

394 Herpetology Conservation III, Highland C, Sunday 15 July 2018

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Reintroduced and Resident Amphibian Community Dynamics and Health Response to Oak Woodland Restoration

We are examining amphibian demographic, community, and health responses to oak restoration via canopy gap management and invasive understory removal in northern Illinois. Objectives include monitoring reintroduced Wood Frog (*Lithobates sylvaticus*) demography, changes in community structure of resident amphibians, changes in incidence of *Batrachochytrium dendrobatidis* (*Bd*) and amphibian stress as restoration progresses. As habitat improves, we expect increased catch per unit effort (CPUE) and diversity, and decreased mean cortisol (CORT) levels and incidence of *Bd* across sites and species. Using drift fences, noninvasive CORT swabs, and *Bd* swabs, we are sampling five restoration sites and one control site. Three sites had both gap management and understory removal, while two had only gap management. Gap and understory treatment sites had greater CPUE, diversity, richness, evenness, and hydroperiods than gap-only sites. Wood Frog representation in the reintroduction site increased from 5.6% of the total catch in 2016 to 20% in 2017, with the greatest number of egg masses observed since translocation in 2010. We observed a north-south gradient of low to high representation of Spring Peepers (*Pseudacris crucifer*). Blue-Spotted Salamanders (*Ambystoma laterale*) had consistent representation across sites in both years. *Bd* sample prevalence slightly decreased from 17.5% in 2016 (n = 194) to 13% in 2017 (n = 313). *Bd* was detected in four of six sites, and in six of nine species in both years. CORT levels of each species were similar among sites and management treatments, but Northern Leopard Frogs (*Lithobates pipiens*) had greater CORT levels with *Bd*-positive status.

449 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018

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Abiotic Correlates of Calling activity of the Southern Crawfish Frog

The crawfish frog has suffered declines across much of its range and is currently considered for state protection in five of the twelve states where it occurs. It is a secretive species that spends most of its time in or near crawfish burrows, making it difficult to detect outside of the breeding season. During the breeding season, however, they 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 2017. Our analyses suggest that several abiotic factors are important predictors of crawfish frog calling activity. 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 behave quite differently than their northern con-specifics with regard to calling phenology, daily calling activity, and possibly their relationships with abiotic factors that influence calling activity.

607 General Ichthyology II, Grand Lilac Ballroom South, Sunday 15 July 2018

Norma Salcedo

Francis Marion University, Florence, South Carolina, USA

***Hemiancistrus platyrhynchus* Fowler 1943 (Siluriformes: Loricariidae): the little catfish that could.**

Hemiancistrus platyrhynchus Fowler 1943 is a small armored catfish that was described based on four specimens donated by Brother Nicéforo María to the Academy of Natural Sciences of Philadelphia. This species has been assigned to *Peckoltia* and *Cordylancistrus*, relying on external morphology, and to *Chaetostoma* after a phylogenetic study that used morphological characters. The genus *Chaetostoma*, has been diagnosed based on: "loss of suture between the pterotic-supracleithrum and hyomandibula, loss of the hyomandibula angled mesially so that the opercle is held almost perpendicular to the body axis, the anterior process of pterotic-supracleithrum is slightly deflected mesially, narrow ventral process of sphenotic, and tip of transverse process of the complex centrum of the Weberian apparatus not contacting the pterotic-supracleithrum". Could this species be closely related to *Dolichancistrus*, *Leptoancistrus*, or *Cordylancistrus* species? It shares a flared anterior tip of the mesethmoid, in contact with dermal plates with *Cordylancistrus torbesensis* and *Dolichancistrus fuesslii*; a short process of the sphenotic with *Lipopterichthys carrioni*, and several *Cordylancistrus*, *Dolichancistrus*, and *Chaetostoma* species; and, a short ossified second basibranchial with *Cordylancistrus torbesensis* and several *Chaetostoma* species. Could this species be, in fact, the only *Chaetostoma* species with dermal plates on the snout? It shares a suture between the hyomandible and the pterotic-supracleithrum that extends half the length of the posterior border of the hyomandible with *Chaetostoma lobarhynchus*, type species of the genus *Chaetostoma*. This species has not been included in recent phylogenetic studies using molecular nor morphological information. Therefore, its generic assignment still could be a surprise.

22 Herpetology Systematics, Highland B, Saturday 14 July 2018

Christopher Samuelson¹, Utpal Smart¹, Eric Smith¹, Mahmood Sasa Marin² and Alejandro Solorzano³

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Systematics of the Central American coralsnakes allied to *Micrurus alleni* (Squamata:Elapidae)

The Pacific population of the Isthmian Central American coralsnake currently recognized simply as *Micrurus alleni* has been variously proposed as a distinct taxon in the past (e.g., *M. a. yatesi*, *M. nigrocinctus yatesi*, or *M. yatesi*). In this study we revisit the validity of this population as a distinct taxon, using the mitochondrial gene fragment ND4 to estimate its phylogenetic placement with respect to closely related species; including populations currently recognized as *M. alleni* from Costa Rica, Honduras, Nicaragua, and Panama, and *M. stewarti*, from Panama. This last relationship call the *M. alleni* complex. After garnering molecular evidence for the phylogenetic distinctness of the Pacific populations from Costa Rica and Panama (which we henceforth recognize as *M. yatesi*) we also employ Discriminant Function Analyses (DFA) using meristic counts and number of bands to investigate whether the observed genetic distinctness is supported by external morphology. Beyond confirming our phylogenetic allocation, the statistical analysis of morphological data reveals that Atlantic populations near the Costa Rica and Panama border (for which we lacked molecular data) can also be assigned with confidence to the taxon *M. yatesi*, which was previously only suspected to occur on the Pacific coast. Although, morphologically diagnosable when examining males, *M. yatesi* is very similar to and difficult to distinguish from its nominal form based on the external morphology of females.

44 SSAR SEIBERT ECOLOGY II, Highland A, Friday 13 July 2018

Mark Sandfoss and Harvey Lillywhite

University of Florida, Gainesville, Florida, USA

Water relations of an insular population of pit viper in Florida.

Seahorse Key (SHK) is a continental island near coastal Florida that lacks permanent sources of fresh water and is inhabited by a large population of Florida Cottonmouth snakes, *Agkistrodon conanti*, that share an interesting relationship with colonial nesting waterbirds. Because cottonmouths on the mainland are strongly associated with freshwater habitats, conspecifics on SHK likely have developed alternative strategies for maintaining water balance. We used a mix of field and laboratory experiments to investigate the possible stresses and adaptations related to dehydration within the cottonmouth population on SHK. Our objectives were to 1) measure

hydration status of free-ranging snakes in relation to rainfall patterns, 2) compare the drinking threshold of dehydrated cottonmouths from SHK and mainland Florida and 3) determine if cottonmouths drink sea water (SW) when in a dehydrated state. We predicted cottonmouths on SHK are using rainfall to maintain water balance, and hypothesized that SHK and mainland snakes differ in their drinking behavior. Preliminary results show 1) cottonmouths captured on SHK were more likely to be in a dehydrated state as time progressed since a substantial rainfall event (>2.5mm/h), 2) snakes from SHK and mainland populations showed little difference in drinking threshold and 3) no cottonmouths from either population voluntarily ingested 100% SW. Cottonmouths on SHK appear to have behaviorally adapted to use of rainfall to maintain water balance. We found little difference in the drinking threshold and avoidance of SW between mainland and SHK populations, suggesting these behaviors may represent innate traits in cottonmouths.

193 Lightning Talks I, Grand Lilac Ballroom North, Thursday 12 July 2018

Marcella Santos¹, Leandro Sousa² and Brice Noonan¹

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Population Genomics and Evolution of Catfishes of the Genus *Hypancistrus* in the Highly Imperiled Xingu River, Brazil

With an incredibly diverse fish fauna and unique landscape, the Xingu River is suffering massive changes due to the construction of the Belo Monte hydroelectric megadam. This Amazonian tributary is still largely unknown by scientists, but ongoing genomic analyses are showing this is an exceptional system for the study of evolutionary processes, comprising a variety of patterns with examples of geographically isolated populations, introgression among related species, and sympatric cryptic lineages. This project focuses on three species of pleco catfishes co-occurring in the Xingu River: the critically endangered *Hypancistrus zebra* and two undescribed species belonging the same genus. We will obtain genomic sequence and phenotypic data to investigate diversity and structure of *Hypancistrus* spp. in the Xingu River with samples collected prior to the construction of the dam, using population genetics, phylogeography, and landscape genetics approaches. We are investigating three non-exclusive hypotheses: 1) existence of a general pattern of downstream increase in diversity; 2) waterfalls act as barriers to gene flow; 3) environmental variables associated with rapids habitat (e.g. water velocity and substrate) are important selective agents for this species. We have obtained 211 tissue samples of Xingu *Hypancistrus*, and constructed restriction-site associated DNA libraries to generate genomic single nucleotide polymorphism data. To estimate the association between genotypes and color phenotypes we photographed the voucher specimens and will quantify color variation with the aid of imaging software.

581 ASIH STOYE GENERAL HERPETOLOGY, Highland C, Friday 13 July 2018

Neha Savant and Matthew Palmer

Columbia University, New York, NY, USA

Genomic Structure & Connectivity of the threatened Long-tail Salamander (*Eurycea longicauda*) Across Ponds and Streams

Understanding population genetic structure and connectivity of imperiled species across habitats is vital not only to understand their natural history, but also to inform management strategies. Amphibians are a model system for many population genetic studies, yet few have explored gene flow of species that occur in multiple habitats such as streams and ponds. Using genomic methods, we explored the genetic structure of the threatened long-tail salamander, *Eurycea longicauda*, across both pond and stream habitats in New Jersey. We compared the species' genetic structure within a stream vs. within a pond complex and among streams vs. among ponds. We collected 94 samples from ponds and 161 samples from streams across similar spatial extents. Population density was higher along pond margins than along streams where salamanders were found in aggregations of fewer individuals. To assess the genetic structure of populations, we are analyzing ddRAD sequencing data with F_{ST} metrics and cluster analysis. We expect to see evidence for isolation by distance with similar genetic structuring among both pond and stream populations. We also expect to find less genetic structure among populations within a stream than within a pond network due to the higher degree of habitat connectivity offered by streams. Studies on *E. longicauda* population connectivity in New Jersey are especially timely as a natural gas pipeline is proposed to be built across many of these stream habitats. Results from this study will bring managers closer to understanding how to best manage impacts from this disturbance and conserve this threatened species.

3 ASIH: If Salamanders Could Speak Symposium, Grand Lilac Ballroom North, Saturday 14 July 2018

Alan Savitzky¹ and Akira Mori²

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Anointed and Sequestered: Diverse Sources of Defensive Cardiotonic Steroids in Tetrapods

A number of tetrapod vertebrates co-opt the chemical defenses of other organisms for redeployment against their predators. An early study of this phenomenon by E. D. Brodie, Jr., in 1977, demonstrated that hedgehogs (Erinaceidae) "self-anoint" their integumentary spines with bufadienolide toxins from toads (Bufonidae). In an interesting parallel, the African crested rat (*Lophiomys*) self-anoints with pharmacologically related cardenolide toxins derived from plants. We have studied a group of Asian natricine snakes that possess defensive glands in the skin of

the neck (nuchal glands) or the full length of the body (nucho-dorsal glands). In the most extensively studied species, *Rhabdophis tigrinus*, the glands contain bufadienolides sequestered from toads consumed as prey. Phylogenetic analysis confirms that all natricines with nuchal or nucho-dorsal glands comprise a single lineage, with toads as the ancestral source of defensive steroids. The discovery of chemically distinctive bufadienolides in a derived, earthworm-eating clade, the *R. nuchalis* Group, led to the search for an alternative dietary source of the toxins in these species. Aside from bufonids and *Rhabdophis*, the only animals known to be defended by bufadienolides are fireflies (Lampyridae), and gut contents of *R. pentasupralabialis*, a member of the *R. nuchalis* Group, frequently contain lampyrine firefly larvae (*Diaphanes* sp.). *R. pentasupralabialis* and *Diaphanes* contain several identical bufadienolides. Thus, the dietary shift from vertebrate to invertebrate prey in the *R. nuchalis* Group involved a shift in the source of defensive toxins from toads to fireflies. As in the self-anointing mammals, alternative exogenous sources provide chemically similar defensive compounds.

69 Poster Session II, Empire Hall South – JF Rochester Riverside Convention Center, Saturday 14 July 2018

Christopher Schalk¹, Nicholas Schiwitz¹ and Daniel Saenz²

¹Stephen F. Austin State University, Nacogdoches, Texas, USA. ²USDA Forest Service, Nacogdoches, Texas, USA

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

The activity rate-predation risk tradeoff is a pattern 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. Dry, 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. 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, and then alarm cues produced from a consumed conspecific. We found that 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 species, providing insight to how it affects the organization of ecological communities.

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Joshua Schwartz

Pace University, Pleasantville, NY, USA

The Influence of Aggressive Calls on Mate Choice by Female Gray Treefrogs

In response to loud calls or physical intrusions by male conspecifics, males of many species of frogs produce aggressive calls. Although the acoustic features of aggressive vocalizations may be well-described, we are largely ignorant of their utility and potential costs to the producing and nearby males. In this study, I investigated whether or not production of aggressive calls would compromise the attractiveness of males of the treefrog, *Hyla versicolor*, to potential mates. I also investigated whether females exposed to simulated aggressive vocal exchanges, would discriminate in favor of putative winners. Using both natural and synthetic aggressive calls, I found that aggressive calls are unattractive relative to advertisement calls although they possess an ability to elicit phonotaxis by a subset of females in single speaker tests. In three-speaker tests, I found that female choice behavior is not affected when a simulated male giving advertisement calls vocalizes near one giving aggressive calls if there is no acoustic interference. However, aggressive calls overlapping with advertisement calls have the potential to reduce the attractiveness of the latter relative to unobscured advertisement calls. Finally, females failed to discriminate between a simulated winner and retreating loser suggesting that such outcomes are irrelevant to females or that their ability to eavesdrop is limited. Results also suggest that retreat and return to advertisement calling may be beneficial because they reduce the probability that an adjacent male would intercept an approaching female.

403 ASIH STOYE CONSERVATION, Highland D, Friday 13 July 2018

Jason Selwyn¹, John Johnson¹, Alan Downey-Wall², Adam Bynum¹, Rebecca Hamner¹, J. Derek Hogan¹ and Christopher Bird^{1,3}

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Veni Vidi Vici: How Many Lionfish Came to Conquer the Atlantic

While likely too late, given current technology, to eradicate the Indo-Pacific red lionfish (*Pterois volitans*) from the invaded range in the western Atlantic Ocean efforts informed by the lionfish invasion can be taken to prevent subsequent invasions. One unclear aspect of the invasion is how many initial colonists were needed at the outset to lead to the current state of the invasion. It is well-established that at least ten lionfish were initially introduced, based on the number of

mitochondrial haplotypes present. However, this is not an assessment of the true number of colonists. To estimate the number of colonists, we used a population genetic model of the mitochondrial control region in concert with a demographic life-history model to simulate the invasion from the Indo-Pacific given the source population diversity. Assuming a balanced sex-ratio and no reductions in fecundity due to Allee effects our results indicate 118 (54-514, 95% HPD) lionfish initially colonized the Atlantic. Incorporating the likely Allee effects experienced by the founding population leads to increased estimates of the number of colonists required to spur the invasion. These results suggest that rather than an introduction by a single individual or small group of individuals the invasion was caused by a systemic failure of the marine ornamental aquarium industry, likely at all levels, from individual aquarists to distributors and wholesalers. Efforts to prevent future invasions need to focus on education of the costs of animal dumping, providing options for humane disposal of unwanted animals, and sufficient penalties for releasing animals.

182 ASIH STOYE GENETICS, DEVELOPMENT, & MORPHOLOGY II, Highland C, Friday 13 July 2018

Gayani Senevirathne and Neil Shubin

University of Chicago, Chicago, Illinois, USA

Ontogeny of the urostyle, a structural innovation in frogs

The urostyle, an apparent key novelty in the anuran (frogs and toads) radiation, is considered an evolutionary enigma. Formed at the onset of metamorphosis, urostyle is a composite structure of dual origin: a mesoderm-derived coccyx and an endoderm-derived hypochord. Despite the importance of the structure, which first appeared in the fossil record during the early Jurassic (depicted in the fossil *Prosalirus bitis*) and still retained in all extant anurans, the cell differentiation of the coccyx and hypochord formation remains obscure, and has not been studied in detail to date. Further, the ossification patterns of the two structures remain to be discussed. Here, we highlight the ontogenetic changes during the urostyle formation in two lineages of frogs, *Xenopus tropicalis* (Mesobatrachia, Pipidae) and *Phylllobates aurotaenia* (Neobatrachia, Dendrobatinae), occupying different habitats, aquatic and terrestrial, respectively. Attention is given to changes at metamorphic climax. Using Alizarin Red and Alcian Blue staining to detect bone and cartilage, and Haematoxylin and Eosin staining to detect cell differentiation, we note the formation of the coccyx as a pair of initial ossification centers (replacing the cartilaginous precursors of the postsacral vertebra 1), which extends its ossification both anteriorly and posteriorly throughout the metamorphosis. The hypochord, in contrast, appears to undergo direct ossification within the notochordal sheath, where ossification progresses ventral to the notochord and the cells appear to be migrating from the notochordal sheath. Further scrutiny on the cell lineages contributing to the coccyx and hypochord will shed light on the novelty of this structural innovation in frogs.

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Daniel Sequeira, Andrea Giraldo and Laine Giovanetto

NJCU, Jersey City, NJ, USA

Roadkill Survey of Amphibians and Reptiles of Great Swamp National Wildlife Refuge, Pigeon Swamp State Park, and Hoboken, New Jersey.

Populations of amphibians and reptiles living in urban and suburban environments face threats that are either unique or intensified compared to those faced by non-urban populations. New Jersey populations are subjected to high rates of road mortality whenever individuals move from feeding grounds to breeding sites and when they move to and from hibernacula. We collected DOR (Dead on Road) amphibians and reptiles from two suburban areas (Great Swamp National Wildlife Refuge and Pigeon Swamp State Park) and one urban area (Hoboken) in New Jersey to help census these areas and to identify possible roadkill hotspots. Between September 2016 and August 2017 we encountered 215 DOR amphibians and reptiles. At PSSP there were 127 species including 116 frogs (4 species), 3 salamanders (2 species), 6 snakes (3 species), and 2 turtles (2 species). At GSNWR there were 83 species including 51 frogs (6 species) 23 turtles (4 species), and 9 snakes (7 species). In Hoboken there were 5 snakes (2 species). We found 36 predated turtle nests in July at GSNWR (34 in a single survey). The overall numbers of DOR specimens at GSNWR would probably have been much higher if one of the student researchers had not avoided surveying the road with the heaviest traffic. The low numbers for salamanders may be due to our surveys beginning too late in the winter months.

606 Lightning Talks III, Highland B, Sunday 15 July 2018

Katherine Sgouros

Tulane University, New Orleans, LA, USA

Gene Partitioning in Catostomidae as a Means of Ecological Adaptation

My dissertation will assess expression partitioning of duplicate transcripts of the homeostatic regulator gene creatine kinase (Ck-B) and glycolytic pathway/neuronal development gene glucose-6 phosphate isomerase (Gpi-A) of smallmouth buffalo (*Ictiobus bubalus*) and spotted sucker (*Minytrema melanops*) living in coastal rivers of Louisiana to determine if these gene copies, which resulted from an ancient hybridization event, have subfunctionalized to play different roles in adapting these species to changes in salinity, dissolved oxygen, and temperature. The talk will outline an experimental study of expression partitioning in wild caught suckers and suckers exposed to different salinities, dissolved oxygen concentrations, and temperatures in the laboratory.

649 Herpetology Conservation II, Highland C, Sunday 15 July 2018

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When Listing Isn't Enough: Can We Prevent the Extinction of an Endangered Amphibian?

