturity, ovocites's diameter and fecundity were estimated. It was found 132 females, 93 males and 3 undifferentiated individuals, with sexual proportion female: male 1.4:1, differently than expected. The Cachana is a fish with total spawning, with spawning season extending from February to December, performing lateral migration in the cienaga. Length at first maturity estimated in 31.1, 25.9 and 29.3 cm TL for females, males and both sexes, respectively, oocites's diameter was 938 µm and average fecundity was 35084 oocites.

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710 AES Symposium: The Sensory Biology of Elasmobranch Fishes, Rendezvous A&B – The Snowbird Center, Saturday 27 July 2019

Jayne Gardiner

New College of Florida, Sarasota, FL, USA

Multisensory Integration in Elasmobranchs: Recent Advances and Future Directions

Our understanding of elasmobranch sensory systems has increased dramatically over the past several decades, but much of this knowledge comes from studying individual senses. In the natural environment, animals must generally attend to multiple sensory cues simultaneously. Different sensory cues disperse over different spatial scales and an animal at a great distance from the source may encounter a sensory cue in isolation, but as it approaches the source, multiple sensory signals. The ability to integrate information from multiple sensory channels, considered a fundamental characteristic of the brain, can enhance detection, identification, or localization of stimuli. For example, two spatially coincident sensory signals may converge at the same neuron in the brain, resulting in a response that is greater than the additive responses to the two individual signals. As a result of sensory plasticity, animals can also perform sensory switching to focus on the most reliable signal or to compensate for signal loss. Studying these phenomena in elasmobranchs has historically proven challenging, but significant progress has been made in recent years. This presentation will review current knowledge of multisensory integration in elasmobranchs garnered from behavioral and neurobiological studies and discuss how new technologies may offer opportunities to increase our understanding of multimodal guidance of complex behaviors in both the laboratory and the field.

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739 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Jayne Gardiner[1], Alexa Baldino[1], Lukas Heath[1], Danielle Zeris[1], Joel Beaver[1], Tonya Wiley[2]

[1]New College of Florida, Sarasota, FL, USA, [2]Havenworth Coastal Conservation, Palmetto, FL, USA

The effects of red tide (*Karenia brevis*) on elasmobranchs in a southwest Florida estuary

Red tide events, blooms of toxic microalgae (*Karenia brevis*), occur regularly along the Gulf coast of Florida. *K. brevis* blooms produce brevetoxins, potent neurotoxins that cause convulsions, paralysis, and respiratory failure in fish, resulting in massive fish kills. These fish kills affect a wide variety of bony fish species and can severely disrupt the structure of teleost communities for months to years after the bloom subsides, but the effects of red tide on elasmobranchs are poorly understood. Because red tide-associated shark mortalities are rarely observed, it has been suggested that these animals are capable of detecting and avoiding *K. brevis*. For the past three years, we have been conducting a standardized gillnet survey to assess elasmobranch diversity and abundance in two adjacent nursery areas, Sarasota Bay and Terra Ceia Bay. Extremely high *K. brevis* cell counts were recorded in Sarasota Bay from August 2018 to January 2019, as were mass mortalities of fish, dolphins, manatees, and sea turtles. Red tide was not observed in Terra Ceia Bay, likely due to its lower salinity, and no fish kills or mortalities of other marine life were reported. We documented significant decreases in the relative abundance of sharks and rays in Sarasota Bay, but not Terra Ceia Bay, during the red tide event and a negative correlation between elevated *K. brevis* cell counts and both diversity and abundance of elasmobranchs. Acoustic telemetry evidence suggests that at least one species, the blacktip shark, *Carcharhinus limbatus*, succumbed to, rather than evaded, the bloom.

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643 ASIH STORER ICHTHYOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Jennifer Gardner[1], James Orr[2], Luke Tornabene[1]

[1]University of Washington, Seattle, Washington, USA, [2]NOAA National Marine Fisheries Service, Alaska Fisheries Science Center, RACE Division, Seattle, Washington, USA

Two new species of snailfish (Liparidae) from the Aleutian Islands, Alaska, and the status of *Temnocora*

Worldwide, over 430 species of liparids have been described and allocated to about 32 genera. The diversity in the North Pacific is particularly high, with more than 150 species of snailfishes in 17 genera. *Careproctus* is the most specious genus in the region, containing over 60 species, though it has been shown to be paraphyletic both globally and locally in the North Pacific. Three species of *Careproctus* from the Aleutian Islands, Alaska, all with variegated coloration have been described recently. These species (*C. comus, C. faunus,* and *C. staufferi*) were recovered in a well-supported clade with *Careproctus (Temnocora) candidus* in recent molecular phylogenetic hypotheses and prompted our reevaluation of the status and diagnosis of *Temnocora*. Presently recognized as a subgenus of *Careproctus,* the monotypic genus *Temnocora* had been primarily diagnosed by the presence of a lobed dorsal fin and a slitted pupil, characters that these species lack. Here we will describe two new species from the Aleutian Islands that appear most similar to *C. candidus* in having a variegated coloration, a slit pupil, and a partially lobed dorsal fin. They differ based on vertebral counts, morphometrics, and characteristics of the dorsal fin. We discuss the resurrection of the newly diagnosed genus *Temnocora* and the allocation of these species to the genus. The description of new species related to *C. candidus* and the potential resurrection of *Temnocora* will provide important steps to resolving the paraphyly of *Careproctus,* the most diverse genus within a diverse marine fish family.

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226 ASIH STOYE ECOLOGY & ETHOLOGY AWARD I, Cottonwood A-D – The Snowbird Center, Friday 26 July 2019

Chance Garrett, Ginny Adams, Reid Adams

University of Central Arkansas, Conway, AR, USA

Habitat Associations Of Riffle Fishes In An Ozark River Having A Dynamic Gravel Bed Load

Streams of the Arkansas Ozarks have experienced extensive erosion and gravel intrusion due to land use change. As a result, modifications to instream habitat have resulted in an increase in transverse and diagonal gravel bars along with associated transient, shallow, low velocity riffles. This study was conducted to determine if variation in riffle habitat affects riffle fish communities. For this study, 37 riffles were sampled across fall and spring in the Kings River, Arkansas using seines and kick-set methods. Additionally, physical and chemical environmental characteristics were measured. Riffles in the Kings River exhibited a gradient in available habitat with two extremes, one being shallower, slower riffles with smaller substrate (unstable riffles) and the other deeper, faster riffles with larger substrate (stable riffles) (PCA). Two-way ANOVA's were used to evaluate differences in relative abundances of benthic fishes based on riffle type and season. During spring, stable riffles had greater richness than unstable riffles, but during fall there was no difference. *Noturus albater*, *N. exilis*, *Etheostoma euzonum*, and *E. zonale* were found in greater abundances and/or frequency in stable riffles during at least one season. These findings indicate gravel intrusion has altered riffles in the Kings River and could be influencing population sizes of benthic fishes.

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478 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Jacob Gastelum, Dalton Leibold, Rory Telemeco

California State University, Fresno, Fresno, California, USA

Effects of Metabolic Demand on Thermal Preference Across Oxygen Environments

The mechanism by which animals lose function at high temperatures is poorly understood for many species. Predicting how animals will respond to climate change through acclimation and

future evolutionary processes requires a mechanistic understanding of the traits that underlie thermal tolerance. The Hierarchical Mechanisms of Thermal Limitation (HMTL) Hypothesis proposes that respiratory capacity and the marginal stability of proteins and membranes interact hierarchically to determine thermal performance and limits. A fundamental, yet untested, prediction of the HMTL hypothesis is that behavioral anapyrexia (i.e. seeking reduced body temperature when exposed to hypoxia) will be exacerbated when metabolic demand is high, with individuals reducing body temperature at higher oxygen partial pressures. We tested this prediction of the HMTL hypothesis using western fence lizards (*Sceloporus occidentalis*). We exposed animals to 16 oxygen environments (6-21 kPa) and allowed animals to select body temperature within a thermal gradient. Metabolic demand treatments included recovery from exercise (high metabolic rate) and animals at rest (low metabolic rate). Lizard body temperatures were recorded every 15s using temperature data loggers and we estimated Preferred Body Temperature (PBT) and the Voluntary Thermal Maximum and Minimum. These data provide insights into how thermal preference and performance are affected by reduced oxygen partial pressures when animals have ecologically relevant metabolic demands. Given numerous species are predicted to migrate to higher elevation where oxygen partial pressures are reduced in response to warming environments, understanding the relationships between temperature, oxygen, behavior, and performance are critical for predicting the effects of climate change on reptiles.

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232 ASIH STOYE ECOLOGY & ETHOLOGY AWARD I, Cottonwood A-D – The Snowbird Center, Friday 26 July 2019

George Gavrielides, Ginny Adams, Reid Adams, Matthew Connolly

University of Central Arkansas, Conway, AR, USA

Potential Effects of Land Cover Change on Fish Assemblages in the Eleven Point River Basin

The Eleven Point River is a spring-fed, karst-dominated stream flowing through the Salem Plateau of the Ozarks ecoregion in southeast Missouri and northeast Arkansas. Limited research has been conducted on the Arkansas stretch of the river despite growing concerns about the existing and projected expansion of the poultry industry in the watershed. Land cover within the watershed is approximately 69% forest, 30% agriculture, and 1% development. Increased poultry production in the lower watershed may result in increased deforestation, water withdrawal and effluent which may negatively affect fish assemblages. Overall land cover change may also alter channel morphology and water chemistry of the stream. Johnson and Beadles (1977) collected 90 species of fish from 1976-1977 prior to the land cover change. In order to examine changes in fish assemblage, we replicated Johnson and Beadles' sampling method using similar seine dimensions and scope of habitat selection (riffles, runs, pools). NMDS of their historical fish collections will be compared with National Wall-to-Wall Anthropogenic Land Use Trends (NWALT) from 1974-2012 to examine changes in contemporary assemblages. Persistence and stability were calculated on fish collections at contemporary tributary sites. Geomorphology data will be collected at each site to further our examination of physical change in the stream. Water table fluctuation and in-stream habitat alterations due to land use are expected to be the main causes of assemblage changes since the Johnson and Beadles study. However, analyses of future collections will determine how the land cover disturbances within the watershed have affected fish biota.

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400 AES Physiology II, Alpine A,B,C – The Snowbird Center, Sunday 28 July 2019

Jim Gelsleichter[1], R. Dean Grubbs[2], John Carlson[3]

[1]University of North Florida, Jacksonville, FL, USA, [2]Florida State University Coastal and Marine Laboratory, St. Teresa, FL, USA, [3]NOAA Fisheries Service Southeast Fisheries Science Center, Panama City, FL, USA

Mercury in blood of the endangered smalltooth sawfish, *Pristis pectinata*

Due to overfishing and human destruction of its habitat, the smalltooth sawfish (*Pristis pectinata*) became listed as “endangered” under the U.S. Endangered Species Act (ESA) in 2003 and remains one of very few U.S. domestic marine fish to hold this undesirable designation. Because of this, a recovery plan was established for this species and is regularly updated to continually assess the status of remnant U.S. sawfish populations, identify threats to population rebuilding, and refine strategies for ESA delisting. One potential category of threats that has not been well studied to date is the effect of environmental pollution on sawfish populations. In this study, we describe the first examination of pollutant exposure in smalltooth sawfish in Florida, conducted by assessing concentrations of the non-essential toxic metal mercury (Hg) in erythrocytes obtained from routine blood sampling. Total mercury (THg) concentrations were measured in erythrocytes of 40 smalltooth sawfish, ranging in size from neonates to full-size adults. Data were compared with THg concentrations in erythrocytes from other elasmobranch species collected from the same general location to gauge the relative level of Hg bioaccumulation in *P. pectinata*. Although range in data was considerable, smalltooth sawfish were shown to be capable of accumulating Hg to concentrations as high as 3 mg/kg dry weight in erythrocytes; levels comparable with those observed in large coastal and pelagic sharks. Based on these results, Hg accumulation has the potential to pose health risks to smalltooth sawfish, particularly in larger individuals.

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277 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Michael Ghedotti[1], Matthew Davis[2]

[1]Regis University, Denver, Colorado, USA, [2]St. Cloud State University, St. Cloud, Minnesota, USA

Anatomy and Evolution of the Greeneye Bioluminescent Organ (Teleostei: Chlorophthalmidae)

The greeneyes (*Chlorophthalmus*) are deep-water fishes with enlarged eyes that are their namesake and a light organ surrounding the anus that houses bacteria in the genus *Photobacterium*. In this study we seek to closely determine the anatomic structure of the bioluminescent organ in multiple species of *Chlorophthalmus* and compare this anatomy to that in the non-bioluminescent sister taxon, *Parasudis.* We used histological sectioning and gross dissection to explore the anatomy of the bioluminescent organs. We generated and used a DNA-sequence based phylogeny for the group to explore the evolution of bioluminescence. The bacterial bioluminescent organs in the greeneyes, as in at least two other unrelated bioluminescent groups, are derived from in-pouching of ectodermal tissue derived from the proctodeum around the anus. The anatomy in the context of the phylogeny suggests that the bioluminescent organs of the greeneyes evolved once. The study also suggests that the proctodeal region provides a repeated opportunity for the evolution of bioluminescent symbiosis in teleost fishes.

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549 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Sam Ghods, Luke Tornabene

University of Washington, Seattle, WA, USA

Evolution and Developmental Morphology of Male Deep-Sea Anglerfishes (Teleostei, Ceratioidei): Investigating the Features Enabling Sexual Parasitism.

This project aims to describe differences in the development and specialization of skeletal elements in male deep-sea anglerfish (Suborder Ceratioidei). While some studies have investigated the origin and development of the characteristic lure of the female anglerfish, few studies have examined the homologous elements of this structure, or lack thereof, in males of this group. Parr, 1930, theorized that the rostral structure of male anglerfish is homologous to the illicium of the female, labeling his observations as “an example of the extreme phylogenetic economy of morphological parts”. To test this hypothesis, our study will describe the origin and development of the specialized rostral jaws in male anglerfish of the genus *Melanocetus* and examine how this relates to female development. We will examine both the skeletal elements as well as musculature in developing males, and then describe any homologies to elements found in the opposite sex. Our goal is to CT scan and subsequently clear and double-stain a complete developmental series of *Melanocetus johnsonii* and examine the metamorphosis of the upper jaw and dorsal-fin elements from larvae to sexually mature adults.

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641 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Nureen Ghuznavi[1], Dahiana Arcila[2], Lily Hughes[1], Ricardo Betancur-R[2], Guillermo Ortí[1]

[1]George Washington University, Washington, District of Columbia, USA, [2]University of Oklahoma, Norman, Oklahoma, USA

Resolving Ancient Fish Radiations with Phylogenomic Data Using Targeted Filtering and Gene Genealogy Interrogation

Phylogenomic datasets are composed of hundreds to thousands of gene fragments of varying length, typically exons or ultraconserved loci. Conflicting phylogenetic signals among loci have been reported in many studies including fishes and other organisms, with several explanations accounting for the discordant resolutions of gene trees. These range from biological processes such as incomplete lineage sorting, hybridization, and paralogy, to statistical artifacts originating from random or systematic errors in the estimation process, to data errors incurred by bioinformatics pipelines during matrix assembly. New methodological approaches to address these issues are in active development but, currently, there is no general consensus about the best way to analyze complex pylogenomic datasets. We here contrast two approaches to gauge the degree of conflict among loci and test their effects in resolving recalcitrant nodes in the Tree of Life of fishes. One approach involves targeted filtering of loci as a function of their phylogenetic information content to maximize signal and minimize noise (homoplasy); the other involves Gene Genealogy Interrogation (GGI), a method that assesses the relative support for alternative hypotheses using topology tests on a locus-by-locus basis. We apply these approaches to shed light on recalcitrant resolutions at the base of the teleost radiation, among otophysan lineages, and at the base of the percomorph radiation. In addition to advancing our knowledge of the fish Tree of Life, this study is a contribution to better understanding the advantages and disadvantages of different methods of analysis.

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475 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Melissa Gibbs, Anna Thornton, Samantha Pasko, Ashley Gamba, Kahri Smith

Stetson University, DeLand, Florida, USA

Patterns of Aerial Respiration in Hypoxic Conditions by Juvenile *Pterygoplichthys* sp. (Loricariidae)

Volusia Blue Spring, a hypoxic freshwater spring in central Florida, has been home to the invasive armored catfish *Pterygoplichthys disjunctivus* (Loricariidae) since 1999. Adult *P. disjunctivus* are common in the spring run, and able to handle the low oxygen conditions by air-breathing using their modified stomach. Nearly all catfish reproduction occurs in the adjacent St. Johns River, and juveniles under 20 cm SL are rarely found in the spring run. We assumed that smaller, less well-armed fish were less common in the spring because they would be more vulnerable to predation in the clear water of the spring, especially if they had to come to the surface to breathe, but we also hypothesized that smaller juvenile fish would be more sensitive to lower oxygen levels than larger juvenile fish and adults, which would lead to elevated air-breathing rates in smaller fish and thus put them at even greater risk of predation. We measured air-breathing behavior (breaths/hour) in the lab, using 12 small (5-7.9 cm) and 24 large (8-13 cm) juvenile armored catfish housed in a range of dissolved oxygen (hypoxic, transitional, and normoxic). The data were compared with an ANOVA, and as expected, we found a significant negative effect of both dissolved oxygen and fish size on air-breathing rates. Smaller juvenile catfish relied significantly more heavily on aerial respiration than did larger juveniles under all dissolved oxygen conditions.

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573 General Ichthyology II, Cottonwood A-D – The Snowbird Center, Saturday 27 July 2019

Sarah Gibson[1], Andrew Milner[2], Paul Olsen[3]

[1]St. Cloud State University, St. Cloud, Minnesota, USA, [2]St. George Dinosaur Discovery Site at Johnson Farm, St. George, Utah, USA, [3]Lamont-Doherty Earth Observatory of Columbia University, Palisades, New York, USA

Revisiting †*Tanaocrossus kalliokoskii* (Osteichthyes, Actinopterygii), an Enigmatic Fish from the Upper Triassic Chinle Formation of the Southwestern United States

†*Tanaocrossus kalliokoskii* is a monotypic extinct stem actinopterygian taxon from the Upper Triassic Chinle Formation (210–201 Ma) of the southwestern United States. It possessed a distinctive elongate dorsal fin, vertical jaw suspensoria, and ganoid scales, but its original description was limited to a single specimen lacking an anterior portion of the skull. Its evolutionary relationships to other stem actinopterygian taxa have remained elusive for decades due to the lack of additional specimens and key morphological data. Prior studies have placed †*T. kalliokoskii* in several different groups of extinct and extant ray-finned fishes, including the †Perleidiformes, †Scanilepiformes, †Palaeoniscimorpha, and Polypteriformes. Recent collecting efforts in the Chinle Formation of San Juan County, Utah have produced a trove of fossil fishes, including multiple complete specimens of †*Tanaocrossus*. These new specimens provide complete skull and jaw information, and allow us to revisit this enigmatic taxon and its relationships to other early ray-finned fishes. Herein we redescribe †*T. kalliokoskii* based on new anatomical and morphological information gained from the addition of new specimens. We examine previous phylogenetic studies and provide a new, more comprehensive hypothesis of evolutionary relationships of †*T. kalliokoskii* among stem actinopterygian lineages.