The California tiger salamander, *Ambystoma californiense*, is one of the most intensively studied endangered amphibians in the world, with decades of landscape ecology, rangewide genomic analyses of population substructure, and field, experimental mesocosm, and genomic analyses of hybridization dynamics. Three separate listings of Distinct Population Segments have led to rangewide protection, and a great deal of recent work has focused on the extremely fragile, endangered population segment in Santa Barbara County at the southern extreme of the species' range. Field and molecular work from the last two years clearly indicate that 1) census and effective population sizes are extremely low, 2) inbreeding coefficients are 5-10 times greater than in other parts of the species' range, and 3) occupancy of historically reliable breeding sites is starting to fail. Given the fragmented landscapes on which populations still occur, it is increasingly clear that regulatory protection alone will not save the species, and more active interventions are necessary. Fortunately, our federal agency partners agree. We discuss the currently available data from mark-recapture studies of breeding adults and molecular estimates of population size and connectivity, and the active management strategies that may serve to reduce or eliminate inbreeding depression and enhance species survival. Although this work is restricted to a single species on a single landscape, the Santa Barbara California tiger salamander represents a compelling example of an increasingly common situation where active, manipulative management is necessary to avoid extinction.

233 Herpetology Genetics II, Highland D, Sunday 15 July 2018

Brian Shamblin¹, Blair Witherington², Shigetomo Hiramama², Robert Hardy³ and Campbell Nairn¹

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Genetic Analyses Support Population-scale Dispersal Consequences of Active Swimming by "Lost Years" Green Turtles

Dispersal is a key driver of population connectivity and dynamics, but dispersing life stages are often cryptic and difficult to study *in situ*. The initial "lost year" model proposed for surface-pelagic juvenile marine turtles assumed that they passively drifted following a brief swim-

frenzy stage. However, mounting evidence indicates that these juveniles engage in directed swimming that affects their trajectories. How this individual behavior affects connectivity at a regional scale is unclear. Dispersal modeling (DM) can predict connectivity, but empirical data are needed to test model assumptions. We sequenced mitochondrial DNA from 121 surface-pelagic juvenile green turtles (*Chelonia mydas*) collected in the northern Gulf of Mexico (GoM) from 2009 to 2015 and conducted genetic mixed stock analyses (MSA) to estimate population contributions. Most juveniles originated in the four Mexican GoM populations, although moderate Costa Rican contributions could not be excluded due to poor marker resolution. Despite these resolution caveats, MSA estimates were markedly divergent from published dispersal modeling (DM) predictions that assumed passive drift. DM predictions for the western GoM stock fell well below their MSA 95% credible intervals (DM: 2%, MSA point estimates: 49-58%), whereas DM predictions for Caribbean Mexico exceeded the MSA upper credible limits (DM: 51-65%, MSA point estimates: $\leq 5\%$). Therefore, the genetic evidence supports population-scale connectivity effects of active dispersal behavior recently demonstrated through paired satellite telemetry and drifter experiments. These results emphasize the value of additional *in situ* studies of this life stage, and the need to collect and integrate behavioral data into DM.

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Coleman Sheehy, Leroy Nuñez, Matthew Fedler, Max Nickerson and David Blackburn

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Progress in the Herpetology Collections at the Florida Museum of Natural History

The Division of Herpetology at the Florida Museum of Natural History has a long and rich legacy of research, education and outreach. For over 100 years, our research collection has grown to contain over 280,000 individual specimens from over 150 countries, making it one of the 10 largest herpetological collections in the US. Particular strengths of the collection are in the geographic areas of the southeast US, Latin America, the Caribbean, Pakistan, Indonesia, and Africa. The collection also contains the largest number of non-native amphibians and reptiles and the second-largest number of dry specimens in the US. Taxonomic strengths include turtles and tortoises, crocodylians, and varanid lizards, and the collections of turtles is the third largest in the US. Museum staff lead regional and international field collecting trips each year, resulting in large acquisitions of specimens, photographs, and tissue samples. Over 20,000 specimens have been accessioned over the past 10 years, with an average of 1,544 specimens accessioned annually. Concerted efforts are underway to build our tissue collection for facilitating studies of the genetic diversity of amphibians and reptiles from Florida and internationally. The number of outgoing specimen loans is increasing rapidly (currently over 50 annually). We are working to make digital specimens from our collections freely available for research and education, in part through CT-scanning for the oVert Thematic Collections Network. These efforts represent our continued efforts to play a leading role in growing and

curating a world-class herpetology collection available for research, teaching, and outreach activities.

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Christopher Sheil¹, Arwen Mohr², Daniel Portik³, Aaron Bauer², Sean Harrington⁴ and Gregory Watkins-Colwell⁵

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Heterochrony of Cranial Bones in Lepidosaurs

A meta-analysis of ossification sequence data for lepidosaurs was conducted to explore heterochrony in cranial bones. New ossification sequence data were collected from 22 lab-incubated embryos of *Paroedura picta* (Gekkonidae); these data were compared to existing ossification sequences that were mined from literature for tuatara and 14 other lizard species across 8 families (Anguidae; Dactyloidae; Gekkonidae; Gymnophthalmidae; Iguanidae; Lacertidae; Scincidae; and Varanidae). Ossification sequences were mapped onto an existing phylogenetic hypothesis with Parsimov-based Genetic Inference (PGi), which reconstructs ancestral ossification sequences at each node and identifies instances of sequence heterochrony (i.e., bones shifting to earlier or later positions along individual tree branches). Results were explored for different classes of bones (endochondral vs dermal) and structural units of the skull (e.g., maxillary arcade, palatal series, and temporal series). The hypothesis that geckos present morphology that is paedomorphic is explored.

237 Herpetology Conservation III, Highland C, Sunday 15 July 2018

Alexander Shepack¹, Dana Morin², Twan Leenders³ and Alessandro Catenazzi¹

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Multi-species recovery in a Bd enzootic habitat

The arrival of the amphibian chytrid fungus (*Batrachochytrium dendrobatidis*) led to declines and disappearances of amphibian species around the world. In Central America these declines were often well documented, and in many cases resulted in heavily changed communities. At Rara Avis Rainforest Lodge in Sarapiquí, Costa Rica many species disappeared in the late 1980s including the Variable Harlequin Toad (*Atelopus varius*). Yearly surveys conducted since the

early 1990s have documented the community level changes at this site, and beginning in 2007 several species have been rediscovered. These species, including the Rufous-eyed Stream Frog (*Duellmanohyla rufiocularis*), Ghost Glass Frog (*Sachatamia ilex*), and Crowned Tree Frog (*Anotheca spinosa*), have become increasingly more common and appear to be recolonizing habitats within the reserve. Mark-recapture surveys indicate high localized densities of these species, high site fidelity, and yearly recruitment. Concurrent surveys for Bd suggest an enzootic state in the community, and individuals of recovering species are infected as well. Our results suggest that while species are recovering within Rara Avis, they are still susceptible to infection by Bd and may face additional challenges due to the modified post-epizootic amphibian community.

139 Herpetology Biogeography II, Highland B, Saturday 14 July 2018

Donald Shepard, Ryan Philobos, Cameron Robicheaux and Pedro Simoncini

Louisiana Tech University, Ruston, LA, USA

Phylogeography and Cryptic Diversity of Slimy Salamanders (*Plethodon glutinosus* complex) in the Interior Highlands

The presence of cryptic species results in underestimates of biodiversity and can hamper conservation efforts. The 16 species of Slimy Salamanders (*Plethodon glutinosus* complex) are distributed throughout the eastern United States and show little to no morphological variation, having been described primarily using genetic data. Three species, *P. albagula*, *P. kiamichi*, and *P. sequoyah*, are known from the Interior Highlands (Ouachita Mountains and Ozark Plateau), but our knowledge of species diversity and distributions in this region is based on genetic analysis of only 15 populations. To better understand biodiversity patterns, we collected salamander tissue samples from >200 localities throughout the Interior Highlands of Arkansas, Missouri, and Oklahoma and sequenced the mitochondrial *ND2* gene. Phylogenetic analysis revealed that: 1) the range of *P. kiamichi* is broader than previously recognized, 2) *P. sequoyah* is nested within *P. albagula*, 3) the range of *P. kisatchie*, a species from the West Gulf Coastal Plain of Louisiana and southern Arkansas, may extend into the region, and 4) an undescribed cryptic species may be present. Species divergences occurred during the Pleistocene, beginning ~2.5 million years ago. Our results indicate that the current understanding of diversity and distributions of species of the *P. glutinosus* complex in the Interior Highlands is inaccurate and in need of revision. Future work will incorporate nuclear loci and employ explicit analyses for delimiting species.

11 Herpetology Reproduction, Highland C, Sunday 15 July 2018

Rick Shine¹, Thomas Madsen² and Greg Brown¹

¹*University of Sydney, Sydney, NSW, Australia.* ²*Deakin University, Geelong, Vic, Australia*

Environmental Sex Determination in a Snake: Dry Nests Produce More Sons

All snakes have been thought to exhibit genotypic sex determination (GSD), but we show that in slatey-grey snakes (*Stegonotus cucullatus*, Colubridae), the role of heteromorphic sex chromosomes can be overridden by hydric conditions during incubation. Dry nests produce sons, especially from small eggs. Dry substrates reduce hatchling size, and male embryos are less affected in this respect than are female embryos (as reflected in hatchling mass relative to initial egg mass). In the field, hatchling size is under strong positive selection (based on mark-recapture data). Hence, environmental sex determination (ESD) enhances the fitness of offspring from small eggs that incubate in dry nests, by producing the sex whose fitness is less impaired by such conditions. This is the first report of environmental sex determination in a snake, of hydric-driven sex determination in a squamate reptile, and of the heterogametic genotype (ZW) developing as both sexes in a reptile.

295 Neotropical Ichthyological Association Talks, Highland E, Saturday 14 July 2018

Brian Sidlauskas^{1,2}, Casey Dillman^{2,3}, Kendra Hoekzema^{1,4}, Bruno Melo⁵, Michael Alfaro⁶, Michael Burns¹, Benjamin Frable^{1,7}, Claudio Oliveira⁵, Mark Sabaj⁸ and Brant Faircloth⁹

¹Oregon State University, Corvallis, OR, USA. ²Smithsonian Institution, Washington, DC, USA. ³Cornell University, Ithaca, NY, USA. ⁴University of Washington, Seattle, WA, USA. ⁵Universidade Estadual Paulista, Botucatu, SP, Brazil. ⁶University of California, Los Angeles, CA, USA. ⁷University of California, San Diego, CA, USA. ⁸Academy of Natural Sciences of Drexel University, Philadelphia, PA, USA. ⁹Louisiana State University, Baton Rouge, LA, USA

Vari's Morphological Legacy in the Light of a Molecular Phylogeny for Anostomoidea

Richard Vari's osteological papers have stood nearly forty years as definitive works on the relationships within the characiform superfamily Anostomoidea. New comprehensive phylogenies based on ultraconserved elements and Sanger sequencing allow re-examination of those classic works through a molecular lens. These strongly supported genetic phylogenies support the monophyly of all four families and nearly all genera that Vari recognized, with paraphyly occurring primarily in taxa lacking clear synapomorphies (*Leporinus*, *Cyphocharax*) or based on single putative synapomorphies (*Curimatella*). In interfamilial and intergeneric relationships, the molecular results agree frequently with a synthesis of nearly 500 characters drawn from Vari's papers. Yet, molecular reconstructions differ from the morphological solution by placing Chilodontidae within the clade containing Curimatidae and Prochilodontidae, rather than as sister to Anostomidae. In Curimatidae, *Curimata* and *Pseudocurimata* appear in unexpected positions and within Anostomidae, molecules do not support the monophyly of two clades previously unified by the orientation of the oral jaws. While anatomical convergence can explain some conflict, re-examination of Vari's

character discussions reveals numerous instances in which he debated alternative codings or hypotheses of homology, some of which are congruent with the molecular tree. Such juxtaposition of new and old data emphasizes the necessity of reciprocal illumination, in which apparent conflict can prompt the re-evaluation of analytical choices, reveal alternative interpretations, and deepen understanding. Vari's comprehensive work will continue to catalyze new discoveries if we treat his legacy as a source of data, hypotheses and ideas to be examined and discussed, not as a final inarguable word.

41 CHS: Effects of Climate Change Symposium, Grand Lilac Ballroom North, Friday 13 July 2018

Barry Sinervo¹ and Donald Miles²

¹University of California, Santa Cruz, CA, USA. ²Ohio University, Athens, OH, USA

Range expansion of North American herpetofauna all the way to the Canadian Arctic and Extinctions in the US and Mexico

Ongoing extinctions due to climate warming since 1975 and future extinctions of reptiles and amphibians due to climate change present a biodiversity crisis. We develop new models to predict phenology and risk of extinction under rapidly changing "climate". Standard species distribution models (SDM) use climate layers to determine a species "climate" niche and then project the species distribution to future time points as climate warms or dries, but such models do not take into account evolved physiological or ecological differences among species that might impact resistance to warm spells and / or long-term droughts. We will describe the relationships between climate layers and operative thermal and hydric environments for reptiles and amphibians. We have derived general models that can be used in SDMs which allow for evolved changes in physiology to be incorporated in the modeling. These models have been applied to North American reptiles and amphibians and we will discuss extinctions at the southern and low elevation margins of the species range in Mexico, and new potential range expansions into Canada. We will also discuss paleoclimate since the Eocene warming, the warmest period in the last 65 million years. Similar conditions are expected under several future warming scenarios allowing herps to expand to the Arctic. We will discuss an analogue of the modern-day climate crisis during the Triassic-Jurassic extinction event and its impact on synapsids, diapsids and anapsids. The results of this analysis are a harbinger of projected extinctions and range expansions of modern day vertebrates in these groups.

101 ASIH STOYE GENERAL ICHTHYOLOGY III, Highland E, Friday 13 July 2018

Randy Singer^{1,2}, Shari Ellis² and Lawrence Page^{1,2}

¹Florida Museum, Gainesville, Florida, USA. ²iDigBio, Gainesville, Florida, USA

Fishy Feud: What the Survey Says About How Fish Biologists Interact with Biological Collections

Professionals in the fish collections community have their own assumptions as to what types of data, which specimens and what types of specimen preparations are the most important to the research community. How do these assumptions align with what fish biologists actually say? How can collections personnel best meet the data needs of the research community? What kinds of exposure have fish researchers had to collections? These questions and more are addressed in a recent survey targeted at all disciplines of fish biology. The goal of this survey was to give the collections community tools and data to guide them in their stewardship of biological collections. As we progress further into the digital age of collections management and data sharing it is important that the community keeps up with the ever growing and expanding needs of its stockholders.

395 SSAR SEIBERT ECOLOGY II, Highland A, Friday 13 July 2018

Shashwat Sirsi¹, Andrew R. MacLaren¹, Daniel H. Foley III² and Michael R.J. Forstner¹

¹*Department of Biology, Texas State University, San Marcos, TX, USA.* ²*Department of Natural and Behavioral Sciences, Sul Ross State University - Rio Grande College, Del Rio, TX, USA*

Determining Population Size and Home Range of Rio Grande Cooters (*Pseudemys gorzugi*) for the Devils River in Texas

Rio Grande Cooters (*Pseudemys gorzugi*) are a freshwater turtle species, restricted to the Rio Grande River and its tributaries. Modification to in-stream flow rates of this river system is likely to have caused reductions in the extent of occurrence and populations. In response to these putative declines, the species has been petitioned to be listed as federally endangered or threatened. However, this turtle is among the most data-depauperate freshwater turtle species in North America. Obtaining baseline information on species status is critical to inform the listing process and future management. We attempted to address this knowledge gap by estimating population size and individual movement patterns through concurrent Capture-Mark-Recapture and satellite GPS telemetry studies at the Devils River in Texas. We analyzed Capture-Mark-Recapture data from multiple years (2011 and 2014-2017) using Pollock's Closed Robust Design Model to arrive at a population estimate of 486 114 turtles. We constructed home ranges for ten turtles (6 females and 4 males) tagged with GPS-enabled VHF transmitters using nonparametric kernel methods. These suggest the entire Devils River, at minimum, be considered a single, contiguous management unit for the species. Additionally, long-range individual movements detected from our telemetry study indicate that while the population estimate is derived at a single site it may arguably represent a useful exemplar for the population of the Devil's River.

397 Lightning Talks III, Highland B, Sunday 15 July 2018

Phillip Skipwith, Frank Burbrink and Christopher Raxworthy

American Museum of Natural History, New York, New York, USA

Ecology shapes phenotypic diversification in Malagasy gem snakes (Lamprohiidae: Pseudoxyrhophiinae) as revealed through phylogenomics and 3D geometric morphometrics

The pseudoxyrhophiine lamprophiid snakes are a diverse group of ~85 species in 19 genera representing a radiation endemic to Madagascar. Very little is known about the ecology and morphological diversity of this exceptional clade. What is known is that, since the late Paleogene, this clade has colonized a number of niches resulting in fossorial, terrestrial, and arboreal forms with accompanying variation in size and shape. Previous studies attempting to account for morphological diversity have been largely descriptive in nature. Moreover, this clade represents the only insular snake radiation where there has been extensive *in situ* diversification. Using a new genomic dataset of hundreds of anchored tag loci in conjunction with 3D CT scanning of the musculoskeletal system, we attempted to address the extent of ecomorphological diversification in this clade. Specifically, the tempo of phenotypic diversification and its relationship with speciation, the presence of determinism and convergence, and the ecological correlates underlying all of these processes. Preliminary analyses reveal staggering amounts of ecomorphological diversity with heterogeneous rates corresponding to different ecomorphs. However, we find that different elements not only show different patterns of diversification, but also different rates. This pattern strongly suggests that modularity has influenced which traits diversify along particular axes and rates. We also found that substrate rather than diet and evolutionary history seems to govern overall cranium shape, but not that of other elements. These patterns imply that complex ecological processes are at play in shaping phenotypic diversification in the world's most diverse insular snake radiation.

226 Ichthyology Conservation, Grand Lilac Ballroom South, Saturday 14 July 2018

Peter Smiley Jr. and Kevin King

USDA Agricultural Research Service, Columbus, Ohio, USA

Fish Community and Population Responses to Planting Grass Filter Strips Adjacent to Channelized Agricultural Headwater Streams

Grass filter strips are a widely used agricultural conservation practice in the United States for reducing nutrient, pesticide, and sediment inputs into agricultural streams. Only a limited amount of information is available on the ecological effects of planting grass filter strips adjacent to agricultural streams. Our previous studies evaluating the ecological effects of grass filter strips indicate that grass filter strips simply widen the riparian habitats of channelized

agricultural headwater streams. In this study we expand upon our previous assessments by evaluating the long term fish community and population responses to planting grass filter strips adjacent to channelized agricultural headwater streams. Our research question is what is the long term effect of planting grass filter strips on fish community and population structure within channelized agricultural headwater streams in central Ohio? We conducted annual sampling of riparian habitat and seasonal sampling of instream habitat, water chemistry, and fishes from three channelized headwater streams without grass filter strips, three channelized headwater streams with planted grass filter strips, and two unchannelized headwater streams with forested riparian habitats in central Ohio from 2006 to 2015. Our preliminary results indicated that planting grass filter strips did not influence fish species richness, evenness, abundance, and the abundance, mean length, and biomass of creek chub (*Semotilus atromaculatus*), green sunfish (*Lepomis cyanellus*), and orangethroat darter (*Etheostoma spectabile*). Our preliminary results suggest that planting grass filter strips will not contribute to the restoration of fishes within channelized agricultural headwater streams.

625 Ichthyology Systematics I, Grand Lilac Ballroom South, Saturday 14 July 2018

Leo Smith¹, Matthew Davis² and Michael Ghedotti³

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

³Regis University, Denver, CO, USA

Phylogeny of Enigmatic Acropomatiform Fishes with a Preliminary Assessment of Morphological Support

Recent molecular studies have placed a diversity of primarily deep-sea fishes from the traditional "percid" and "trachinoid" fishes in a new clade variously referred to as the Acropomatiformes or Pempheriformes. In this study, we use the results of an analysis of UCE (ultraconserved elements) and individual gene fragment sequence data to guide a preliminary morphological investigation of this recently circumscribed clade. In particular, we focus on the placement of some of the more enigmatic acropomatiform families to assess whether the novel molecular placements have more or less morphological support than their placements in traditional classifications.