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163 Ichthyology Reproduction, Development, and Morphology, Cottonwood A-D – The Snowbird Center, Sunday 28 July 2019

M Chaise Gilbert[1], Alberto Akama[2], Cristina Cox Fernandes[3,4], R Craig Albertson[5]

[1]University of Massachusetts, OEB, Amherst, Massachusetts, USA, [2]Museu Paraense Emílio Goeldi, Belém, Pará, Brazil, [3]University of Massachusetts Amherst, Amherst, Massachusetts, USA, [4]Instituto Nacional de Pesquisas da Amazônia, Manaus, Amazonas, Brazil, [5]University of Massachusetts, Amherst, Massachusetts, USA

Rapid Changes in Native Cichlid Populations following Anthropogenic Alteration to a Major Clearwater River in the Amazon

The Tocantins River serves as the major drainage for the Tocantins and Araguaia watershed and was once a large (2,450km), contiguous system. The construction of the Tucuruí Hydroelectric Dam in 1984 established a large (~2,850km^2) ‘permanent’ reservoir, eliminating the once historic streams, floodplains, and rapids that occupied this length of the Tocantins river. Such dramatic anthropogenic change can either lead to the extirpation of local flora and fauna, or species may be able to adapt to local environmental changes. To explore the latter possibility, we used geometric morphometrics to evaluate changes in native cichlids, incorporating both

museum specimens collected prior to the closure of the hydroelectric dam (≤ 1984) and specimens collected during 2017-18. A total of six species across four genera were included to represent distinct ecomorphs, varying from large piscivorous fishes to relatively small opportunistic omnivores. While some lineages expressed subtle changes, more drastic morphological shifts were documented in others. Moreover, documented morphological changes tended to be associated with functional aspects of anatomy, including head, fin and body shape. Notably, morphological data collected from large predatory *Cichla* samples suggested that reservoir populations may be hybridizing. A comparison of mtDNA sequences supports the idea that resident *Cichla* constitute a hybrid swarm. These data suggest that native cichlid populations have undergone rapid (≤ 50 years), and in some instances dramatic, morphological changes since the closure of the dam, and provide insights as to the ways that different fish ecotypes and reservoir populations may respond to sudden, large scale hydrological alterations.

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142 Ichthyology Genetics, Cottonwood A-D – The Snowbird Center, Sunday 28 July 2019

Matthew Gilg, Emily Kerns, Natalia Gutierrez, Catherine Kooyomjian, Natasha Hinojosa

University of North Florida, Jacksonville, FL, USA

Dynamic Cohort Analysis Reveals Evidence of Directional Selection in a Killifish Hybrid Zone.

Hybrid zones are excellent places to study evolutionary processes due to the presence of distinguishable recombinant genotypes that often differ in fitness. Also, since they typically involve species that are recently diverged they provide insight into the early stages of speciation. The strength of reproductive barriers and whether the fitness of various genotypes within a hybrid zone are related to environmental differences are key questions to address to understand the evolutionary dynamics of the zone. We conducted a dynamic cohort analysis at a location within a hybrid zone between the killifish species, *Fundulus heteroclitus* and *F. grandis*, over the course of three years to determine the extent at which hybridization occurs, whether hybrids have low fitness, and whether patterns of selection observed are likely tied to environmental differences or are simply intrinsic. Samples were genotyped at three nuclear loci and one mitochondrial locus and separated into a pair of age classes each year by size differences. Populations at this location were dominated by parental and second generation hybrid genotypes with few likely F1 genotypes observed. While older age classes tended to show hybrid deficiencies, selection appears to be directional with a sharp decline in the frequency of *F. grandis* alleles at all nuclear loci between the two age classes in all years. The allele frequency change between ages 1 and 2 suggests a likely environmental component.

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336 Ichthyology Life History/NIA, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Victor Giovannetti, Mônica Toledo-Piza

Departamento de Zoologia, Instituto de Biociências da Universidade de São Paulo, São Paulo, SP, Brazil

Morphological Variation of Characiform Dentition and its Phylogenetic Significance

It has been repeatedly highlighted in the literature that the dentition of the Characiformes is extremely variable. An expected consequence of this variation is that this anatomical complex could provide informative characters that contribute to elucidate the relationships between the major taxa within the order. Variation of the dentition has been phylogenetically explored in sub groups of the order, however, to this date, this anatomical complex was not fully explored at the order level with adequate sampling and detail. In this study we aim to describe and illustrate in detail the adult dentition of representatives of the Characiformes regarding tooth morphology; tooth implantation mode; number, arrangement and identity of teeth rows; replacement teeth formation modes and temporal sequence of the replacement. So far, 74 taxa covering all the families within the order, except the edentulous Curimatidae and the recently described Tarumaniidae, were described and illustrated based on examination of cleared and stained specimens and histological sections. In addition, we describe and illustrate morphological changes such as teeth number, arrangement and tooth morphology on the dentition throughout the ontogeny of selected taxa (*Hydrocynus forskahlii*, *Brycinus ferox*, *Astyanax lacustris*, *Ctenolucius hujeta*, *Leporinus* sp., *Prochilodus* sp., *Brycon orthotaenia* and *Colossoma macropomum*). Along with the descriptions and illustrations, some shared general patterns were identified, as well as new interpretations regarding teeth rows identity and their homology between related taxa. The new data and interpretations along with their implications are discussed considering the current knowledge of the phylogenetic relationships within the Characiformes.

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655 ASIH STOYE GENERAL ICHTHYOLOGY AWARD II, Cottonwood A-D – The Snowbird Center, Friday 26 July 2019

Matthew Girard

University of Kansas, Lawrence, KS, USA

Morphological support for the relationships among carangiform fishes

Beginning in the early 21st century, researchers using DNA-based analyses hypothesized novel sets of relationships among percomorph fishes. These hypotheses of relationships have been repeatedly tested using different scales of molecular data—from single loci and hundreds of basepairs, to hundreds or thousands of loci and hundreds of thousands of basepairs—and the same major clades have been repeatedly recovered and refined in subsequent DNA-based studies. However, few of these DNA-based and ordinal-scale clades have been evaluated from an anatomical perspective. While few studies have noted anatomical traits in light of their recovered

topology, novel morphological characters have largely been unexplored for these phylogenetic hypotheses. Given the lack of a comparative morphological dataset for any of these recently recognized clades, the objective of this study is to investigate the relationships among the carangiform fishes from a combined morphological and molecular perspective. The morphologically diverse carangiform fishes, which has been called numerous names since being recovered by analyses of DNA data (e.g., Clade L, Carangimorpha, Carangaria), consists of more than one thousand species and thirty families, including, but not limited to, the Carangidae, Latidae, Istiophoridae, and all pleuronectoid flatfishes. To investigate the relationships and anatomical support among these fishes, I will show the results of a combined phylogeny of the Carangiformes that is based on osteological characters, Sanger-based loci, and ultraconserved elements.

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269 ASIH STORER HERPETOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Cody Godwin[1], Christopher Murray[1], Alejandro Grajal-Puche[2], Matthew Grisnik[2], Alexander Romer[2], Donald Walker[2]

[1]Tennessee Technological University, Cookeville, TN, USA, [2]Middle Tennessee State University , Murfreesboro, TN, USA

Testing the Febrile Response of Snakes Inoculated with *Ophidiomyces ophiodiicola* (*O.o*), the Causative Agent of Snake Fungal Disease

Snake Fungal Disease (SFD) is a fungal pathogen of wild snakes populations, predominantly in the Eastern and Midwestern United States. SFD is characterized by heterophilic granulomas that can form around the mouth and eyes with severe cases causing weight loss, impaired vision and eventual death. Researchers, making field observations, have noted early season basking from severely infected snakes. This may suggest that snakes are attempting to raise their body temperature, inducing a febrile response, to combat the mycosis. This study tested the hypothesis that the causative agent of snake fungal disease (*Ophidiomyces ophiodiicola*) induces a febrile and behavioral response of seeking differential basking temperature to regulate body temperature. Eastern ribbon snakes (*Thamnophis sauritus,* n=30) were sham or *O.o* inoculated. Seven days after inoculation, snakes were tested on a thermal gradient that ranged from 40°C to 18°C. The internal body temperature of each snake was measured every 30 minutes for eight hours with a thermal probe inserted into the cloaca of each snake. Additionally, substrate temperatures, where the snake was basking, were measured every 30 minutes, using a laser temperature gun. Experiments are still in progress and results are still pending. Results will be presented at JMIH.

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411 Reptile Conservation, Ballroom 2 – Cliff Lodge, Saturday 27 July 2019

Scott Goetz[1], Eric Hileman[2], Melia Nafus[3], Amy Yackel Adams[3], Robert Reed[3], Shane Siers[1]

[1]USDA APHIS WS National Wildlife Research Center, Hilo, HI, USA, [2]U.S. Geological Survey, Brown Treesnake Project, Dededo, GU, USA, [3]U.S. Geological Survey, Fort Collins Science Center, Fort Collins, CO, USA

Brown Treesnake survivorship in relation to aerial applications of toxicant-laced baits

Aerial application of toxic baits has proven to be a cost-effective means to control invasive species at the landscape scale. A recently developed toxicant baiting system that delivers dead neonatal mice (bait), each affixed with an 80 mg acetaminophen tablet (toxicant) has been shown to be a humane form of lethal control capable of suppressing invasive Brown Treesnake (*Boiga irregularis*) abundance. To gain a better understanding of individual variation in susceptibility to this control tool, we monitored two test groups of Brown Treesnakes using radio-telemetry in a 55-ha snake exclosure in northern Guam. We investigated survival probability in relation to two series of toxicant applications, applied on 01 and 04 October 2018 (N = 12,686 baits) and 09, 12, and 15 March 2019 (N = 19,800 baits) using known-fate models. To evaluate the influence of sex, snout-vent-length, and mass on treatment susceptibility, we used multimodel inference and Akaike's information criterion for model selection. Survival estimates during the ten-day toxicant activity period were significantly lower than non-treatment periods. Our results provide estimates of mortality in relation to the aerial application of Brown Treesnake toxicants and allow for better parameterization of models predicting suppression outcomes.

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410 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Scott Goetz[1], Amy Yackel Adams[2], Shane Siers[1]

[1]USDA APHIS WS National Wildlife Research Center, Hilo, HI, USA, [2]U.S. Geological Survey, Fort Collins Science Center, Fort. Collins, CO, USA

Validating performance of an aerially-delivered Brown Treesnake control tool using distance sampling

Aerial application of management tools provides a cost-effective means to conserve or control wildlife populations at the landscape scale. Large spatial scales present difficulties when assessing *in situ* reliability and integrity of the devices. We demonstrate a novel application of distance sampling density estimation to assess performance of a newly-developed toxicant bait system for control of invasive Brown Treesnakes (*Boiga irregularis*). Bait cartridges were designed to open in flight to expose the toxicant-laced bait, and to tangle in the forest canopy via a plastic ribbon. Following application of a total of 12,686 bait cartridges from an automated aerial delivery system over a 55-ha site on Guam, USA, we employed distance sampling to evaluate cartridge performance. We performed 22 line transect surveys for a total distance of 10.3 km. While thoroughly searching the ground for bait cartridge components that did not hang in the canopy as designed, we recorded all observations of unopened bait cartridges, instances of

cartridge ribbon failure, and carcasses of Brown Treesnakes and nontarget species. Too few undeployed bait cartridges (*n* = 6), Brown Treesnake carcasses (*n* = 1), or nontarget carcasses (*n* = 0) were observed during surveys to support additional analysis. We detected 299 instances of ribbon failure. Using distance sampling analyses, we estimate that ribbon failure occurred in 3,376 ± 351 (95% CL = 2,746 – 4,150) cartridges or 26.6% of the total applied. Our results demonstrate the utility of distance sampling density estimation to validate performance and reliability of aerially-applied management tools.

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727 ASIH STOYE CONSERVATION AWARD, Cottonwood A-D – The Snowbird Center, Friday 26 July 2019

Marta Gomez-Buckley[1], Luke Tornabene[1], Ryan Kelly[1], Ramon Gallego[2], Raymond Buckley[1]

[1]University of Washington, Seattle, WA, USA, [2]NOAA NWFSC, Seattle, WA, USA

Using eDNA to Detect Species of Cryptobenthic Reef Fishes in Shallow Coral Ecosystems in Vava'u, Kingdom of Tonga

Cryptobenthic reef fishes (CRF) are an important and often overlooked faunal component of coral reef ecosystems. Their cryptic nature and very small size (average < 20 mm TL), makes them very difficult to assess using visual transect methods. The current method to determine the species composition of CRF is to use enclosures to collect the fishes after an ichthyocide or anesthetic is applied. This study is the first to do comparative collections of underwater eDNA and corresponding samples of the actual fishes collected from the same habitat. The objective of this study was to determine if the diversity of unique DNA sequences from eDNA sampling would reflect the CRF species composition from anesthetic collections. Assessing CRF species composition using eDNA samples would be a faster and non-lethal method, and it would allow participation of citizen scientists in local communities through collection of eDNA water samples. CRF were collected between December of 2018 and January 2019 in Vava'u, Tonga. A total of 596 CRF were collected from shallow (2-5 m) coral heads and coral rubble habitats using quinaldine solution as fish anesthetic, and an underwater airlift sampling device. Before the CRF were collected, modified 200 ml syringes were used to extract water and sequester samples from the coral habitats. A total of 50 eDNA samples were collected at the same stations as CRF. Ongoing analyses of eDNA samples, including use of bioinformatics, is revealing the presence of fish DNA sequences.

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70 SSAR SEIBERT ECOLOGY AWARD II, Ballroom 2 – Cliff Lodge, Thursday 25 July 2019

Hayley Crowell, Sebastian Gonzales, Emily Taylor

Cal Poly, San Luis Obispo, CA, USA

A Comparative Study of Home Range and Movement Patterns of Pacific Rattlesnakes (*Crotalus oreganus*)

Few studies have compared spatial ecology among different populations of a single snake species. In this study, we compared the home range sizes and daily movement patterns of two coastal and two inland populations of adult, male Pacific rattlesnakes (*Crotalus oreganus*) with the goal of exploring potential variation among populations. Using radio-telemetry, we tracked 26 snakes (n/coastal=13, n/inland=13), from June to October of 2017. Individuals were tracked 4-5 times per week at various times throughout the day, and location was recorded via handheld GPS. Individuals from inland populations had larger minimum convex polygon home ranges than individuals from coastal populations, while there was no difference among populations for 95% or 50% kernel density home ranges. No difference in mean daily movement was observed between inland and coastal populations; however, there was a significant difference in mean daily movement between the two inland populations. Potential causes for the observed differences in spatial ecology among these populations include varying food availability, thermal quality, and topography. Our study highlights the fact that studying a single population does not adequately capture the complexity of spatial patterns for a given species.

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810 Reptile Conservation, Ballroom 2 – Cliff Lodge, Saturday 27 July 2019

Matt Goode

University of Arizona, Tucson, AZ, USA

Ecology and Conservation of King Cobras in India and Southeast Asia

The king cobra is the world's longest venomous snake, reaching lengths of up to 5-6 m. These charismatic snakes have long captured the imagination of people throughout the world, putting fear in the hearts of some, while inspiring awe in others. When we began studying King Cobras in India in 2008, there had never been an in-depth study of the species' ecology in the wild. Using radiotelemetry, we learned a great deal about these amazing snakes, publishing several shorter papers on our research. Obviously, with such a small sample size, we needed to do more. We began research on King Cobras in Thailand in 2013. To date, we have radio tracked over 20 individuals, publishing a series of papers based on more robust sample sizes. Our talk will focus on King Cobra spatial ecology, habitat use, diet, and reproductive activity, including data from juvenile snakes. And finally, I will discuss our newly begun research in Indonesian Borneo (Kalimantan), where we are studying King Cobras associated with an oil palm plantation in an effort to learn more about how to conserve this flagship species in the face of dramatic environmental degradation. In addition to research findings, I will also discuss our extensive outreach efforts designed to engage local communities in the conservation of King Cobras and the habitats on which they depend.

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492 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Miranda Goss, Kirsten Nicholson

Central Michigan University, Mount Pleasant, Michigan, USA

Thermal and Foraging Ecology of *Nerodia sipedon* at Two Insular Sites in Lake Michigan

Recent studies have shown that *Nerodia* species foraging in the Great Lakes are larger in size now than in the past. These changes have been attributed to the presence of the invasive Round Goby (*Neogobius melanostomus*) as a new food source. Both past and present studies also show that inland snakes feed primarily on amphibians and are smaller than coastal snakes that feed primarily on fish. No attempts have been made to investigate changes in foraging behavior that may have resulted from the availability of Round Goby, or a fish versus an amphibian diet. Due to their cryptic nature, quantifying snake behavioral ecology, such as foraging effort, with traditional methods can be extremely difficult. We used a novel technological method (temperature and pressure sensitive archival tags) to quantify foraging effort in Northern Watersnakes (*Nerodia sipedon)* at an inland (4) and a coastal (4) site on Beaver Island, Lake Michigan, from May, 21st-June, 21st 2018. We characterized 520 foraging bouts over the course of 32 days. Total foraging effort over the course of our study for all tagged snakes was 9.70 ± 1.14%, significantly higher than previous estimates using traditional methods. No significant difference was found in foraging bout length, timing of bouts, or total overall foraging effort between sites. Overall, our results do not support our hypotheses concerning the differences in foraging behavior between our two sites. They do, however, support our assertion that archival tag data can be used to accurately quantify foraging effort in a cryptic species.

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621 SSAR RABB UNDERGRADUATE AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Parker Gottsch, Neil Balchan, Stephen Mackessy

University of Northern Colorado, Greeley, Colorado, USA

Predator-prey interactions between the Desert Massasauga Rattlesnake (*Sistrurus tergeminus edwardsii*) and the Tiger Centipede (*Scolopendra polymorpha*)

Centipedes are recorded as a dietary component of several viperid snakes, and rattlesnakes (genera *Crotalus* and *Sistrurus*) are well-documented predators of large centipedes (*Scolopendra spp*.). Published dietary records identify centipede consumption in the Baja California Rattlesnake (*C. enyo*), Ridge-nosed Rattlesnake (*C. willardi*), Rock Rattlesnake (*C. lepidus*), Pigmy Rattlesnake (*S. miliarius*), and Western Massasauga (*S. tergeminus*). Behavioral aspects of this predation have been documented extensively in the Pigmy Rattlesnake but remain largely unstudied in other rattlesnake species. A dietary study conducted on the Desert Massasauga Rattlesnake (*S. t. edwardsii*) found *Scolopendra* centipedes comprised 9.1% of the snake's diet. We document predation on and handling of Tiger Centipedes (*Scolopendra*

polymorpha) by the Desert Massasauga Rattlesnake through captive feeding trials conducted in a laboratory setting. Initial results indicated that Desert Massasaugas actively pursue and strike centipedes; centipedes are immediately released following envenoming, and not approached by the snake until motionless, at which point consumption commences. We are testing centipedes for venom resistance using syntopic rattlesnakes and centipedes and will compare results to a model invertebrate system using domestic crickets (*Acheta domesticus*). Because venom composition may be affected by selection pressures favoring toxins that target non-vertebrate prey, invertebrate-specific toxins may be present, in turn leading to greater venom complexity. Studying interactions involving less frequently consumed prey items allows us to understand better the chemical ecology of rattlesnakes as well as potential coevolution between these interacting species.

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687 Herpetology Biogeography II, Ballroom 3 – Cliff Lodge, Friday 26 July 2019

Andrew Gottscho[1,2], Kevin de Queiroz[1]

[1]*Smithsonian Institution, Washington, DC, USA,* [2]*Merritt College, Oakland, CA, USA*

Diversification and Dispersal in Baja California: Phylogeography of Zebra-tailed Lizards (Phrynosomatidae: *Callisaurus draconoides*)

Zebra-tailed lizards (Phrynosomatidae: *Callisaurus draconoides* species complex) have a large, varied geographic distribution that begs for detailed inquiry and analysis. They occur on both sides of the Gulf of California, including several of its islands, as well as the Sonoran, Mojave, and much of the Great Basin deserts. This distribution spans from the Tropic of Cancer in Baja California and Sinaloa, Mexico, to beyond 40 N latitude in the Black Rock Desert of Nevada, and as far east as the Gila River in New Mexico near the edge of the Chihuahuan Desert. Eleven subspecies have been described, but their taxonomic status remains uncertain, as does the general evolutionary history of zebra-tailed lizards. Here, we use genomic data (ddRADseq and target sequence capture of exons and UCEs) to evaluate the historical biogeography of this species complex. We confirmed the presence of several well-defined clades with small ranges distributed along the Baja California peninsula and its islands. However, all lizards outside of Baja California are nested within the northern Baja clade, implying a range expansion out of the peninsula at the beginning of the Pleistocene. Estimated effective migration surfaces indicate high diversity within Baja California and the rest of the Sonoran Desert and low diversity elsewhere, especially at the limits of the range in Nevada, New Mexico, and Sinaloa. We interpret these data in light of unresolved taxonomic issues and outline future areas for productive research, especially for insular populations in the Gulf of California.

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594 Reptile Ecology, Primrose A&B – Cliff Lodge, Saturday 27 July 2019

Stephen Mackessy[1], Emily Grabowsky[1,2]

[1]University of Northern Colorado, Greeley, CO, USA, [2]Washington Department of Fish and Wildlife, Ephrata, WA, USA

Venom composition in a high elevation lizard specialist, *Crotalus pricei* (Twin-spotted Rattlesnake)

The Twin-spotted Rattlesnake (*Crotalus pricei*) is a small lizard specialist restricted to montane habitat in the Sky Islands of Arizona and México. This species' distribution is disjunct and isolated to higher elevations, and few studies have investigated the venom composition of *C. pricei.* Furthermore, *C. pricei* preys primarily on Yarrow's Spiny Lizard (*Sceloporus jarrovii*), and the predator-prey dynamic between these species is similarly unknown. This study characterized the venom composition of *C. pricei* from several different Sky Island mountain ranges and its relationship with *S. jarrovii* by using venom protein analyses and comparative lethal toxicity assays. Venoms were evaluated using reverse-phase high performance liquid chromatography, SDS-PAGE, and enzyme assays to identify compounds present and evaluate potential geographic variation in composition. Lethal toxicity assays were performed on *S. jarrovii* (from populations both allopatric and sympatric with *C. pricei*) to determine if local adaptation to a specific predator exists. Results indicated that there is minor geographic variation in venom composition, mainly between *C. pricei* from Durango, México and *C. pricei* from Arizona. Lethal toxicity results revealed that *S. jarrovii* has not developed resistance specific to *C. pricei* venom but does display a general tolerance to venoms of several species of *Crotalus* (relative to a model lizard species). These results provide insight into the evolutionary relationship between a lizard specialist and its natural prey, in addition to detailing information on the venom composition of a little-studied habitat specialist with a limited distribution in the United States.

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216 AES Conservation & Management I, Rendezvous A&B – The Snowbird Center, Sunday 28 July 2019

Jasmin Graham[1], R. Dean Grubbs[2], John K. Carlson[3], Andrea Kroetz[3]

[1]Florida State University, Tallahassee, Florida, USA, [2]Florida State University Coastal and Marine Laboratory, St. Teresa, Florida, USA, [3]NOAA Southeast Fisheries Science Center, Panama City, Florida, USA

Analysis of smalltooth sawfish (*Pristis pectinata*) bycatch risk in Florida

The smalltooth sawfish (*Pristis pectinata*) is a critically endangered species endemic to the Atlantic Ocean. The only known viable populations have been found along the coast of Florida as well as in the coastal areas of the Bahamas. In this study, we use passive acoustic telemetry as well as satellite telemetry to track the movements of the sawfish. For the acoustic telemetry part of this study, we make use of hundreds of receivers in the i-Tag, FACT and ACT arrays along the U.S. Atlantic and Gulf coasts to track the movements of adult and large juvenile *P. pectinata*. From 2016-2018, eighteen large juvenile and adult sawfish were implanted with V16

transmitters. Sixteen have been detected on more than 170 receivers in the arrays as far north as Brunswick, Georgia. For the satellite data, we analyze eighteen mk10 and PATF satellite tags deployed from 2011-2017. In this study, we identify areas of high sawfish density based on our telemetry data. We also use observer data from the shrimp, shark bottom longline and gillnet fisheries to identify areas of high fishing pressure based on fishing effort. Using Geographic Information Systems (GIS), we identify areas of high bycatch risk based on sawfish densities and fishing effort. We also analyze the differences in exposure risk based on demographics within the population to determine if any demographic is more vulnerable. This information can be used to assess the success of the current protections provided for the species and the critical habitats on which they depend.

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286 ASIH STOYE ECOLOGY & ETHOLOGY AWARD II, Primrose A&B – Cliff Lodge, Friday 26 July 2019

Alejandro Grajal-Puche[1], Christopher M. Murray[2], Jonathan K. Warner[3], Mark Merchant[4], Christopher Nix[5], Mathew Kearley[6], Tania Datta[2], Donald M. Walker[1]

[1]Middle Tennessee State University, Murfreesboro, TN, USA, [2]Tennessee Technological University, Cookeville, TN, USA, [3]Texas Parks and Wildlife, Port Arthur, TX, USA, [4]McNeese State University, Lake Charles, LA, USA, [5]Alabama Wildlife and Freshwater Fisheries Division, Montgomery, AL, USA, [6]Auburn University, Auburn, AL, USA

Microbial assemblage dynamics within the American Alligator (*Alligator mississippiensis*) nesting microbiome

Disentangling the ecological processes which underlie observed assemblage patterns is central to community ecology. The scale at which assemblages are studied may lead to distinct process-driven conclusions. Pattern-process assemblage dynamics are scale-relative and occur at macro- and microscopic scales. Micro-environmental differences allow for distinct microbial assemblages to occur within close spatial proximity. For example, an individual host may harbor unique microbial assemblages across their bodies, the sum of which is defined as a host's microbiome. Here, I compare bacterial assemblages within the American Alligator (*Alligator mississippiensis*) nesting microbiome, across micro-, meso-, and macro-scales, to infer the class of ecological processes shaping these observed patterns. We defined the micro-scale as microbial assemblages among distinct depths within nests, the meso-scale as whole microbial assemblages within individual nests, and the macro-scale as entire microbial assemblages sampled within a geographic site. Across all scales, Simpson's bacterial diversity did not statically differ ($p > 0.05$). By comparison, differences among bacterial assemblages, i.e. species turnover, strongly differed across nearly all focal scales, with individual nests predicting the largest degree of bacterial variation ($p < 0.005$, $R^2 = 0.438$). Therefore, bacterial patterns within the Alligator nest microbiome are likely subject to both dispersal and/or selective processes. For example, Alligator nests are likely colonized by dispersal-limited bacteria. These bacterial colonizers may radiate to fill a similar number of available niches and are maintained by redundant selective factors. Results of this study advance pattern-process dynamics within community ecology and describe factors influencing the nesting microbiome of the American Alligator.

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4 Session Honoring Contributions and Retirement of Pat Gregory, Ballroom 3 – Cliff Lodge, Sunday 28 July 2019

David Green

McGill University, Montreal, Quebec, Canada

Pat disperses to the west, bringing herpetology with him.

Until the mid-1970s, herpetologists in British Columbia, Canada, were a rare and lonely breed, and professional herpetologists were nonexistent. Then Pat Gregory arrived and, suddenly, there was one. Born in England, raised in southern Ontario and awarded a PhD in Manitoba, Pat completed his westward journey at the University of Victoria in 1973, an advent that I, an undergraduate student and wannabe amphibian biologist at UBC, managed to be entirely unaware of. As Pat dispersed west, I prepared to disperse to the east. It's an enigma, dispersal. In animal populations, dispersal is a necessity as it enables gene flow, range expansion, metapopulation dynamics, out-breeding and, ultimately, species survival. From burrowing asps to budding academics, dispersal kernels all look about the same. Yet dispersal is not particularly conducive to the survival of the individual dispersers because of the risks inherent in traveling to new sites, and the low probability of successful relocation. Efforts to reconcile this contradiction have achieved limited success, potentially because dispersal, currently, is variously defined in the context of particular evolutionary or ecological models rather than first principles.

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180 Session Honoring Contributions and Retirement of Pat Gregory, Ballroom 3 – Cliff Lodge, Sunday 28 July 2019

Patrick Gregory

University of Victoria, Victoria, BC, Canada

Prey-Size vs. Snake-Size Relationships and Variation in Diet in Three Species of Gartersnakes (*Thamnophis*) on Vancouver Island

Because snakes swallow their prey whole, there is an upper limit to the size of prey that a given snake can consume. However, larger snakes also can eat smaller prey, so that variance in prey size, as well as mean prey size, typically increases with snake size (i.e. telescoping plot). Changes in prey size, however, are likely often accompanied by changes in prey type. How important are variations in prey type in contributing to the typical telescoping prey-size distribution seen in snakes? One clue comes from piscivorous snakes, which eat one prey type; in this case, prey size is more tightly matched to snake size (i.e. monotonic relationship with little change in variance). Thus, for generalist species, the telescoping pattern might be due to a combination of prey-size vs. snake-size relationships for different prey. I tested this hypothesis for 3 species of gartersnakes (*Thamnophis*) on Vancouver Island and found strong support for it, especially in *T. elegans* and *T. sirtalis*. Both species feed on small invertebrates (slugs or earthworms) when young and continue eating those small prey as they grow, while adding larger vertebrate prey. Why large snakes of these two species continue eating energetically low-value slugs and earthworms is unclear, but the third species, *T. ordinoides*, eats only these kinds of prey. Besides gape-limitation, multiple other factors should influence dietary differences between species and between conspecific populations. These include habitat preferences, prey availability, specializations for handling different prey, and interspecific competition. I briefly touch on some of these issues.

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381 AES Genetics/Ecology, Rendezvous A&B – The Snowbird Center, Friday 26 July 2019

Henriette Grimmel[1,2], Robert Bullock[3,2], Simon Dedman[4], Guttridge Tristan[2], Bond Mark[2,5], Samuel Gruber[5,2]

[1]University of Ghent, Ghent, Belgium, [2]BBFS, Bimini, Bahamas, [3]Hull International Fisheries Institute, Hull, United Kingdom, [4]Independent Researcher, San Carlos, CA, USA, [5]Department of Biological Sciences, Florida International University, Miami, FL, USA

Assessment of Faunal Communities and Ecosystem Interactions within a Shallow Water System using Non-invasive BRUVs Methodology

Seagrass and mangrove habitats are critical for multiple species at various life-stages, particularly as nursery grounds. Despite their intrinsic value, these ecosystems are increasingly threatened by anthropogenic activities. In Bimini, Bahamas, baited remote underwater video (BRUV) surveys were used to examine faunal communities in seagrass and mangrove habitats, and the open shallow water lagoon system. We aimed to assess species abundances and spatial distribution, and improve knowledge of faunal community structure. 140 BRUV deployments, conducted over 13 months, recorded 62 species including teleost fishes, invertebrates and elasmobranchs from 27 families. Maximum Number (MaxN) assessed species relative abundances, and multivariate analyses (i.e. MDS, PCA, PERMANOVA) investigated differences in community composition across a range of factors and environmental variables. Boosted Regression Trees (BRTs) explored influences of environmental variables on chosen response variables. Results showed distinct habitat preferences across species and faunal groups. This emphasized the importance of mangrove edge and seagrass habitat in Bimini for sharks and coral reef fishes. Open lagoon habitat was preferred by other family groups, reflecting species habitat preferences based on life stages, physical determinants, and predator-prey interaction behaviors. Although typically employed in deeper-water environments, BRUV surveys proved effective in identifying fish species and distinct habitat use patterns. Even in a shallow water environment they can serve as a scalable, non-invasive instrument to assess certain community structures (e.g. teleosts, elasmobranchs). If employed in a monitoring survey design, e.g. for an MPA, results could document impacts of coastal development, specifically mangrove degradation or removal, on fish communities.

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15 General Herpetology II, Primrose A&B – Cliff Lodge, Sunday 28 July 2019

Ashley Grimsley[1], Cheryl Eamick[2], Leslie Carpenter[2], Michael Ingraldi[1], Daniel Leavitt[1,3]

[1]Arizona Game and Fish Department, Phoenix, Arizona, USA, [2]Tucson Electric Power Company, Tucson, Arizona, USA, [3]U.S. Navy-Naval Air Weapons Station, China Lake, California, USA

Comparisons of Reptile Assemblages in Two Subdivisions of the Sonoran Desertscrub Biotic Community

Anthropogenic disturbances can have negative effects on species assemblages. This study was established to form baseline data on the environmental structure and reptile assemblages within a planned energy corridor in Pinal County, Arizona, prior to construction. We emphasized evaluating the differences in reptile assemblages in two subdivisions of the Sonoran Desertscrub, the Lower Colorado River Valley (LCV) and Arizona Uplands (AZU). Surveys were conducted on 50 sites (LCV = 15; AZU = 35) along the proposed 67.1-km long energy corridor through environmental surveys and 50 drift-fence trapping arrays with 400 box funnel traps. Vegetation height, number of burrows, and percent rock, ground cover, and coarse woody debris were significantly higher in the AZU than in the LCV. Eighteen reptile species (n = 995 captures) were detected on the energy corridor including 8 lizard species (n = 952 captures) and 10 snake species (n = 43 captures). Species richness, evenness, and capture rates were not significantly different between the LCV and AZU; however, species diversity was significantly higher in the LCV. Reptile abundance (LCV = 281; AZU = 714) differed in the two subdivisions, yet rank-abundance curves revealed no difference in dominance of species. Post hoc examination revealed that the geographic separation of sites within the LCV and the location of the study area (along the ecotone) may have contributed to our results. We conclude that both subdivisions are equally important to the maintenance of local biotic diversity and recommend that any future land set-asides consider both subdivisions.

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182 Herpetology Conservation and Disease, Ballroom 3 – Cliff Lodge, Saturday 27 July 2019

Matthew Grisnik[1], Donald Walker[1], Jacob Leys[2], Alejandro Grajal-Puche[1], Christopher Murray[2], Matthew Allender[3]

[1]Middle Tennessee State University, Murfreesboro, Tennessee, USA, [2]Tennessee Technological University, Cookeville, Tennessee, USA, [3]University of Illinois at Urbana-Champaign, Champaign, Illinois, USA

The Snake Fungal Disease Pathogen is Predictive of the Skin Microbiome Across Spatial Scales.

Understanding how biological patterns translate into functional processes across different scales is a central question in ecology. Within a spatial context, extent is used to describe the overall geographic area of a study, whereas, grain describes the overall unit of observation. This study aimed to characterize the snake skin microbiome (grain) and to determine host- microbiome-pathogen effects across spatial extents within the Southern United States. The causative agent of snake fungal disease, *Ophidiomyces ophiodiicola*, is a fungal pathogen threatening snake populations. We hypothesized that the skin microbiome of snakes differs from its surrounding environment, by host species, spatial scale, season, and in the presence of *O. ophiodiicola*. We collected snake skin swabs, soil samples, and water samples across six states in the Southern U.S. (macroscale extent), four Tennessee ecoregions (mesoscale extent), and at multiple sites within each Tennessee ecoregion (microscale extent). These samples were subjected to DNA extraction and quantitative PCR to determine the presence/absence of *O. ophiodiicola*. High-throughput sequencing was also utilized to characterize the microbial communities. We concluded that the snake skin microbiome was partially distinct from environmental microbial communities. Snake host species was strongly predictive of the skin microbiome at macro-, meso- and microscale spatial extents, however, the effect was variable across geographic space and season. Lastly, the presence of the fungal pathogen *O. ophiodiicola* is predictive of the microbiome across macro- and meso-spatial extents and particular bacterial taxa associate with *O. ophiodiicola* fungal copy number. Our results highlight the importance of scale regarding wildlife host-pathogen-microbiome interactions.

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514 AES Conservation & Management I, Rendezvous A&B – The Snowbird Center, Sunday 28 July 2019

R. Dean Grubbs[1], John Carlson[2], Andrea Kroetz[2], Mark Bond[3]

[1]Florida State University Coastal and Marine Lab, St. Teresa, FL, USA, [2]NOAA Fisheries Service, Southeast Fisheries Science Center, Panama City, FL, USA, [3]Florida International University, Miami, FL, USA

Comparative Relative Abundance of Smalltooth Sawfish and Coastal Sharks in Two Mangrove Dominated National Parks in Florida and the Bahamas

The smalltooth sawfish (*Pristis pectinata*) is *Critically Endangered* in the IUCN Red List of Threatened Species and *Endangered* under the U.S. Endangered Species Act. The species is restricted to the Atlantic Ocean and populations declined throughout the range due to overfishing and habitat loss. Southwest Florida in the U.S. and the west side of Andros Island in the Bahamas are the only known regions with viable smalltooth sawfish populations. Both of these regions include substantial national parks (Everglades National Park – ENP; Andros West Side National Park - AWSNP) that offer protection of critical habitats and are characterized by extensive mangrove estuaries with highly variable salinity and proximity to relatively deep shelf-

edge habitats that are buffered from seasonal temperature extremes. Telemetry data suggest there is little movement of sawfish between these systems. We used fishery-independent longline surveys employing identical methods to assess relative abundances of sawfish and sharks in ENP (2011-present) and AWSNP (2014-present). To date, nearly 3,000 elasmobranchs from 15 species, including more than 60 large smalltooth sawfish, have been captured. Whereas catch rates and community structure of coastal sharks were similar between ENP and AWSNP, relative abundance of smalltooth sawfish was more than 10 times higher in ENP than in AWSNP despite higher apparent fishing mortality in the Florida population. These patterns may be driven by differences in habitat complexity and productivity as well as densities of sawfish prey, competitors and predators. We will discuss the implications of these patterns for recovery efforts for this critically endangered species.

CANCELLED

807 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Maggie Grundler[1,2], Sonal Singhal[1,3], Mark Cowan[4], Daniel Rabosky[1]

[1]University of Michigan, Ann Arbor, MI, USA, [2]University of California, Berkeley, Berkeley, CA, USA, [3]CSU Dominguez Hills, Carson, CA, USA, [4]Department of Biodiversity, Conservation and Attractions, Kensington, WA, Australia

Is genomic diversity a useful proxy for census population size? Evidence from a species-rich community of desert lizards

Species abundance data are critical for testing ecological theory, but obtaining accurate empirical estimates for many taxa is challenging. Proxies for species abundance can help researchers circumvent time and cost constraints that are prohibitive for long-term sampling. Under simple demographic models, genetic diversity is expected to correlate with census size, such that genome-wide heterozygosity may provide a surrogate measure of species abundance. We tested whether nucleotide diversity is correlated with long-term estimates of abundance, occupancy, and degree of ecological specialization in a diverse lizard community from arid Australia. Using targeted sequence capture, we obtained estimates of genomic diversity from 30 species of lizards, recovering an average of 5,066 loci covering 3.6 Mb of DNA sequence per individual. We compared measures of individual heterozygosity to a metric of habitat specialization to ask whether ecological preference exerts a measurable effect on genetic diversity. We find that heterozygosity is significantly correlated with species abundance and occupancy, but not habitat specialization. Demonstrating the power of genomic sampling, the correlation between heterozygosity and abundance/occupancy emerged from considering just one or two individuals per species. However, genetic diversity does no better at predicting abundance than a single day of traditional sampling in this community. We conclude that genetic diversity is a useful proxy for regional-scale species abundance and occupancy, but a large amount of unexplained variation in heterozygosity suggests additional constraints or a failure of ecological sampling to adequately capture variation in true population size.