102 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018

Margaret Smith¹, Jayme Waldron¹, Shane Welch¹ and Jeff Holmes²

¹Marshall University, Huntington, WV, USA. ²Amphibian and Reptile Conservancy, Nashville, TN, USA

Determining Presence of Carolina Gopher Frogs and Frosted Flatwoods Salamanders Using eDNA and Conventional Surveys

Frosted Flatwoods Salamanders (*Ambystoma cingulatum*) and Dusky Gopher Frogs (*Rana capito*)

are two species endemic to the imperiled longleaf pine savanna ecosystem, consequently, both species have been reduced in abundance and range. Both species have life histories that largely limit surveys to the breeding season when adults and larvae may be found in ephemeral, upland isolated wetlands. The species' use of aquatic habitats suggests that survey data may be improved by including environmental DNA (eDNA) as protocol. In this ongoing study, we conducted eDNA surveys in combination with traditional trapping, auditory, and visual surveys to examine the presence of *A. cingulatum* and *R. capito*. Survey sites were located in the South Carolina coastal plain, and include areas where these species have historically been found as well as new sites that have been selected based on land use history and habitat characteristics. Currently, twenty-five sites have been surveyed using eDNA. Of these, only one site yielded results positive for *Rana capito*, which was confirmed by several other survey methods. We plan to conduct further surveys throughout 2017 and 2018. We hope to gather further information on the reliability of eDNA data and survey new sites to determine the presence of gopher frogs and flatwoods salamanders within their historic range.

323 Herpetology Habitat & Environment, Highland A, Saturday 14 July 2018

Sierra Smith^{1,2}, Elyse Fritas^{1,2}, Jessa Watters³ and Cameron Siler^{1,4}

¹Herpetology Department, Sam Noble Museum, Norman, OK, USA. ²Biology Department, University of Oklahoma, Norman, OK, USA. ³Herpetology Department, Norman, OK, USA.

⁴Biology Department, Norman, OK, USA

Comparison of Infectious Disease Presence between Thailand and Philippine Populations

There are numerous factors contributing to the global decline of amphibians, with infectious disease as one of the most pressing. The pathogen *Batrachochytrium dendrobatidis* (chytrid fungus or *Bd*), is linked with declines and extinctions of numerous amphibian populations around the world. Unfortunately, there remain many regions on the planet for which information on the distribution and prevalence of *Bd* is lacking, hindering empirical studies of the global threat of chytrid fungus. To date, few studies have screened for this pathogen among wild amphibian populations in Southeast Asia, including in the Philippines and Thailand. I am completing a screening effort of amphibian populations in Thailand and the Philippines for *Bd* infection from samples collected in 2016 and 2017. The results will allow for comparisons of disease prevalence and load between three provinces in Thailand (Chiang Mai, Mae Hong Son, and Tak) and two islands in the central and northern Philippines (Luzon and Negros). Our dataset consists of 484 skin swabs collected in the field from which I extracted DNA and screened for the presence and quantity of *Bd* using quantitative PCR (qPCR). Interestingly, although recent studies suggest that these two countries have suitable climates and environmental conditions for *Bd* to flourish, our preliminary data reveal low infection rates among the sampled species. The results of this study will add significant baseline information on infectious diseases in the Old World tropics and will provide better context for global assessments on the impact of chytrid fungus.

499 Herpetology Systematics, Highland B, Saturday 14 July 2018

Edward Stanley, Daniel Paluh and David Blackburn

Florida Museum of Natural History, Gainesville, FL, USA

Diversification of dermal armor in squamates.

The order Squamata contains over 10,000 species, many of which are small-bodied and occupy a low trophic position. As a result, the group displays a bewildering diversity of anti-predation defenses. All squamates are protected by toughened, keratinized scales but in some lineages these scales are buttressed by osteoderms: bony subdermal plates which strengthen the integument, provide additional ornamentation in the form of spines or keels, and may play a role in calcium sequestration and thermoregulation. Osteoderms are found in several orders of fish, mammals, amphibians, archosaurs, turtles and in 13 extant families of squamates. This study employs comparative phylogenetic analyses of microcomputed Tomography (μ CT) data to quantify and investigate the diversity of dermal armor across Squamata, with deep sampling in the families that are known to possess osteoderms. Our analysis reveals multiple independent origins of osteoderms within the order, with three clades – Cordylidae, Anguillidae and egeine skinks – displaying increased rate-shifts in the distribution and extent of their armor. There are repeated losses and gains of ossified armor within these three lineages, and variations in the extent and distribution of osteoderms are shown to be correlated with microhabitat but not climate.

23 Lightning Talks I, Grand Lilac Ballroom North, Thursday 12 July 2018

C. Tristan Stayton

Bucknell University, Lewisburg, PA, USA

The Turtle Shell as a Prestressed Structural Element: Preliminary Observations

Individual turtle carapaces experience a change in shape when physically separated from their plastrons. In most cases, the lateral margins of the carapace move away from one another once their connections to the plastron are cut, reducing the curvature of the plastron, although in some cases the carapace may become more curved after the connections to the bridge are severed. These shape changes occur instantly after the carapace is detached from the plastron, even in fresh specimens; subsequent drying may enhance or reduce this pattern but cannot entirely explain the changes in shape in all specimens. This phenomenon of immediate shape change after the connections between shell parts are broken suggests the possibility that turtle shells develop and are maintained as "prestressed" structures. Prestressing can increase the strength of structures, increasing the loads which they can bear before failure occurs. Given the function of the turtle shell as a load-resisting structure, such prestressing could be adaptive. I discuss evidence for prestressing in turtle shells and describe the types of loads for which such prestressing would and would not be beneficial. I conclude with a request for additional observations or ideas regarding the potential benefits of and developmental mechanisms which could produce prestressing in turtle shells.

241 SSAR: Coloration in Fish, Amphibians, & Reptiles Symposium, Grand Lilac Ballroom North, Sunday 15 July 2018

John Steffen

Shepherd University, Shepherdstown, WV, USA

How and why do animals color themselves? A Painted Turtle's response.

Animal coloration is a fundamental trait that is shaped by natural and sexual selection and is a field of biology that is experiencing a surge in interest among scientists. Current research on animal coloration is highly integrative and collaborative and has made many advances in our understanding of biology. Fields as diverse as sensory ecology, behavior, development, evolution, chemistry, mathematics and nano-structural physics are employed to answer questions about how and why animals use the colors they do. This 'Color in fish, amphibians, and reptiles' symposium sponsored by SSAR brings together nine integrative biologists to present the latest research findings from North American darters, coral reef fish, zebrafish, spotted salamanders, turtles, snakes, and lizards. My own research will present the latest findings of how and why Painted Turtles color themselves. This research has implications for understanding broader patterns of evolution in vertebrates.

51 Reptile Ecology II, Highland A, Sunday 15 July 2018_

Leyna Stemle, Kristen Martinet and Gabriel Langford

Florida Southern College, Lakeland, Florida, USA

Life History Traits and Spatial Ecology of the Striped Mud Turtle, *Kinosternon baurii*, in Central Florida

The ecology of the striped mud turtle (*Kinosternon baurii*), a member of the Kinosternidae, has been studied in only a few locations within Florida. Previous studies have consistently found that these mud turtles have a small home range, but they observed varied nesting periods and habitat preference. We conducted a mark – recapture and radio telemetry study at Circle B Bar Reserve (CBR), a restored wetland in Polk County, Florida, to assess the population size, health, and movement of *K. baurii*. Our data indicates that these mud turtles have a small home range (1,111.2-14,395.5 m²) with some males and gravid females having a larger area that they frequent. The health of the turtles was generally good, as our marked turtles had clear eyes, energetic movements, and undamaged bodies. Our population was small (38 adult individuals) and we recaptured many of the same turtles. However, unmarked turtles were caught occasionally, and multiple age classes were found, and the sex ratio of the studied population was female skewed (65.4 % females). Given the low population size a female-biased sex ratio, the future of *K. baurii* at CBR must be carefully monitored, especially with encroaching urbanization and increased attendance at the reserve. If numbers of *K. baurii* continue to decline, management practices will be the key to conserving mud turtles. Overall, our study provides additional knowledge on *K. baurii* ecology, population size, and movements, which local reserves can use to better protect the turtles and their habitat.

613 Amphibian Ecology II, Highland A, Sunday 15 July 2018

Kenzi Stemp, Thomas Anderson and Jon Davenport

Southeast Missouri State University, Cape Girardeau, MO, USA

Food web ecology and keystone effects of an endemic pond-breeding salamander

Keystone species have disproportionately large effects on communities relative to their abundance. One way keystone predators affect communities is by decreasing the relative abundance of superior competitors, relieving competitive pressure and increasing relative abundance of inferior competitors - and consequently, increasing local biodiversity. Thus, their identification and management is of great conservation concern. Additionally, functional redundancy explains how different species in a trophic level can have either additive or redundant effects on communities. In pond communities, the fall-breeding marbled salamander (*Ambystoma opacum*) can serve a keystone role and increase tadpole diversity via selective predation. A congeneric endemic species, the ringed salamander (*Ambystoma annulatum*), can co-occur with *A. opacum* in Missouri, and has a similar fall-breeding phenology. To evaluate the conditions under which these salamanders act in keystone roles and the potential for functional redundancy, we conducted an artificial pond experiment with a diverse assemblage of anuran prey in four different experimental food webs. We found that *A. annulatum* may have significant effects on local tadpole assemblage. Food webs with *A. opacum* alone showed no significant increase in tadpole diversity (i.e. no keystone effect) thus reducing the possibility for functional redundancy between these two predators. The similarities in life history and phenology of *A. annulatum* to *A. opacum* suggested that they should have similar effects on tadpoles; however, the observed lack of redundancy between the species indicates the importance of geographic variation. In the future, a better understanding of the ecosystem-level impacts of keystone predators can facilitate management decisions to promote biodiversity.

576 Herpetology Conservation IV, Highland C, Sunday 15 July 2018

Anne Stengle¹, Thomas Tynning² and Lou Perrotti³

¹*Holyoke Community College, Holyoke, MA, USA.* ²*Berkshire Community College, Pittsfield, MA, USA.* ³*Roger Williams Park Zoo, Providence, RI, USA*

Headstarting of the Timber Rattlesnake in Massachusetts

Timber Rattlesnake (*Crotalus horridus*) populations have become increasingly fragmented and isolated during the past 300 years, and probably most pronounced near the northeastern edge of their distribution in Massachusetts. Currently, five populations exist in the state, with only one site large enough to be considered a metapopulation. The state began a small-scale headstarting program in 2011 with the Roger Williams Park Zoo, Providence, RI with the first release in 2012. All neonates were wild caught, although the state is exploring the option of

captive breeding in the future. Following releases were done in 2013 and 2014, with future releases planned. Sample sizes were small and the protocol for both the release and husbandry were adjusted with each release. Individuals were released with implanted radiotransmitters and the most recent release was the most successful. Here we will describe how our protocols changed with each release to optimize survivorship, and the results of each release. Headstarting has been widely successful with several turtle species, but there are few reports of its use with snake species, and even fewer that were successful with snake species. These results will guide not only future work with this species in this region, but can be applied to other species in other regions.

123 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018

Natasha Stepanova and Molly Womack

UC Berkeley, Berkeley, CA, USA

Morphological Convergence in Anuran Limbs

When faced with shared selective pressures, animals frequently converge on phenotypes that increase their fitness. For instance, species from different lineages living in similar habitats often evolve similar body shapes. Frogs have transitioned to various ecotypes including burrowing and fully aquatic morphs multiple times, making them an excellent system to study patterns of morphological convergence. Given the role of limbs in locomotion, it seems likely that limb shape would vary based on the locomotor requirements of different microhabitats (burrowers, arboreal, terrestrial, etc.). We used 3D morphometrics on micro-CT scans of over 250 frog species to collect shape data for each limb bone. We also assembled ecological data for every species. Taking body size into account, we used this data to identify patterns of shape variation in limbs across microhabitat and test the hypothesis that similar morphologies arise in similar microhabitats across different lineages. We also predicted that distal bones would show more variation than proximal elements. While there was not much variation between limb bones across most microhabitats, the limbs of burrowing species showed a high degree of variation in shape from those of other ecotypes. Our study suggests that adaptation to different environments can lead to convergence of traits within and between clades.

469 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018

Phillip Sternes and Kenshu Shimada

DePaul University, Chicago, IL, USA

Geometric morphometric analysis of caudal fin shapes in lamniform sharks (Chondrichthyes: Elasmobranchii) and its evolutionary implications

Lamniformes is a small order of sharks consisting of only 15 extant species but a highly diverse group, including a wide interspecific variation range in their caudal fin shape. A previous study has suggested that caudal fins of lamniforms can be grouped into two types. Type 1 fins have a high aspect ratio and high heterocercal angles, characterized by Cetorhinidae and Lamnidae. Type 2 fins are those with a moderate heterocercal angle and a moderate to well-developed subterminal lobe and are found in Mitsukurinidae, Odontaspidae, Pseudocarchariidae, Megachasmidae, and Alopiidae where an exceptionally elongate alopiid tails representing an extreme end of Type 2 spectrum. Based on non-embryonic specimens housed in various museums, we quantitatively examined the caudal fin shape of all 15 species using a principal component analysis. Whereas Type 2 is generally regarded as a plesiomorphic condition in Lamniformes, our analysis clearly shows two evolutionary pathways emerging from Type 2, one representing the Alopiidae clade and another the Type 1 clade. What is particularly intriguing is the sequence of taxa within each clade. In the Alopiidae clade, the plot for *A. superciliosus* is situated closest to the center of the Type 2 cluster, suggesting the species is less derived compared to *A. pelagicus* and *A. vulpinus*. In the Type 1 clade, Cetorhinidae is placed closest to the Type 2 taxa, followed successively by *Lamna* and '*Isurus + Carcharodon*.' These specific taxonomic sequences based purely on the caudal fin morphology broadly agree with their evolutionary sequences predicted by molecular-based phylogeny.

21 Lightning Talks I, Grand Lilac Ballroom North, Thursday 12 July 2018

Annie Stevens

SUNY ESF, Syracuse, NY, USA

Dermal Bacteria of *Ambystoma maculatum* and *Ambystoma jeffersonianum*

Dermal bacterial communities have been shown to be important in amphibians and may keep pathogenic organisms such as the chytrid fungus under control. However, few studies have looked at naturally occurring bacterial communities in salamanders, and no studies have examined these communities in ambystomid salamanders. We investigated the cutaneous bacterial communities of the spotted salamander, *Ambystoma maculatum* and Jefferson salamander, *Ambystoma jeffersonianum*. In March 2017, we captured 5 male and 7 female spotted salamanders as well as 3 female Jefferson's salamanders during the annual migration to breeding pools at Mendon Ponds Park in Pittsford, NY. Captured salamanders were measured, weighed, and rinsed three times in distilled water after sex was determined. Skin swabs were taken on both dorsal and ventral sides and cultured on TSA plates. Subcultures were taken to obtain pure cultures, then gram stained and examined using BioMerieux API 20E test kits to determine identity of bacteria. The average number of bacterial species on spotted salamanders was 3.08. Significantly more bacterial colonies were found on males than females. The most common bacterial species present on both species was the gram negative bacterium

Pseudomonas aeruginosa, which has been shown to have antifungal properties in previous studies.

505 ASIH Stoye General Ichthyology III, Highland E, Friday 13 July 2018

Donald Stewart¹, Juliette Pouzadoux² and Christelle Tougard²

¹SUNY Coll. Envir. Sci. & For., Syracuse, NY, USA. ²ISEM, CNRS, Université de Montpellier, IRD, EPHE, Montpellier, France

505 IS NOT A STUDENT COMPETING IN STOYE AWARD

Phylogeography of *Arapaima* spp. (Osteoglossidae) Based on Complete Mitogenomes and Morphological Divergences, Including Type Specimens for Three Nominal Species

Diversity within *Arapaima* (Osteoglossidae) remains poorly resolved; published perspectives range from monotypy (based on ND1+ATPase), to 5 species (based on morphology), and sympatric species (based on microsatellites). *Arapaima* today suffer overexploitation and even extirpations; *Arapaima gigas* is listed under CITES Appendix II (Endangered). To better understand these important fishes, we sequenced complete mitogenomes for 24 specimens from across the range, including holotypes of *A. gigas*, *A. mapae* and presumptive holotype of *A. arapaima*. For type specimens (ages ~225, ~181 and ~180 yr, respectively) and other ancient museum materials, we used a protocol to build and sequence shotgun Illumina libraries from small quantities of degraded genomic DNA on a laboratory platform dedicated to such analyses. Fresh tissues were sequenced using standard protocols. Genetic relationships were evaluated using maximum likelihood and rooted with African *Heterotis* as outgroup. Morphology of available preserved specimens was analyzed using multivariate analyses of morphometric and meristic data. Monophyly of *Arapaima* and two lineages within *Arapaima* were highly supported (bootstraps= 100, 98, 70), and as a minimum, refute monotypy. Genetic distances, however, were about 0.1-0.2% within each lineage, and 0.3% between lineages. These slight genetic differences contrast notably with phenotypic divergences among *Arapaima* specimens; the latter suggest multiple taxa within each mitogenomic clade. Results include association of *A. mapae* holotype with Peruvian materials, and association of both *A. gigas* and *A. arapaima* types with Guyanese materials. We suggest full resolution of *Arapaima* diversity may require integrative analyses of mitogenomes, nuclear markers and morphology.

319 ASIH: If Salamanders Could Speak Symposium, Grand Lilac Ballroom North, Saturday 14 July 2018

Amber Stokes¹, Brian Gall², Peter Ducey³, Lorin Neuman-Lee⁴, Susannah French⁵, Charles Hanifin⁶, Michael Pfrender⁷, Edmund Brodie III⁸ and Edmund Brodie, Jr.⁵

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The Presence and Function of Tetrodotoxin (TTX) in Terrestrial Organisms

Tetrodotoxin (TTX) is a low molecular neurotoxin most well known from puffer fish. It is of particular interest as it is found in a taxonomically disparate array of organisms, most of which are marine. Within terrestrial systems, much of the work and understanding of TTX has focused on the clade of modern newts that includes *Taricha*, *Cynops*, and *Notophthalmus*. However, in recent years, TTX has been documented in a wider array of terrestrial organisms, with a diversity of functions. This presentation outlines two such examples. *Taricha* are preyed on by garter snakes of the genus *Thamnophis*. However, early life history stages suffer predation by invertebrate predators. Caddisfly larvae can consume newt eggs, and have been shown to sequester that TTX in their bodies, and in some cases retain the TTX through emergence as an adult, where it is likely used as an antipredator mechanism. In another system, *Bipalium kewense* and *Bipalium adventitium*, two species of terrestrial Turbellarians, have been shown to have TTX. These two species were compared, and TTX in the eggs of *Bipalium adventitium* was also quantified. In these two species there is evidence to suggest that TTX is being used offensively to subdue large earthworm prey, yet likely has an antipredator function as well, especially in the eggs. Both of these systems help us to better understand the diversity of organisms with TTX as well as the many functions of the toxin, which may all lead to a better understanding of the origins of TTX.

527 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018

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Phenotypic variation and allometry in the endangered Barton Springs salamander (Plethodontidae: *Eurycea sosorum*)

The Barton Springs salamander (*Eurycea sosorum*) is a neotenic plethodontid species restricted to only a few interconnected springs and seeps of the Barton Springs segment of the Edwards Aquifer in central Texas. Anecdotal evidence indicates that *E. sosorum* is morphologically intermediate between surface and subterranean forms of central Texas *Eurycea*. However, aside from preliminary information provided at the time of its description in 1993, very little is known of phenotypic variation within the species. Here, we leveraged a large database of standardized photographs to perform a detailed geometric morphometric analysis of head

shape in *E. sosorum*, and evaluated allometry of head shape and trunk length within and between various known populations in order to elucidate ontogenetic patterns. Furthermore, we used this geometric morphometric dataset with complimentary data from photographs of the Austin blind salamander (*E. waterlooensis*), a more extreme subterranean form, to evaluate the potential for identifying hybrids between these two sympatric species.