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721 ASIH STORER HERPETOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Miranda Gulsby, Thomas McElroy

Kennesaw State University, Kennesaw, GA, USA

Upland Snake Community in Montane Longleaf Pine Habitats of Northwest Georgia

The Paulding and Sheffield Wildlife Management Areas (WMA) in northwest Georgia have been undergoing montane longleaf pine ecosystem restoration for the past 15 years. Habitat management using prescribed fire and hardwood removal have been shown to benefit reptile communities allowing increasing diversity of species. The two WMAs differ in their management history, while Paulding was converted into a monoculture of loblolly pines and Sheffield underwent fire suppression over decades. It's known that many reptile communities are in decline however, no surveys have been conducted to determine snake community within these WMAs undergoing restoration. This study serves as an initial survey of the upland snake community after many years of ecosystem restoration occurring. This community includes the northern pine snake (*Pituophis melanoleucus melanoleucus*), a species of concern in Georgia, however, this species was thought to be expatriated from these state-managed properties. We utilized drift fence arrays and road cruising to survey the upland snake community in both WMAs during two seasons, May - June, and Late-August - Late-October in 2018. This survey confirmed the presence of northern pine snakes in these WMAs. Sheffield contained a higher species diversity during both seasons. Seasonal variation was observed with higher species richness and evenness in Sheffield during the first season then higher in Paulding during the second season. We found that the mosaic of disturbance-maintained habitats in these WMAs are supporting high species diversity and can be used as a baseline for future studies of managed habitats in northern Georgia.

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751 Ichthyology Conservation, Cottonwood A-D – The Snowbird Center, Saturday 27 July 2019

Jennifer Gumm, Mitchell Stanton, Olin Feuerbacher

US Fish & Wildlife Service, Amargosa Valley, NV, USA

Captive Breeding of the Devils Hole Pupfish (*Cyprinodon diabolis*)

Captive propagation is a vital component to the recovery and management of many imperiled fishes. With a total wild population of fewer than 200 fish that are restricted to a single geothermal pool in the Mojave desert, the federally endangered Devils Hole pupfish, *Cyprinodon diabolis*, seems a prime candidate for captive propagation. However, despite decades of attempts, propagation in aquaria has never been fully successful. While refuge populations have fared slightly better, ultimately all ended in failure. Since 2013, the Ash Meadows Fish Conservation

Facility (AMFCF) has maintained a backup population of Devils Hole pupfish, *Cyprinodon diabolis*. To establish the population in a state-of-the-art 100,000 gallon refuge tank, Devils Hole pupfish eggs were recovered from Devils Hole and brought to the lab at AMFCF for rearing and culturing. Herein, we discuss recent advances that have led to successful breeding by Devils Hole pupfish in both the refuge tank and in aquaria. Specifically, we highlight management of predation by diving beetles in the refuge tank that resulted in fertilized eggs being collected from the refuge population and breeding trials in aquaria that produced fertilized eggs. Finally, we present results of a comparative analysis of eggs collected from the three sources (wild, refuge tank and lab aquaria) comparing egg production, hatching success and survival to adulthood. Understanding differences in reproduction between wild and captive fish is critical for recovery of the Devils Hole pupfish and will help inform management of this and other species.

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157 AES Ecology, Rendezvous A&B – The Snowbird Center, Friday 26 July 2019

Brianna Hall[1], Jennifer Bigman[2], Christine Bedore[1]

[1]Georgia Southern University, Statesboro, GA, USA, [2]Simon Fraser University, Vancouver, BC, Canada

Scaling and ecological relationships in the visual ecology of sharks

Visual adaptations such as eye size, acuity (the ability to discern detail), and sensitivity (the amount of light needed for image formation) can infer the relative importance of vision to an organism. Eyes and the visual processing system are metabolically costly to maintain, suggesting that large relative eye size (as it relates to body length) may have a significant ecological or evolutionary role, such as mate selection, predator avoidance, and foraging strategy. Elasmobranchs comprise a morphologically diverse group that has filled a wide range of marine and freshwater niches with several species exhibiting different niches across their lifetime as ecological demands shift, yielding a wide range of visual habitats. As eye size changes with body length ontogenetically, they represent an ideal group for examining scaling relationships, such as eye growth rate and eye size at a given body length within the context of visual habitats. In this study, we quantified the relationship of eye size and body length in 9 species of sharks and compared this scaling across species that differ in ecological lifestyle (i.e. activity level, habitat, and maximum size). Eyes of all species scaled hypoallometrically with body size, however larger and more active species (e.g. the white shark *Carcharodon carcharias*) had larger relative eye sizes than smaller, less active species (e.g the Atlantic sharpnose shark *Rhizoprionodon terraenovae*). Larger eyes for active predators may provide either greater sensitivity or greater visual acuity which would enable these species to carry out visually-guided behaviors across a wide range of visual habitats.

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385 Reptile Conservation, Ballroom 2 – Cliff Lodge, Saturday 27 July 2019

Brian Halstead, Jonathan Rose, Gabriel Reyes, Glenn Wylie, Michael Casazza

U.S. Geological Survey, Western Ecological Research Center, Dixon, California, USA

Conservation Reliance of a Threatened Snake on Rice Agriculture

Conservation-reliant species require perpetual management by humans to persist. But do species that persist largely in human-dominated landscapes actually require conditions maintained by humans? Because most extant populations of giant gartersnakes (*Thamnophis gigas*) inhabit the highly modified rice agricultural regions of the Sacramento Valley, we sought to evaluate whether giant gartersnakes are indeed a conservation-reliant species dependent on maintenance of rice agriculture and its infrastructure for their continued existence. Specifically, we examined the extent to which giant gartersnakes use rice fields themselves, and whether survival of adult giant gartersnakes was influenced by the amount of rice grown near their home ranges and daily movements. We found that although giant gartersnakes only use rice fields minimally and then only between mid-June and early September, their survival was lower when less rice was available near the areas they inhabited. Survival was particularly low in early spring, when giant gartersnakes emerge from brumation but rice fields are not yet flooded. The incongruity between the phenology of rice cultivation and giant gartersnake foraging requirements suggests that although giant gartersnakes are reliant on the rice agroecosystem, rice is likely suboptimal habitat for giant gartersnakes. Giant gartersnakes' reliance on the rice agroecosystem challenges the notion of preservation-based conservation, but provides opportunities for win-win scenarios benefitting both rice farmers and giant gartersnakes. Our study highlights that in addition to land use, the timing of land management might be crucial for conservation-reliant species.

`CANCELLED`

~~204 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019~~

~~Paul Hampton~~

~~Colorado Mesa University, Grand Junction, CO, USA~~

~~Evidence for adaptations of the axial skeleton as a factor influencing relative organ position in snakes~~

~~For snakes, organ position is typically determined as a linear measurement relative to body length. Disparities in organ position among species have been associated with common ancestry and habitat use. I used a novel approach to measuring organ position in snakes to explore the possibility that the axial skeleton is exhibiting adaptations that would influence relative organ position. I found that in Hydrophiidae and Viperidae, the axial skeleton is labile whereas organ position is comparably constrained relative to the cloaca. Specifically, the number of vertebrae between the cranium and the heart exhibited high variation among species and was dissociated from the number of vertebrae between the atrium and cloaca for hydrophiids. In viperids, trunk vertebrae were dissociated from tail vertebrae which also showed high variation. Relative to the cloaca, the vertebral position of the heart and pyloric sphincter were phylogenetically~~

~~constrained for both hydrophiids and viperids. I conclude that variation in snake organ position is the result of regional adaptations to the axial skeleton.~~

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9 ASIH STOYE GENERAL HERPETOLOGY AWARD I, Primrose A&B – Cliff Lodge, Thursday 25 July 2019

Donglin Han, Lynnette Sievert

Emporia State University, Emporia, KS, USA

The effect of temperature on activity of the digestion and hopping behavior of *Anaxyrus woodhousii*

Anaxyrus woodhousii occupies an extensive range of habitats in the United States. However as an ectotherm, temperature regulation plays a critical role in digestive physiology of *A. woodhousii.* We were interested in whether temperature affects the rate of a toad's digestion. To test that, we used 20 male and female Woodhouse's toads individually acclimated in stable temperature chambers at 16 ºC, 21ºC, 26ºC and 31ºC, We fed toads crickets with a different colored bead at 12:00pm for 7 days. Each toad was acclimated and tested at the 4 different temperatures. Every day we gave each toad 2 crickets and one bead. We checked toads 3 times every day to find the beads until we found all 7 beads.

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258 ASIH STORER HERPETOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Ryan Hanscom[1,2], Stephen Dinkelacker[2], Aaron McCall[3], Adam Parlin[4]

[1]Tennessee Technological University, Cookeville, TN, USA, [2]Framingham State University, Framingham , MA, USA, [3]The Nature Conservancy, Kill Devil Hills, NC, USA, [4]Miami University, Oxford, OH, USA

Demographic Traits of Freshwater Turtles in a Maritime Forest Habitat

Local demographics of freshwater turtle populations are necessary in order to understand their natural history and assess population status. To examine whether maritime forest populations display different demographic traits compared to other populations, we studied the freshwater turtle community at Nags Head Woods Ecological Preserve (NHWEP), located on the barrier islands of North Carolina. We determined specific demographic traits such as sex ratio, size distribution, somatic growth, annual survival (ϕ), annual abundance ($\hat{n}$), and population growth rate (λ) of Yellowbelly Sliders (*Trachemys scripta*), Common Snapping Turtles (*Chelydra serpentina*), Chicken Turtles (*Deirochelys reticularia*), and Northern Red-bellied Turtles (*Pseudemys rubriventris*). *Deirochelys reticularia* showed apparent annual survivorship similar

to that of a typical turtle species, contradicting previous studies reporting low annual survival due to reduced longevity. We determined that most demographic traits of freshwater turtle populations at NHWEP are structured similarly to other populations studied. We found that the population growth rates for all four species analyzed are increasing, indicating expanding populations. Analyzing multiple demographic traits of different freshwater turtle species within a maritime forest community on a barrier island provides an important baseline on freshwater turtle demographics in unique habitats that are subject to intense environmental stochasticity.

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507 AES Conservation & Management III, Rendezvous A&B – The Snowbird Center, Sunday 28 July 2019

Alex Hansell[1], Tobey Curtis[2], John Carlson[3], Enric Cortes[4], Gavin Fay[1], Steve Cadrin[1]

[1]UMass Dartmouth, New Bedford, MA, USA, [2]NMFS, Gloucester , MA, USA, [3]NMFS, Panama City, FL, USA, [4]NMFS, Panama City , FL, USA

Stock Assessment of the Lemon Shark (*Negaprion brevirostris*) in U.S. Waters of the Northwest Atlantic

The lemon shark is a large coastal shark that commonly occurs in the shallow nearshore waters of the tropical western Atlantic Ocean. Lemon shark life history and ecology have been studied extensively, but little is known about its population dynamics. The International Union for the Conservation of Nature lists the lemon shark as near threatened, but no quantitative assessment of stock status is available. There are conservation concerns for this species due to fisheries exploitation, low productivity, anthropogenic disturbance at nursery sites, and the depleted status of other large coastal sharks. We synthesized all available data to develop a stock assessment of the lemon shark in U.S. waters of the northwest Atlantic. Abundance of lemon sharks was estimated from 1981–2016 using a Bayesian state-space surplus production model. The model incorporated prior knowledge of lemon shark demography and a combination of nine fishery-dependent and fishery-independent indices of abundance. Markov chain Monte Carlo methods were used to estimate ranges for the values of model parameters and stock status-related derived quantities. Preliminary model results suggest that stock biomass decreases in the 1980s and then remains relatively stable during the 1990s and 2000s. Results from our study provide the first estimates of lemon shark population trends and provide valuable information for fisheries managers.

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568 ASIH STOYE ECOLOGY & ETHOLOGY AWARD II, Primrose A&B – Cliff Lodge, Friday 26 July 2019

Maggie Hantak, Shawn Kuchta

Ohio University, Athens, Ohio, USA

Spatial Variation of Correlated Trait Complexes in the Polymorphic Eastern Red-backed Salamander, *Plethodon cinereus*

An open question in color polymorphic species is why morph frequencies are variable among populations. Little work has been done to examine geographic patterns in polymorphisms, with most studies focusing on a single population. The Eastern Red-backed Salamander, *Plethodon cinereus*, has a widespread distribution in the northeastern United States and southeastern Canada, and is color polymorphic throughout portions of its range. Two color morphs are common: a 'striped' morph that has a red stripe overlaid on a black dorsum, and an 'unstriped' morph that is completely black. Previous studies on single populations of *P. cinereus* have suggested that the two color morphs differ in elements of their ecology, behavior, and physiology, yet a mechanistic understanding of the ecological differences between the morphs, and the evolutionary processes that maintain the polymorphism, remains unclear. In northern Ohio, many populations with varying morph frequencies of *P. cinereus* exist. Here, we established six sites that varied in morph frequency, including two populations that are monomorphic for unstriped (95-100% unstriped), two that are polymorphic, and two that are striped. We gathered ecological data from each site to determine whether morphs assortatively mate by color, and if they were divergent in temperature associations, territoriality, and their response to predation. Our results demonstrate strong geographic variation in assortative mating and ecological differences between the morphs. Overall, this study provides essential data for understanding variation in ecological interactions between the morphs over space and time, and contributes to our understanding of the relationship between polymorphism and diversity.

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207 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Yuichiro Hara[1], Kazuaki Yamaguchi[1], Mitsutaka Kadota[1], Yoshinobu Uno[1], Osamu Nishimura[1], Kiyonori Nishida[2], Keiichi Sato[3], Susumu Hyodo[4], Shigehiro Kuraku[1]

[1]RIKEN BDR, Kobe, Japan, [2]Osaka Aquarium Kaiyukan, Osaka, Japan, [3]Okinawa Churaumi Aquarium, Motobu, Japan, [4]AORI Tokyo University, Kashiwa, Japan

Molecular Evolution of Elasmobranchs through a Genomic Lens

Modern cartilaginous fishes are divided into elasmobranchs (sharks, rays, and skates) and chimaeras, and the paucity of reliable whole genome sequence information for the former has prevented our understanding of early vertebrate evolution and the unique phenotypes of elasmobranchs. To overcome this situation, we have conducted *de novo* genome sequencing for two egg-laying shark species, namely the brownbanded bamboo shark *Chiloscyllium punctatum* and the cloudy catshark *Scyliorhinus torazame*, and reported various findings, taking advantage of our own expertise in large-scale DNA sequence data production (Hara, et al., 2018. *Nat. Ecol. Evol.* 2:1761-1771). Including the whale shark for which we improved an existing assembly, the obtained sequences have been elongated by Hi-C scaffolding to achieve a chromosome-level continuity. Their relatively large genomes, of up to 6.67 giga basepairs, contain sparse distributions of protein-coding genes and putative regulatory elements and exhibit reduced molecular evolutionary rates. Our thorough genome annotation revealed distinct gene repertories of visual opsins and olfactory receptors that would be associated with adaptation to variable habitat depths. We also show the early establishment of the genetic machinery governing the homeostatic gut-brain axis and reproduction at the jawed vertebrate ancestor. This study, supported by an unprecedented set of genomic, transcriptomic and epigenomic resources, provides a foundation for the comprehensive, molecular-level exploration of elasmobranch evolution and ecology.

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575 Herpetology Biogeography II, Ballroom 3 – Cliff Lodge, Friday 26 July 2019

Sean Harrington, Riley Parks, Robert Thomson

University of Hawaii, Honolulu, HI, USA

Tip-dated phylogenetics and biogeography of *Xenosaurus*

The knob-scaled lizards of the genus *Xenosaurus* are flattened, rock dwelling lizards endemic to Central America. Xenosaurs are deeply diverged from the remaining anguimorph lizards, but little is known about the age and geographic origin of the clade. We used a Bayesian tip dating approach to analyze a dataset of DNA and morphological data for both extant *Xenosaurus* and extinct relatives under the fossilized birth-death model. We used the resulting tree to perform biogeographic analyses in RevBayes. We demonstrate that crown Xenosaurus originated approximately 35 million years ago in northern Mexico and has since expanded southward.

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474 ASIH STORER ICHTHYOLOGY AWARD, Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Pamela Hart[1], Matthew Niemiller[2], Jonathan Armbruster[3], Prosanta Chakrabarty[1]

[1]Louisiana State University, Baton Rouge, LA, USA, [2]University of Alabama, Huntsville, Huntsville, AL, USA, [3]Auburn University, Auburn, AL, USA

Population Genomics of a Cavefish Species Complex: Implications for Conservation and Aquifer Connectivity

Cave-obligate aquatic organisms are difficult to monitor for conservation needs due in particular to cryptic diversity and unknown cave and water source connectivity. The promise of Next Generation genomic sequencing could offer an unprecedented ability to accurately determine the diversity and relatedness of aquatic cave-obligate organisms (e.g., cavefishes). The Southern Cavefish (*Typhlichthys subterraneus*), found in karst regions of the Southeastern U.S., has the largest range of any cavefish known, but probably represents a species complex (i.e., encompassing multiple species). Several of the known genetic lineages are reported as Vulnerable, Critically Imperiled, or Imperiled. However, the extent of introgression, hybridization, and connectivity of these lineages remains unclear. Thus, the Southern Cavefish is a great subject to test the application of Next Generation sequencing to cave-obligate species complexes, in particular those with lineages of conservation concern. We use population genomic analyses on a dataset of Single Nucleotide Polymorphisms (SNPs) harvested from Ultraconserved Element (UCE) loci to determine diversity and phylogeography of the Southern Cavefish species complex. By using this contemporary technique to assess relationships, status, and population sizes of Southern Cavefish lineages, we can help protect these North American endemic cavefishes, determine the applicability of this technique to other aquatic cave-obligate species complexes, and increase our understanding of aquifer and cave connectivity.

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115 Herpetology Morphology and Systematics, Ballroom 1 – Cliff Lodge, Friday 26 July 2019

Jordan Hartley, Dustin Siegel

Southeast Missouri State University, Cape Girardeau, MO, USA

Modification of genital kidney nephrons for sperm transport in *Eurycea longicauda*

The kidneys of male salamanders possess nephrons that function in urine formation/transport (pelvic kidney nephrons) and nephrons that transport sperm to the Wolffian ducts (genital kidney nephrons). Genital kidney nephrons possess the same regionality as those of pelvic kidney nephrons and, thus, it was previously hypothesized that genital kidney nephrons possess dual functionality; i.e., sperm transport and urine formation/transport. In the current study we highlight modifications of genital kidney nephrons for sperm transport by comparing the ultrastructure of the filtration barrier, proximal tubule, and distal tubules between the pelvic and genital kidney nephrons from *Eurycea longicauda* (Plethodontidae). We found no differences in ultrastructure between the filtration barrier of the two regions, though the glomeruli of genital kidney nephrons are significantly smaller than those of pelvic kidney nephrons. Genital kidney proximal tubules possess epithelial linings that are highly ciliated, a feature lacking in pelvic kidney nephrons. Basal membranes of genital kidney proximal and distal tubules lack the extensive folding that is stereotypical of pelvic kidney proximal and distal tubules. These results are similar to studies published previously on male salamanders from other families with one major deviation; i.e., the genital kidney proximal tubule epithelium is comprised of only one cell type that possesses both cilia and microvilli. In contrast, previous studies on ambystomatids and salamandrids described two cell types; one possessing an extensive microvillus brush border and one possessing cilia.

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45 Amphibian Ecology, Ballroom 2 – Cliff Lodge, Friday 26 July 2019

Kristen Hecht[1], Amber Pitt[2], Joseph Mitchell[1]

[1]University of Florida, Gainesville, Florida, USA, [2]Trinity College, Hartford, Connecticut, USA

Evaluation of the Diet of Two Native and Two Introduced Fish Species for Presence of Hellbender Salamander Larvae and Eggs

Hellbender salamander (Cryptobranchus alleganiensis) populations have declined precipitously in recent decades. Population declines have been attributed to a wide variety of factors, including predation by fish. We examined the diet of four fish species to determine if they consumed Hellbenders or their eggs. The fish species included two native species (Ozark Sculpin Cottus hypselurus) and two introduced species, Banded Sculpin (C. carolinae) and two introduced species (Rainbow Trout Onchorhynchus mykiss and Brown Trout Salmo trutta). We examined the diet of Ozark and Banded Skulpin from an Ozark Hellbender (C. a. bishopi) stream including the stream reach with the most densely populated Ozark Hellbender population ever recorded. We collected dietary data in every month of the year and across multiple years. Additionally, we evaluated dietary data for Rainbow and Brown Trout collected by state agency personnel. We also surveyed the literature concerning the diets of these fish species. Field and published data encompassed the time span of 1968-2013 and included four Ozark and four Eastern Hellbender (C. a. alleganiensis) streams in Missouri and seven Eastern Hellbender streams outside of Missouri. We found no evidence supporting these fish species as predators of Hellbenders.

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588 Herpetology Physiology, Ballroom 3 - Cliff Lodge, Saturday 27 July 2019

Tanner Harvey, Stephen Mackessy

University of Northern Colorado, Greeley, Colorado, USA

Cytotoxicity of Argentine Racer and the Sonoran Lyre Snake venoms

With few exceptions, rear-fanged snake venoms are not usually considered dangerous or particularly toxic. Toxicity of the venoms of the Argentine Racer (*Philodryas baroni*) and Sonoran Lyre Snake (*Trimorphodon biscutatus lambda*), two rear-fanged “colubrid” snakes, was evaluated toward several immortal cell lines. The Argentine Racer is a South American species related to snakes known to cause medically significant human envenomation (*P. olfersii*), while the Sonoran Lyre Snake, a North American species, is not known to have caused significant human bites. The enzymatic activities of the venoms have been profiled, as well as assays for toxicity toward different cancer cell lines (melanoma A-375, breast cancer MCF-7 and colon cancer Colo-205). Both venoms show metalloprotease activity (as measured by an azocasein substrate assay), with *P. baroni* venom having a higher activity than *T. b. lambda* venom. *Trimorphodon b. lambda* venom also has phospholipase A_2 activity, which the venom of *P. baroni* lacks. The venom of *T. b. lambda* caused cytotoxicity at similar doses in all three cell lines. The venom of *P. baroni* caused cytotoxicity even at low doses in the breast and colon cancer cell lines but was not cytotoxic to the melanoma at higher doses. Previous research has shown that *P. baroni* venom causes local hemorrhagic activity in mice, and lethal toxicity (LD_{50}) assays are currently in progress using both mouse and lizard models. This research suggests that *P. baroni* venom is highly cytotoxic but has a selectivity which may be indicative of components with potential utility in anti-cancer therapies.

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448 Ichthyology Life History/NIA, Alpine A,B,C – The Snowbird Center, Saturday 27 July 2019

Heidi Heim-Ballew[1,2], Kristine Moody[3], Peter McIntyre[4], Michael Blum[3], Derek Hogan[1]

[1]*Texas A&M University - Corpus Christi, Corpus Christi, Texas, USA,* [2]*Texas Parks and Wildlife Department, Palacios, Texas, USA,* [3]*University of Tennessee - Knoxville, Knoxville, Tennessee, USA,* [4]*Cornell University, Ithaca, New York, USA*

Reproductive isolation and genetic differentiation between migrant and non-migrant forms of the Hawaiian River Goby Awaous stamineus (Gobioidei: Oxudercidae)

The Hawaiian River Goby (Awaous stamineus) exhibits two distinct migration life-histories with migratory and non-migratory individuals existing sympatrically within stream populations. Migrants are amphidromous, where larvae hatch in freshwater and drift to the ocean where theydisperse, and then return to freshwater to eventually spawn. In contrast, non-migrants complete their life cycle in their natal streams. Here we demonstrate that migrants and non-migrants exhibit genetic differentiation within and among stream populations despite a lack of obvious barriers to gene flow. Otolith aging analysis reveals that the timing of hatching, and therefore spawning, differed between migrants and non-migrants. Migrants tend to hatch around the full moon and non-migrants around the new moon. ddRAD SNP assays provided evidence of strong genomic differentiation between co-occurring migrants and non-migrants. Differences in selection pressures between migrants and non-migrants may be driving the variation in hatching timing, where shifts in breeding phenology may be acting as a pre-zygotic isolating mechanism resulting in genetic differentiation between sympatric migratory forms.

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617 Herpetology Ecology & Behavior, Primrose A&B – Cliff Lodge, Saturday 27 July 2019

Matthew Heinicke[1], Melissa Bowlin[1], Juan Daza[2], Tony Gamble[3], Cameron Siler[4]

[1]*University of Michigan-Dearborn, Dearborn, Michigan, USA,* [2]*Sam Houston State University, Huntsville, Texas, USA,* [3]*Marquette University, Milwaukee, Wisconsin, USA,* [4]*University of Oklahoma, Norman, Oklahoma, USA*

Evaluating Aerial Descent in the Flap-legged Geckos (Genus *Luperosaurus*) of the Philippines

Gliding or parachuting behavior has evolved numerous times in squamate reptiles, including independently in several lineages of geckos. Morphological and behavioral traits associated with aerial descent and gliding have been especially well studied in the “flying” geckos, *Ptychozoon* spp., and in the flat-tailed house gecko, *Hemidactylus platyurus*. In contrast, only anecdotal evidence of gliding or parachuting exists for other putative gliding gecko lineages. *Luperosaurus* is one such genus containing putatively gliding species. *Luperosaurus* species are Southeast Asian arboreal geckos closely related to or nested within the genus *Lepidodactylus*, but differ from members of this genus in having skin flaps and webbing that may aid in aerial descent. On a recent field expedition in the Philippines, we collected individuals of two *Luperosaurus* species (*L. macgregori* and *L. angliit*), as well as exemplars of the arboreal gecko genera *Gehyra*, *Gekko*, *Hemidactylus*, and *Lepidodactylus*, and observed aerial descent behavior in each of these taxa. Our data suggest that at least the *Luperosaurus* species found in the northern Philippines do not have gliding capabilities equivalent to those of the better known *Ptychozoon* spp. and *Hemidactylus platyurus*. Phylogenetic, morphological, and behavioral correlates of gliding in geckos are discussed.

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161 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Max Henderson

Tennessee Technological University, Cookeville, Tennessee, USA

Ecotoxicology at a Population Level: The Impact of Endocrine Disruption on Crocodilian Population Viability

Organisms subject to environmental sex determination (ESD) are particularly susceptible to endocrine disrupting contaminant (EDC) exposure, with high doses leading to complete or partial sex reversal. Crocodilian embryos exhibit heightened sensitivity to endocrine disturbance, even when xenobiotics are at environmental levels that may otherwise be negligible, and thus serve as key sentinel species for monitoring health of EDC exposed ecosystems. A classic EDC case study elucidated the feminizing effects of p,p'-DDE, a major persistent metabolite of commercial pesticide DDT, of American alligators in Lake Apopka, Florida. Alligators at Lake Apopka showed evidence of permanent morphological and physiological gonadal alterations such as smaller phalli and poorly organized testes. Such alterations are likely to lead to cryptic effects on population structure, however such effects have yet to be tested. Here, I propose to assess the population-scale effects of EDCs using effective population size (N_e). Estimated using multi-locus diploid genotypes, N_e represents the effective number of reproductive individuals. Census population size (N_c) will be obtained from capture-mark-recapture data to standardize N_e between different populations. I hypothesize that N_e/N_c will be significantly reduced in populations historically exposed to EDCs.

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477 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Valencia Henderson, Pamela Hart, Prosanta Chakrabarty

Louisiana State University, Baton Rouge, LA, USA

Complete Mitochondrial Genomes of the Southern Cavefish (*Typhlichthys subterraneus*), Eigenmann's Cavefish (*T. eigenmanni*), and the Swampfish (*Chologaster cornuta*)

Cave-obligate organisms have fascinated the world for centuries, yet it is only recently that we have begun to examine the modes of subterranean adaptation and evolutionary history of these animals. Most of the literature on cave-adapted fishes focuses on the model Mexican Blind Cave Tetra, *Astyanax mexicanus*. The limited work on non-model fishes suggests that the modes of cave adaptation for the tetras are not mirrored in other fishes. The North American amblyopsid fishes have been suggested as a good group to examine different modes of subterranean invasions. Members of this family represent all three states of troglomorphy (characteristics associated with cave adaptation), including epigean (surface), stygophilic (facultative cave-dwelling), and stygobiotic (cave-obligate) . However, the evolutionary relationships within this family are still debated. The goal of the project is to recover the mitogenomes of species in the Amblyopsidae for phylogenetic investigation. In this study, we recovered and annotated the complete mitochondrial genomes for three species: the Southern Cavefish (*Typhlichthys subterraneus*), Eigenmann's Cavefish (*Typhlichthys eigenmanni*) and the Swampfish (*Chologaster cornuta*). We used Geneious to align and annotate the mitochondrial genomes and we performed a multiple alignment of raw sequence data to the phylogenetically closest complete reference genome (*Aphredoderus sayanus*). We then transferred the annotations from the reference genome to the aligned consensus sequence. Examining the mitochondrial genomes provides a more complete genetic history of this fascinating group of fishes and gives us valuable insight into multiple modes of subterranean adaptation.

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547 SSAR SEIBERT ECOLOGY AWARD II, Ballroom 2 – Cliff Lodge, Thursday 25 July 2019

Kodiak Hengstebeck[1], Christina Romagosa[1], Paul Andreadis[2], Ian Bartoszek[3]

[1]University of Florida, Gainesville, Florida, USA, [2]Denison University, Granville, Ohio, USA, [3]Conservancy of Southwest Florida, Naples, Florida, USA

Burrow Use and Selection by Invasive Burmese Pythons (*Python bivittatus*) in Florida

Burmese pythons (*Python bivittatus*) are established invaders of natural ecosystems in southern Florida and are affecting many native species with which they co-occur. Pythons have been implicated in the severe declines of meso-mammal populations throughout the southern Everglades, and are also likely affecting populations of large mammals and birds. The python population has expanded from the core population in the southern Everglades into other regions of southern Florida. In southwestern Florida, Burmese pythons have access to dry upland hammock and scrub habitats, which are uncommon throughout most of their current Florida range. Pythons commonly use animal burrows within these upland habitats as thermal refuge, as well as for breeding and nesting sites. This behavior could negatively impact native burrow-dwelling species, such as the state-listed gopher tortoise. Additionally, the thermal refuge provided by burrows may facilitate the northern range expansion by pythons in the southeastern United States. In this study, we used radio telemetry-tagged pythons to assess burrow use by Burmese pythons in southwestern Florida, and discuss the implications of this burrow use on native burrowing species.

CANCELLED

~~449 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019~~

~~Andrea Hernandez, Marianne Porter~~

~~*Florida Atlantic University, Boca Raton, FL, USA*~~

~~Fancy Fish Bits: Morphology of Soft Cranial Projections of the Red Lionfish, *Pterois volitans*~~

~~Since their introduction to the Western Atlantic in the 1980s, lionfish have become a successful invasive predator, causing negative effects on these ecosystems. One characteristic trait of lionfish (sub-family Pteroinae) is the soft cranial projections that decorate their eyes, nostrils, and mouth. The function of these projections remains unknown, but some are hypothesized to aid in defense, attract prey, or attract mates. A few studies have shown that the projections above the eyes, the supraocular tentacles, decrease in length with increasing fish length, while some of the projections around the mouth increase with fish length. Information on the morphological variation of these projections between sexes and among other cranial projections is missing. To~~

~~address this gap in knowledge, we quantified the morphology of soft cranial projections on the red lionfish (*Pterois volitans*), and hypothesized that there would be variations among head region and between sexes that scale with size. Comparative analyses on the number, size, and shape of the projections were used to characterize variation in cranial projection morphology. Preliminary data collected from females (n=5) suggests that projection morphology varies among head regions. Projection morphology in males will be quantified and compared with that of females. These morphological analyses on lionfish soft cranial projections, along with studies on their basic biology and ecology are crucial to create effective management programs to control the invasive population.~~

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634 Amphibian Disease, Ballroom 3 – Cliff Lodge, Sunday 28 July 2019

Obed Hernandez-Gomez[1], Erin Kenison[2], Jeffrey Briggler[3], Rod Williams[4]

[1]University of California, Berkeley, Berkeley, CA, USA, [2]U.S. Fish and Wildlife, Boise, ID, USA, [3]Missouri Department of Conservation, Jefferson City, MO, USA, [4]Purdue University, West Lafayette, IN, USA

Captivity-induced changes in the skin microbial communities of hellbenders (*Cryptobranchus alleganiensis*)

Captive environments often lack natural microbial reservoirs, have filtration systems that remove microbes, and are maintained in hygienic ways to prevent the spread of infectious disease. Aseptic conditions can negatively influence the establishment and maintenance of “wild-type” microbiotas within captive animals. Alternative microbial communities can result in the proliferation of disease among captive stock or upon reintroduction. Hellbenders (*Cryptobranchus alleganiensis*) are a threatened salamander for which extensive captive management is currently employed. Using metabarcoding, we characterized the skin microbiota of wild and captive-reared individuals from two subspecies in the state of Missouri, the eastern (*C. a. alleganiensis*) and the Ozark hellbender (*C. a. bishopi*). We also tracked changes in the skin microbiota of captive-reared eastern hellbenders exposed to river water from an intended re-introduction site in Indiana. Captive eastern hellbenders possessed richer communities than wild cohorts, whereas the opposite pattern was observed within the Ozark subspecies. We found significant microbial community structure between wild and captive populations of both subspecies. Eastern hellbenders exposed to river water in captivity had higher skin microbial diversity and distinct community composition on their skin, compared to control hellbenders. Exposing hellbenders to river water in captivity was an effective method to increase bacterial colonization and produced similar changes as release into the river. Our study provides a baseline for the effect of captivity on the skin microbial communities of hellbenders, and highlights the need to incorporate microbiota management in current captive-rearing programs.

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745 SSAR SEIBERT SYSTEMATICS AND EVOLUTION AWARD II, Ballroom 2 – Cliff Lodge, Friday 26 July 2019

Mark William Herr[1], Christian Cox[2], Adrian Nieto[3], Rafe Brown[1]

[1]University of Kansas Biodiversity Institute, Lawrence, Kansas, USA, [2]Georgia Southern University, Statesboro, Georgia, USA, [3]UNAM MZFC, Mexico City, Mexico

Comparative phylogeography of the North American Centipede Snakes (*Tantilla*)

The centipede snakes of the genus *Tantilla* are a diverse group of small- to medium-sized, New World snakes, uniquely specialized as predators of centipedes. *Tantilla* presently contains over 60 described species, making it the third most speciose snake genus in the world, widely distributed from Argentina to the central United States. The clade's species diversity and expansive distribution would seem to position *Tantilla* as a tempting subject for biogeographers. However, such inquiries have been hampered by a poor understanding of the interspecific relationships within the genus. Indeed, no published studies have yet examined the molecular phylogenetics of *Tantilla*. In order to explore the biogeography of this group, we generated nuclear and mitochondrial DNA sequences from genetic material sourced from the field and natural history collections. Here we present the first molecular phylogeny of North American *Tantilla species,* which we use to explore range evolution of the genus across space and time. In this presentation we present results of biogeographic inference (ancestral area reconstructions) and temporal framework for diversification (analyses of variation in rates of lineage accumulation) for the genus, and we discuss our results in the context of the broader biogeographic history of North America.

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823 Herpetology Morphology and Systematics, Ballroom 1 – Cliff Lodge, Friday 26 July 2019

Amanda Hewes, Kurt Schwenk

University of Connecticut, Storrs, Connecticut, USA

Multiple origins of a complex phenotype: morphology, kinematics, and phylogenetics of tongue-feeding in squamate reptiles

Despite rapid advances in our understanding of molecular evolution, much is still unknown about how complex phenotypes evolve. Feeding is an excellent model system in which to address this question because it entails the precise functional integration of many characters (e.g., senses, jaws, tongue, etc.) to ensure a successful outcome. Lizards exhibit a dichotomy of prey capture modes, in which small prey are apprehended with either the jaws or tongue, with the latter putatively ancestral. Recent work, however, shows that tongue-feeding occurs in several species nested within three, otherwise jaw-feeding clades, suggesting that this complex phenotype has evolved multiple times. I propose to study several tongue-feeding species within the families Cordylidae and Scincidae using gross anatomy, histology, high-speed videography, and materials testing methods. I will compare my results to the purely tongue-feeding taxon, Iguania, possibly representing the ancestral condition. A particular focus will be the biomechanics of the lingual adhesive mechanism, as effective adhesion is critical for successful prey capture. I will consider tongue kinematics and lingual shape change, papillary histology, the histochemistry of the lingual and other salivary glands, and the rheology (stickiness, viscoelasticity) of the salivary secretions. All results will be examined in light of competing phylogenetic hypotheses to infer character state transitions, discern overarching patterns of phenotypic change, and test the hypothesis that the evolution of tongue-feeding has occurred through parallel transformations in a set of common characters.

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548 Herpetology Ecology & Behavior, Primrose A&B – Cliff Lodge, Saturday 27 July 2019

Diana Hews[1], Duje Lisičić[2], Marko Glogoški[2], Sofia Blažević[2], Dubravka Hranilović[2]

[1]Indiana State University, Terre Haute, IN, USA, [2]University of Zagreb, Faculty of Science, Zagreb, Croatia

Do Island and Mainland Populations of *Podarcis sicula* Mirror Typical Within-Population Personality Differences?

Animal “personality” or “stress-coping styles” are consistent behavioral differences of individuals in multiple contexts or consistent within-individual behavioral correlations. Personalities also include differences in behavioral and neuroendocrine stress responses or “reactivity”. Personality types have been described for many vertebrate species, but the ecological contexts favoring animal personality are unclear. We present a study of adult males in an island and a mainland population of the Italian Wall Lizard, *Podarcis sicula.* We asked if personality styles that typically are described for a single population could represent extremes of a continuum, with one personality (less reactive) expressed on the island and the other (more reactive) on the mainland. In the field, we measured antipredator behavior (flight initiation distance, hiding duration), and breeding-season plasma testosterone and corticosterone (baseline and 30-min post capture stress levels); laboratory trials on a second set of males measured activity, aggression, and brain monoamines post-sacrifice. Island males had shorter hiding duration following a simulated predator approach, lower testosterone, and lower norepinephrine and epinephrine but not dopamine and serotonin. Analysis of corticosterone, open field activity trials and aggression trials are underway. Future work should examine more populations to determine if this is a general pattern, and identify selective factors, such as difference in predators, that favor expression of different stress-coping styles in different populations.