238 Poster Session I, Empire Hall South - JF Rochester Riverside Convention Center, Friday 13 July 2018

John P. Sullivan, Stacy Ciufu, Shobha Sharma and Conrad Schoch

NCBI-GenBank, Bethesda, MD, USA

Fish & Herp Species Representation and Underappreciated Features, Tools & Resources in GenBank

Representation of reptile, amphibian and fish species in the GenBank nucleotide sequence database (National Center for Biotechnology Information/National Library of Medicine/U.S. National Institutes of Health, Bethesda MD, USA) continues to grow apace. These sequences are integral to phylogenetic, evolutionary, ecological, medical and conservation-related study of these organisms and are among most valuable research products of ichthyology and herpetology collections. Yet many GenBank users, submitters and collection managers remain unaware of various GenBank features and resources – some old, some new – that can facilitate more effective use of the database, improve the research value of submitted sequences, and provide attribution back to source collections. In this poster we highlight four of these underappreciated features/resources: (1) the two methods of linking GenBank records to specimen data in collection databases, (2) annotation of type material in GenBank records, (3) the newly public BioCollections Database of institution codes, and (4) the MOLE-BLAST tree-building tool.

268 ASIH STOYE GENERAL HERPETOLOGY, Highland C, Friday 13 July 2018

Alexandra Sumarli and Tod Reeder

San Diego State University, San Diego, CA, USA

Phylogeography of the Plateau Striped Whiptail (*Aspidoscelis velox*): A Spatial Diffusion and Ecological Niche Modeling Approach

Whiptails (*Aspidoscelis*) are a widely distributed group of North American teiid lizards distinguished by their relatively high number of unisexual lineages. We investigate the biogeographic history of the Colorado Plateau unisexual *A. velox* by applying a continuous

Bayesian phylogeographic approach and ecological niche modeling (ENM). The continuous Bayesian phylogeography incorporated georeferenced occurrence data and a random walk model to explore the spatiotemporal history of *A. velox* while estimating the timing and location of ancestral mtDNA haplotype populations. Paleoclimatic and current ENMs estimated areas of climatic suitability for *A. velox* and its currently allopatric bisexual ancestors, *A. costatus barrancorum* and *A. inornatus arizonae*. Our time-calibrated Bayesian phylogeny reconfirms the maternal ancestor of *A. velox* as *A. c. barrancorum*, and suggests they diverged in the mid-Pleistocene and strongly supports the presence of substructure within *A. velox*. The continuous Bayesian phylogeography inferred that ancestral populations of *A. velox* initially occurred in northeastern Arizona approximately 400 kya and then expanded into northeastern and west-southwestern populations. ENMs demonstrate areas of climatic suitability for *A. velox* were restricted to east-northeastern Arizona during the Last Glacial Maximum whereas both *A. i. arizonae* and *A. c. barrancorum* had more expansive ranges in northwestern Mexico and parts of Arizona. These hindcast ENMs of the parental species support that their populations were likely in contact during periods of glacial maxima during at least some of the glacial cycles of the mid-Pleistocene. None of these lineages have statistically similar niches, even though *A. velox* is of hybrid origin.

106 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: ECOLOGY, NATURAL HISTORY, DISTRIBUTION & BEHAVIOR, Empire Hall South - JF Rochester Riverside Convention Center, Friday 13 July 2018

Meredith Swartwout and John Willson

University of Arkansas, Fayetteville, AR, USA

Effects of Leaf Litter Depth on *Anolis humilis* Egg Survival

Reduced leaf litter depth, driven by changes in climate and vegetation, negatively affects reptiles and amphibians directly through habitat loss, and indirectly through changes in food web interactions. Lizard eggs are immobile and therefore the most vulnerable life stage to changes in litter depth. The primary objective of this study was to test how litter depth affects egg survival of a tropical leaf litter lizard (*Anolis humilis*). At La Selva Biological Station in Costa Rica, I set up 30 experimental plots and manipulated litter in three treatments (n = 10 each): litter removal (L-), litter addition (L+), and control (L0). Ants can be important predators of lizard eggs, so I used a combination of Berlese, pitfall, and sticky trap samples to assess ant abundance and activity in experimental plots. I also used mass removal from tuna bait stations to estimate ant predation pressure. To monitor lizard egg mortality across treatments, I placed *A. humilis* eggs collected from gravid females in randomized plots, and monitored each egg every other day until mortality or hatching occurred. Litter depth manipulations were successful, but lizard egg mortality was not significantly affected by litter depth or ant abundance. However, probability of lizard egg mortality and bait mass removal from tuna bait stations were positively correlated, suggesting that ants may be important predators of lizard eggs at La Selva. Observations of bait mass removal from tuna bait stations could be a viable method for rapid assessment of ant predation pressure on lizard eggs.

405 Poster Session II, Empire Hall South – JF Rochester Riverside Convention Center, Saturday 14 July 2018

Alyssa Swinehart¹, Krista Larson² and Katherine Greenwald¹

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Population Genetics of Mudpuppy Salamanders (*Necturus maculosus*) in Minnesota Rivers and Lakes

Mudpuppy Salamanders are listed as a Species of Special Concern in Minnesota. Over-collection, habitat modification, and exposure to contaminants are major threats to Minnesota populations which have possibly led to declines. Small and isolated populations are vulnerable to loss of genetic diversity and stochastic local extinction. We genotyped over 600 mudpuppies from 8 river systems in Minnesota using DNA microsatellite markers to determine population genetic structure. We analyzed genetic variability and connectivity within and among river systems, as several of the rivers contain numerous dams which may act as physical barriers and lead to population isolation. We are also investigating two potentially introduced lake populations, with an aim of better understanding their origin and history. Preliminary data show significant genetic differentiation among river systems, and point to dams as a potentially important isolating factor. We predict that populations isolated by dams will have lower genetic variation and lower effective population size, and will show signatures of recent declines. Identifying which populations are genetically isolated, as well as which may be introduced, will help in allocating limited conservation resources to target at-risk populations and develop future management plans.

370 Ichthyology Genetics, Reproduction, and Development, Highland E., Friday 13 July 2018

Milton Tan¹, Al Dove² and Timothy Read³

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Comparative Genomics of the Whale Shark and the Evolution of Vertebrate Gigantism

The whale shark (*Rhincodon typus*) is by far the largest species of fish. Recently, the whale shark genome was published, representing the second published genome for a chondrichthyan and the first published genome for an elasmobranch. We report on a new *de novo* genome assembly for the whale shark derived from PacBio long read sequences, and its improvement over the previous version. The whale shark genome is a resource that can allow for studies into the evolution of vertebrate gene families and the origin of jawed vertebrates, the evolution of gigantism in the whale shark, and the biology of the whale shark itself. We demonstrate a low level of heterozygosity in the whale shark genome, which has implications for the conservation of this species. We compared the whale shark genome to other vertebrates, and inferred a large number of gene families that originated prior to the most recent common ancestor of jawed vertebrates. Finally, we quantify rates of duplication and loss in these gene families, and test for

whether these rates differ between giant vertebrate taxa and other vertebrates. Such gene families may have a potential role in the evolution of gigantism in vertebrates.

154 Poster Session II, Empire Hall South – JF Rochester Riverside Convention Center, Saturday 14 July 2018

Manette Tanelus^{1,2}, Guha Dharmarajan² and Melissa Pilgrim^{1,2}

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Parasites as Potential Indicators of Ecosystem Health: A Case Study with Largemouth Bass (*Micropterus salmoides*)

Anthropogenic activities (e.g. the burning of fossil fuels) have greatly increased the amount of mercury (Hg) cycling in the environment. Mercury is highly toxic to organisms and poses a threat to wildlife and human health. Research suggests that heavy metals and generalized ‘disturbance’ negatively affect parasites. Thus, parasites may serve as indicators of environmental degradation. In this study, we collected parasites (internal and external) from eighteen largemouth bass (*Micropterus salmoides*) captured at PAR Pond - a former nuclear cooling reservoir with a history of Hg contamination. Our goals were to determine if parasite load was negatively related to bass mercury concentrations and quantify mercury concentrations among parasite taxa. We collected 253 parasites (24 leeches, 71 lice, 19 trematodes, and 139 nematodes) from eighteen Largemouth bass. Regression analyses revealed no significant association between mercury concentration and parasite load. In addition, lice had significantly higher mercury concentrations relative to leeches, trematodes, and nematodes. Our results indicated that largemouth bass parasites were not reliable bioindicators of mercury pollution in PAR Pond. In the future, it would be interesting to see if a different host-parasite system (e.g., alligators and their parasites) in PAR Pond might be useful as an indicator of mercury pollution.

587 Poster Session II, Empire Hall South – JF Rochester Riverside Convention Center, Saturday 14 July 2018

Kevin Tang, Rebecca Farr and Siobhan Ingersoll

University of Michigan-Flint, Flint, MI, USA

Phylogenetic Relationships of Ophidiiformes

Fishes of the order Ophidiiformes are an enigmatic group of marine bony fishes with a worldwide distribution. The group is divided into six families, with over 100 genera and more than 500 species. Representatives from all six families were included in this study, encompassing more than 60 genera and 120 species. Ten genes were used for phylogeny reconstruction: six mitochondrial (12S, 16S, ATPase 8/6, cytochrome *b*, cytochrome *c* oxidase I) and four nuclear (ectodermal-neural cortex 1, histone H3, recombination activating gene 1, and zic family member 1). The results of these analyses found support for the monophyly of the

order and some of its constituent taxa. Their evolutionary relationships, and how they might affect the classification and taxonomy of the group, will be presented.

404 Herpetology Systematics, Highland B, Saturday 14 July 2018

Rory Telemeco¹, Brian Lavin² and Chris Feldman³

¹California State University, Fresno, CA, USA. ²Sonoma State University, Rohnert Park, CA, USA. ³University of Nevada, Reno, NV, USA

An integrative taxonomic analysis of the southern and panamint alligator lizard complex: Combining morphological, ecological, and molecular evidence

Genetic tools provide immense power to explore phylogenetic relationships – a prerequisite for analyses ranging from phylogenetic independent contrasts to conservation planning, but these tools have limitations. By integrating multiple datasets, we can better resolve phylogenetic history, delineate species boundaries, and increase understanding of ecological divergence. We used such an integrative approach to test predictions from competing phylogenetic hypotheses for southern and Panamint alligator lizards (*Elgaria multicarinata* and *E. panamintina*, respectively). Recent DNA evidence contradicts the traditional taxonomy of these lizards, calling the species status of *E. panamintina* into doubt, and suggesting that *E. multicarinata* is composed of 2–4 cryptic species. First, we expanded sampling to improve molecular phylogenies and analyze population structure. Second, we examined the morphology of specimens used for molecular analyses and ~200 others. We examined male genital morphology for evidence of reproductive isolation, and head morphology to assess ecological divergence. Finally, we used species distribution modeling to further explore ecological divergence. Our results support components of traditional and DNA phylogenies. All morphological data support the species status of *E. panamintina*, and we suggest that the aberrant mtDNA phylogeny results from incomplete lineage sorting after peripatric speciation. Morphological data, population structure, and species distribution modeling confirm two divergent cryptic clades within *E. multicarinata*. We recommend treating these as separate operational taxonomic units for management. By integrating morphometric analyses and species distribution modeling with molecular data, we obtained phylogenetic inferences that were impossible with any available dataset in isolation.

222 Poster Session I, Empire Hall South - JF Rochester Riverside Convention Center, Friday 13 July 2018

Stéphanie Tessier and Kamal Khidas

Canadian Museum of Nature, Ottawa, Ontario, Canada

The Herpetology and Ichthyology Collections of the Canadian Museum of Nature: An Overview of Two Unique and Rich Repositories

The ichthyology and herpetology collections of the Canadian Museum of Nature (Ottawa, Ontario) together hold over one million specimens, which were collected recently to as far

back as 1846. Although comprised of material from around the globe, the collections' focus is on Canadian species. The curation of the Fish Collection began in 1958, and now includes the world's most extensive Canadian Arctic fish and North American lamprey collections. The Amphibian and Reptile Collection, established in 1914, has been built primarily to represent geographic and life history variation in Canadian species, and is the most important collection of Canadian herpetological material. Specimens are preserved following current best practices. The collections consist predominantly of whole fluid-preserved specimens, as well as skeletons, dried skins, mounted specimens, and frozen tissue samples. All records for both collections can be accessed via the Global Biodiversity Information Facility and VertNet. Our current objective is to maximize usability by adding scientific value to already digitized records. This will be completed by consolidating and digitizing associated collection data as well as imaging specimens and adding georeferencing data. Future directions will include furthering the development of the tissue collection to be housed in the museum's new cryogenic facility, making our collections useful for both morphological and molecular studies. Used nationally and internationally, these irreplaceable collections document patterns of diversity across and within taxa, temporally and spatially, and are essential to research ranging from evolution, ecology to conservation.

79 Reptile Ecology I, Highland A, Sunday 15 July 2018

Christopher Thawley and Jason Kolbe

University of Rhode Island, Kingston, RI, USA

A Trick of the Light: Impacts of Human-Produced Light at Night on Anoles

As anthropogenic habitat disturbance increases, one aspect of urbanization that affects many species worldwide is artificial light at night (ALAN). Current research shows that ALAN can impact survival, physiology, and behavior of many taxa, yet we lack a clear understanding of how ALAN affects reptiles. Anoles are considered to be strongly diurnal and are adapted to specific photic environments. However, many anole species thrive in human-altered environments where ALAN is prevalent. Previous research with brown anoles (*Anolis sagrei*) in the lab shows that exposure to ALAN may induce onset of reproduction and increase growth and reproductive output, while work in the field shows that exposure to ALAN can increase wariness and decrease endurance. To illuminate the impacts of ALAN in a real-world scenario, we conducted a field experiment introducing a common form of ALAN, landscape lighting, into a previously unlighted habitat within an urban matrix. Over a two-month period, we assessed whether two species, brown anoles and crested anoles (*Anolis cristatellus*), experienced higher levels of light at night at their sleep perches and whether they behaviorally avoided exposure to ALAN. We also followed marked lizards to assess whether exposure to ALAN impacted survival, growth, body condition, and physiology. As urban areas continue to grow, artificial lighting will increasingly affect anoles and other urban-tolerant organisms. Considering the ecological impacts of this evolutionarily novel disturbance will be important to future studies of urban ecology and conservation.

385 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: EVOLUTION, GENETICS, & SYSTEMATICS, Poster Session I, Empire Hall South - JF Rochester Riverside Convention Center, Friday 13 July 2018 AND Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center; part of ASIH symposium: If Salamanders Could Speak, Saturday 14 July 2018

Vicki Thill, Mike Teglas and Chris Feldman

University of Nevada, Reno, NV, USA

You Lose, Spidey! Untangling Venom Resistance in Reptiles

Black widow spiders have evolved a potent venom that is effective against a variety of prey, including small vertebrates, and is also used defensively. While the effects of black widow spider venom (BWSV) on mammals is well understood, effects on reptiles have never been investigated. Lizards can be major predators of spiders, and at least two species (*Elgaria multicaudata* and *Sceloporus occidentalis*) are syntopic with, and prey upon, black widows in the western US. We sought to determine resistance to BWSV in these two species and a presumed susceptible species, *Uta stansburiana*, which is occasional prey of black widows, through whole-animal performance trials and tissue histology. We obtained baseline sprint speeds, then injected lizards with control (saline), low, or high mass-adjusted venom treatments. We then obtained post-injection sprint speeds for treatment and control groups. Following whole animal trials, tissue samples at injection sites were taken for histological examination. We found no statistical decrease in sprint speed between control and treatment groups, though we detected a potential decrease in sprint speed for *U. stansburiana* in the high dose treatment. Tissue damage was present in all three species, but both *E. multicaudata* and *S. occidentalis* appear highly resistant to BWSV at the whole animal level. These data suggest that predator-prey relationships between lizards and spiders are potentially more complex than previously imagined, and involve several physiological and molecular adaptations that allow lizards to tolerate the effects of arachnid venoms.

219 SSAR SEIBERT ECOLOGY I, Highland A, Friday 13 July 2018

Cassandra Thompson and Viorel Popescu

Ohio University, Athens, Ohio, USA

Withering Waters & Teetering Temperatures: How one frog copes with Pool Permanency

Environmental variation during development can have profound, variable effects on an organism's phenotype, physiological attributes, and overall fitness. With increasing environmental temperatures and higher frequency of extreme events, ectotherms across the globe are expected to experience thermal ranges and extreme heat events beyond their physiological capacity. Anurans have a dual life cycle, raising the question of whether detrimental environmental conditions experienced in the aquatic (larval) stage are carried over in the terrestrial (juvenile and adult) stage, and whether the negative impacts on growth and survival in the larval stage are exacerbated by changes in temperature and moisture availability in the terrestrial realm. Notably, while many studies have focused on the effects of pool

permanency on developmental rates and survival of larval amphibians, few have considered carryover effects into the metamorph life stage. We evaluated the impact of hydro-period length on wood frogs (*Lithobates sylvaticus*), a model forest specialist. Our specific objectives were to (1) evaluate the impacts of drying conditions on larval development and survival, (2) evaluate carryover effects from the aquatic stage on locomotor performance (endurance) of metamorphs, and (3) evaluate carryover effects into the terrestrial habitat on growth and survival. While we found significant differences in larval survival and size at metamorphosis between hydro-period treatments, we found no significant differences in terrestrial growth and survival. Our future research will integrate the biological and physiological insights from this work with existing occurrence, demographic, and future climate, hydrological, and land use change models to create spatial rankings for conservation prioritization.

31 HL GRADUATE RESEARCH AWARD, Highland A, Friday 13 July 2018

Jessica Tingle¹, Brian Sherman² and Timothy Higham¹

¹University of California, Riverside, CA, USA. ²NA, Riverside, CA, USA

Scaling of Morphology and Locomotion in the Sidewinder Rattlesnake, *Crotalus cerastes*

Body size affects morphology, physiology, and even behavior across the tree of life, including locomotion ranging from invertebrate peristaltic crawling to tetrapod running. Previous studies on scaling of terrestrial locomotion have shown that kinematics scale inter- and intraspecifically for walking, running, and jumping. However, many animals move terrestrially without limbs, and they face different locomotor challenges than do limbed animals. Because limbless terrestrial animals range across orders of magnitude in size, and because they move so differently than limbed animals do, studies of scaling of limbless locomotion would deepen our understanding of the diversity of effective movement on land. We examined the scaling of sidewinding locomotion in the rattlesnake *Crotalus cerastes* by collecting various morphological measurements and high-speed video of 74 sidewinder rattlesnakes ranging in size from 8 g to 272 g. Many morphological characters scale isometrically, meaning large and small sidewinders have similar shapes despite their size differences. However, a few do not scale isometrically, pointing to some changes in body shape as sidewinders grow. In addition to the subtle body shape changes, we expected changes in the kinematics of sidewinding motion, perhaps mediated in part by body shape. Preliminary results suggest that certain kinematic variables, such as the height to which the snakes lift their bodies as they move forward, may also scale isometrically, but others, such as speed of individual points, do not show such a clear relationship. Scaling of the sidewinding motion could have ecological consequences for sidewinders as they grow.

513 Reptile Ecology I, Highland A, Sunday 15 July 2018

Brian Todd and Evan Eskew

UC Davis, Davis, CA, USA

Environmental Drivers of Snake Movement and Activity

Many biologists report having better success capturing snakes some nights than others, and generally suspect that weather plays a role. However, there are still very few studies that have unambiguously identified environmental influences on snake movement and activity. Here, we investigate environmental drivers of terrestrial snake activity in a temperate community in the Atlantic Coastal Plain region of South Carolina, USA. Our analyses included nearly 1,000 captures of 23 species from over three years of pitfall and box funnel trapping representing over 500,000 trap nights. Activity was strongly seasonal, with primarily fossorial species showing unimodal activity peaks in summer, whereas several aquatic species showed increased terrestrial movements to and from a wetland in both spring and fall. After controlling for seasonal activity, temperature and precipitation had consistent effects on snake movement, with activity of snakes increasing with temperature and decreasing with precipitation. The influence of moon illumination was more ambiguous, but appeared to have a weak, negative effect on snake activity. These environmental factors likely drive snake movements because of physiological constraints and trade-offs between foraging success and predation risk. Our results contribute to general knowledge of snake natural history and ecology and may help improve sampling of these elusive organisms that are increasingly in need of conservation attention.

616 ASIH STORER HERPETOLOGY, Empire Hall South - JF Rochester Riverside Convention Center, Friday 13 July 2018

Erin Toffelmier and H. Bradley Shaffer

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

Conservation and Landscape Genomics of the Endangered Santa Barbara Distinct Population Segment of the California Tiger Salamander, *Ambystoma californiense*

The Santa Barbara County population of California tiger salamanders (CTS), *Ambystoma californiense*, has experienced intense human development across its limited range and is federally protected under the US Endangered Species Act as a distinct population segment (DPS). Ample field-based evidence suggests that populations of this species are declining due to habitat fragmentation and destruction, but little is known about the population genetic effects of anthropogenic disturbance or current levels of connectivity among intact habitats. Using genome-wide molecular markers, we examine the genetic consequences of human habitat alteration. We find that relative to other CTS populations, effective population sizes are reduced and intra-population inbreeding is high, which suggests that populations within this DPS are becoming more isolated.

611 ASIH STOYE GENETICS, DEVELOPMENT, & MORPHOLOGY III, Highland C, Friday 13 July 2018

Erin Toffelmier¹, Adam Clause² and H. Bradley Shaffer¹

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USA. ²Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA

Landscape Genetics and Connectivity in the Panamint Alligator Lizard, *Elgaria panamintina*

The Panamint alligator lizard, *Elgaria panamintina*, has an extremely limited range and restricted habitat requirements in several arid mountain ranges in eastern California. The species is listed as “Sensitive” by the Bureau of Land Management, is a California Species of Special Concern, and is currently undergoing a status review for listing under the US Endangered Species Act. However, relatively little is known about its natural history and even less about its population genetic structure, overall levels of genetic diversity or population connectivity. In this study we use genome-wide molecular markers and landscape modelling to examine the population genetic structure and associated landscape variation in this enigmatic species. We find that while inter-population genetic differentiation is high, geographic distance appears to be the largest contributing factor to genetic isolation.

421 General Ichthyology II, Grand Lilac Ballroom South, Sunday 15 July 2018

Luke Tornabene¹, Carole Baldwin² and D. Ross Robertson³

¹University of Washington, Seattle, WA, USA. ²National Museum of Natural History, Smithsonian Institution, Washington, DC, USA. ³Smithsonian Tropical Research Institute, Balboa, Panama

Community structure of Caribbean deep-reef fishes

Mesophotic reefs extend from the lower limits of traditional SCUBA depths (~50 m) down to approximately 150 m in some locations. Mesophotic reefs harbor a unique assemblage of reef fishes that differs taxonomically and ecologically from fishes occurring on shallow reefs. The lower depth limits of mesophotic reef-fish communities have yet to be rigorously investigated, largely due to logistical challenges in deep diving. The present dataset represents the most extensive record of fish communities from 50-300 m, which was obtained using manned submersibles at four localities throughout the Caribbean. Based on more than 12,000 fish observations, reef-fish community structure was compared across sites and along the deep-reef slope. These data suggest that while the taxonomic composition of deep reefs may differ somewhat between sites across the Greater Caribbean, the overall patterns of zonation and the depth at which faunal shifts occur (including the end of the mesophotic zone) are surprisingly similar across sites. Collectively these results serve as a robust baseline for comparing other deep-reef fish communities beyond the Caribbean, and for monitoring ongoing changes to deep-reef fish communities over time.

553 SSAR SEIBERT SYSTEMATICS & EVOLUTION II, Highland B, Friday 13 July 2018

Javier Torres

The University of Kansas, Lawrence, Kansas, USA

Possible hybridization among Cuban Trunk-Ground anoles (*Anolis*, Dactyloidae) evidenced by testicular anomalies

Four trunk-ground anole species are sympatric in western Cuba: *A. allogus*, *A. homolechis*, *A. mestrei* and *A. sagrei*. In one location where they co-occur I have collected males that I could not identify at the species level due to the presence of unusual phenotypic traits, mainly in dewlap (an extensible skin fan with importance in located on the throat used in displays to potential mates) coloration and size. My aim is to prove that the unusual specimens are interspecific hybrids through the comparison of external characters and indicators of gonadal reproductive activity. To test the reproductive fitness hypothesis, I measured testicles size and counted the different cell types at the germinal. The putative hybrids were sexually mature based on size and the presence of sperms cells in the reproductive tract. They had smaller testicles and seminiferous tubules and less sperm cells than non-hybrids. Contrary to the non-hybrids, in the putative hybrids was not possible to identify the spermatogenic stage due to the presence of only spermatogonia in the seminiferous tubules and the existence of spermatozoa in very low quantities in the epididymis. Based on the previous evidences I conclude that the putative hybrids are interspecific hybrids due to the identification of the reproductive isolation mechanism of hybrid sterility. One parental species was identified based on external phenotypic traits while the other remains unknown.

508 SSAR SEIBERT SYSTEMATICS & EVOLUTION I, Highland B, Friday 13 July 2018

Claire Tracy^{1,2}, Kin Onn Chan² and Rafe Brown²

¹*Villanova University, Villanova, PA, USA.* ²*University of Kansas, Lawrence, KS, USA*

Phylogenetics and Morphometrics of Philippine Tree-hole Frogs of the Genus *Kaloula*

The genus *Kaloula*, family Microhylidae, is found throughout Southeast Asia, and has undergone an adaptive radiation within the Philippines. Taxa from the radiation within this archipelago generally occupy three different ecotypes: terrestrial ground frogs, scansorial shrub frogs, and tree-hole breeding frogs. One clade within the Philippine radiation that exemplifies the tree-hole ecotype is the *K. kalingensis* complex, which is comprised of species across the Luzon and West Visayan subregions of the northern and central Philippines. Currently, there are two described species within this group: *Kaloula kalingensis* from northwestern Luzon and *K. kokacae* from southern Luzon. Recent studies, however, have identified two additional putatively distinct lineages within this clade that have not yet been formally described: an East Luzon species and a species from Panay Island. In this study we examine morphological and genetic diversity in this clade across Luzon Island using standard external morphometric data and Sanger sequencing of the highly informative 16S gene. We identify additional species supported in both morphological and phylogenetic analyses, demonstrating higher species-level diversity within the *K. kalingensis* tree-hole clade than assumed previously. These data provide fertile grounds for future analyses of genomic variation.

557 Poster Session II, Empire Hall South – JF Rochester Riverside Convention Center, Saturday 14 July 2018

Scott Trageser¹, Paul Hamilton¹, Ross Maynard¹ and Juan Guayasamin²

¹The Biodiversity Group, Tucson, Arizona, USA. ²Universidad San Francisco de Quito, Quito, Ecuador

Herpetofaunal Survey Results in Manduriacu Reserve, Ecuador

The Tandayapa Andian Toad (*Rhaebo olallai*) was recently rediscovered within the 530 ha of protected primary Ecuadorian cloud forest of the Manduriacu Reserve on the western slope of the Andes. As part of The Biodiversity Group's ongoing mission to document life overlooked, 180 person-hours of visual and eDNA surveys were conducted to map the range of *R. olallai* and estimate relative abundances of the herpetofaunal community. In addition, two novel anurans were discovered, along with a population of one of the rarest lizards in Ecuador, and the rediscovery of a glass frog species not officially recorded in Ecuador since 1984. Populations of several critically endangered reptiles and amphibians were discovered to be locally abundant and warrant further protection through the expansion of the Manduriacu Reserve.

414 Herpetology Conservation I, Grand Lilac Ballroom South, Friday 13 July 2018

Scott Trageser¹, Shahriar Caesar Rahman¹ and Stephen Spear²

¹Creative Conservation Alliance, Dhaka, Bangladesh. ²The Wilds, Cumberland, Ohio, USA

Human-Python Conflicts: A Radio Telemetry Study of Burmese Pythons (*Python bivittatus*) in Bangladesh

Burmese pythons are rarely studied in their natural range, despite their Vulnerable status. Herein we present the results of the first radio-telemetry study of ten *Python bivittatus* in South Asia demonstrating the effects of translocation of conflict pythons. Our study has resulted in best practice recommendations for conservation managers as part of our organization's ongoing efforts to mitigate human-python conflicts range-wide. Movement patterns have been assessed and comparisons can now be made to the invasive population in Florida. Various natural history aspects are also reported on as well as range within Bangladesh and habitat preferences.

432 ASIH STOYE PHYSIOLOGY & PHYSIOLOGICAL ECOLOGY, Highland D, Friday 13 July 2018

Catherine Tylan and Tracy Langkilde

Pennsylvania State University, University Park, PA, USA

Local and Systemic Immune Responses to Different Types of Phytohemagglutinin in the Green Anole: Lessons for Field Ecoimmunologists

The phytohemagglutinin (PHA) skin test is commonly used by ecologists to assess cell-mediated immune function of wild animals. It can be performed quickly and easily in the field, involving injection of PHA and measurement of the resultant swelling. There are multiple formulations of PHA used in ecological studies, with potentially differing outcomes that could produce inconsistent results. We tested two common types of PHA in the green anole (*Anolis carolinensis*) to identify local and systemic immune responses underlying the resultant swelling at 6, 18, 24, and 48 hours post injection. There were differences in both local (injection site) and systemic (blood) leukocyte responses to PHA-L vs. PHA-P. PHA-P injection produced a greater overall increase in local heterophil count at the injection site compared to PHA-L, and this response was greatest at 6 and 24 hours post injection. Systemically, heterophil percentage was higher in the blood of PHA-P vs. PHA-L injected anoles at 24 hours post injection; the time point at which heterophil percentage peaked in PHA-P injected anoles. These results indicate that, while both PHA types are effective tests of immune function in green anoles, the PHA-P swelling response invokes a much stronger heterophilic response. PHA-L is a more specific test of lymphocyte function, particularly at 24 hours post injection, making it preferable for ecoimmunology studies.

218 Poster Session I, Empire Hall South - JF Rochester Riverside Convention Center, Friday 13 July 2018

Karen Underkoffler¹, Luers Meagan², John Hyde³ and Matthew Craig³

¹NOAA National Marine Fisheries Service, Seattle, WA, USA. ²NOAA National Marine Fisheries Service, Gloucester, MA, USA. ³NOAA National Marine Fisheries Service, La Jolla, CA, USA

A taxonomic review of *Lampris guttatus* (Brünnich 1788) (Lampridiformes; Lampridae) with descriptions of three new species.

The genus *Lampris* (Lampridae) currently comprises two species, *Lampris guttatus* (Brünnich 1788) and *L. immaculatus* (Gilchrist 1905) commonly known as Opah and Southern Opah, respectively. Hyde et al. (2014) presented DNA sequence data which revealed the presence of five distinct, monophyletic lineages within *L. guttatus*. In this paper, we present morphological and meristic data supporting the presence of five species previously subsumed within *L. guttatus* (Brünnich 1788). We restrict *Lampris guttatus* (Brünnich 1788), resurrect *L. lauta* (Lowe 1838), and describe three new species of *Lampris*. A key to the species of *Lampris* is provided.

310 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018

Yasel Urgelles Alfonso¹, Leroy Nunez¹, Ansel Fong² and Javier Torres³

¹Division of Herpetology, Florida Museum of Natural History, University of Florida, Gainesville, Florida, USA. ²Centro Oriental de Ecosistemas y Biodiversidad (BIOECO), Museo

de Historia Natural "Tomas Romay", Santiago de Cuba, Cuba. ³*Department of Ecology and Evolutionary Biology, The University of Kansas, Lawrence, Kansas, USA*

Evolutionary history of the Antillean gecko *Tarentola americana* (Phyllodactylidae) based on mitochondrial and nuclear DNA sequences

The genus *Tarentola* (Family Phyllodactylidae) comprises 31 species distributed across the Mediterranean Basin and on many Macaronesian islands, including Madeira, the Selvages, the Canary and Cape Verde islands. In the New World, three species are recognized as representative of the subgenus *Neotarentola*: *Tarentola americana* (Cuba and the Bahamas), *T. albertschwartzi* (the largest and probably extinct) from Jamaica, and the recently described *T. crombiei* (Cuba). Earlier phylogenetics analysis in the Cuban *Tarentola* suggest 11.4 (7.2–15.2) Ma for the split between *T. a. americana* and *T. crombiei* and 5.5 (2.8–9.1) Ma for the split between the central and eastern Cuban populations of *T. a. americana*. Previous data indicate a long occupation and diversification (~15 million years) of this genus of geckos on Cuba. In the present work we have re-examined the phylogenetic and phylogeographic relationships between *T. a. americana*, *T. crombiei* and we included the Bahamian taxon *T. a. warreni*. We have investigated the sequence variation of three mitochondrial genes (12S rRNA, 16S rRNA, and cytochrome b), and one nuclear gene (amelogenin) for 22 populations reaching their geographic distribution. The phylogenetics results obtained for population of *Tarentola americana* between Cuba (eastern and western) and Bahamas provide deep split between them and may warrant recognition as a separate species, after further morphological study.

436 ASIH STOYE GENERAL ICHTHYOLOGY III, Highland E, Sunday 15 July 2018

Diego Vaz and Eric Hilton

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

Comparative Anatomy of the Jaws, Suspensorium, and Gill Arches of Toadfishes (Batrachoidiformes)

The toadfishes (Batrachoidiformes) are a monophyletic group of mostly benthic, ambush-predatory fishes. Although the external morphology of toadfishes is conservative, their gill arches, jaws, and suspensorium are highly variable. Characters related to these complexes have been used in phylogenetic analyses, although these hypotheses were based on relatively low species coverage, and without assessing intraspecific variation or making comprehensive outgroup comparisons. Fifty-five species representing all four subfamilies of Batrachoidiformes and more than 50 species of Acanthomorpha were examined using CT-scans and cleared-and-stained specimens with the goal of identifying characters from the jaws, suspensorium and gill arches that may be phylogenetically informative for the interrelationships of Batrachoidiformes. The length of the maxilla varies intergenerically (longer in taxa with relatively flattened heads, such as *Perulibatrachus*, Halophryninae). Batrachoidinae and Halophryninae have a subopercle with one or two spines, whereas in Porichthyinae and Thalassophryninae the subopercle is spineless. The endopterygoid is hexagonal and extends posteriorly, articulating with the metapterygoid in Batrachoidinae, Porichthyinae, Thalassophryninae, and *Triathalassothia*. In Halophryninae the endopterygoid is either reduced to small triangular bone (*Halobatrachus*) or

absent (*Halophryne*). *Colletteichthys* and *Bifax* (Halophryninae) share a unique epibranchial one, in which its anterior tip is separated from the main body of the element by connective tissue. In Thalassophryninae, the reduced ossification of the basibranchials and the first pharyngobranchial suggests that some species of *Thalassophryne* may be more closely related to *Daector* spp., resulting in a paraphyletic *Thalassophryne*. The implications of these and other characters for reconstructing the phylogenetic relationships of Batrachoidiformes will be discussed.

192 Poster Session II, Empire Hall South – JF Rochester Riverside Convention Center, Saturday 14 July 2018

Tyara Vazquez, Ian Clifton, Jeanine Refsnider-Streby and Madison Zimmerly

University of Toledo, Toledo, Ohio, USA

Acute and Prolonged Heat-stress Effects on Performance and Heat-shock Protein Expression in Greater Short-horned Lizards (*Phrynosoma hernandesi*)

The southwestern desert ecosystems of the United States are one of the most sensitive areas to climate change. Warmer temperatures and increased droughts put desert reptiles at higher risk because many already live at the edge of their physiological limits. Heat-stress and dehydration may decrease performance and subsequent survival in reptiles, however, less is known about the underlying cellular mechanisms behind this. Cellular heat-stress protections such as heat-shock protein (HSP) expression may serve to mitigate heat-stress damage, however, there may be potential costs such as decreased performance. My research examines acute and prolonged heat-stress effects on performance and heat-shock protein expression in the desert, montane Greater short-horned lizards (*Phrynosoma hernandesi*). I captured lizards at one low-elevation site and one high-elevation site in the Abajo Mountains, Utah. I quantified performance (i.e. sprint speed and endurance), then lizards were randomly assigned to either acute, prolonged or control groups. Juveniles were heat-shocked at 36°C for two hours and adults were heat-shocked for four hours to simulate acute heat-stress. Adults were reciprocally transplanted between elevations for a week to simulate prolonged heat-stress. I quantified performance again after heat-stress treatment, then collected a tail tip and toe clip from each lizard. Toe clips were used to determine gravimetric water content and tail tips were used to determine HSP60, -70, and -90 expression. Acute heat-stressed juveniles from the high-site had lower endurance and lost more water than low-site juveniles. Desert, montane lizards from high-elevation sites may be more vulnerable to warmer, drier climates.

84 Poster Session II, Empire Hall South – JF Rochester Riverside Convention Center, Saturday 14 July 2018

Matthew Venesy¹, Joseph DeMarchi², Rachel Marbach¹, Keva Pariyar¹, Cari-Ann Hickerson² and Carl Anthony²

¹*Allegheny College, Meadville, PA, USA.* ²*John Carroll University, University Heights, OH,*

USA

Female salamanders experience higher parasitism compared to males: a cost of female reproduction?

Males tend to experience higher rates of parasitism compared to females because they engage in risky behaviors and because testosterone is known to be immunosuppressive. However, females could experience higher rates of parasitism if energy is allocated from costly immune responses towards producing eggs. We used data from laboratory experiments to investigate sex-specific differences in salamander (*Plethodon cinereus*) resistance to the emerging fungal pathogen *Batrachochytrium dendrobatidis* ("Bd"). Contrary to our predictions, we found that female salamanders had a higher prevalence of infection and carried a higher Bd infection burden compared to male salamanders. We also found that female reproductive investment (i.e., mass of eggs) positively correlated with Bd infection burden. Collectively, our findings might indicate that female salamanders experience a cost of reproduction in the form of decreased disease resistance.

624 Lightning Talks III, Highland B, Sunday 15 July 2018

Calvin Vick¹ and Kelly J. Irwin²

¹Benton High School, Benton, Arkansas, USA. ²Arkansas Game & Fish Commission, Benton, Arkansas, USA

An Eastward range expansion and new ecoregion for the Four-toed Salamander (*Hemidactylum scutatum*) in Arkansas.

We report a new locality of the Four-toed Salamander (*Hemidactylum scutatum*) in Saline County, Arkansas. This represents a range expansion of the Four-toed Salamander to the East of any known localities in Arkansas, as well as the first time this species has been found in the Gulf Coastal Plains of Arkansas. Four-toed salamanders generally inhabit valleys of the Ouachita Mountains in Arkansas. The documentation of the species outside of the mountain range, in a different ecoregion, indicates they may have a larger range in Arkansas than previously thought. Further sampling efforts will be conducted in the Saline River basin, South of where these specimens were located.

627 Herpetology Behavior, Grand Lilac Ballroom South, Friday 13 July 2018

Richard C. Vogt¹ and Camila Ferrara²

¹INPA, Manaus, Amazonas, Brazil. ²WCS-BRAZIL, Manaus, Brazil

Vocalizations in Seaturtles

We have been documenting underwater vocalizations in both freshwater and marine turtles in nature for the last decade. We use the term vocalizations in that we now have video recordings of turtles vocalizing underwater and simultaneous muscle movements on the inferior posterior cephalic region suggesting the sounds are being produced in the buccal cavity. Although our

most extensive work has been with one freshwater species, the Giant South American River Turtle (*Podocnemis expansa*) in the Brazilian Amazon Basin we have also documented vocalizations in many other freshwater species from both suborders in North and South America, Mexico, Australia and China. Documentation of all species of sea turtles has now been documented in different life history stages, eggs, hatchlings, and adults, on land and in the water. The propagation of low frequency sound underwater is an excellent media for long distance communication. We now have comparative data from different populations of *Chelonia mydas* and as well as vocalizations from both species of *Lepidochelys*, so that we can compare intra and interspecific characteristics of the structure and frequency of the sounds produced.