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587 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Coral Gardner[1], William Heyborne,[1,2]

[1]Southern Utah University, Cedar City, UT, USA, [2]The Nature Conservancy, Cedar City, UT, USA

Herpetological Inventory of the Grand Staircase Escalante National Monument, Utah, USA

The Grand Staircase Escalante National Monument was established in 1996. The 1.9 million acre monument includes a diverse array of high desert habitats. Monument staff, tasked with management of an unknown resource, solicited proposals for conducting monument-wide herpetological inventories in 2016. Our team has been conducting inventories for the last two field seasons, with a focus on visual encounter surveys, night drives, and acoustic surveys. Thus far, we have 4,246 unique observations of 27 species. However, there are seven species, encountered in museum records from the monument area, which have not been encountered during the course of the current project. Additionally, the project has been complicated by a reduction in monument size in 2018. Herein we present the findings of this ongoing project and hypothesize regarding the implications of monument boundary realignment.

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692 ASIH/HL/SSAR Symposium: Citizen Science in Herpetology: Productive Past and Promising Future, Ballroom 2 – Cliff Lodge, Sunday 28 July 2019

Toby Hibbitts[1,2], Danielle Walkup[2], Kevin Skow[2], Wade Ryberg[2]

[1]Biodiversity Research and Teaching Collections, Texas A&M University, College Station, Texas, USA, [2]Natural Resources Institute, Texas A&M University, College Station, Texas, USA

On the Road Again: Using Citizen Science Data to Understand Patterns of Amphibian and Reptile Road Mortality

Transportation planning is complicated by natural resource and environmental issues. Project planning and delivery are more efficient when environmental impacts are known early. Many environmental impacts involve state and federally listed threatened and endangered (TE) species. GIS-based habitat models can overestimate TE species' occurrence in environmental impact assessments. Overestimated TE species' occurrence can lead to ineffective prioritization and allocation of resources. Wildlife-vehicle collision (WVC) data can improve environmental impact assessments for TE species. Accurate WVC data has been collected for amphibian and reptile species on Texas roadways since 2012, in the form of observations in the "Herps of Texas" project on the citizen science platform iNaturalist. These data were used to create a database of species of greatest conservation need (SGCN) recorded and verified in the state that was joined with Texas road data from the Texas Department of Transportation (TxDOT) and used to evaluate SGCN species on and near roads. Our approach was to use previous collisions to find "hotspots" or seasonal collisions to find "hot moments" of conflict. These predictions can improve accuracy and effectiveness of transportation environmental impact assessments and mitigation for TE species over species distribution modeling approaches, because they are based on evidence that the species was actually present and struck by a vehicle.

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151 Herpetology Biogeography II, Ballroom 3 – Cliff Lodge, Friday 26 July 2019

Eric Hileman[1], Patrick Barnhart[1], Bradley Eichelberger[2], Jill Liske-Clark[2], Robert Reed[3], Amy Yackel Adams[3], Melia Nafus[3]

[1]U.S. Geological Survey, Brown Treesnake Project, Dededo, Guam, [2]Commonwealth of the Northern Mariana Islands, Division of Fish and Wildlife, Tanapag, Saipan, Northern Mariana Islands, [3]U.S. Geological Survey, Fort Collins Science Center, Fort Collins, CO, USA

Predictors of Lizard Distribution on Saipan

Vicariance and dispersal are primary drivers of species distributions in space and time. However, once species are established, persistence and abundance are governed by local conditions, available resources, and interspecific interactions. Introduced species are a primary cause of extinction on islands and can result in altered community membership, i.e., changes in multispecies occupancy, through competition for space and other resources. Consequently, understanding how introduced species affect native species and their distributions is important for conservation efforts. Saipan is an island in the Commonwealth of the Northern Mariana Islands with a long history of herpetofauna introductions, some as recent as the last several decades, others dating back to the arrival of Chamorro islanders ~3,500 years ago. However, the distribution of native and introduced herpetofauna on Saipan is poorly understood, and the effects of introduced species on Saipan's native herpetofauna are largely unknown. In 2018, we randomly selected sites on Saipan from established island-wide transects and used repeated surveys to account for imperfect species detection. We used multiple survey methods and single- and multispecies occupancy models to investigate the role ecological factors and species interactions have in explaining occupancy and detection of the herpetofauna. We recorded 2,568 observations representing 1 amphibian and 11 reptile species, including one species (*Perochirus ateles*) revealed to be less rare than previously thought. In general, introduced species were more widely distributed and frequently detected than native species. Visual surveys yielded the largest number of observations (1,872), followed by glue boards (655) and closed-cell foam covers (41).

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300 ASIH/HL/SSAR Symposium: The Expanding Role of Natural History Collections, Ballroom 1 – Cliff Lodge, Sunday 28 July 2019

Eric Hilton[1], Gregory Watkins-Colwell[2], Sarah Huber[1]

[1]Virginia Institute of Marine Science, William & Mary, Gloucester Point, VA, USA, [2]Yale Peabody Museum of Natural History, New Haven, CT, USA

The Expanding Role of Natural History Collections

Museum specimens are the bedrock of systematic and taxonomic research and provide the basis for repeatability or reinterpretation of observations. Specimens are also fundamental to fields such as ecology, behavior, and development. Each specimen is a record of biodiversity, and

documents a particular species present at a particular place at a particular time. As such, specimens can provide key evidence for biodiversity and conservation initiatives. Four aspects of natural history specimens that bear on their intrinsic importance can be circumscribed: 1) collection, curation, and use of specimens, particularly non-traditional specimens; 2) the use of specimens and technological advances in morphology, ontogeny, systematics, and taxonomy; 3) specimen use in other fields of biology and ecology; and 4) specimen use in education and outreach. Collections, and their vitality, depends on both their continued roles in traditionally supported fields (e.g., taxonomy) as well as emerging arenas (e.g., epidemiology). Just as a library that ceases buying books becomes obsolete, or at least has diminished impact and relevance, a natural history collection that does not continue to grow by bringing new specimens limits its utility. This presentation, and others in this symposium, will describe these roles of specimens, and speak directly to the need to increase the visibility of the inherent and critical value of natural history museums and the care of the specimens they protect for future generations.

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257 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Jessica Hobbs[1], Jennifer Schmidt[2], Jennifer McKinney[3], Eric Hoffmayer[4], Dení Ramírez-Macías[5], Jessica Dutton[1]

[1]Texas State University, San Marcos, TX, USA, [2]The Shark Research Institute, Princeton, NJ, USA, [3]Louisiana Department of Wildlife and Fisheries, New Orleans, LA, USA, [4]National Marine Fisheries Service, NOAA, Pascagoula, MS, USA, [5]Tiburón Ballena México, La Paz, Mexico

Mercury Concentrations in Whale Sharks (*Rhincodon typus*) from the Gulf of Mexico and Gulf of California

Mercury (Hg) is a toxic global pollutant that is well known to biomagnify up marine food webs, so top predators including sharks have the highest body burden. Most shark species are apex predators and can have a muscle Hg concentration that exceeds the Food and Drug Administration (FDA) and World Health Organization (WHO) action limit of 1 µg/g wet weight. In comparison, whale sharks (*Rhincodon typus*), the largest fish in the sea, are planktivorous and little is known about the concentration of Hg in their tissues. This study measured the concentration of total Hg in skin biopsied from primarily male juvenile whale sharks in the Gulf of Mexico (GoM; n = 17) and Gulf of California (GoC; n = 23) using a Direct Mercury Analyzer. The initial findings indicate that whale sharks in the GoM have a 3.14-times higher average Hg concentration than whale sharks in the GoC, which is attributed to differences in age and environmental Hg concentrations. However, within a region, there was a much wider range in Hg concentrations in GoM whale sharks compared to GoC whale sharks, possibly as a result of differences in age and migration patterns. This study is the most comprehensive regional assessment of Hg in whale sharks to date and the findings from these two areas will be compared to skin samples collected from other whale shark aggregations around the world that are currently undergoing Hg analysis.

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680 Herpetology Biogeography I, Ballroom 3 – Cliff Lodge, Friday 26 July 2019

Eric Hoffman[1], Nicholas Christodoulides[1], Anna Farmer[2], Kevin Enge[2], Alexa Trujillo[1], Steve Johnson[3]

[1]University of Central Florida, Orlando, FL, USA, [2]Florida Fish and Wildlife Conservation Commission, Gainesville, FL, USA, [3]University of Florida, Gainesville, FL, USA

Contrasting molecular markers and connectivity in an imperiled salamander

The striped newt (*Notophthalmus perstriatus*) is an imperiled species of salamander endemic to northern Florida and southern Georgia, USA. Individuals primarily inhabit sandhill, scrub, and scrubby flatwood communities and breed exclusively in isolated wetlands that lack predatory fishes. The species has declined throughout most of its range due to habitat loss and degradation (e.g., fire suppression), which appears to have reduced landscape-scale habitat connectivity. During the past two decades, the species has primarily been detected at "stronghold" sites that consist of multiple breeding ponds embedded within fire-maintained uplands or isolated populations throughout its historical range. We used ddRADSeq to generate 12,720 SNP loci to evaluate how contemporary patterns of gene flow and genetic diversity influence population dynamics and connectivity among 15 populations found throughout the species' range. We sought to answer two main questions: A) were the patterns of genetic differentiation consistent with our previous work (May et al. 2011 and an unpublished microsatellite dataset); and B) would geographically isolated populations be re-founded if a population became extirpated? Our data indicated that little gene flow occurs between isolated populations. Indeed, STRUCTURE indicated that all isolated populations represented unique genetic units, whereas two stronghold regions showed high levels of connectivity. Our results provide unique insight into the mechanisms influencing patterns of gene flow among populations of *N. perstriatus*. Understanding the cause of patterns observed for striped newts is important for conservation and effective management of this and other species with similar life history characteristics.

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421 AES Symposium: The Sensory Biology of Elasmobranch Fishes, Rendezvous A&B – The Snowbird Center, Saturday 27 July 2019

Sarah Hoffmann

Applied Biological Services, Biomark, Inc., Boise, ID, USA

Past, Present, and Future of Sensor Tags: Applications for Elasmobranch Research and Management

Biologging and biotelemetry facilitate the study animal movement at spatially and temporally applicable scales for conservation and management, but are limited in their inference of animal behavior. The incorporation of sensor tags for direct measurements of physiological processes combined with movement data can clarify how animals interact with different environments and provide insight into mechanisms and drivers of behavior. Tags that record feeding (gastric temperature/pH), stress (heart rate, glucose), and energetics (acceleration, muscle contraction, body temperature) are used successfully among many taxa to describe physiological processes as they relate to ecology. Elasmobranchs are a diverse group including cryptic and highly mobile species that vary in behavior and physiology; factors that exaggerate data acquisition issues associated with sensor tags. Most current physiological tags log data due to the amount of information recorded, requiring that tags be recovered for data acquisition. Onboard data processing, compression, and transmission are essential steps forward in the recovery of data for animals that are unlikely to be reencountered. Accelerometer data are frequently used to infer behavioral states (i.e., mating, foraging, respirating) but must be secondarily validated, which is not feasible for many elasmobranch species. The use of multisensory tags may overcome this challenge by pairing physiological data with triaxial accelerometry to confirm inferred behavior from movement. The combination of empirical physiological and movement data provides a validated description of behavior and may illuminate potential drivers thereof. Understanding where, how, and why elasmobranchs interact with their habitat is critical to effective species conservation and management.

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252 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Michael Holden, Joseph Barron II, Jeffery Feaga, Emmanuel Frimpong, Carola Haas

Virginia Tech, Blacksburg, Virginia, USA

Understanding the Interactions between Development and Nest Depredation in Bog Turtles

Animals such as raccoons, skunks, and opossums are documented to depredate a wide variety of terrestrial nests. These mesocarnivores are also known to persist in artificially inflated densities in relation to human activity, subsidized by anthropogenic food sources and refuse material. While studies show that these animals both depredate terrestrial nests, and persist at augmented population densities along an urban gradient, there is a lack of understanding on how these factors interact. While numerous species face these depredation pressures, I plan to conduct this research within the context of bog turtle (*Glyptemys muhlenbergii*) conservation. This species is a prime candidate for this research for a number of reasons. *G. muhlenbergii* is declining across much of its range, requiring a thorough understanding of the primary drivers of decline for this species. Additionally, they lay terrestrial nests, with documented depredation by mesocarnivores. These nests are easily replicated, as they are non-randomly placed, small in clutch size, and shallowly lain. To investigate these interactions, I plan to construct artificial nests in conjunction with camera traps during the 2019 field season. These nests will be placed at varying distances to human developments such as residential structures and roads. Furthermore, by mid-February I plan to conduct a GIS analysis assessing the potential anthropogenic impact on *G. muhlenbergii* wetlands. I will use available spatial data and a previously developed GIS-based habitat model to

identify what proportion of wetlands predicted to be suitable for bog turtles in southwest Virginia occur in close proximity to established human infrastructure.

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450 Herpetology Genetic Diversity, Ballroom 1 – Cliff Lodge, Thursday 25 July 2019

Matthew Holding[1,2], Jason Strickland[2], Rhett Rautsaw[2], Andrew Mason[2], Erich Hofmann[2], Michael Hogan[1], Schyler Ellsworth[1], Gunnar Nystrom[1], Mark Margres[2], Timothy Colston[1], Miguel Borja[3], Christoph Grünwald[4], Jason Jones[4], Gamaliel Castañeda[3], Luciana Sousa[5], Ana Moura da Silva[5], Inácio Azevedo[5], Felipe Grazziotin[5], H. Lisle Gibbs[6], Darin Rokyta[1], Christopher Parkinson[2]

[1]Florida State University, Tallahassee, FL, USA, [2]Clemson University, Clemson, SC, USA, [3]Universidad Juárez del Estado de Durango, Gómez Palacio, Durango, Mexico, [4]Herp.mx, Colima, Colima, Mexico, [5]Instituto Butantan, Sao Paulo, Brazil, [6]Ohio State University, Columbus, OH, USA

Assessing the relationship between venom complexity and diet diversity in rattlesnakes using a novel, genome-wide phylogeny

The rattlesnakes (*Crotalus* and *Sistrurus*) are the most speciose group of vipers, consisting of ~50 currently described species. Rattlesnakes are medically important as they contribute the majority of snakebites in North America, additionally they are flagships for curiosity, culture, and conservation of snakes. Despite being the focus of countless phylogenetic studies, the evolutionary history of rattlesnakes remains clouded and the phylogenetic placement of many species is uncertain, limiting studies of adaptive evolution and toxicity of venoms. We have collected tissue of 147 individuals snakes, representing all putative rattlesnake lineages. We use > 1000 nontoxin sequences from venom gland transcriptomes to infer the phylogeny of rattlesnakes, and characterize the composition and complexity of toxin expression in the transcriptomes and in chromatographic profiles of whole venom. We provide strong evidence for 3 major clades within *Crotalus*, the dusky and rock rattlesnakes, the montane rattlesnakes including *C. willardi*, and the large-bodied rattlesnakes such as *C. durissus* and *C. scutulatus*. Interestingly, we support *C. horridus* as sister to the rest of the clade of large-bodied *Crotalus* species, which differs considerably from its place in previous phylogenies. Finally, we use our venom gene expression, published diet data, and phylogenetic comparative methods to test the hypothesis that more complex venoms evolve in response to a more taxonomically complex diet. Our work provides new insight into the evolutionary history of this complex and iconic group, and relates complexity in patterns of gene expression to the complexity of ecological interactions an organism must face.

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443 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Matthew Holding[1], Vivian Trevine[2], Oleksandr Zinenko[3], Jason Strickland[4], Rhett Rautsaw[4], Andrew Mason[4], Erich Hofmann[4], Michael Hogan[1], Christopher Parkinson[4], Felipe Grazziotin[2], Adam Summers[5], Sharlene Santana[6], Mark Davis[7], Darin Rokyta[1]

[1]Florida State University, Tallahassee, FL, USA, [2]Instituto Butantan, Sao Paulo, Brazil, [3]V. N. Karazin Kharkiv National University, Kharkiv, Ukraine, [4]Clemson University, Clemson, SC, USA, [5]University of Washington, Friday Harbor, WA, USA, [6]University of Washington, Seattle, WA, USA, [7]Illinois Natural History Survey, Champaign, IL, USA

Fang length evolution in vipers is predicted by furred and feathered diets

Fangs, stingers, spines, and harpoons are used by diverse animal taxa to inject venom into their prey. Strong selection on venom composition has been repeatedly documented, and we might expect the venom injection apparatus to be under similarly strong selection to meet specific functional demands. Snakes in the family Viperidae (true vipers and pitvipers) consist of ~320 species widely studied by both ecologists and evolutionary biologists. Vipers provide an opportunity to determine how the venom injections systems evolve in response to functional demands of prey killing. Utilizing museum collections, we obtained measurements of fang length in >2000 individual specimens representing 200 viper species. We document the mode and tempo of fang length evolution across this diverse family, and test for relationships between ecology and the rate of fang length evolution across clades. We then leverage data collected from over 100 published diet studies to test the hypothesis that longer fangs evolved in response to demands associated with feeding on prey with coverings of fur or feathers. We find support for this hypothesis, where the percentage of mammals and birds in viper diets is positively correlated with relative fang length. Finally, when controlling for head size, the Gaboon Viper is dethroned as the snake species with the longest fangs, and overtaken instead by the Speckled Forest Pitviper of South America. Venom and the venom delivery system merit further work to determine if they are part of a broader functional and evolutionary module that facilitates feeding in venomous animals.

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508 Herpetology Biogeography I, Ballroom 3 – Cliff Lodge, Friday 26 July 2019

Bradford Hollingsworth[1], Alexandra Sumarli[2], Melissa Stepek[1], Jorge Valdez-Villavicencio[3], Tod Reeder[2]

[1]San Diego Natural History Museum, San Diego, CA, USA, [2]San Diego State University, San Diego, CA, USA, [3]Conservación de Fauna de Noroeste, Ensenada, Baja California, Mexico

Genomic Perspective of the Species Boundaries and Phylogenetic Relationships within the Baja California Gophersnake (*Pituophis vertebralis*)

The Baja California Gophersnake is distributed across Baja California from the northern regions of the Municipality of Ensenada to the tip of the peninsula at Cabo San Lucas, Mexico. Previous phylogenetic studies have focused primarily on the interspecific relationships within *Pituophis* and have not specifically dedicated efforts towards relationships within *P. vertebralis*.

Studies using mitochondrial data place the southern populations of *P. vertebralis* with *P. catenifer* populations in mainland Mexico, while northern samples group with *P. catenifer* to the north. We use a genomic approach to explore the phylogenetic affinities of *P. vertebralis* populations using 24 samples from across the peninsula and an equal number of samples from *P. catenife*r and other outgroup taxa. We assess the species boundaries and phylogeographic structure within *P. vertebralis* with respect to *P. catenifer* using SNP's (1300-1500 loci) obtained from RADseq data. Phylogenetic and population membership analyses support *P. vertebralis* and place it with a southwestern lineage of *P. catenifer* (~*P. c. annectans*) with limited introgression between the two in areas nearest to their geographic contact zone. Within *P. vertebralis*, we found no patterns to support the previously recognized subspecies (*bimaris* or *vertebralis).* We also found no indication that any part of *P. vertebralis* is closely related to *Pituophis* populations in mainland Mexico and our analyses support the continued recognition of *P. vertebralis* as a distinct species.

CANCELLED

530 AES Trophic Ecology I, Alpine A,B,C – The Snowbird Center, Sunday 28 July 2019

Lisa Hoopes[1], Tonya Clauss[1], Nicole Browning[2], Alexa Delaune[1], Bradley Wetherbee[3,4], Mahmood Shivji[4], Jessica Harvey[5], Guy Harvey[4]

[1]Georgia Aquarium, Atlanta, GA, USA, [2]Brenau University, Gainesville, GA, USA, [3]University of Rhode Island, Kingston, RI, USA, [4]The Guy Harvey Institute, College of Natural Sciences and Oceanography, Nova Southeastern University, Dania Beach, FL, USA, [5]Guy Harvey Ocean Foundation, George Town, Cayman Islands

Seasonal Patterns in Stable Isotope and Fatty Acid Profiles of Southern Stingrays (*Hypanus americana*) at a Popular Tourist Interaction Site

Ecotourism opportunities in the marine environment often rely heavily on provisioning to ensure the viewing of cryptic species by the public. However, intentional feeding of wildlife can impact numerous aspects of an animals' behavior and ecology. Southern stingrays (*Hypanus americana*) provisioned at Stingray City Sandbar (SCS) in Grand Cayman have altered diel activity patterns and decreased measures of health. This study looked at seasonal changes in stable isotope (SIA) and fatty acid (FA) profiles of provisioned stingrays at SCS. Plasma δ^{15}N was enriched in male stingrays compared to females. Depleted values for δ^{15}N in males and females were measured in October during the low tourist season, suggesting stingrays may be forced to rely on more depleted native prey items to supplement the decreased amount of provisioned squid available during this time. Plasma FA profiles were significantly different between sexes and across sampling time points. Dietary FAs primarily contributed to differences between males and females lending further evidence to differences in foraging patterns at SCS, likely due to intraspecific competition. Patterns in FA profiles suggest similar diets during peak tourist season (January) and differences in diet between males and females during the low season (October). This study demonstrates alterations in feeding ecology in stingrays at SCS which is of critical importance for well-informed and effective management of the SCS aggregation.

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713 Poster Session I, Event Center – The Snowbird Center, Friday 26 July 2019

Lisa Hoopes[1], Alisa Newton[2], Christopher Fischer[3]

[1]Georgia Aquarium, Atlanta, GA, USA, [2]Wildlife Conservation Society, New York Aquarium, Brooklyn, NY, USA, [3]OCEARCH, Park City, UT, USA

Fatty Acid Profiles of White Sharks (*Carcharodon carcharias*) in the Western North Atlantic

Reductions in the abundance of apex or mesopredators such as sharks can cause changes in ecosystem dynamics through competitive release, making it imperative to understand the trophic ecology of sharks to evaluate the consequences of their absence. Fatty acid (FA) profiles provide a non-lethal, minimally invasive technique to evaluate prey consumption given that long chain FAs pass from prey to carnivore consumers relatively unchanged, allowing for the reflection of a prey's FA profile to be represented in the tissues of the consumer. In addition to dietary information in elasmobranchs, FAs can also provide information on bioenergetics, body condition, life history and physiology. This project examined FA profiles of white sharks (*Carcharodon carcharias*) within the Western North Atlantic population to evaluate dietary differences across life history stages and geographic regions. Plasma FA profiles from 37 white sharks (19 young of year [YOY], 11 subadults, 7 adults) were dominated (>5% of total fatty acids) by FAs 22:6n3, 16:0, 20:5n3, 18:1n9 and 18:0. Distinct FA profiles were evident for both life history stage and geographic local. Unsurprisingly, FA ratio estimates of trophic position (18:1n9/18:1n7) and of nutritional condition (20:4n6/20:5n3) increased as animals progressed from YOY to subadult to adult life history stages. These preliminary results provide insight into the feeding ecology of white sharks and demonstrate the utility of FAs as biomarkers of diet.

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469 ASIH STOYE GENERAL HERPETOLOGY AWARD II, Primrose A&B – Cliff Lodge, Thursday 25 July 2019

Andrew Hopkins, Tiffany Schriever

Western Michigan University, Kalamazoo, Michigan, USA

Herpetofauna Species Composition and Environmental Variation in Interdunal Wetlands of Lake Michigan Coastline

Dune habitats feature unique species assemblages; however, little is known about how the environment shapes these communities. To date a survey of the herpetofauna associated with interdunal wetlands along the Eastern coastline of Lake Michigan has not been conducted. We surveyed 38 wetlands from April to October in five parks spanning four degrees of latitude separated into the southern ecoregion (3 parks, 21 wetlands) and northern ecoregion (2 parks, 17

wetlands). We hypothesized that species richness and diversity will be higher in the Southern sites compared to the Northern sites, following the prediction of latitudinal diversity gradient. Visual encounter surveys were carried out diurnally each month at 17 of the 38 total wetlands and nocturnally at 7 wetlands each month. We calculated beta diversity between wetlands and parks, tallied species richness, and tested significance of different components of environmental variation on community richness across both parks and sites. In all, we recorded 305 sightings of eight different species. Green frogs, *Lithobates clamitans*, were the most commonly found with an occupancy of 86% and a detection chance of 63% across all wetlands. Species richness ranged from 1 - 4 species across sites with a maximum Shannon Diversity index of 0.99. Our data supports our hypothesis with Southern diversity being significantly higher compared to northern sites ($p=0.03067$). Our field survey shows herpetofauna communities vary from southern to northern ecoregions and that environmental conditions influence species richness. This data can help inform conservation practices of coastal dune and wetland ecosystems.

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688 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Gareth Hopkins[1,2], Liz Yoon[3], Susannah French[2], Edmund Brodie, Jr.[2]

[1]Western Oregon University, Monmouth, OR, USA, [2]Utah State University, Logan, UT, USA, [3]Western Oregon University, Monmouth, OR, USA

Non-NaCl basedroad deicing salts: An underappreciated threat to amphibians?

Millions of tons of deicing salts (commonly NaCl, $MgCl_2$, $CaCl_2$, and commercial blends) are applied to roads every winter in North America. These salts run-off into aquatic environments, resulting in the salinization of freshwater. This salinization can affect the survival and development of osmotically-sensitive organisms in these environments, such as amphibians. While the effects of NaCl on amphibians is well understood, less tested are the effects of non-NaCl based salts. We reviewed the literature to determine our state of knowledge of the effects of non-NaCl salts on freshwater organisms, and found that surprisingly little is known. What little data exist, however, point to $MgCl_2$, the second most commonly applied salt in North America, being particularly potent to aquatic life, with greater effects on average than NaCl. To gain more data in this area, we tested the effects of different concentrations of both pure $MgCl_2$ and a commercial $MgCl_2$-based salt blend on the embryonic survival and development of a common western amphibian, the rough-skinned newt (*Taricha granulosa*). Our results show that commercial $MgCl_2$ was significantly more toxic than pure $MgCl_2$ to newt embryos, resulting in increased mortality, decreased size at hatching, and higher incidence of developmental deformities. These results highlight that studies examining only pure salts may underestimate the real-world impacts of commercially-applied deicers, and point to the significant potential impact of $MgCl_2$ application on amphibians. Non-NaCl based salts are an underappreciated threat to amphibian survival, and the serious dearth of knowledge on the conservation impacts of these chemicals should be addressed.

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625 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Tanden Hovey[1], Matthew Davis[2], Michael Ghedotti[1]

[1]Regis University, Denver, Colorado, USA, [2]St. Cloud State University, St. Cloud, Minnesota, USA

Histology of the Opercular Bioluminescent Organ of *Astronesthes* Snaggletooth Fishes (Teleostei: Somiidae)

The snaggletooths (*Astronesthes*) are predatory mesopelagic fishes with a diversity of intrinsic light organs including a luminous barbel, sequential ventral photophores, and orbit-associated photophores. Some species of *Astronesthes* also have luminous tissue on the opercle. Although the presence of this tissue has long been noted, its anatomical structure has not been documented. In this study we seek to closely determine the anatomic structure of the opercular bioluminescent organ in *Astronesthes.* We used histological sectioning in *A. formosana*, which has an opercular organ, and *A. lucifer*, which lacks an opercular organ, to document the anatomy of this organ. The opercular organ is of dermal origin and photocytes exhibit similarities to the more organized photocytes in other *Astronesthes* bioluminescent organs. Examination of additional species would provide a more comprehensive understanding of opercular bioluminescent organ anatomy and evolution.

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298 SSAR SEIBERT CONSERVATION AWARD II, Ballroom 1 – Cliff Lodge, Friday 26 July 2019

Hunter Howell[1], Caitlin Mothes [1], Stephanie Clements [1], Shantel Catania [1], Betsie Rothermel [2], Christopher Searcy [1]

[1]University of Miami, Coral Gables, FL, USA, [2]Archbold Biological Station, Venus, FL , USA

Amphibian Responses to Livestock use of Wetlands: New Empirical Data and a Global Review

As the global human population continues to increase, the amount of land devoted to livestock production will continue to rise. To mitigate the loss of global biodiversity because of ever-expanding land-use for livestock grazing, an understanding of how livestock impact wildlife is critical. While previous reviews have examined the impact of livestock on a wide variety of taxa, there have been no reviews examining how livestock grazing affects amphibians. We conducted both an empirical study in Florida examining the impact of cattle on amphibian communities and a quantitative literature review of similar studies on five continents. Our empirical study analyzed amphibian community responses to cattle as both a binary (presence/absence) or stocking rate (improved vs. semi-native pasture) variable, and as a continuous variable. Across all analysis, we were unable to find any evidence that cattle negatively affected the amphibian community at our study site. Of the studies included in the literature review, 15 found positive

effects of livestock on amphibians, 21 found neutral/mixed effects, and 10 found negative effects. Our analysis of these data indicates that amphibian species that historically occurred in closed-canopy habitats are generally negatively affected by livestock presence. In contrast, open-canopy amphibians are likely to experience positive effects from the presence of livestock, and these positive effects are most likely to occur in locations with cooler climates and/or greater precipitation seasonality. Collectively, our empirical work and literature review demonstrates that under the correct conditions well-managed rangelands are able to support diverse assemblages of amphibians.

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231 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Kelly Hoyer, Aaron Geheber

University of Central Missouri, Warrensburg, MO, USA

Impacts of Stream Temperature Gradient on Reproductive Capacity and Population Densities of Banded Sculpin, *Cottus carolinae*

Environmental stressors influence the life histories of organisms by altering amounts of energy invested in maintenance, growth, and or gonadal production. Temperature increase is a known environmental stressor, and as climate warms life history alterations are a possible consequence. In freshwater stream systems increases in water temperature may pressure fishes to invest less energy into (or reallocate energy for) reproduction, and this can potentially lead to smaller egg sizes and lower fecundity. The banded sculpin, *Cottus carolinae,* is an ideal organism for studying the effects of temperature on life history characteristics because of its sedentary lifestyle and its known low heat tolerance threshold. The aim of this study was to determine whether (and to what extent) reproductive capacity and population density of *C. carolinae* varies along stream temperature gradients. Surveys for banded sculpins were conducted in multiple tributaries of the Niangua River (Missouri) where man-made warm water inputs generate artificial temperature gradients. Reproductive qualities including egg size, egg counts per clutch, fecundity, and gonadosomatic index (GSI) were measured from individuals collected from stream sites. We hypothesized that warmer stream temperatures would affect *C. carolinae* reproductive output, and potentially lead to smaller eggs, lower fecundity, lower GSI, and lower population densities compared to colder stream reaches. Our results suggest that temperature gradient has some influence on both population density and reproductive output of *C. carolinae*. The implications of these findings in relation to climate change and life history strategy will be discussed.

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682 ASIH STOYE ECOLOGY & ETHOLOGY AWARD II, Primrose A&B – Cliff Lodge, Friday 26 July 2019

Steven Hromada[1], Todd Esque[2], Amy Vandergast[3], Corey Mitchell[1], Kirsten Dutcher[1], Kenneth

Nussear[1]

[1]*University of Nevada, Reno, Reno, NV, USA,* [2]*US Geological Survey, Henderson, NV, USA,* [3]*US Geological Survey, San Diego, CA, USA*

Habitat selection by Mojave Desert Tortoises (*Gopherus agassizii*) in Altered Landscapes

Understanding the movements and habitat preferences of animals is important in making informed conservation decisions because it can provide insight into the influences of anthropogenic activities. The Mojave desert tortoise (*Gopherus agassizii*) is a federally threatened species found broadly across the Mojave desert.. Urban expansion, increased incursion of recreation (e.g. OHV use), and utility scale solar facilities are all increasing in tortoise habitat. Understanding how these impacts influence tortoise populations is critical in conservation planning. To elucidate how tortoises use available habitat and interact with human infrastructure we used GPS dataloggers to record successive localities and to infer fine-scale movement of individuals (~130) at ten 1-km^2 study sites centered in the Ivanpah Valley area, near the California/Nevada border. Our sites encompass a variety of habitats, including mountain passes that serve as important corridors connecting neighboring valleys and have a variety of anthropogenic alterations (e.g. roads, powerline right-of-ways). We used step-selection functions and autocorrelated kernel density estimates of home range overlap to quantify habitat use. Our results indicate that both natural and human-created features shape desert tortoise activity patterns. Understanding these influences on desert tortoise movements can help to develop management strategies for future development within desert tortoise habitat.

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642 Reptile Conservation, Ballroom 2 – Cliff Lodge, Saturday 27 July 2019

Diego Huerta, Alexus Cazares, John Bosak, Jonathan Gould, Matt Goode

The University of Arizona, Tucson, AZ, USA

Ecology of Three Sonoran Desert Rattlesnake Species at an Urbanizing Site

Among snake species, rattlesnakes are one of the most studied groups. However, there exist significant gaps in our knowledge of how urban development affects rattlesnakes. Understanding anthropogenic impacts associated with urban development is critical for developing effective conservation strategies. We examine responses to urban development among three rattlesnake species, Western Diamondback Rattlesnakes (*Crotalus atrox*), Tiger Rattlesnakes (*Crotalus tigris*) and Black-tailed Rattlesnakes (*Crotalus molossus*). Since 2002, we conducted repeated surveys at Stone Canyon, an urbanizing residential development located at the base of the Tortolita Mountains near Tucson, Arizona. Making use of our long-term dataset, we compare relative abundance, growth rates, reproduction, body size, and other aspects of rattlesnake ecology. We discuss our results as they relate to rattlesnake ecology in general, and to the influence of anthropogenic factors populations over time.

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505 AES Conservation & Management II, Rendezvous A&B – The Snowbird Center, Sunday 28 July 2019

Robert Hueter[1], Bryan Franks[2], Christopher Fischer[3]

[1]Center for Shark Research, Mote Marine Laboratory, Sarasota, FL, USA, [2]Department of Biology and Marine Science, Jacksonville University, Jacksonville, FL, USA, [3]OCEARCH, Park City, UT, USA

The North Atlantic White Shark Study: Interdisciplinary, International, Collaborative Research on the White Shark in the Western North Atlantic

The white shark (*Carcharodon carcharias*) has been the focus of a number of studies in the eastern Pacific, South Africa and Australia, but our knowledge of this species in the Western North Atlantic (WNA) is still in its early stages. Recent findings indicate the WNA white shark population is rebuilding, raising concerns about increasing human-shark interactions and calling for a more comprehensive understanding of this shark's life history, behavior and ecology and the effects of climate change and environmental contaminants on these sharks in the WNA. This collaborative, multi-institutional, international research program involves more than 25 principal investigators from 25 institutions collecting data for 17 projects using the research capabilities of the nonprofit organization OCEARCH. Ten expeditions in U.S. and Canadian Atlantic waters have been completed to date, with the goal of sampling and tagging 60 WNA white sharks comprising 20 each of young-of-the-year, immature/subadults, and adults, with approximately equal numbers of males and females in each category. About two-thirds of this sampling goal has been achieved, with gains made in studies of population genetics, body and eye morphology, microbiology, parasitology, reproductive and stress physiology, health assessment and nutrition, trophic ecology, ecotoxicology, and movement behavior and ecology of WNA white sharks. We review findings to date of these integrated studies and present plans for conducting an additional eight expeditions, with a call for participation by other collaborators who can utilize OCEARCH facilities and expeditions, at no cost to the researcher, to further our knowledge of the white shark.

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482 Ichthyology Systematics II, Cottonwood A-D – The Snowbird Center, Sunday 28 July 2019

Lily C. Hughes

George Washington University, Washington, DC, USA

Exon-based phylogenomics of the fish clade Ovalentaria

Ovalentaria is a clade of more than 5,000 living fish species, first defined by analysis of molecular data and later diagnosed by a combination of morphological characters. This group includes a high diversity of forms and well-supported groups such as atherinomorphs, cichlids, damselfishes, blennies, clingfishes, glassfishes, mullets, and many others. Internal relationships among ovalentarian lineages remain uncertain as is the ordinal status of nine families within this clade. Additionally, molecular studies sometimes render certain families non-monophyletic. To address these uncertainties, we present phylogenomic analyses of Ovalentaria based on more than 1,100 exon markers, combining available data from transcriptomes and genomes, plus newly obtained sequences using a targeted exon-capture approach. Phylogenetic analyses of more than 400 species representing 43 of 44 ovalentarian families, were based on a matrix of half a million base pairs to resolve this large radiation. We find a well-supported backbone for major divergences in this clade, as well as the relationships among families, clarifying the phylogenetic position of pomacentrids, ambassids, pseudochromids, and other lineages that have been difficult to place.

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141 ASIH STOYE GENERAL ICHTHYOLOGY AWARD II, Cottonwood A-D – The Snowbird Center, Friday 26 July 2019

Jonathan Huie, Luke Tornabene

University of Washington, Seattle, WA, USA

Co-evolution of cleaning and morphology in Caribbean neon gobies

Cleaning is a mutually beneficial relationship, where cleaners remove and consume ectoparasites from their clients. Among fishes, the cleaning behavior has evolved several times as a juvenile or facultative feeding strategy, and is often lost in adults. Moreover, taxa that clean almost exclusively across their ontogeny (obligate cleaners) are relatively rare. The largest radiation of obligate cleaners are the Caribbean neon gobies (*Elacatinus*), that evolved with several congeneric non-cleaners, and in parallel with a closely related lineage of facultative cleaners (*Tigrigobius*). We suspect that obligate cleaning is a specialized trophic ecology tied to an equally specialized feeding morphology that facilitates improved cleaning performance. We coupled micro-CT scanning with the clearing and staining of museum specimens to compare several functional predictors of feeding performance between cleaner gobies and non-cleaners in a phylogenetic context. We also used geometric morphometrics to compare relative changes in head shape and mouth orientation. Obligate cleaning in gobies has evolved once, and is characterized by a specialized scraping dentition, stouter cranial features, and a more subterminal mouth position relative to non-cleaners. Meanwhile, facultative cleaning evolved at least 2-3 times, and their overall morphology reflects their intermediate feeding ecology. All cleaners are also converging on a similar, less sexually dimorphic dentition pattern, suggesting that the demand for an efficient cleaning morphology trumps sexual selection.