645 Amphibian Ecology I, Grand Lilac Ballroom North, Friday 13 July 2018

Rudolf von May and Daniel Rabosky

Museum of Zoology & Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, Michigan, USA

Phylogenetic Community Structure of Amazonian Amphibian Assemblages

Lowland Amazonian rainforests exhibit high levels of amphibian and reptile diversity, with local communities often housing over 80 species of each group. How do so many species coexist in relatively small areas is a question that remains unresolved and motivates further scientific research. Previous work has shown that species richness, composition, and abundance differ across forest types in western Amazonia. However, the role of phylogenetic relatedness on species co-occurrence and abundance across habitats remains unclear. In this study, we assembled a species-level phylogeny and used trait-and-habitat data to infer the role of niche divergence and evolutionary history in community assembly. Our trait-and-habitat data included species abundance, body size, habitat use, and substrate use across multiple lowland rainforest sites in Amazonian Peru. In addition to floodplain forest and terra firme forest, our surveys included other poorly studied habitats such as bamboo forest and palm swamp. We tested for pairwise correlations in species abundance across habitats, and quantified the degree of phylogenetic clustering and overdispersion across forest types. Our analyses shed light on the potential role of contemporary and historical species interactions underlying community structure across multiple amphibian assemblages.

646 Poster Session I, Empire Hall South - JF Rochester Riverside Convention Center, Friday 13 July 2018

Rudolf von May¹, Edgar Lehr² and Daniel Rabosky¹

¹*Museum of Zoology & Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, Michigan, USA.* ²*Department of Biology, Illinois Wesleyan University, Bloomington, Illinois, USA*

Evolutionary Radiation of Earless Frogs in the Andes: Molecular Phylogenetics and Habitat Shifts in High-Elevation Terrestrial Breeding Frogs

The loss of hearing structures and loss of advertisement calls in terrestrial breeding frogs (Strabomantidae) living at high elevations in South America are common and intriguing phenomena. The Andean frog genus *Phrynopus* has undergone an evolutionary radiation in which most species lack the tympanic membrane and tympanic annulus, yet the phylogenetic relationships among species in this group remain unclear. We present an expanded molecular phylogeny that includes *Phrynopus peruanus*, the type species of the genus, and 10 other species for which genetic data were previously unavailable. Using X-ray computed tomography imaging, we demonstrate that the absence of external hearing structures is associated with complete loss of the auditory skeletal elements (columella) in at least one member of the genus. We mapped the tympanum condition on to a species tree to infer whether the loss of hearing structures took place once or multiple times. We identified a single evolutionary transition that involved the loss of both the tympanic membrane and tympanic annulus, which in turn is correlated with the absence of advertisement calls. We also identified several species pairs where one species inhabits the Andean grassland and the other montane forest. When accounting for phylogenetic relatedness among species, we detected a significant pattern of increasing body size with increasing elevation. Additionally, species at higher elevations tend to develop shorter limbs, shorter head, and shorter snout than species living at lower elevations. Our findings strongly suggest a link between ecological divergence and morphological diversity of terrestrial breeding frogs living in montane gradients.

574 SSAR: Coloration in Fish, Amphibians, & Reptiles Symposium, Grand Lilac Ballroom North, Sunday 15 July 2018

Mitchell Vu¹, Sami R. Cherikh¹, Shai Meiri² and Peter Uetz¹

¹Virginia Commonwealth University, Richmond, VA, USA. ²Tel Aviv University, Tel Aviv, Israel

Color patterns in snakes: a phylogenetic and geographic analysis

Color and pattern are the most conspicuous features of snakes (and most other larger animals). However, both have turned out to be of little value for systematic purposes, given their tremendous variation across (and often within) species. We started to collect color and pattern information of snakes on a global scale, both to analyze their relationship to phylogenetics but also to geographic distribution. A database of snake colors and patterns will help us to identify snakes more easily, help with systematics and basic biology (such as mimicry). Importantly, color and pattern data will also assist with the identification of venomous snakes and help with conservation efforts (e.g. in import control). The colors and patterns of snakes will be deposited in the Reptile Database (<http://www.reptile-database.org>) and made available for searches, together with other characters such as size and geographic distribution.

500 Herpetology Conservation III, Highland C, Sunday 15 July 2018

Hardin Waddle¹, Jenny Keterlin² and Frank Mazzotti³

¹U.S. Geological Survey, Gainesville, FL, USA. ²National Park Service, Homestead, FL, USA.
³University of Florida, Ft. Lauderdale, FL, USA

A Model of Daily Capture Probability for Management of an Invasive Reptile

The Argentinian black and white tegu (*Tupinambis meriana*) is an introduced lizard species in Florida that is a major threat to native species due to its high reproductive rate and generalist carnivorous diet. To mitigate this threat, research and management agencies have been conducting trapping efforts to remove tegus. The goal of this trapping is to reduce the population size and reduce the spread of tegus in the region. To understand the effectiveness of various trapping techniques (e.g. trap type, bait, etc.) and conditions (e.g. sites, time of year, etc.) it is important to have a useful metric of trap effectiveness. Catch per unit effort (CPUE) is one such measure, but it is difficult to model the effects of various technique and condition parameters on CPUE. To assist managers in evaluating trapping success, we developed a Bayesian model to estimate capture probability directly from trapping data when using single- close live traps checked daily. This model makes it possible to estimate daily capture probability as a function of any combination of covariates. Using this model at one research site we determined the daily capture probability throughout the activity season, and the type of trap that maximized capture probability. By adding other sites into the model, it is simple to compare capture rates among sites. The information generated from this model will directly benefit managers by helping to guide decisions about the trap type, trap location, timing, and effort that is most efficient.

239 Herpetology Biogeography I, Highland B, Saturday 14 July 2018

Brian Waldron¹, Shawn Kuchta², Maggie Hantak², Cari Hickerson¹ and Carl Anthony¹

¹John Carroll University, University Heights, Ohio, USA. ²Ohio University, Athens, Ohio, USA

Genetic Analysis of Distinct Clades of the Red-backed Salamander (*Plethodon cinereus*) at a Northeast Ohio Contact Zone

Contact zones between species, subspecies, or incipient lineages offer important insights into the processes that maintain reproductive isolation. *Plethodon cinereus*, a highly abundant and wide-ranging terrestrial salamander found in the northeast United States and southeast Canada, provides an excellent model system for studying secondary contact zones. Six distinct clades have previously been identified with mtDNA across the range of *P. cinereus*. Populations of two such clades, the Ohio (OH) clade, which dispersed through central Ohio following receding glaciers of the Last Glacial Maximum, and the Pennsylvania (PA) clade, which dispersed through Pennsylvania and then west through northern Ohio, can be found approximately 9.6 km apart in Lorain County, Ohio. We analyzed ten microsatellite loci and one mitochondrial locus from 16 sites along a ~53 km east-west transect. While we found a clinal transition of mtDNA within the transect, microsatellite markers revealed little differentiation and weak population structure. A lack of linkage disequilibrium suggests that the nuclear hybrid zone lies outside of our sampling region. We discuss the observed population genetics compared to other studies on *P. cinereus* and pose potential causes of mito-nuclear discordance.

522 Herpetology Habitat & Environment, Highland A, Saturday 14 July 2018

Danielle Walkup¹, Wade Ryberg², Toby Hibbitts³ and Lee Fitzgerald¹

¹Department of Wildlife and Fisheries Sciences, Texas A&M University, College Station, Texas, USA. ²Natural Resources Institute, Texas A&M University, College Station, Texas, USA.

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Microhabitat variables drive within breeding season colonization/extinction dynamics in a specialist lizard.

The persistence of habitat specialists at the landscape scale is strongly tied to the persistence, configuration, and quality of habitat. *Sceloporus arenicolus* (dunes sagebrush lizard) is a habitat specialist endemic to the Mescalero-Monahans Sandhills ecosystem of West Texas and southeastern New Mexico. Interconnected subpopulations of *S. arenicolus* are made up of demographic “neighborhoods” that are influenced by the configuration of landscape features. Understanding the linkages between microhabitat used by the lizards and landscape scale features may help us to better understand what ultimately determines the distribution of *S. arenicolus* across broad landscapes, as well as dispersal and diffusion processes. We trapped lizards during four years (April-August 2012-2015) in two large “super-grids” consisting of 324 pitfalls arranged in a grid of 36 sub-grids that covered 13.69 ha. Microhabitat data collected at each trap included slope, substrate compaction, and percent cover for different substrates (i.e., sand, oak, yucca, forb, grass, caliche, shrub). Trapping data were aggregated for use in a multi-season occupancy model to examine microhabitat use in relation to colonization/extinction dynamics for *S. arenicolus*. Results indicate that extinction and colonization dynamics across the landscape are linked to slope, substrate compaction, percent cover oak, and percent cover sand at the microhabitat scale.

540 Herpetology Conservation II, Highland C, Sunday 15 July 2018

Susan Walls

U.S. Geological Survey, Gainesville, FL, USA

What Constitutes Conservation Success and How is it Achieved?

A fundamental challenge in conservation and management of imperiled species is defining what constitutes success, along with identifying metrics by which it may be measured. Population recovery, or some other biological measure of population viability, is the ultimate measure of conservation success; more intermediate metrics based on project-specific objectives are beneficial but are rarely explicitly defined. Conservation success depends not only on knowing what strategies work, but also on using adaptive management to learn critical lessons – both positive and negative – that can reduce uncertainty and foster effective conservation. Learning is therefore pivotal to conservation and management of natural resources and understanding what constitutes a lack of success can improve conservation effectiveness. My objectives are to identify elements of successful conservation of amphibians and reptiles, two of the most imperiled biodiversity groups; identify strategies for addressing

challenges and mitigating threats; highlight key case studies that illustrate successful conservation with at-risk species; and provide “lessons learned” from past conservation efforts that could help steer current and future conservation towards more effective outcomes, therefore strengthening the prospects of species recovery. Conservation successes need to be celebrated in this era of escalating rates of population declines, species’ extinctions, and shortfalls in conservation funding. Clarifying what qualifies as success and how it can be achieved is a first step towards increasing effectiveness in conservation of amphibians and reptiles.

626 ASIH STOYE GENETICS, DEVELOPMENT, & MORPHOLOGY II, Highland C, Friday 13 July 2018

Danielle Wasserman

City University of New York, New York, NY, USA. Queens College, Flushing, NY, USA

The practicality of using vertebra number to gauge hyoid position in anguimorph lizards

Hyoid position on the anterior-posterior axis is known to have transformed over evolutionary time across Lepidosauria. In anguimorphs, hyoidal elements occur along the throat in the territory below and between vertebrae two through nine. Ancestral state reconstruction of position can be made simple if a piece of hyoid bone or cartilage can be characterized by the number of the vertebra above it. Following random sub-sampling and resampling from a total sample of thirty two species and fifty four individuals, length based measurements varied significantly between closely related taxa. However, character reconstructions of length measurements and vertebra position, when compared, were more or less congruent on all but a few branches, where shifts to from fossorialism are thought to have occurred. Niche divergence was found to be a reliable predictor of position change, much more so than phylogenetic distance. Using vertebra number is an acceptable approach to characterizing hyoid position, so long as ecomorphology is conserved.

495 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018

Jessica Watson¹, Michelle Lawing² and Jesse Meik¹

¹Tarleton State University, Stephenville, Texas, USA. ²Texas A&M, College Station, Texas, USA

Preservation Effects and Geometric Morphometrics of Head Shape in Western Rattlesnakes

Patterns of phenotypic variation are vital for informing studies of taxonomy, systematics, and evolution. However, elucidating these patterns, and distinguishing between different sources of variation (i.e., noise from signal), is not trivial given the complexity of biological structures. We used geometric morphometrics to reanalyze a large landmark dataset of head shape morphology obtained from museum specimens that was used previously to inform taxonomy

of the western rattlesnake (*Crotalus viridis*) complex, a widespread polytypic species with nine recognized subspecies. Our motivation was to use objective Bayesian clustering algorithms to identify and assign specimens to species (i.e., species discovery methods) rather than to 'test' *a priori* hypotheses of species limits based on subspecies designations. Our results suggest that in contrast to findings from previous analyses, head shape represented by landmarks on images of preserved specimens was not a useful character for delimiting species within the *C. viridis* complex. Furthermore, while some biologically relevant variation in head shape could be attributed to head size allometry, thin plate spline deformations revealed substantial variation caused by preservation effects on head shape.

604 SSAR SEIBERT SYSTEMATICS & EVOLUTION II, Highland B, Friday 13 July 2018

Jeffrey Weinell¹, Daniel Paluh² and Rafe Brown¹

¹University of Kansas and Biodiversity Institute, Lawrence, Kansas, USA. ²Florida Museum of Natural History, University of Florida, Gainesville, Florida, USA

Morphological specialization and molecular phylogenetic history of the Philippine-endemic snake subfamily Cyclocorinae

The Philippines includes at least 112 species of terrestrial snakes (74% of which are endemic to the archipelago) in 41 genera (12% endemic). The majority (80%) of the Philippine-endemic snake genera belong to the subfamily Cyclocorinae (Lamprophiidae), an enigmatic, primarily fossorial group with seven described species in four genera: *Cyclocorus*, *Hologerrhum*, *Myersophis*, and *Oxyrhabdium*. We present X-ray computed tomography (CT) data for each of these genera, and highlight dramatic cases of morphological specialization in this group. Furthermore, we used a multilocus DNA dataset, sampling broadly across the geographic ranges of all cyclocorine species, to provide an updated estimate of species diversity and phylogenetic relationships within this subfamily. Lastly, we address the question: What are the closest relatives to Cyclocorinae?

408 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018

Jessica Wells and John Peterson

University of Wisconsin Platteville, Platteville, WI, USA

Soundscape Ecology of State-endangered Blanchard's Cricket Frog Communities in Wisconsin

Frogs are important indicators of environmental conditions. Understanding what influences their breeding vocalizations can help scientists better report on population dynamics. Previous studies have documented that the soundscape at wetlands can influence vocalizations, but fewer studies have looked at how the soundscape changes throughout the day and how the

soundscape may bias surveys. Recording devices were utilized to record the soundscape at 6 wetlands during the month of June from 1300h to 300h. Occurrence of Gray Treefrogs (*Hyla versicolor*), Green Frogs (*Lithobates clamitans*), and Blanchard's Cricket Frogs (*Acris blanchardi*, an endangered species in Wisconsin), traffic, birds, wind, rain, thunder, running water, construction, and insects were quantified. Birds, traffic, and wind dominated the soundscape during the day and frogs dominated at night. Sites with high occurrences of birds, traffic, and frogs tended to have lower occurrence of other sounds, suggesting bias in assessment of quieter aspects of the soundscape. At a site next to a four lane highway bird call occurrence was higher and occurred later into the evening and *L. clamitans* occurrence was low. It is unclear whether this variation was caused by the traffic or other factors in the environment. Also, the low frequency sounds of the traffic may have biased the assessment of *L. clamitans* calls.

550 Herpetology Systematics, Highland B, Saturday 14 July 2018

Rachel Welt and Chris Raxworthy

American Museum of Natural History, New York, NY, USA

Dispersal, not Vicariance, Explains the Biogeographic Origins of Iguanas on Madagascar

As a primarily New World group, the presence of Iguanidae (*sensu lato*) on the isolated Indian Ocean island of Madagascar (family Opluridae) has long been a biogeographic mystery. Previous work has attributed this disjunct extant distribution to (1) a widespread Gondwanan distribution of iguanids and their subsequent extinction on Africa, and potentially other Gondwanan landmasses, (2) vicariance following a once contiguous distribution via land bridge connection between South America, Antarctica, and Madagascar, present until about 80 Ma, or (3) long-distance overwater dispersal between South America and Madagascar. Each of these explanations has received some support through molecular analyses of divergence dating, thus this biogeographic pattern has not yet been well resolved. Here we utilize sequences of ultraconserved elements for the majority of genera, and all families of Iguanidae, as well as morphological data on extant and fossil taxa in divergence dating analyses, resulting in the most comprehensive dataset to address this question to date. We find strong support for a sister relationship between Opluridae (Madagascar) and Leiosauridae (South America), and for post-Gondwanan dispersal of the Opluridae lineage to Madagascar. We discuss potential dispersal routes from South America, but additional fossil or paleobiogeographic information is needed to confirm any of these scenarios. Further work will focus on the evolution of this unique family of iguanas since their arrival on Madagascar.

566 ASIH STOYE ECOLOGY & ETHOLOGY I, Highland C, Thursday 12 July 2018

Florence Wen

Southeastern Louisiana University, Hammond, LA, USA

Investigating Sea Turtle Hatchling Sex Ratios and Methods to Mitigate Climate Change Effects at an Arribada 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 high 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, we built 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 to these thermal zones will be determined using histological examination of hatchling gonads. Temperature loggers were also placed throughout the main nesting area of the beach to determine sand temperatures throughout the study period. Sex ratio information from the hatchery will be extrapolated to estimate the 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.

614 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018

Sarah M Wenner¹, Jeanne M Robertson¹ and Katy Delaney²

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Conservation Genetics of an Emblematic Reptile in Urban Southern California

In the highly urbanized greater Los Angeles area, the Blainville's horned lizard (*Phrynosoma blainvillii*) has experienced an immense reduction in range. My study will use principles of conservation genetics to estimate effective population sizes, quantify genetic diversity, and infer patterns of gene flow within remaining populations in this area. Further, previous work identified Los Angeles and Ventura counties as the contact zone between two evolutionary clades of Blainville's horned lizards. If there is evidence of genomic introgression in this area, it may be considered a genetic hot spot and a priority for future conservation work. I will analyze up to 300 non-lethal tissue samples from individual horned lizards throughout the Santa Monica Mountains and the adjacent Transverse Ranges. I will use RADseq to generate a dataset to calculate genetic diversity, population genetics structure and effective population sizes. I will also test for recent and historical genetic bottlenecks in these populations, and determine the extent of introgression between populations of the two evolutionary clades at the putative contact zone. Together, these data will be used to delineate conservation units for the Blainville's horned lizard in this urban region.

262 Lightning Talks I, Grand Lilac Ballroom North, Thursday 12 July 2018

Steven Werman and Rebecca Bryan

Colorado Mesa University, Grand Junction, Colorado, USA

DNA sequence information of concolor toxin genes in midget faded rattlesnakes near Grand Junction, Colorado

The Midget Faded Rattlesnake, *Crotalus oreganus concolor*, found in western Colorado and eastern Utah, is known to possess a beta-neurotoxin (PLA₂) known as concolor toxin. To assess genetic variation among individuals, blood was collected from several specimens from the vicinity of Grand Junction, CO. Portions of both the acidic (A) and basic (B) subunit genes were amplified, sequenced and compared. The amplified *C. o. concolor* acidic and basic subunit gene regions show a very high sequence identity among individuals and to corresponding regions of Mojave toxin A and B genes from *C. scutulatus*. Based on preliminary data, concolor toxin is essentially Mojave toxin.

119 Lightning Talks I, Grand Lilac Ballroom North, Thursday 12 July 2018

Aundrea Westfall, Jamie Oaks and Tonia Schwartz

Auburn University, Auburn, AL, USA

The Evolution of Viviparity and the Insulin and Insulin-like Signaling Network in *Sceloporus* Lizards

Transitioning from egg-laying to live birth has occurred approximately 140 times across vertebrate evolution, 115 of which have occurred within lizards and snakes. In contrast, the mammalian lineage experienced this change one time with the evolution of the mammalian placenta followed by rapid diversification of structures and mechanisms to maintain fetuses. This transition is a major life history change requiring the coordinated evolution of mechanisms that retain the egg, lose the eggshell, and begin provisioning maternal resources to the fetus via a placenta-like structure. A major gene network implicated in the development, growth, and function of the mammalian placenta is the insulin and insulin-like signaling (IIS) network. However, the role of this molecular network in placental function in other groups is poorly understood. There is strong evidence that squamate reptiles have experienced significant positive selection in major regulators of the IIS network such as insulin growth factor 1 (IGF1), IGF1 receptor, and insulin receptor, but this selection has not yet been investigated in the context of the repeated evolution of viviparity. *Sceloporus* is a genus of lizards that is ancestrally oviparous but has experienced three or more unique transitions to viviparity. Partial genomes for 35 different species in the genus were recently published, and I have isolated IIS network genes from each species. Using analyses of molecular evolution, I am testing for unique patterns of selection in IIS network genes that may promote the lability of parity mode in this genus.

507 SSAR: Coloration in Fish, Amphibians, & Reptiles Symposium, Grand Lilac Ballroom North, Sunday 15 July 2018

Michael Westphal^{1,2} and Theodore Morgan²

¹US Bureau of Land Management, Marina, CA, USA. ²Kansas State University, Manhattan, KS, USA

When gartersnakes go dark: pigment knockouts and the unfulfilled promise of xanthine dehydrogenase

A decades-old physiological model based on histological evidence provided a compelling argument that the protein xanthine dehydrogenase (XDH) could be a locus of major effect for garter snakes (genus *Thamnophis*) that express blue markings that are normally colonized by bright red or yellow pteridine-containing pigment cells. We conducted a survey of unpigmented garter snakes and identified a number of recognizable color syndromes all of which could be loosely characterized as “melanistic” but were clearly distinct from each other and likely of different genetic origin. We sampled integumental tissue from some morphs and assayed them with a chemical test to detect the presence of XDH. We also retrieved sequence data representing most of the coding region of XDH from a set of dark and wild type garter snakes and tested for correlation between haplotypes and color syndrome. Our chemical assay confirmed the presence of XDH even in snakes displaying putative pteridine-knockout phenotypes, and we saw no correlation between sequence polymorphisms and dark phenotypes. We conclude that, if XDH is at all involved in pigment-knockout phenotypes, regulatory genes are the likely targets.

518 ASIH STORER HERPETOLOGY, Empire Hall South - JF Rochester Riverside Convention Center, Friday 13 July 2018

Courtney Weyand, James C Godwin and Jon Armbruster

Auburn University, Auburn, Alabama, USA

Using Environmental DNA to Detect Species Found within the Black Warrior River Basin after a Flash Drought Event

The southeastern US has been under one of the most extreme flash droughts in at least 10 years. In Alabama, exceptional drought conditions started in September 2016 and persisted unabated until late December 2016, drying numerous waterways with many large rivers reading 5% or less of typical flow. The drought reached historic levels with 98% of Alabama experiencing severe drought; 73% extreme drought, and 20% exceptional drought. The areas recently experiencing exceptional drought conditions directly correspond to watersheds with the highest occurrences of endemic taxa groups. How aquatic organisms respond to atypical and quickly-occurring disturbances such as the current flash drought are unclear. In this study, we focused on three endemic taxa of high conservation concern across 50 sites throughout the Black Warrior system, the Black Warrior Waterdog (*Necturus alabamensis*), Flattened Musk Turtle (*Sternotherus depressus*), and the Tuskaloosa Darter (*Etheostoma douglasi*). By utilizing

environmental DNA (eDNA) techniques, through comparisons from both pre and post-drought data were completed to compare eDNA signatures before and after the drought. Presence/absence accounts were then determined for these three species of special concern. Because the drought is centered on an area with high taxonomic and functional diversity, our results are broadly applicable to drought effects on aquatic species elsewhere.

272 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: PHYSIOLOGY & MORPHOLOGY, Empire Hall South - JF Rochester Riverside Convention Center, Friday 13 July 2018

James Whelan, Hayley Crowell, Malory Harmel and Emily Taylor

Cal Poly, San Luis Obispo, CA, USA

Preferred body temperature of inland and coastal Pacific Rattlesnakes (*Crotalus oreganus*).

Internal body temperatures of ectotherms are affected by their environment, size, sex, and food availability. In the wild, factors such as predation, food resources, and refugia availability may restrict an animal's ability to reach their preferred internal body temperature (T_{set}). Bearing this in mind, this trait may be plastic among populations, and the underlying factors that affect an ectotherm's T_{set} are unclear. Geographic variation in T_{set} is rarely assessed. In this study, we aimed to determine the T_{set} of Pacific rattlesnakes (*Crotalus oreganus*) on the central coast of California, specifically testing the hypothesis that T_{set} varies among snakes from four different populations that differ dramatically in climate, despite being relatively close together geographically. To do this we placed freshly captured snakes from each field site in a thermal gradient and monitored their body temperatures via cloacal thermocouples over a 12-hour period. We predicted that snakes at coastal sites will have lower T_{set} than inland snakes, which would potentially make them more thermally constrained under the projected rise in temperatures as predicted by future California climate change models. Preliminary data suggest no significant difference in T_{set} among sites, despite major climatic differences among the sites. These preliminary results suggest that preferred body temperature is not plastic among populations and will remain similar between geographically separated populations.

156 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018

Mary White¹ and Mark Merchant²

¹*Southeastern Louisiana University, Hammond, LA, USA.* ²*McNeese State University, Lake Charles, LA, USA*

Expression of Immune System Genes in Alligators

Crocodylians have potent antimicrobial activity in their tissues and blood, attributed in large part to their serum complement proteins and other components of the innate immune system. Our previous work shows that crocodylians have evolved two very different genes for complement C3, a vital component of complement activation. Birds and mammals have only a single C3 gene, and although snakes have multiple C3 genes, they encode highly similar proteins. Among vertebrates, only fish are known to have such diverse C3 genes, and it was hypothesized that the diversity expanded the recognition repertoire of the innate immune system. A preliminary liver transcriptome from *Alligator mississippiensis* revealed expression of both complement C3 genes, along with all other known complement genes, as well as a wide variety of antimicrobial peptides. Quantitative expression of these immune system genes will be compared with a mouse liver transcriptome to shed light on the evolution of the powerful immune function of alligator serum.

52 Poster Session I, Empire Hall South - JF Rochester Riverside Convention Center, Friday 13 July 2018

Matthew White, Brianna Baer, Kathleen Cook and Sam McGee

Ohio University, Athens, OH, USA

Genetic diversity in the Least Brook lamprey

The Least Brook lamprey, *Lampetra aepyptera*, is a nonparasitic species widespread throughout the eastern and central US. It displays little inter-population morphological variation and some life history variation. We used DNA sequences from three mitochondrial (ND3, Control region, CytB) and one nuclear gene (ABCB9 intron 2) to assess phylogenetic relationships among 39 populations. Extensive differentiation was observed among populations from different drainages (Ohio River, Obion, Forked Deer, Hatchie, Yazoo, Tennessee) suggesting multiple undescribed taxa. However, the additional sequence data did not provide the resolution needed to understand the relationships among clades. Our data suggests several instances of stream capture and a couple of relationships that perhaps don't make as much sense as we would like.

209 Herpetology Conservation I, Grand Lilac Ballroom South, Friday 13 July 2018

Steven Whitfield¹, Frank Ridgley¹, Nicole Atteberry¹, Daniel Valle², Adrian Figueroa², Johnny Iglesias² and Brianna Chin²

¹Zoo Miami, Miami, FL, USA. ²Florida International University, Miami, FL, USA

Ecology and Conservation of Gopher Tortoises in Pine Rocklands Habitat in Miami, Florida

Gopher Tortoises (*Gopherus polyphemus*) are the only tortoise native to the southeastern United States, and are listed by Florida's state wildlife agency as a threatened species and a species of greatest conservation need. In extreme southern Florida, gopher tortoises face challenges from unique geology (seasonally flooded and/or shallow rocky soils); biology (introduced species and emerging infectious diseases); and human impacts (urbanization and habitat loss, fire suppression, anthropogenic displacement). Here, we characterize population biology, ecosystem role, and management challenges for gopher tortoises with the Richmond Pine Rocklands - an ~450 ha isolated habitat fragment harboring a large number of threatened and endangered species in Miami-Dade County, Florida. Burrow surveys indicate a large number of apparently active burrows distributed throughout the property, yet relatively few burrows are occupied compared to other published studies. The current population apparently consists of few adults and many small juvenile tortoises. Camera traps at burrow entrances indicate that burrows provide important refugia for a wide assemblage of mammals, reptiles, and amphibians - including both native and invasive species. We dissected 54 tortoise scats to understand patterns in seed dispersal, and tortoises ingested both native and invasive seeds, primarily grasses. We report exposure to two *Mycoplasma* pathogens among individuals within this isolated population, though we report no clinical symptoms of disease. While the tortoise population apparently serves important ecological functions for the critically endangered pine rocklands habitat, it is unclear whether the population is sustainable without more intensive management.

597 Ichthyology Genetics, Reproduction, and Development, Highland E., Friday 13 July 2018

Abby Wicks¹, Trevor Krabbenhoft² and Thomas Dowling¹

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

Variation in gene expression of round goby and Johnny darter in two Southeastern Michigan streams

Organisms vary in their response to abiotic and biotic factors, with environmental heterogeneity leading to variation in physiological responses. We used RNA-seq to test the hypothesis that invasive round goby (*Neogobius melanostomus*) exhibit different responses to environmental heterogeneity as compared to native Johnny darter (*Etheostoma nigrum*). By characterizing variation in gene expression we can understand the contribution of historical structure, demographics, and environmental factors to variation in patterns of gene expression and organismal response to these environments. Our prediction was that the native darter would exhibit greater variation in gene expression among rivers than round goby because as a recent colonizer, we expect limited divergence in ecology and physiology among round goby populations. Differential expression analysis was applied to these two common fishes from two

Southeastern Michigan drainages, the Rouge and Clinton rivers. Sites were chosen to represent a gradient in habitat quality and fishes were collected over three consecutive years. Greater differences in patterns of gene expression were observed in Johnny darter than in round goby, with major differences attributable to variation between sexes and between rivers. Differences between sites within the same river were minimal. Environmental data were collected concurrent with fish collection and will be analyzed for correlation with expression patterns. We also identified SNPs from the RNA-seq data, finding more genetic variation between populations of the two rivers in round goby than in Johnny darter. The observed genetic differences between round goby populations may be due to founder effects given round goby's recent invasion.

419 Ichthyology Conservation, Grand Lilac Ballroom South, Saturday 14 July 2018

Mark Wildhaber¹, Lynsey Whitacre², Gary Johnson², Justin Downs³, Tendai Mhlanga-Mutangadura², Vernon Tabor⁴, Daniel Fenner⁵ and Jared Decker²

¹USGS, Columbia Environmental Research Center, Columbia, Missouri, USA. ²University of Missouri, Columbia, Missouri, USA. ³The Peoria Tribe of Indians of Oklahoma, Miami, Oklahoma, USA. ⁴USFWS, Kansas Ecological Services Field Office, Manhattan, Kansas, USA. ⁵USFWS, Oklahoma Ecological Services Field Office, Tulsa, Oklahoma, USA

Neosho Madtom (*Noturus placidus*) Genetic Variation and Population Structure in Support of Species Recovery

The Neosho madtom (*Noturus placidus*) is a catfish generally less than 3 inches in length that was Federally listed as threatened in 1990. The Neosho madtom is unique to the Neosho-Spring River system within the Arkansas River Basin, designated as critical habitat by the state of Kansas. Neosho madtom threatened status is likely connected to reservoir construction, gravel mining, water extraction, zinc-lead mining, agricultural runoff, urbanization, and industrialization. Since its listing, ongoing efforts have been working toward removing low-head dams, evaluating increased water storage, understanding population genetics, and developing propagation and reintroduction capabilities. Supporting the latter two efforts, whole genome sequence data (39X coverage) were generated from ten Neosho madtom from each of three geographically separated populations to evaluate genetic diversity and population structure. One stonecat (*Noturus flavus*) was also sequenced as an outgroup. Single nucleotide polymorphisms were assessed de novo and via reference alignment with the channel catfish (*Ictalurus punctatus*) reference genome. Weak population structure was found, suggesting the three populations represent one panmictic population. This research in a threatened species provides novel genetic information to guide current and future conservation efforts, especially reintroduction. Furthermore, it demonstrates the utility of new genomic approaches to conservation of non-model organisms which previously had few genetic resources available. From an ecological perspective, Neosho madtom status seems to reflect the overall health of its aquatic community. Having genomic resources for the Neosho madtom will allow managers to

better monitor and conserve populations, which may in turn improve conditions of its aquatic community.

638 ASIH: If Salamanders Could Speak Symposium, Grand Lilac Ballroom North, Saturday 14 July 2018

Becky Williams¹, Jake Richardson¹ and Susan Durham²

¹Utah State University Uintah Basin, Vernal, UT, USA. ²Utah State University, Logan, UT, USA

Comparison of Epithelial Microbial Communities of the Tetrodotoxin-Bearing Rough-skinned Newts and Non-Tetrodotoxin Bearing Pacific Tree Frog from a Common Pond

We sequenced microbiomes of two sympatric amphibians in a common pond in Western Oregon, USA, the Pacific Tree Frog (*Pseudacris regilla*) and the Rough-skinned Newt (*Taricha granulosa*). The Rough-skinned Newt contains a powerful neurotoxin, tetrodotoxin (TTX). Some have suggested TTX is produced by bacteria in marine organisms. Others contend that there is no evidence for bacterial production of TTX in terrestrial organisms. We investigated whether bacterial communities of TTX-bearing and non-TTX bearing amphibians from a common pond differ in their microbial communities. Some similarities exist between these two amphibians in that *Sediminibacterium* spp. and *Pseudomonas* spp. occur in high abundance and *Herbaspirillum* spp. occur in low abundance, which may be due to a common habitat; however there is variation in microbial communities between individuals and species. There is no difference in total bacterial counts ($t = 0.756$, $df = 14$, $p = 0.766$). We also assess whether TTX levels of individual Rough-skinned Newts are related with their microbial communities. Whether microbial communities influence TTX levels or vice versa is unknown.

640 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018

Danielle Williamson, Macy Elwell, Victoria Brady, Jonathan Malinski and Matthew Bealor

Rowan University, Glassboro, New Jersey, USA

What's on the Menu: Assessing the Dietary Preferences of Introduced Italian Wall Lizards via Chemosensory Assay

Italian Wall Lizards (=IWLs), *Podarcis sicula*, are native to Italy and the Balkan Peninsula, but introductions have resulted in the establishment of breeding populations in at least four U.S.

cities (Topeka, KS, Long Island, NY, Los Angeles, CA and Mount Laurel, NJ). We examined the feeding patterns and dietary preferences of wild-caught, hatchling IWLs from the NJ population, which was established from intentional release of captive-bred lizards 35 years ago. Hatchlings were presented with five different chemical stimuli presented on cotton tipped applicators. We recorded the number of tongue flicks and latency to bite (in trials where lizards bit the applicator) for each lizard in response to chemical cues from crickets, mealworms, earthworms, dandelion flowers and distilled water as a control. We then used these data to calculate a tongue flick attack score (TFAS), which is a composite score based on the number of tongue flicks, but that assigns heavier weighting to trials where lizards bit the applicator. We will compare our results with published dietary accounts on this species from the New York population as well as with dietary data from native populations in Italy.

524 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018

Stuart C. Willis¹, Hudson T. Pinheiro¹, Carlos E. L. Ferreira², Ronaldo Francini-Filho³, Paulo M. Affonso⁴ and Luiz A. Rocha¹

California Academy of Sciences, San Francisco, CA, USA. ²*Universidade Federal Fluminense, Rio de Janeiro, RJ, Brazil.* ³*Universidade Federal da Paraíba, João Pessoa, Paraíba, Brazil.* ⁴*Universidade Estadual do Sudoeste da Bahia, Vitória da Conquista, Bahia, Brazil*

Low genetic diversity promotes phenotypic diversification? Genomic investigations of the unusual Queen Angelfish (*Holocanthus ciliaris*) of St. Paul's Rocks

Queen Angelfish (*Holocanthus ciliaris*), a common reef fish in tropical waters from the United States to Brazil, are large omnivores feeding primarily on sponges. Despite having high fecundity and abundant food sources, population density is generally low among adults that exist solitarily or in pairs, suggesting important social interactions to defend territory and acquire mates. Adults show a relatively consistent phenotype despite distribution over thousands of kilometers: yellow color with extensive blue edging and with dorsal and anal fin extensions that reach past the caudal fin. St. Paul's Rocks (Arquipélago de São Pedro e São Paulo; SPR), a group of small islands (~15,000 m²) that lie 1,010 km from the Brazilian coast, hosts a population of Queen Angelfish that exhibit unusual phenotypic patterns. These include all-yellow, all-blue, and all-white color patterns, and intermediates; shortened dorsal and anal fins rarely reaching past the caudal; and occasional 'pug-nose' jaw abnormalities. Anecdotal evidence also suggests unusually high population densities, which is odd considering the sharp relief and limited area of contemporary shallow-water habitat. However, deep, submerged banks may have provided greater habitat during sea-level low-stands, and supported a historically substantially larger population size. Using ddRAD sequencing, we examined the genetic diversity of Queen Angelfish from SPR, and found that SPR fish exhibit lower genetic diversity than coastal populations. Using these data, we test the hypotheses that the SPR population is genetically isolated from other populations and has undergone a bottleneck since the glacial age.

401 Neotropical Ichthyological Association Talks, Highland E, Saturday 14 July 2018

Stuart C. Willis¹, David E. Saenz², Gang Wang³, Christopher M. Hollenbeck⁴, Luiz A. Rocha¹, David S. Portnoy⁴, James J. Cai² and Kirk O. Winemiller²

¹California Academy of Sciences, San Francisco, CA, USA. ²Texas A&M University, College Station, TX, USA. ³MD Anderson, Houston, TX, USA. ⁴Texas A&M University-Corpus Christi, Corpus Christi, TX, USA

Osmoregulation in freshwaters: Gene expression in the gills of a Neotropical cichlid in contrasting pH and ionic environments

Freshwater habitats of the Neotropics exhibit a gradient from relatively ion-rich whitewater to acidic, ion-poor blackwater. Closely related species often show complementary distributions among ionic habitats, suggesting that adaptation to divergent osmoregulatory environments may be an important driver of Neotropical fish diversity. However, little is known about the evolutionary tradeoffs involved in osmoregulation across distinct freshwater environments. Here, we surveyed gill RNA expression of *Cichla ocellaris* var. *monoculus*, a Neotropical cichlid, to examine cellular and physiological responses to experimental conditions mimicking whitewater and blackwater. Expression patterns indicated that the gills were remodeled during both osmotic challenges, with changes biased towards the cellular membrane. We observed expression of signaling pathways from both the acute and extended response phases, including evidence that growth hormone may mediate osmoregulation in whitewater through paracrine expression of IGF-I, but not through the GH receptor, which instead showed correlated expression with the prolactin receptor and IGF-II in blackwater. Differential expression of genes related to paracellular tight junctions and transcellular ion transport showed responses similar to euryhaline fishes in fresh versus salt water, with some exceptions, suggesting that selective ion excretion via the gills, probably mediated by the GH/IGF-I axis, is likely a critical osmoregulatory process in whitewater and one which blackwater-adapted fishes may not be able to reproduce effectively. In each osmoregulatory pathway, we also saw examples of contrasting differential expression of duplicated genes, indicating that adapting to diverse osmotic challenges by fishes has utilized diversification at the genomic level.

236 Lightning Talks I, Grand Lilac Ballroom North, Thursday 12 July 2018

John Willson

University of Arkansas, Fayetteville, AR, USA

Rapid growth and flexible reproduction in semi-aquatic snakes inhabiting seasonal prairie wetlands

Flexible patterns of growth, survival, and reproduction are keys to success in dynamic habitats, such as seasonal wetlands. Long-term monitoring of four sympatric semi-aquatic snake species inhabiting a seasonal wet prairie in Northwest Arkansas, USA, has yielded exciting preliminary data on ways that snakes succeed in a habitat that is characterized by seasonally and annually variable resource pulses. Specifically, *Regina grahamii* are only surface active for a few months a year, but display astounding growth rates during their short activity window. *Thamnophis proximus* also grow rapidly during resource pulses (amphibian reproduction) and display flexible patterns of size at maturity and timing of parturition. *Nerodia erythrogaster* grow relatively slowly and are longer-lived. These data provide insight on flexibility of snake life history characteristics and the selective forces that shape them.