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614 General Ichthyology II, Cottonwood A-D – The Snowbird Center, Saturday 27 July 2019

Elizabeth Hunt[1], Kathryn Hamilton[1], Shannon O'Leary[1], Kyle Piller[3], Jeremy J. Wright[4], Kevin Conway[2], David Portnoy[1]

[1]Texas A&M University - Corpus Christi, Corpus Christi, Texas, USA, [2]Texas A&M University, College Station, Texas, USA , [3]Southestern Louisiana University, Hammon, LA, USA, [4]New York State Museum, Albany, NY, USA

Molecular phylogenetics of the genus *Erimyzon* (Family Catastomidae) based on mitochondrial and nuclear loci

Erimyzon is a genus in the family Catastomidae, comprised of four currently described species: *E. oblongus* (Eastern creek chubsucker), *E. claviformis* (Western creek chubsucker), *E. sucetta* (Lake chubsucker), and *E. tenuis* (sharpfin chubsucker) native to North America. Phylogenetic studies of Catostomids have been focused on resolving relationships of higher taxonomic groups, with little investigation into species level relationships within genera. Unlike other cypriniform fishes, Catostomids are tetraploid, leading to a limitation in the molecular markers available to use for phylogenetic inference. Previous studies have focused on mitochondrial markers, finding very limited success with nuclear markers. Inconsistencies in recovered relationships between various studies are mostly likely due to a combination of loci used and limited taxon sampling. While the genus *Erimyzon* is consistently recovered as a monophyletic group, in a recent study, *E. oblongus* did not form a monophyletic group. This could be due to misidentification of samples, presence of cryptic species, incomplete lineage sorting, lateral gene transfer or hybridization/introgression. The genus *Erimyzon* has not been thoroughly examined for more detailed morphological and genetic variation, and there may be unrecovered species in the genus. Here, we used mitochondrial and nuclear markers amplified in multiple individuals of each species, across reported ranges, to reconstruct phylogenetic relationships and better understand evolutionary relationships within the genus.

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498 Ichthyology Conservation, Cottonwood A-D – The Snowbird Center, Saturday 27 July 2019

Sarah Hylton[1], Woon Yuen Koh[1], Gail Wippelhauser[2], James Sulikowski[1]

[1]University of New England, Biddeford, Maine, USA, [2]Maine Department of Marine Resources , Augusta, Maine, USA

Sex and Foraging Ecology of Endangered Shortnose Sturgeon (*Acipenser brevirostrum*) in the Merrimack River, MA

Understanding reproductive biology and foraging ecology are imperative to the recovery of endangered species such as shortnose sturgeon (*Acipenser brevirostrum*), which require management specific to each distinct population segment (DPS). As shortnose sturgeon (SNS) exhibit no external sexual dimorphism, reproductive data is difficult to obtain without invasive or lethal sampling methods. The analysis of steroid hormones, however, has been effective in

determining sex for multiple species of captive and wild sturgeon. Existing descriptions of SNS diet are geographically sparse and dated, and must be updated in each DPS for effective management. To better understand population dynamics of SNS, seasonal trends in sex ratios and sex-specific diet in the Merrimack River DPS in the Gulf of Maine were identified using a novel combination of steroid hormone analysis and gastric lavage between 2016-2018. Testosterone (T) and 17β-Estradiol (E_2) values from 30 females identified via borescope and 28 males identified by release of milt were used to identify sex in 72 individuals via binomial logistic regression. Results of the study identified female-dominated aggregations in summer, fall, and winter with male:female ratios ranging from 1:1.5 - 1:3. In addition, a heavily male-dominated spring spawning aggregation of 50:1. Gammarid amphipods held the highest percent Index of Relative Importance (IRI) to diet in all seasons for males and females with the exception of summer 2017, when female diet was dominated by polychaete worms and Haustorid amphipods.

65 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Arturo Acero[1], Michelle Scharer Umpierre[2], Jose Tavera[3], Monruedee Chaiyapo[4]

[1]Universidad Nacional de Colombia sede Caribe, Santa Marta, Magdalena, Colombia, [2]Universidad de Puerto Rico, Río Piedras, Puerto Rico, Puerto Rico, [3]Universidad del Valle, Cali, Valle del Cauca, Colombia, [4]University of Chiang Mai, Muang, Chiang Mai, Thailand

A New Species of Grunt (Lutjaniformes: Haemulidae) from the Puerto Rican Upper Slope

A new species of the haemulid genus *Rhonciscus* Jordan & Evermann, 1896 was found in the upper slope and deep shelf of the northeastern Caribbean island of Puerto Rico. The new species is separated from the other three species of the genus [the western Atlantic *R. crocro* (Cuvier, 1830) and the Eastern Pacific *R. bayanus* (Jordan & Evermann, 1898) and *R. branickii* (Steindachner, 1879)] by having seven scale rows between the dorsal fin and the lateral line; *R. crocro* and *R. branickii* have six or less scale rows above the lateral line, while *R. bayanus* has eight scale rows above the lateral line. It differs clearly from its western Atlantic relative by having 50 lateral-line scales (vs 53-55 in *R. crocro*) and 11 short lower gill rakers (vs 7-9 in *R. crocro*). Habitat is another evident difference between the two western Atlantic species: *R. crocro* inhabits shallow waters, not deeper than 20 m and is frequently found in the mouth of short, rapid rivers; the new Puerto Rican species, on the other hand, inhabits the deep portion of the island shelf and the upper segment of the slope. The new species may be clearly separated from its two Eastern Pacific congeners by having a well serrated preopercle, with 2-3 large spines in the angle and 20-21 relatively small spines in the vertical border; the preopercle is weakly or not serrated in both Eastern Pacific species.

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538 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

Cory Adams, Daniel Saenz

USDA Forest Service, Southern Research Station, Nacogdoches, Texas, USA

Impacts of Native and Invasive Leaf Litter on Larval Anuran Behavior

Recent studies have demonstrated that Chinese tallow (*Triadica sebifera*) leaf litter can cause changes in behavior in anuran larvae by causing drastic changes in water chemistry. The effects of the leaf litter on water chemistry is attributed to the rapid decomposition of leaves causing a high biological oxygen demand. This reduction in oxygen impacts the behavior of tadpoles, forcing them to increase surfacing frequency to obtain aerial oxygen. It is unclear if the decomposition of native tree species leaf litter will have a similar effect on water chemistry and tadpole behavior. To test this, we compared the sub lethal effects of invasive Chinese tallow leaf litter to seven native tree species leaf litter. We exposed Bronze frog larvae (*Lithobates clamitans*) to three concentrations (0.15g/L, 0.25g/L and 1.0g/L) of Chinese tallow leaf litter and to one concentration (1.0g/L) of seven native tree species leaf litter and measured water

chemistry and tadpole behavior. We found significant differences in water chemistry between the species of leaf litter. Tadpoles exposed to red maple, Chinese tallow and sweetgum treatments had the highest frequency of air-gulping behavior; while tadpoles exposed to loblolly pine and water oak leaf litter made the fewest trips to the water's surface. While some species of native plants leaf litter had little effect on water chemistry, other species caused drastic changes in dissolved oxygen which impacted tadpole behavior. More work needs to be done to understand the impact native and invasive plants have on water quality and their effects on wildlife.

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343 Poster Session II, Event Center – The Snowbird Center, Saturday 27 July 2019

David Adams[1], Matthew Gifford[2]

[1]Vilonia High School, Vilonia, Arkansas, USA, [2]University of Central Arkansas, Conway, Arkansas, USA

Lizards Modulate Foraging Behavior in Response to Environmental Variation

Movement is an important determinant of an animal's fitness because it underlies all tasks necessary to survival, yet the basis on which animals choose varying speeds is still largely unknown. Speeds chosen by animals while preforming tasks, like predator evasion and foraging, are dependent on numerous external and internal factors. Environmental conditions and functional constraints should have influence over movement speeds of animals. Understanding the relationships between these factors and how they contribute to movement would help us better predict the speeds used during survival-dependent tasks. We video recorded Prairie Lizards (*Sceloporus consobrinus*) in experimental enclosures and analyzed the speeds and attack initiation distances lizards used while foraging. We predicted that, in more cluttered habitats, animals would use slower speeds and initiate prey capture attempts from shorter distances due to reduced visibility. Secondly, we predicted that average attack velocities during successful foraging attempts would be slower than unsuccessful attempts. Further, we predicted that increasing habitat complexity would reduce the difference of speeds between successful and unsuccessful attempts. Overall, attack speeds and distance were dependent on habitat type. Regardless of enclosure type, attack velocity was positively and significantly correlated with the attack distance, indicating that animals modulate attack speed based on distance prey is from them. Successful foraging attempts were significantly slower than unsuccessful ones, and the difference in successful and unsuccessful attempts was dependent on habitat configuration. Finally, this study emphasizes that functional constraints dominate in simple environments and that environmental constraints become more important with increasing habitat complexity.

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796 Ichthyology Reproduction, Development, and Morphology, Cottonwood A-D – The Snowbird Center, Sunday 28 July 2019

Mia Adreani[1], Casey Benkwitt[2], Scott Hamilton[3], Will White[4], Mark Steele[5]

[1]*California State University Northridge, Northridge, CA, USA,* [2]*Lancaster University, Lancaster, United Kingdom,* [3]*Moss Landing Marine Lab, Monterey, CA, USA,* [4]*Oregon State University, Corvallis, OR, USA,* [5]*California State University, Northridge, CA, USA*

Effects of size-selective fishing on population dynamics of blackeye gobies

Size-selective removal of individuals from populations, either via natural processes (e.g., predation) or humans (e.g., fishing) can influence the population dynamics of many species. However, it is unclear how selective removal influences fishes that change sex as part of their lifecycle. Therefore, we examined the influence of varying levels of removal intensity (0%, 50%, 80%) and size-selection (small removal, large removal, random removal) on a model species, blackeye gobies. We measured rates of growth, sex change, reproduction, recruitment, and immigration over the course of two experiments in summer 2017. The effect of removal treatments on demographic rates varied throughout the season. In the first experiment, rates of growth and sex change increased when larger individuals were removed from the population. These effects occurred regardless of removal intensity. In the second experiment, rates of growth and sex change only increased when there was both selective removal of large individuals and high removal intensity. Recruitment and immigration was similar among all reefs, regardless of treatment. Applying these results to commercially-important sex-changing fishes may help determine the most effective management strategy for preventing over-harvesting.

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646 ASIH STOYE GENERAL HERPETOLOGY AWARD II, Primrose A&B – Cliff Lodge, Thursday 25 July 2019

Justin Agan, Matthew Lovern, Jennifer Grindstaff, Stanley Fox

Oklahoma State University, Stillwater, Ok, USA

Use of Hatchling Orange Bars in Male-Male Interactions of *Crotaphytus collaris*

Collared lizards, *Crotaphytus collaris,* are sexually dimorphic; males use their sexually selected traits to defend territories against rival males and to attract females. Collared lizards are different from other animals in that they are sexually dichromatic as both hatchlings and adults, but the dichromatism is distinct during these stages. Hatchling males develop orange dorsolateral bars (HOB) that are lost as the lizards become sexually mature. Juvenile males are aggressive toward other juvenile males and use HOB in this aggressive context. We conducted behavioral trials that separated the effect of HOB from aggressive behavior. Lizards either had their HOB removed (masked with paint) or enhanced (increased area of bars with spectrally similar paint) and received either a hormone implant that increased dihydrotestosterone (DHT) levels and aggressive behavior, or a blank implant. Treatment lizards were placed in a neutral arena with an unaltered and size-matched stimulus male and behaviors of both lizards were recorded and scored to measure relative aggression. HOB and aggressive behavior were linked in behavioral

trials and increasing one, either HOB or aggression, negatively altered the outcome of male-male interactions. Lizards with increased aggression via hormone implants were significantly more aggressive in comparison to blank implanted lizards; lizards with only enhanced HOB or enhanced aggression received more aggression from opponents as retaliation for signal discordance. This result means that lizards police and punish those that act outside of the bounds of their signal.

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718 Herpetology Physiology, Ballroom 3 – Cliff Lodge, Saturday 27 July 2019

Mickey Agha, Yuzo Yanagitsuru, Nann Fangue, A. Justin Nowakowski, Laura Kojima, Joseph Cech, Melissa Riley, Janna Freeman, Dennis Cocherell, Brian Todd

University of California, Davis, Davis, CA, USA

Physiological consequences of rising water salinity for a declining freshwater turtle

Sea level rise, drought, and water diversion can all lead to rapid salinization of freshwater habitats, especially in coastal areas. Increased water salinities can in turn alter the geographic distribution and ecology of freshwater species including turtles. The physiological consequences of salinization for freshwater turtles, however, are poorly known. Here, we compared the osmoregulatory response of two geographically separate populations of the freshwater Western Pond Turtle (*Actinemys marmorata*) — a species declining across its range in western North America — to three constant salinities: 0.4, 10, and 15‰ over two weeks. We found that turtles from an estuarine marsh population regulated their plasma osmolality more efficiently than their conspecifics from a freshwater creek population 45 km away. Plasma osmolalities were consistently lower in estuarine marsh turtles than the freshwater creek turtles over the entire two-week exposure to 10 and 15‰ water. However, individuals from both populations exhibited body mass loss in 15‰ water, with significantly greater loss in estuarine turtles. We suggest the greater capacity to osmoregulate by the estuarine marsh turtles may be explained by their greatly reduced feeding and drinking in elevated salinities that was not exhibited by the freshwater creek population. However, due to rapid mass loss in both populations, physiological and behavioral responses exhibited by estuarine marsh turtles may only be effective adaptations for short-term exposures to elevated salinities, such as those from tides and when traversing saline habitats, and are unlikely to be effective under long-term exposure to elevated salinity as is expected if sea levels rise.

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636 AES Trophic Ecology I, Alpine A,B,C – The Snowbird Center, Sunday 28 July 2019

Matthew Ajemian[1], Catherine Lamboy[2], Ali Ibrahim[3], Breanna DeGroot[1], Kimbrough Bassos-Hull[4], Laurent Cherubin[1]

[1]FAU Harbor Branch Oceanographic Institute, Fort Pierce, Florida, USA, [2]Florida Institute of

Technology, Melbourne, Florida, USA, [3]Florida Atlantic University, Boca Raton, Florida, USA, [4]Mote Marine Laboratory, Sarasota, Florida, USA

Breaking ground with underwater sound: a novel approach to remotely measure hard prey consumption in durophagous predators

The elusive behaviors of durophagous (shell-crushing) aquatic predators creates challenges to observing predation *in situ* and thus quantifying their impacts on prey communities. Passive acoustics, or the remote monitoring of underwater sounds with sensitive hydrophones, provides an opportunity to observe shell fracture with sound, which travels over considerable distances in the aquatic environment. Despite these potential advantages in long-distance predation detection, researchers have not utilized this approach in ecological studies. Here, we report on results from an experiment where whitespotted eagle rays (*Aetobatus narinari*) were fed an assortment of hard-shelled mollusks and shell fracture events were recorded by a hydrophone coupled to a video camera. From April to May 2018, a total of 462 unique recordings were created from four captive rays. Overall, shell fracture events were short-lived (<0.1 sec) with a dominant frequency centered around 2.4 kHz, characteristics that make feasible feature identification and extraction from long-term acoustic recordings. Additionally, a multivariate analysis of variance of fracture frequency characteristics found differences between representative bivalve (hard clam, *Mercenaria mercenaria*) and gastropod (banded tulip, *Cinctura lilium*) prey (Pillai's Trace, $F_{3,137} = 4.627$, $P < 0.0001$) with significantly lower minimum frequencies for fracturing banded tulips. Further, significant variation in processing behavior was observed between the prey types; hard clams required significantly more processing time (39.0 ± 2.8 sec) than similarly sized banded tulips (mean = 15.5 ± 1.3 sec). While additional field testing is required, these findings indicate the potential to remotely quantify foraging in durophagous species via passive acoustics.

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545 Amphibian Conservation, Ballroom 2 – Cliff Lodge, Saturday 27 July 2019

Nathaniel Akers, Brian Arbogast

University of North Carolina Wilmington, Wilmington, NC, USA

Assessing Geographic Patterns of Genetic Variation and Gene Flow in North Carolina Populations of the Gopher Frog (*Rana capito*)

The gopher frog (*Rana capito*) is considered an endangered species in North Carolina. This species primarily occurs in long leaf pine forests, which have suffered a 97% reduction in distribution due to fire suppression and development over the last century. Now, many species associated with this habitat type are listed as threatened or endangered. Prior studies have produced broad-scale genetic information for gopher frogs from across their range in the southeastern United States, but little fine-scale genetic data are available for populations of gopher frogs in North Carolina. Thus, there is a need to obtain such information on gopher frogs in North Carolina in order to effectively manage the species in the state. Understanding the genetic architecture of gopher frogs will provide critical information necessary for conservation practices, including potential translocation of frogs between sites or augmentation of populations

that have relatively low levels of genetic diversity with individuals from more genetically diverse populations of this species. Here, we present our analyses of nucleotide sequence variation in the mtDNA ND2 gene for North Carolina populations of *R. capito*. Our results indicate that mtDNA sequence variation within and among the NC populations is relatively small. We have also genotyped individuals from these populations using microsatellite markers in order to assess finer-scale geographic patterns of genetic variation as well as relatedness of individuals sampled from a given site. Overall, this genetic information can be used as a framework for guiding conservation and management decisions for gopher frogs in North Carolina.

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428 Ichthyology Systematics I, Cottonwood A-D – The Snowbird Center, Sunday 28 July 2019

Fernando Alda[1], Diego Elias[2], William Ludt[3], Caleb McMahan[4], Prosanta Chakrabarty[2]

[1]University of Tennessee at Chattanooga, Chattanooga, LA, USA, [2]Louisiana State University, Baton Rouge, LA, USA, [3]National Museum of Natural History, Smithsonian Institution, Washington DC, USA, [4]The Field Museum of Natural History, Chicago, IL, USA

Compared Performance of Hybrid-Target Capture Methods in Resolving the Phylogeny of Heroine Cichlids: Are All Markers Good for All Nodes?

Phylogenomic studies are struggling to develop computational protocols scalable to the amount of genomic data generated by massive parallel sequencing technologies. Therefore, we usually rely on the analysis of datasets containing reduced representations of the genome. These datasets can be obtained through hybrid target capture of hundreds to a few thousand orthologous loci (e.g. exon capture, ultraconserved elements, anchored enrichment), with desirable properties such as low paralogy, easy alignment, high consistency across studies, and proven utility at multiple evolutionary timescales. However, there are also differences inherent to the nature of these markers that may potentially affect their performance. Alignment length, polymorphism, or nucleotide substitution rates and models, can result in different amounts of phylogenetic informativeness relative to systematic error, and therefore alter the inference of species trees. The information content of the markers in a study is rarely interrogated. Let alone, comparing different types of markers to decide which one is more suitable to resolve the relationships of interest. Here, we inferred the phylogenetic relationships of Central American heroine cichlids using—novel—ultraconserved elements and—previously published—exon data. We compared topologies and support between species trees inferred using concatenation and coalescent methods, and related estimates of phylogenetic informativeness across the tree for each type of marker with the consistently recovered nodes at each particular period of time. We also evaluated heterogeneity among gene trees of different molecular markers, and draw conclusions on the relative effect of incomplete lineage sorting vs. systematic errors in obtaining accurate species trees.