561 ASIH: If Salamanders Could Speak Symposium, Grand Lilac Ballroom North, Saturday 14 July 2018

Natasha Wilson and Craig Williams

University of South Australia, Adelaide, South Australia, Australia

A Critical Review of Freshwater Crayfish as Predators of Toxic Amphibians

Consumption of amphibian eggs and larvae by crayfish has been widely reported despite many amphibians being unpalatable and/or toxic to other predators. This review sought to collate and evaluate reports of interactions between freshwater crayfish and the eggs and larvae of purportedly toxic anurans and caudates. The extent of toxin consumptive ability was also explored in the context of crayfish phylogenetic history to speculate as to the evolutionary history of this trait. Tolerance of toxic prey was broad in terms of the diversity of both predators and prey. Freshwater crayfish consumed a range of toxic amphibians including both anurans (nine species across two families) and caudates (four species across three families). Meta-analysis indicated ontogenetic variation in palatability; with amphibian eggs were more likely to be unpalatable to freshwater crayfish than larvae. All three extant freshwater crayfish families were represented in accounts of the consumption of toxic amphibians and this feeding behaviour has been observed across several continents, which suggests that tolerance to amphibian toxins may be a primitive trait in freshwater crayfish.

445 SSAR: Coloration in Fish, Amphibians, & Reptiles Symposium, Grand Lilac Ballroom North, Sunday 15 July 2018

Monica Winebarger^{1,2}, Worth Pugh^{1,2}, Michael Osbourn² and Lynn Siefferman²

¹*University of Alabama, Tuscaloosa, AL, USA.* ²*Appalachian State University, Boone, NC, USA*

Conspicuous Coloration May Function to Deter Avian Predators in Appalachian Salamanders

In the Southern Appalachian Mountains, several species of salamander display conspicuous coloring and patterning that may have evolved via aposematic signaling. We used three complementary approaches to investigate the potential for aposematic signaling in two conspicuous salamanders: *Ambystoma maculatum* (large black-bodied salamanders with large bright yellow to orange spots on their dorsal side) and *Plethodon yonahlossee* (which have a red dorsal patch that covers ~40% of their dorsal region). First, we used avian vision models to quantify the conspicuousness of *P. yonahlossee* and *A. maculatum* to avian predators. We found that both species are distinguishable from typical forest backgrounds and are chromatically distinct from two duller sympatric heterospecifics (*P. montanus* and *P. cylindraceus*). Second, we used plasticine models of *P. yonahlossee* and *P. montanus* to experimentally test whether predators depredate conspicuously colored models less frequently than dull models. Predation rates on grey models were significantly higher compared to that of red models, suggesting that the red dorsal coloration of *P. yonahlossee* is interpreted as a warning signal that deters predation. Third, we used a comparative approach to investigate associations between body size and conspicuous coloration in the genera *Ambystoma* and *Plethodon*. We found that increased conspicuous coloration co-evolved with increased body size in *Ambystoma*, but that evolution in *Plethodon* salamanders has favored a negative relationship between these two traits. These results suggest that both *P. yonahlossee* and *A. maculatum* possess traits consistent with aposematism, but more information on unpalatability is needed for each species to further explore this hypothesis.

107 HL GRADUATE RESEARCH AWARD, Highland A, Friday 13 July 2018

Sean Wineland¹, Shane Welch¹, Thomas Pauley¹, Jeff Holmes², Joseph Apodaca³ and Jayme Waldron¹

¹Marshall University, Huntington, WV, USA. ²Amphibian and Reptile Conservancy, Nashville, TN, USA. ³Tangled Bank Conservation, Asheville, NC, USA

Multi-scale Drivers of Eastern Hellbender (*Cryptobranchus alleganiensis alleganiensis*) Extirpation Assessed Using Environmental DNA and Occupancy Modeling

Amphibian population declines and range constrictions as a result of land-use alteration are widespread but poorly studied. Identifying drivers of change in species distributions is essential to conservation planning. However, conventional detection methods for rare and elusive amphibians are inefficient. Integrating new surveying and modeling techniques may allow for more comprehensive assessment of population declines. We used environmental DNA (eDNA) sampling methods and detailed historical records to identify drivers of extirpation in an imperiled, long-lived giant salamander, the eastern hellbender (*Cryptobranchus alleganiensis alleganiensis*) in West Virginia, USA. We used a site occupancy and detection

modeling framework (SODM) to test the effects of current and historic land use, hydrogeomorphic, and water quality variables on model-based predictions of occupancy and detection. Hellbenders were extirpated from 48% of the 52 historical sampling sites. Our top-ranked model indicated watershed-scale road density was the strongest predictor of hellbender occupancy, and water turbidity and electrical conductivity were the best predictors of detection. All covariates had a strong negative effect on hellbender occupancy and detection. Roads can contribute to sedimentation and increase the salinity and conductivity of freshwater environments, which may limit hellbender reproductive success. Integrating eDNA data within a SODM framework allowed us to rapidly and accurately assess causal changes in hellbender distribution throughout their historical range in West Virginia, which will aid conservation planning. This study emphasizes the impacts of anthropogenic land alterations on freshwater ecosystems and the sensitivity of long-lived amphibian species to rapid environmental change.

477 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018

Whitney Wong¹, Luis Ceriaco¹, David Blackburn², Aaron Bauer³ and Matthew Heinicke¹

¹University of Michigan-Dearborn, Dearborn, MI, USA. ²University of Florida, Gainesville, FL, USA. ³Villanova University, Villanova, PA, USA

Evolutionary Relationships among Sand Frogs (*Tomopterna*) in Southwestern Africa

The genus *Tomopterna* includes 15 species of frogs found across sub-Saharan Africa. These species are among the most common amphibians in many terrestrial habitats, especially grasslands and savanna. However, morphological similarity among species makes them difficult to distinguish and difficult to determine which species occur in which regions. The evolutionary relationships among species are also not fully understood. We have obtained genetic samples of *Tomopterna* from across Southwestern Africa (Angola and Namibia) and performed phylogenetic analyses to determine these frogs' evolutionary relationships and patterns of distribution and diversity. The phylogeny shows that the morphologically conservative "*cryptotis*" complex does not form a monophyletic group even though members of this complex are not easily distinguishable based on external morphology. Our results also show that at least three species occur in Angola, and at least five occur in Namibia. One of these species is undescribed and also occurs more widely in southern Africa, and another, *Tomopterna damarensis*, is also much more widespread than originally believed. Evolutionary patterns are compared with *Sclerophrys*, another terrestrial anuran genus often found in sympatry with *Tomopterna*.

38 Amphibian Disease Ecology, Highland E, Thursday 12 July 2018

Vanessa Wuerthner¹, Obed Hernández-Gómez² and Jessica Hua¹

¹*Binghamton University, Binghamton, NY, USA.* ²*University of California, Berkeley, Berkeley, CA, USA*

Amphibian Host and Skin Microbiota Response to a Common Antimicrobial and Internal Parasite

Disease and anthropogenic influence are two of the major contributors to amphibian declines across the globe. The amphibian skin harbors diverse communities of microbes that are highly interactive with the environment, providing the initial defense against external stressors. Utilizing holistic approaches that characterize responses of both hosts and their microbial symbionts to environmental shifts are imperative to understand the effects of stressors on overall host health. Using the northern leopard frog (*Lithobates pipiens*) as our model, we investigated the effects of a common trematode (family Echinostomatidae), a common agricultural antimicrobial (Sulfadimethoxine; SDM), and their interaction on amphibian skin microbiota (identified through 16S rRNA sequencing) and amphibian health (growth metrics and susceptibility to parasites). We found that both stressors had an effect on the composition of the skin microbiota. Groups treated with SDM, echinostomes, or a combination of the two stressors, had higher abundances of OTUs assigned to *Flavobacterium* and *Acinetobacter*. *Flavobacterium* and *Acinetobacter* species have been associated with infectious disease in northern leopard frogs and other aquatic taxa. An increased abundance of potential amphibian pathogens suggests that exposure to both SDM and echinostomes induced dysbiosis of the skin microbiota. Changes in microbial community composition may have resulted from stress-related disruption of host immunity. Despite changes in the microbiota, we found no effect of echinostomes and SDM on amphibian host health. Given the current disease- and pollution-related threats facing amphibians, our study highlights the need to continue to evaluate the influence of natural and anthropogenic stressors on host-associated microbial communities.

86 Herpetology Conservation I, Grand Lilac Ballroom South, Friday 13 July 2018

Anne Yagi^{1,2} and Glenn Tattersall¹

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Managing an Ecological Trap on an Endangered Species *Massasauga* (*Sistrurus catenatus*) by Using Forced Hibernation

Reptiles use temperature and moisture cues to locate suitable habitats to complete their annual life cycle. Anthropogenic habitats mimic these cues and attract animals. However when habitat quality is not maintained, animals die. Ecological trap theory suggests that the continued presence of a trap will drive populations to extinction. Using an isolated population of *Massasaugas* located in a partially mined peatland in a case study, declining numbers of neonates and gravid females followed a cycle of flooding. This lends support to the notion that

the peatland functions as an ecological trap on the population. "Forced hibernation" is a technique tested during the last four winters and refers to the method of placing neonatal snakes into artificial burrows within ideal subterranean habitat for their first hibernation. This prime habitat must meet the criteria of maintaining an annual "Life Zone", which is a subterranean space that does not freeze or flood completely. The purpose of this experiment is to test whether 'forced hibernation' is a suitable strategy for headstarting neonatal Massasaugas. Preliminary results are favorable with 100% survival of neonatal Eastern gartersnakes (n=23) and 90% survival of neonatal Massasaugas (n=10). The experiment was repeated in the winter of 2017-18 with massasauga (n=41) and gartersnakes (n=23). Forced hibernation will directly manage the ecological trap by eliminating a neonate's naïve selection of a potentially lethal burrow and ensure overwinter survival where the life zone is maintained. Hibernation site fidelity will then ensure winter survivors return to good hibernation sites and the population should increase.

551 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018

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

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How does ontogeny affect changes in the gut microbiome of 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. We would expect dramatic changes in the microbiome of a frog as it undergoes the profound changes associated with metamorphosis. Such changes include completely remodeling the digestive tract while shifting from an herbivorous to a carnivorous diet. We are characterizing changes in the communities of symbiotic microbes living in the guts of American Bullfrogs (*Rana catesbeiana*) as they develop and undergo one of nature's most striking morphological and physiological transformations. A recent study showed that captive-raised leopard frog tadpoles exhibited the highest level of microbial community diversity, followed by adult and subadults (Kohl et al. 2013). Accordingly, we hypothesized that developing eggs and tadpoles undergoing metamorphosis would have the lowest microbiome community diversity and early stage tadpoles the greatest. We dissected the guts of tadpoles and frogs ranging from Gosner stage 25-46 to >0.62 kg adults ($n = 82$ total), sampled their guts for microbes, and extracted DNA from these microbial communities. Following DNA purification, amplification, sequencing, and identification of operational taxonomic units, microbial communities were analyzed with standard bioinformatics packages. Preliminary data ($n = 4$ adults) indicate that Fusobacteriaceae are the most prominent bacteria, suggesting these bacteria play an as-yet unknown role in frog health. Our study will provide insight into the ways that radical developmental changes alter gut microbial communities in organisms with complex lifecycles.

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Lauren Yetter¹, Carlos Rivera², Juan D. Daza¹ and Aaron M. Bauer³

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Are large eyes of geckos paedomorphic?

Gekkotans are big-eyed lizards, developing the proportionally largest eyes among living lizards, matched only by some snakes among squamates (e.g., *Dipsas*, *Leptodeira*, *Ahaetula*). In general terms, gekkotans have been an exemplary group for changes on the onset of development of phenotypic traits or heterochrony, in particular paedomorphosis or the retention of juvenile features in adults. Some characteristic paedomorphic skeletal features of gekkotans (not universal within the group) include paired premaxillae, paired frontals, paired parietals, and amphicoelous vertebrae. Large eyes have been proposed to be result of paedomorphosis in geckos (e.g., *Chatogekko*) and also birds when compared with their non-avian dinosaur ancestors. To test this idea, we studied ontogenetic series of two species of geckos, the sphaerodactylid *Sphaerodactylus townsendi* (diurnal) and the gekkonid *Hemidactylus maboia* (nocturnal). We measured the area occupied by the sclerotic ring in cleared and stained specimens, and regressed it against jaw length. Linear correlation of area versus length is expected to have a slope of 2 if the structures compared are isometrical (~ paedomorphic or constant during the ontogeny). When estimating the regression formula, we found that slope values were not similar or equal to 2 in either species, and found remarkable differences between the two species studied. The *S. townsendi* ontogenetic series yielded a higher value (1.47) than the series of *H. maboia* (0.91), supporting an allometric rather than isometric developmental trajectory in both the nocturnal and diurnal species.

312 Ichthyology Morphology/Collections/Fisheries, Grand Lilac Ballroom South, Sunday 15 July 2018

Hu Yanan^{1,2}, John Majoris³, Peter Buston³ and Jacqueline Webb²

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Ontogeny of the Ear in the Pelagic Larvae of Coral Reef Fishes (Gobiidae, Pomacentridae, Apogonidae)

The ability of pelagic fish larvae to navigate the open ocean and reliably locate suitable settlement sites is a key feature of the life history of most marine fishes with important

implications for their ecology and evolution. Coral reefs are sound-rich environments that present a soundscape that is quite different from that of the open ocean, which allows larvae to orient to them at considerable distances. The role of sound in orientation behavior has been demonstrated in the pelagic larvae of a small number of species, but nothing is known about the structural or functional ontogeny of the ear in these fishes. Here we provide the first developmental anatomy of the ear in coral reef fishes using ontogenetic series (larvae, juveniles) of two gobiids (*Elacatinus lori* and *E. colini*), two pomacentrids (*Amblyglyphidodon leucogaster*, *Amphiprion polymnus*) and an apogonid (*Cheilodipterus quinquelineatus*) reared from demersal eggs in field laboratories. We measured the length, width, and spatial orientation (relative to the dorso-ventral axis) of each of the three sensory maculae (utricle, saccule, lagena) using histological material. Results reveal the conserved features of the ear of percomorphs, with inter-familial variation in the timing of the appearance of the three maculae, the relative sizes and location of the maculae and the sacs containing them, and inter-aural distances. The behavioral and ecological implications of the timing of development and variation in ear morphology are discussed. Funded by NSF grants 1459224 (to JFW) and 1459546 to PMB, and NSF DDIG #1501651 to PMB and JEM.

124 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018

Dara Yiu¹, Luke Tornabene¹ and Mark Erdmann²

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Elucidating species boundaries in the *Eviota atriventris* species complex

The exceptional biodiversity in the Coral Triangle is partially attributed to the elevated rates of evolution that occur in the shallow reefs of the Indo-Pacific Ocean. Its current geographical location and complex oceanographic history have facilitated rapid speciation in many lineages of coral reef fishes. The processes causing these unique evolutionary patterns can be closely studied in *Eviota* (Gobiidae), a widespread lineage of rapidly diverging marine fishes. Their restricted dispersal capabilities, short generation time, and specific habitat preferences have facilitated repeated exploitation of novel niches and thus catalyzed their high species diversity. Here, we examine morphological and genetic diversity in relation to biogeography in the *Eviota atriventris* species complex. This study analyses *E. atriventris* from nine localities across its range spanning the Indo-Australian Archipelago to determine whether recent speciation has occurred at fine scales across the Coral Triangle. Our combined morphological and molecular phylogenetic analysis examines differences in meristic, coloration, morphometrics, and gene sequence data from seven mitochondrial and nuclear genes. Results show strong divergence in mitochondrial DNA sequences in Papua New Guinea and Solomon Islands populations, as compared with a western haplotype from Indonesia. This suggests that lineages within *E. atriventris* are geographically and genetically isolated. However, evidence from nuclear gene sequences show few differences between groups, and morphological data to support the

separation of these populations are inconclusive. These similarities imply that eastern and western haplotypes may be in the early stages of speciation.

293 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: PHYSIOLOGY & MORPHOLOGY, Empire Hall South - JF Rochester Riverside Convention Center, Friday 13 July 2018

Gabriella Zagorski¹, James Trottier², Douglas Boreham³ and Jacqueline Litzgus¹

¹*Laurentian University, Sudbury, ON, Canada.* ²*Ministry of Natural Resources and Forestry, Blind River, ON, Canada.* ³*Northern Ontario School of Medicine, Sudbury, ON, Canada*

A Preliminary Examination of the Effects of Uranium Mining on Long-Lived Turtle Species

The aim of our research is to understand the effects on turtle species exposed to mine tailings during embryological development and at maturity. We will study the impacts of living in proximity to uranium tailings ponds in Algoma District on turtles, a group of animals well known for their great longevity and slow life history. We will assess potential impacts of uranium tailings on turtles by examining body conditions of individuals living within or near tailings ponds (impact sites) and those living far from tailings ponds (control sites). If turtles are negatively impacted by contaminants in tailings, we postulate poorer body conditions in those living in tailings compared to control sites. Radium is a radioactive isotope found in uranium tailings. Radium and calcium are known to act as analogues in their capacity to accumulate in turtle shells, thus we will be examining whether turtles living in tailings exhibit signs of calcium deficiency. We will also collect turtle shell filings, gathered when 'notching' marginal scutes to mark turtles with individual identification codes, and egg shells from predated turtle nests. These calcium-based tissues will be analyzed using alpha dosimetry in the lab to gather information about presence and abundance of radium. If turtles can accumulate radium in tissues from exposure in tailing ponds, regression analysis should indicate a negative relationship between levels of radium in tissues and distance from tailings ponds. Our preliminary investigation can direct future research about impacts of uranium tailings on biodiversity and abundance, and on individual fitness.

296 SSAR SEIBERT CONSERVATION II, Highland B, Thursday 12 July 2018

Gabriella Zagorski¹, James Trottier², Douglas Boreham³ and Jacqueline Litzgus⁴

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Examining Population and Spatial Ecologies of Blanding's Turtles *Emydoidea blandingii* to Inform Mitigation Plans for Quarry Development

Habitat destruction is one of the leading causes of reptile and amphibian declines worldwide. The Great Lakes population of Blanding's turtles was recently up-listed to Endangered in Canada due to many threats; including habitat alteration and destruction. A trap-rock quarry is proposed in known Blanding's turtle habitat in central Ontario, and under the provincial Endangered Species Act, an Overall Benefit Permit and Mitigation Workplan are required for development to proceed. The purpose of our study is to provide data to inform the mitigation plans, and to provide baseline data that can serve as the "before" sampling period in a long-term Before-After-Control-Impact (BACI) study. Mark recapture surveys are being conducted to gather population ecology data, and radio telemetry and GPS tracking are being used to quantify the spatial ecology of turtles at impact and control sites. Movements, habitat use, and temperature selection will be quantified, and nesting and overwintering sites will be identified. In the 2017 field season, we captured 29 individual turtles within a 2 km radius of the impact site. One nesting site and 9 overwintering sites (i.e., critical habitats) were identified, and turtles moved a maximum of 83 m (straight-line distance) from active season wetlands to overwintering sites. Our study is significant because not only will it provide data to inform mitigation at our study site, but will serve as a model for other BACI studies that should be used during development projects in order to assess the risks of extreme habitat alterations to species at risk.

138 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018

Christopher Zobek, Casey Dillman and Harry Greene

Cornell University, Department of Ecology and Evolutionary Biology, Ithaca, NY, USA

Comparative Adaptations for Skink Predation in the Genus *Lampropeltis*

The goal of this study is to test the hypothesis that skink predation, a behavior exhibited in members of the Lampropeltini, is manifest in the jaws and dentition of this lineage. We utilize natural history specimens to compare the skull and tooth structures of the genus *Lampropeltis*. Skinks are known to be difficult prey due to their smooth, hard scales and "rolling" behavior. Examples of scincivory come from many independent lineages, though no direct comparisons with closely related non-skink eating specialists are known. Here we compare *Lampropeltis elapsoides*, a known scincivore, to a closely related species, *L. triangulum*, to investigate potential difference due to the life history associated with scincivory. Further, *L. triangulum* is known to shift its diet from ectotherms, i.e. skinks, to endotherms during ontogeny. *L. triangulum triangulum* is known to focus mostly on mammals, and the diet of *L. triangulum sypila* varies with range and body size (samples used here include Alabama and Kansas). Tooth structure is examined using computerized tomography scans of the skulls of *Lampropeltis triangulum* and *Lampropeltis elapsoides*. Comparing juvenile and adult tooth morphology will therefore provide

an additional test for the hypotheses related to scincivory and may also provide new morphological evidence to support currently controversial Lampropeltine relationships. Results indicate a clear differentiation between the two species, and a more modest difference in life stages.
